Wheat Gene Catalogue

Nov. 2026

This document is a pdf version of
our online implementation at
https://www.wheat-gateway.org.uk/gene_sym.php
of R. A. McIntosh's 2024
edition of his "Wheat Gene Catalogue"
which is available here

Wheat Gene Catalogue, 2024 – Introduction

This Catalogue is a WORD extension of the MACGENE (National Institute of Genetics Japan (http://shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp) that was not continued after 2017. It is updated with all curated material up to 1 September 2024.

The material in the Catalogue has been collated since 1968 and major contributions were made by numerous people including Mike Gale, Gary Hart, Katrien Devos, Olin Anderson, John Rogers, Jorge Dubcovsky, Xianchun Xia, Yukiko Yamazaki, and John Raupp and many others who have discussed individual trait material. This is gratefully acknowledged and appreciated.

The Catalogue is not free from errors in curation and the various cycles of editing over years – please advise problems or suggestions for updating.

The documents presented are working files – items highlighted are for checking or currently cannot be traced.

Some items listed as 'alleles' would currently fit the description 'haplotype' as defined in Boden et al. (2023) 'Updated guidelines for gene nomenclature in wheat'. Theoretical and Applied Genetics 136:72. https://doi.org/10.1007/s00122-023-04253-w.

Until 2017 this Catalogue was prepared and maintained on behalf of the International Wheat Genetics Symposium.

R.A. McIntosh
1 September, 2024

Wheat Gene Catalogue at wheat:gateway

The current document is a pdf version of our online implementation of R. A. McIntosh's 2024 update to the "Wheat Gene Catalogue" which we had initially downloaded the 2017 edition of from http://shigen.nig.ac.jp/wheat/komugi/genes/symbolClassList.jsp.

In general we have followed R. A. McIntosh's 2024 edition adding to, deleting from and editing our previous data accordingly with one exception that in section 3.30 **Reaction to *Tilletia caries* (common bunt)** we have added a new category of data, "markers report" showing marker information from the work of bunt resistance researchers/breeders Anders Borgen and Dennis Kjær Christensen.

As we have moved through the catalogue doing this update we have come across some fairly easily recognisable mis-types that we have taken the liberty of changing, hopefully correcting and these have been communicated to R. A. McIntosh and await his approval.

In general in this pdf where we show section and subsection numbering we have attempted to ensure in general inline with that in R. A. McIntosh's document. However in the 2nd part of the catalogue covering "Proteins" we felt it was appropriate to remove non-storage proteins and enzyme inhibitors into their own sections outside of the storage proteins' section.

All the symbol names in this pdf are clickable to get to that symbol's entry in our online edition.

Andrew Forbes
https://www.wheat-gateway.org.uk
https://www.brockwell-bake.org.uk

Key

Symbols

Q	a symbol at the head of its entry: a link to that symbol's entry in the online catalogue
Gene	a gene: bold
Allele	an allele: bold italic
QTL, *marker*	a QTL or a marker: italic
locus: 5AL	on the symbol's line: its chromosome location
syn:	on the symbol's line: its synonyms

References

text[1048]	R. A. McIntosh's reference number, a link to the reference in the list at the end of the catalogue
reported in ▸ 0324	a reference that is part of the sentence
▲ p.3,17	in the reference list: back to where it is cited, with the pages when more than one
114, 0114, 00114	three different references: the leading zeros matter

Headings and pages

1.78.8 Heading	section and subsection numbers as R. A. McIntosh's; a link back to the contents
1.69a, 1.69b	a number R. A. McIntosh uses twice, until resolved
… > Cg *cont.*	at the top of a page: what continues from the page before

Germplasm and other information

i:	Near-isogenic stocks, with number of backcrosses indicated.	**tv:**	Tetraploid stocks.
s:	Homologous chromosome-substitution stocks, with number of backcrosses indicated.	**tv2:**	Tetraploid stocks with two or more genes affecting the trait.
tr:	Translocation line of common wheat.	**trtv:**	Translocation line of tetraploid wheat.
idv:	Near-isogenic line of diploid wheat.	**v:**	Cultivaral hexaploid stocks in increasing order of genetic complexity.
dv:	Diploid stocks.	**v2:**	Cultivaral hexaploid stocks with two or more genes affecting the trait.
v, tv:	Hexaploid and tetraploid stocks.	**al:**	Alien species.
ad:	Alien chromosome addition line.	**matv:**	Same as **ma:** but for tetraploid wheats.
su:	Alien chromosome substitution line.	**ad, su:**	Alien chromosome addition and substitution lines.
c:	Cloning details and gene structure	**sutv:**	Alien chromosome substitution line of tetraploid stocks
itv:	Near-isogenic tetraploid stocks.	**bin:**	Deletion bin: the chromosome segment the gene has been located to.

CS Chinese Spring wheat.

ma: Reference to mapping information involving agronomic and morphological traits and molecular markers under gene entries will generally be restricted to values of less than 10 cM. Values higher than this would be of less use in genetics and plant breeding and, in any case, should be available from the genetic linkage section of the Catalogue or from genetic maps. Higher values will be used in the case of flanking markers.

Markers reports

BOLD	MAS flank markers
ROMAN	markers for MAS
ITALIC	GWAS markers

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1.1 Gross Morphology: Spike characteristics

Major hexaploid wheat types are categorized into groups with respect to three major gene pairs; viz. **Q**, **C** and ***S1*** [1038].

1. Common wheat **Q** *c* ***S1*** v: vulgare group.
2. Club wheat **Q C** ***S1*** v: compactum group.
3. Shot wheat **Q** *c* ***s1*** v: sphaerococcum group.
4. Spelt wheat **q** *c* ***S1*** and **q C** ***S1*** v: spelta group (including vavilovi).

The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups. Diploid wheat is assumed to be **q**. Durum and carthlicum groups have the genotype **Q** [1049].

1.1.1 Squarehead/spelt

Q

Q [881] locus: 5AL [1293] syn: k [1550], Ap2-5A

bin: 5AL-17 [10541]. **v**: Common wheats. CS; Iranian spelts [140]. **tv**: *T. turgidum* ssp. *carthlicum*, *durum* and *polonicum* [10457]. **ma**: Complete linkage with cDNA clone PtAq22 [0127]. **c**: **Q** was cloned and shown to have similarity to *AtAP2* (APETALA 2), the **Q** allele was more abundantly transcribed than the **q** allele transcription factors [10457]. GenBank AY02956.1.

The speltoid phenotype of at least some spelts may be caused by genes at other loci [0140]. Fine mapping of the 20 cM region possessing Q and delimited by deletions 5AL -7 and -23 is reported in ▸ [0324].

q [881] syn: K [1550]

v: Macha wheats; European spelt wheats [10457]; *vavilovi* wheats. **s**: CS*8/White Spring Spelt 5A [1048]. **tv**: *T. turgidum* ssp. *dicoccum*, *dicoccoides* [10457]. **ma**: Cent - *Xrsq805* (*Empb*) - 4.6 cM - **Q** - 4.3 cM - *Xpsr370-5A* [419]; **Q** was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23 [446]; **Q** - 9.3 cM - *Xpsr370-5A* [9903].

The speltoid phenotype of at least some spelts may be caused by genes at other loci [0140]. Fine mapping of the 20 cM region possessing **Q** and delimited by deletions 5AL -7 and -23 is reported in ▸ [0324].

A nucleotid change in the micro RNA172 binding site of the Q locus played a critical role in wheat domestication and the origin of free-threshing modern wheats [11192].

Pleiotropic features of the **Q** locus include effects on glume toughness, threshability, rachis fragility, spike length, flowering time, and plant height [11342]. Final spike and reproductive morphology is affected by the **Q**/**q** sequence and its regulation by miR172 [11344] along with direct or indirect interaction with the homoeologues [11344].

Homoeologues of **Q** were described in ▸ [11192]. Both have miRNA172 target sites close to the 3' ends of the coding region. These genes were referred to as *Ap2-5B*, a transcriptionally active pseudogene, and *Ap2-5D* that encodes a functional protein that contributes to suppression of the speltoid phenotype [11342]. Reduced height gene **Rht23**, a mutationally derived allele in NAUH164, was caused by a SNP (G3147A, Ala416Thr) within the miR172 target site in 5DL that permitted up-regulation of *Ap2-5D* due to down-regulation of miR172 in leaves, stems and spikes [11345].

1.1.2 Club/Compact spike

C [1517] locus: 2DL [1192, 1517]. probably 2DL [10578]. 2D [1192] syn: Cd [47]

bin: C-2DS1 - C- 2DL3, markers flanking **C** were located on either side of the centromere [10578]. **i**: S-615*11/Elgin [1500]. **s**: CS*6/Poso 2D [1304]; CS*5/Red Egyptian 2D [1304]. **v**: Club wheats; Coda [10578]; Corrigin [10578]. **ma**: Coda/Brundage: *Xwmc144-2D* – 1 cM – **C** – 8 cM – *Xwmc18-2D*; Corrigin/CS (*Ae. tauschii*2D): *Xwmc245-2D* – 1 cM – *Xcfd16-2D*/*Xgwm358-2D*/**C**/*Xcfd116-2D* – 1 cM – *Xbarc145-2D* [10578].

C_g [11114] locus: 2BL [11114]

bin: 2BL-0.48-0.89, near breakpoint 0.69. **v**: Akage Gumbai [11114]; Akage Gumbai 22 [11114]; Gumbai 22 [11114]; Kinoshita Komugi [11114]; Nakote Gumbai [11114]. **ma**: *Xhbg410*/*Xhbg440-2B* – 18.1 cM – C_g – 15.3 cM – *Xgwm47-2B* [11114].

Although gene **C** may be present in some forms of group *macha* [1447] and *spelta* [0623], it is not universally present. Tsunewaki [1500] found that compact spike in one form was controlled by polygenes.

C may be orthologous to gene **Sog** for soft glumes on chromosome $2A^m$ [10578] Tetraploid wheat: A compact spike gene $\mathbf{C}^{17648}$ in mutant line MA 17648 was located in chromosome 5AL [10541]. *Xbarc319-5A* – 9.7 cM – $\mathbf{C}^{17648}$ – 24.8 cM – *Xgwm179-5A* [10541]. $\mathbf{C}^{17648}$ was distal to the **Q** locus [10541].

QTL

Courtot / Chinese Spring: Six QTL for spike compactness were detected but only 4 on chromosome arms 1AL, 2BS, 2DS and 4AS were consistent for at least two years [0114]. Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring [10080] on chromosome arms 5DL (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers *Xcfd26-5D* and *Xcfd38-6D* explained 13.6% and 12.2% of the variance in spike compactness, respectively [10080].

1.1.3 Sphaerococcum

The naturally-occurring sphaerococcum gene in chromosome 3D and various mutant alleles conferring a similar phenotype form a homoeologous series. The sphaerococcoid alleles are either recessive or incompletely dominant. All three mapped loci are closely linked to the respective centromeres [0030]. The "a" alleles are allocated to Chinese Spring or "normal" wheats.

S1

S-A1 [0029] locus: 3A [0056]

v: CS [0029].

S-A1a [0029]

v: CS [0029]; common wheats [0029].

S-A1b [0029] syn: S3 [0056]

v: MS 1453 [0056]. **ma**: *Xgwm2-3A*(S) - 5.1 cM - **S-A1** - 6.6 cM - *Xgwm720-3A* (L) [0030].

S-B1 [0029] locus: 3B [0030]

v: CS [0029].

S-B1a [0029]

v: CS [0029]; common wheats [0029].

S-B1b [0029] syn: s^{16219} [10541], S2 [0030]

v: MSK 2452 [0056]; MSK 2454 [0056]. **tv**: MA 16219 [10541]. **ma**: *Xgwm685-3B* (S) – 4.2 cM – **S-B1** – 0.5 cM – *Xgwm566*/*Xgwm845*/ cent [0030].

S-D1 [0029] locus: 3DL [692] 3D [1292, 0030] 3DS [1193, 1194, 11415]

v: CS [0029].

S-D1a [0029]

v: CS [0029]; common wheats [0029].

S-D1b [0029] syn: s1, sp1 [1286], Tasg-D1 [11415]

i: S-615*11/*T. sphaerococcum* var. *rotundatum* [1500]. **s**: CS*7/*T. sphaerococcum* var. *rubiginosum* 3D [1304]. **v**: Nongda 4332 [11415]; Sphaerococcum wheats [0029]; *T. antiquorum* K056397 & K56398 [10234]. **ma**: Located between markers *Xgwm341-3DS* and *Xgdm72-3DS* [11415]. **c**: The sphaerococcum phenotype is caused by a gain of function mutation in serine/threonine kinase glycogen synthase kinase 3 (STKc_GSK3) that in rice affects the brassinosteroid signaling pathway and grain shape [11415]. There is a Lys286Glu substitution in the ninth exon of *TraesCSD01G137200* [11415].

S-D1c [0029] syn: S1 [0056]

MS 3287 [0056]. **ma**: *Xgdm72-3D* (S) – 8.0 cM – **S-D1** – 2.9 cM – *Xgwm456-3D*/cent [0030].

S2

s2 syn: sp2[1286]

Partially dominant[1286].

v: Sphaerococcoid wheats. "*Sphaerococcum simulator*"[1286].

Sphaerococcum-like tetraploid wheats were reported[122, 475, 1282, 1286], but comparisons between them, or with **s2**, were not made. Whereas Schmidt & Johnson[1281] reported a single recessive controlling the sphaerococcum character in tetraploid wheat, Joppa[621] using the same stock found that two recessive genes were necessary to produce this phenotype.

1.2 Branched spike

Synonyms: branched spike, four-rowed spike, multi-rowed spike, supernumerary spikelet, tetrastichon spikelet.

Branched spike and multi-rowed spike are phenotypes involving the presence of supernumerary spikelets or the presence of additional spikelets at rachis nodes. A similar condition in rye is known as 'monstrosum ear' (reviewed in ▶[10637]). Genetic studies of branched spike in tetraploid and hexaploid wheats indicate that the phenotype is recessive, involves one or more genes, and is strongly influenced by environmental effects. Comparative genetic studies suggest an orthologous gene series in homoeologous group 2[10637].

BH1

bh-A1[10637] locus: 2AS[665] syn: bh[665]

tv: PI 349056[665].

bh-D1[10637] locus: 2DS[10637] syn: mrs[10637]

bin: 2DS5-0.47-1.0[10637]. **v**: Ra1[10637]; Ruc163167-1-02 = Ra1/ZGK242-81[10637]; Ruc163167-1-02 = Alana/3/Ra1/ZGK242-82//Ra1[10637]. **ma**: *Xwmc453-2D*/**bh-D1** – 7.8 cM – *Xgwm988-2D*[10637]; *Xwwm484-2D* – 3.3 cM – *Xwmc453-2D*/**bh-D1** – 3 cM – *Xwgm988-2D*[10637].

Ra1 is a mutant stock maintained at the NI Vavilov Research Institute of Plant Industry, St Petersburg, Russia.
A chromosome 2B gene of minor effect was identified[9907]. In a monosomic analysis of the hexaploid line LYB with supernumerary spikelets, Peng et al.[9908] located recessive genes in chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene in chromosome 2D that prevents their expression.

bh-R1[10637] locus: 2R[10637] syn: mo[10637]

al: *S. cereale* D40[10637]. **ma**: *Xrms056-2R* – 15.7 cM – **bh-R1** – 10.7 cM – *Xcfe209-2R*[10637].

1.3 Elongated glume

Elongated glume is the phenotype associated with the polonicum group of tetraploid wheats. Expression in hexaploid wheat is much reduced compared with tetraploids. Matsumura[911] reported linkage of gene *P* and a gene for red coleoptiles implicating chromosomes 7A or 7B. A different gene was subsequently located in chromosome 7B[9990].

P1 locus: 7AL[922, 1547] 7A or 7B (based on linkage of 02 with a gene for red coleoptile)[922] 7AS[11587, 11606] syn: P-Apol1[0254], P[911], Eg[922], P-Apet1[0254]

i: Saratovskaya29*8//Novsibirskaya 67*2/*T. polonicum*[922, 0066]. NILs developed in ▶[11587, 11606]. Paragon derivative[11606]. **itv**: P-LD222 = LD222*11/*T. turgidum* var. *polonicum*[1546, 1547]. **tv**: *T. polonicum*[0254]; *T. petropavlovskyi*[0254]. NILs developed in ▶[11587]. *T. petropavlovskyi* {add: 11587}; Tall and dwarf (with **Rht22**) Polish wheat accessions from Xinjiang[11587]. **ma**: *Xgwm260* – 7A(S) – 2.3 cM – **P1** – 5.6 cM – *Xgwm1083* -7A (L)[0254]; *Xgwm890* -7A – 2.1 cM – **P1**[0254]; *Xgwm260-7AS* – 2.3 cM – **P1** [pol] – 5.6 cM – *Xgwm1083-7AL*[0254]; *Xgwm890-7AS* – 2.1 cM – **P1** [pet 11587, 0254]. Located between SSR markers *XP25* (128.79 MB) and *XP87* (128.92) in CDSREFSeq_v1[11587]. **c**: An insertion in intron 1 causes alternate splicing and > 50fold up-regulation of the **P1** allele affecting kernel length, glume length and flowering date through the brassinosteroid pathway[11587]. The *VRT-A2a* allele[11606] is present in Chinese Spring and other non-long-glume

tetraploid and hexaploid accessions; The *VRT-A2b* in long-glume accessions has a 160 bp sequence replacing a 563 bp sequence in intron 1 in all *T. polonicum*, *T. petropavlovskyi* and hexaploid Arrancada landraces[11606]. Loss-of- function mutations in both *VRT2* homoeologs in tetraploid wheat delay heading time, reduce plant height and increase number of spikelets per spike[11607].

The loci determining elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* are not homoeologous to the *P* loci in the centromeric region of the group 7 chromosomes[0254]. According to ▶[11606] *T. petropavlovskyi* is hexaploid.

P2[9990] locus: 7BL[9990]

itv: LD222*7/*T. ispahanicum*[9990]. **tv**: *T. ispahanicum*[9990].

According to ▶[0254] the loci of *T. polonicum*, *T. petropavlovsky* and *T. ispahanicum* are allelic ('homoeoallelic') whereas other workers had claimed genes in the first two forms were not allelic. Wang et al.[0254] however concluded that loci bearing alleles for elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* were not part of the above series.

1.4 Ear length

QEl.ocs-5A.1[0068] locus: 5AL[0068]

v: CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population[9903]. **ma**: Associated with *Xbcd9-5A*[0068].

1.5 Multi-gynoecium; Multi-ovary

Synonym: three pistils (TP).

This trait describes a dominant phenotype consisting of 3 kernels within each wheat floret; that is, the flower consists of 3 separate ovaries, 3 anthers and 2 lodicules

Pis1[10636] locus: 2DL[10636]

bin: C-2DL3-0.49[10636]. **i**: CM28TP[11228]. **v**: TP Mutant[10636]. **ma**: *Xgwm539-2D* – 17.6 cM – **Pis1** – 19.5 cM – *Xgwm349-2D*[10636]. *KM69 _132294739* – 3.5 cM – *KM70_136805221* – 3.0 cM – **PIS1** – 1.1 cM – *KM71_140258883*[11228].

1.6 Accumulation of abscisic acid

A QTL was mapped on 5AL between *Xpsr575-5A* (proximal) and *Xpsr426-5A* (distal)[1180].

1.7 Alkylresocinol content in grain

AR

Ar1[0281] locus: 5AL[0281]

High alkylresocinols content is dominant[0281]

tv: Langdon[0281].

ar1[0281]

tv: Ardente[0281]; this cultivar has a low content compared to all tested durum and common wheats[0281].

1.8 Aluminium tolerance

ALT1

Alt1[234]

v: ET3 = Carazinho/4*Egret[234].

alt1[234]

v: ET3 = Carazinho/4*Egret[234].

ungrouped

Almt1 locus: 4DL[11242] 4DL[11242] syn: TaALMT1[11242].

v: CAR3911[11242]. **ma**: *Xwmc457-4D* – 4.0 cM – **Almt1** – 2.0 cM – *Xwmc331-4D*[11242].

Alt2[848] locus: 4DL[848] syn: Alt_{BH}[1213]

su: *T. turgidum* cv. Langdon 4D(4B)[848]. **v**: BH1146[1213, 0115]; IAC-24[0115]; IAC-60[0115]; 13 induced mutants of Anahuac[0115]. **ma**: **Alt2** was mapped to a 4 cM interval flanked by *Xpsr914-4D* and *Xpsr1051-4D*[848]; on a consensus 4B-4D map of *T. aestivum*; **ALT2** – 1.1 cM – *Xbcd1230-4D*[1213]; **Alt2** cosegregated with *Xbcd1230-4D* and fell within the interval *Xgdm125-4D* – 4.8 cM – **ALT2** – *1.1 cM* – *Xpsr914-4D*[248].

Malate transporter *AlMT-D1* gene (GenBank AB081803) is completely linked to aluminium tolerance in chromosome arm 4DL between SSR markers *Xwmc48b* and *Xwmc331* in a similar region to **ALT2**[10285]. **Almt1** transgenic expression in barley conferred and Al-activated efflux of malate with properties similar to those of Al-tolerant wheat[10286]. Allelic variation at the promoter of *Almt-D1* was associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germplasm is derived from several independent sources[10532].

QTL

Atlas 66 / Century: A QTL in the region *Xdgm125-4DL* – *Xwmc331-4DL* accounted for nearly 50% of the phenotypic variation in root growth rate in hydroponic solution[10265]. An Al-activated malate transporter (*LMT1*) was earlier mapped to the same location[10266].

Atlas 66 (insensitive) / Chisholm (sensitive) RILs: One QTL, located in chromosome 4DL, corresponded to **ALMT1** and accounted for 50% of the phenotypic variation[10483]. A second QTL was located on 3BL (R^2= 0.11); nearest marker *Xbarc164-3B*[10483]. Both QTLs were verified in Atlas/Century[10483].

FSW (A1 tolerant) / ND35 (A1 sensitive): 3 QTLs for tolerance, *Qalt.pser-4DL* co-segregating with *Xups4*, a marker for the promoter of the **ALMT1** gene, *Qalt.pser-3BL* (*Xbarc164-3B* – *Xbarc344-3B*) and *Qalt.pser-2A* (*Xgwm515-2A* – *Xgwm296-2A*)[10605].

In D genome introgression lines of Chinese Spring a major QTL was located in the interval *Xgwm125-4D* – *Xgwm976-4D*, R^2=0.31[10598], probably coinciding with **Alt2**. A second QTL from CS, $Qalt_{CS}$*.ipk-3B*, R^2=0.49, occurred in interval *Xgwm1029-3BL* – *Xgwm1005-3BL* in a CS/CS (Synthetic 3B) population[10598].

1.9 Anthocyanin pigmentation

The genetic determinants of anthocyanin pigmentation of various tissues are largely located in homoeologous regions in group 7, viz. 7BS (**Rc-B1**, *Pc-B1, Plb-B1, Pls-B1*) and 7DS (**Rc-D1**, *Pc-d1, Plb-* **D1**), and appear to be linked clusters rather than multiple alleles on each chromosome[10700]. Their relationship with genes for purple auricle and purple pericarp are still not clear.

1.9.1 Purple anthers

A single, dominant factor was reported[1326].

PAN

Pan1[921] locus: 7DS[921]

v: Ilyitchevka[921]; Mironovskaya 808[921]; Novosibirskaya 67[921]; Pyrothrix 28[921]; Saratovskaya 210[921]; Strela[921]; Ukrainka[921]. **tv**: *T. polonicum*[921].

Pan2 locus: 7AS[9959]

tv: *T. turgidum* ssp. *dicoccoides* acc. MG4343[9959]. **ma**: **PAN2** – 9.2 cM – **RC1** – 12.2 cM – *Xutv1267-7A* (proximal)[9959].

1.9.2 Purple/Red auricles. Purple leaf base/sheath

For review see [1641].

Melz and Thiele[983] described a "purple leaf base" phenotype where anthocyanin pigmentation extended to the leaf base as well as auricles. Purple leaf base was expressed only when pigmentation occurred in the coleoptiles.

An5[983] locus: 5R[983]

Pc/Pls/Plb[10692] locus: 7B[10692]

tv: TRI 15744 (IPK GeneBank, Gatersleben)[10692]. **ma**: *Xgwm951-7B* – 6.7 cM – **Pc/Pls/Plb** – 8.2 cM – **Pp1** – 8.9 cM – *Xgwm753-7B*[10692].

Ra1 locus: 1D Gulyeeva[474, 983] 2D[1645] syn: Ra[1645]

v: Kenya 58[1645].

Ra2[983] locus: 4B[983]

Ra3[983] locus: 6B[983]

1.9.3 Red/purple coleoptiles

There is an orthologous gene series on the short arms of homoeologous group 7. The 'a' alleles confer red coleoptiles. In chromosome substitution lines of wild emmer to common wheat both the 7AS and 7AL derivatives had red coleoptiles, placing **Rc-A1** in the centromeric region[10974].

RC-1

Rc-A1[10451] locus: 7AS[3] [10451] syn: Rc

dv: PAU14087[10451]. **ma**: *Xcfa2174-7AS* – 11.1 cM – *RC- A1* – 4.3 cM – *Xgwm573-7A*/*Xwmc17-7AL*[10451].

Rc-A1a[0250] locus: 7A[769, 1293] 7AS[0250] syn: Rc1, R[401]

s: CS*6/Hope 7A[1293]. **v**: Hope ***Rc-B1a***[1293]. **tv**: *T. turgidum* ssp. *dicoccoides* acc. MG4343[9959]. **ma**: **PAN2** – 9.2 cM – *RC- A1* – 12.2 cM – *Xutv1267-7ª* (proximal)[9959]; **RC-A1** (distal) – 11.9 cM – *Xgwm913-7A*[0250].

Rc-B1

Rc-B1a locus: 7BS[250, 401, 769] 7B[742] syn: Rc2, R2[401]

s: CS*6/Hope 7B[769]. **v**: Hope *Rc- A1*. **ma**: *Xgwm263-7B* – 26.1 cM – **RC-B1** – 11.0 cM – *Xgwm1184-7B*[0250].

Rc-D1

Rc-D1a[0250] locus: 7D[596] 7DS[1241, 1444, 0250] syn: Rc 3

v: Gaoyuan 115[11160]; Mironovskaya 808[1444]; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404[1240]; Tetra Canthatch/*Ae. squarrosa* var. *meyeri* RL 5289, RL 5406[1240]; Sears' *T. dicoccoides*/*Ae. squarrosa* = Sears' Synthetic[596]. **ma**: **RC-D1** (distal) – 3 cM – *Xpsr108-7D*[180]; *Xgwm44-7D* – 6.4 cM – **RC-D1** – 13.7 cM – *Xgwm111-7D*[0250]. **c**: *TaMYB-D1* isolated from Gaoyuan 115 was proposed as the candidate gene[11160].

Tahir & Tsunewaki[1453] reported that *T. spelta var. duhamelianum* carries genes promoting pigmentation on chromosomes 7A and 7D and genes suppressing pigmentation on 2A, 2B, 2D, 3B and 6A. Sutka[1444] reported a fourth factor in chromosome 6B and suppressors in 2A, 2B, 2D, 4B and 6A. The **Rc** allele appears to encode a transcription activator of late biosynthesis genes involved in the light- regulation of anthocyanin systhesis (studies carried out on CS(Hope 7A) substitution line)[10317].

1.9.4 Purple/red culm/straw/stem

Purple or red colour is dominant.

Pc/Pls/Plb[10692] locus: 7B[10692]

tv: TRI 15744 (IPK GeneBank, Gatersleben)[10692]. **ma**: *Xgwm951-7B* – 6.7 cM – **PC/PLS/PLB** – 8.2 cM – PP1 – 8.9 cM – *Xgwm753-7B*[10692].

Pc1[743] locus: 7BS[768] 7B[743] syn: Pc[743]

s: CS*6/Hope 7B[743, 768]. **itv**: LD222*11/CS (Hope 7B)[1546]. **ma**: **Pc** (proximal) – 5.7 cM – *Xpsr490* (*Ss1)-7B*.

Pc2[921] locus: 7DS syn: 7DS[921]

v: Ilyitchevka[921]; Mironovskaya 808[921]; Novosibirskaya 67[921]; Pyrothrix 28[921]; Saratovskaya 210[921]; Strela[921]; Ukrainka[921].

1.9.5 Purple grain/pericarp

Genes for purple pericarp were transferred from tetraploid wheats to the hexaploid level[112, 214, 941, 1138]. At the hexaploid level duplicate genes[112, 941] and complementary genes[112, 438, 939, 1138] were reported. At the tetraploid level, duplicate-gene[941] and single-gene[1327] inheritances were observed. Purple colour is dominant and may be affected by environment and genetic background. Complementary genes were located in chromosomes 3A and 7B[1138]. Possible pleiotropic relationships of genes affecting pigmentation of various tissues have not been studied in detail. **Pc2** and ***Rc-B1a*** may be the same gene[769]. Also, complementary genes involved in determination of purple pericarp could be related to culm colour[112]. The location of the second complementary gene is confusing: the three group 7 homoeologues might be involved in different materials. For review, see [1643].

Complementary dominant genes. A purple line PC was obtained from a cross of non-purple Line 821 (a 7S(7B) substitution from *Ae. speltoides*) and Line 102/00, a chromosome 2A introgression from *T. timopheevii*[10946]. Purple grained accessions are unknown in both *Ae. speltoides* and *T. timopheevii*.

PP-1

PP-A1 locus: 7AS syn: Pp-A1

v: Saratovskaya 29 (not purple)[11312].

PP-B1 locus: 7BS syn: Pp-B1

Later renamed as ***Pp3b***.

PP-D1 locus: 7DS[11312] syn: Pp-D1, TaPpm1a[11313]

Pp-D1a

v: Heixiaomai 76 **Pp3**[11313]; Luozhen 1 **Pp3**[11313]; Nongda3753 **Pp3**[11667]. **c**: GenBank KM382421, a purple pericarp MYB 1, is strongly expressed in the pericarp[11313]. GenBank MG066451[11313].

PP1

Pp1[41] locus: 7BL[10392] 6A[41]

i: Saratovskaya 29*8/Purple (Australia) **Pp2**[40]. **v**: Novosibirsk 67 (this cultivar has white pericarp)[10392]. **v2**: Purple K49426 ***Pp3a***[10392]; Purple Feed ***Pp3b***[10392]. **ma**: *Xgwm983-7B* – 15.2 cM – PP1 – 11.3 cM – *Xgwm767-7B*[10392].

PP3

Combinations of **Pp3** and one or other **Pp1** single purple allele gave light purple pericarp whereas combinations involving **Pp3** with multiple purple alleles gave a dark purple phenotype[11312].

Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color[11285]. This may correspond to *TaPpm2* located on chromosome 4BL, one of three *Ppm* genes with no effect on purple pericarp[11313].

PP3 locus: 2AS syn: Pp3, TaMyc1[11312], TaPpb1a[11313]

Pp3a[10392]

v2: Purple K49426 **Pp1**[10392]. **ma**: *Xgwm328-2AS* – 2.7 cM – ***PP3a*** – 3.2 cM – *Xgwm817-2AL*[10392].

Pp3b[10392] syn: Pp2

v2: Purple Feed[66, 10392]. **ma**: *Xgwm328-2A*S – 5.2 cM – ***PP3b***/*Xgwm817*/*Xgwm912-2A* – 3.6 cM – *Xgwm445-2A*[10392].

PP2

Pp2[41] locus: 7A[41]

tv: *T. durum* Desf. subsp. *abyssinicum* Vav[40].

Piech and Evans[1138] located complementary genes on chromosomes 3A and 7B. **Pp2** was renamed ***Pp3b***.

ungrouped

pp1pp3

v: Saratovskaya 29 (this cultivar has red pericarp)[10329].

A set of Saratovskaya 29 NILs is described in [11136]. A homoeologous system was later proposed:

Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color[11285]. This may correspond to *TaPpm2* located on chromosome 4BL, one of three *Ppm* genes with no effect on purple pericarp[11313].

1.9.6 Purple glume

Pg[10692] locus: 2A[10692]

tv: TRI 15744 (IPK GeneBank, Gatersleben)[10692]. **ma**: *Xgwm328-2A* – 19.2 cM – **PG** – 1.4 cM – **PP3** – 5.1 cM – *Xgwm817-2A*[10692].

1.9.7 Purple leaf blade

Plb[10692] locus: 7B[10692]

tv: TRI 15744 (IPK GeneBank, Gatersleben)[10692]. **ma**: *Xgwm951-7B* – 6.7 cM – **PC/PLS/PLB** – 8.2 cM – PP1 – 8.9 cM – *Xgwm753-7B*[10692].

Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color[11285]. This may correspond to *TaPPM2* located on chromosome 4BL, one of three *PPM* genes with no effect on purple pericarp[11313].

1.10 Awnedness

In cereals such as barley and rice awns are conferred by dominant genes. No homologous genes have been reported in wheat.

hd b1 b2

Bearded or fully awned genotype

1.10.1 Dominant inhibitors of awns

Although hooded, half-awned, tip-awned and awnless variants occur among tetraploid wheats, these are relatively infrequent. It has not been established with certainty that the above inhibitors are involved.

The inhibitor alleles have a pleiotropic effect on glume-beak shape[1348]. Acuminate beak is associated with full beardedness and occurs only in **b1 b2** types. **B2** reduces beak length producing an acute beak shape. **B1** reduces beak length producing an obtuse beak shape. In this effect **B1** is epistatic to **B2**.

Hooded

Hd[1551] locus: 4AS[1195, 1293]

i: S-615*11/CS[1500]. **v**: Chinese Spring **B2**[1293]. **ma**: *Xcdo1387-4A* – 8.2 cM – **HD** – 7.2 cM – *Xpsr163-4A*[0047] was mapped as a QTL with a peak on *Xfba78-4A*[0309].

hd

s: CS*6/Hope 4A; CS*5/Thatcher 4A; CS*6/Timstein 4A.

Tipped 1

B1[1551] locus: 5AL[1293, 0242] syn: ALI-1[11581]

B1 was mapped as a QTL with a peak on *Xwmc182-6B*[0309]. Associated with increased number of spikelets per spike and decreased kernel size in a survey of global bread wheat germplasm[11571]. Associated with lower grain length and 1000 grain weight[11581].

i: S-615*11/Jones Fife[1500]. **v**: Timstein[741]; Redman[160]; [10040]. **tv**: LD222[10541]. Glossy Huguenot[11570]. **ma**: *Xgwm410.2-5A* – 8.2 cM – **B1** – 12.2 cM – YR34[10040]; Terminally located[10189]; *Xgwm291-5A.3* – 5.3 cM – **B1**[10330]. **matv**: *Xgwm291-5A* – 8.0 cM – **B1**[10541]. **c**: Functionally confirmed by transforming awned Kennong 199 with a 2,017 bp fragment containing *TraesCS5A02G542800* and UTRs from YMZ[11581].

B1a[42]

s: Saratovskaya 29*8/Festiguay 5A[42].

B1b[42]

s: Saratovskaya 29*8/Aurora 5A[42].

B1c[42]

s: Saratovskaya 29*8/Mironskaya 808 5A[42].

b1 syn: ali-1[11581].

v2: Chinese Spring **B2 Hd**[1293].

In a common genetic background, carriers of ***B1a*** have the shortest tip-awned phenotype; carriers of ***B1b*** and ***B1c*** have awns 2 to 3 times longer depending on environment. In F1 hybrids, differences between the substitution line combinations are significant. The postulation of **B1** in both CS and Courtot[0309] based on the phenotype of a CS deletion stock is not supported by genetic observations

Tipped 2

B2[1551] locus: 6BL[1293, 1297]

i: S-615*11/CS[1500]. **v**: Chinese Spring **Hd**[1293].

b2

s: CS*6/Hope 6B; CS*5/Thatcher 6B; CS*9/Timstein 6B.

A GWAS of 364 wheat accessions identified 26 loci associated with awn length[11581].

Awnless

Genotypes **Hd B2** (e.g., Chinese Spring) and **B1 B2** (e.g., Federation) are awnless. Presumably **Hd B1** is awnless. Watkins & Ellerton[1551] noted the probability of a third allele "***b1a*** " leading to a half-awned condition, and in discussion they considered the possibility of a similar third allele at the **B2** locus. In view of more recent cytogenetic analyses, it seems that the half-awned condition could result from epistatic interactions between the alleles **B1** and/or **B2** and various promotor genes.

1.10.2 Promotors of awns

The effects of (recessive) awn-promoting genes were documented in a number of studies, mainly through monosomic and disomic F1 comparisons, and in tetraploids, whereas Heyne & Livers[549] provided genetic evidence of their effects. A series of a genes was documented, but the evidence for the existence of at least some of these was not well supported. Hence symbols for this gene series are not recognized.

1.10.3 Smooth awns

Smooth-awned tetraploid wheats were reported[16, 45, 690, 1259] and genetic analyses[16, 45, 690] suggested a single recessive factor, with modifiers in most instances, relative to rough awns. The phenotype has not been reported in hexaploid wheats. No gene symbol is applied.

1.11 Basal sterility in speltoids

The presence of gene **Q** ensures the fertility of the first and subsequent florets in wheat spikelets[378]. In speltoids lacking **Q**, fertility of the second and subsequent florets is ensured by the dominant allele *Bs* (designated *A* in [378]) located on chromosome 5D[377]. In the presence of *Bs* the fertility of the first floret is under polygenic control.

In *bs bs* speltoids floret development is under polygenic control, and stocks with varying levels of basal fertility were isolated.

All group *vulgare* genotypes so far studied carry *Bs*. The following stocks were described[378]:

GenotypeApprox. sterile-base scoreGroup *vulgare* ---- *QQ Bs Bs* 0.00Speltoids StFF*qq Bs Bs* 0.00StF*qq Bs Bs* 0.08St1A*qq Bs Bs* 0.39St1*qq Bs Bs* 0.96St2*qq bs bs* 1.41

	Genotype		Approx. sterile-base score
Group *vulgare*	----	*QQ Bs Bs*	0.00
Speltoids	StFF	*qq Bs Bs*	0.00
	StF	*qq Bs Bs*	0.08
	St1A	*qq Bs Bs*	0.39
	St1	*qq Bs Bs*	0.96
	St2	*qq bs bs*	1.41

1.12 Blue Aleurone

The *Ba* allele in *T. monococcum* spp. *aegilopoides* acc. G3116 determines a half-blue seed phenotype and is different from the allele present in *Elytrigia pontica* that determines a solid blue phenotype[282].

They are treated genes. For review see [1643].

Ba1[643] locus: 4B [4BS-4el2][594] syn: Ba[643]

Derived from *Elytrigia pontica* (2n=70).

tr: UC66049B (currently UC66049, PI 633834)[643].

Ba2 locus: 4A^{m}L syn: Ba[10451]

dv: G3116[282]; PAU5088 = G2610 = PI 42783Ie9[10451]. **ma**: **BA2** co-segregated with *Xcdo1387-4A*, *Xmwg677-4A* and *Xbcd1092-4*^{a}[282]; *Xcfd71-4A* – 10.3 cM – **BA** – 16.5 cM – *Xcfa2173-4A*.

1.13 Brittle culm

Three independent mutants with brittle tissues were obtained as EMS-induced mutants in *T. monococcum* accessions PAU 14087[11002]. The mutations likely affected cellulose synthesis and involved all tissues[11002].

brc1[11002] locus: 6AS[11002]

dv: *T. monococcum* mutant **brc3**[11002]. **ma**: *Xbarc37-6A* – 1.9 cM – **BRC1** – 10.3 cM – *Xbarc113-6A*[11002].

brc2[11002] locus: 3AL[11002]

dv: *T. monococcum* mutant **brc2**[11002]. **ma**: *Xcfa2170-3A* – 2.9 cM – **BRC2** – 0.8 cM – *Xcfd62-3A*[11002].

brc3[11002] locus: 1AL[11002]

dv: *T. monococcum* mutant **brc1**[11002]. **ma**: *Xwmc470-1A* – 3.9 cM – **Brc3** – 2.1 cM – *Xgwm135-1A*[11002].

brc5[11505]

A further recessive mutation in *T. monococcum* accession Pau 5088 was named **brc5**[11505]

ma: *Xcfd38-5AL* – 2.6 cM – **BRC5** – 4.8 cM – *Xgwm126-5AL*[11505].

1.14 Brittle rachis

Brittle rachis in *T. durum* was defined as a spike that disarticulated when the tip was bent by 45 degrees relative to the peduncle[10242]. In chromosome substitution lines of wild emmer to common wheat, the 3AS derivative was more brittle than the 3BS derivative[10974].

Wedge (W) type disarticulation is associated with the *Br-1* gene set whereas barrel (B) type disarticulation is caused by a different gene and is limited to species with the D genome[11080].

BR-1

Br-A1[10061] locus: 3A[0130] 3AS[10061] syn: Br2[10061] Br-A2[10280]

sutv: LDN(DIC 3A)[0130]. **itv**: ANW10A=LD222*7/LDN-DIC DS 3A[10242]. **ma**: *Xgwm2-3A* – 3 cM – **BR-A1** – 8 cM – *Xgwm666-3A.1*/*Xbarc356-3A*/*Xbarc19-3A*/*Xgwm674-3A*/*Xcfa2164-3A* [10280].

Br-B1[10061] locus: 3BS[10061] 3B[0130] syn: Br3[0130], Br-A3[10280]

sutv: LDN(DIC 3B)[0130]. **itv**: ANW10B=LD222*7/LDN-DIC DS 3B[10242]. **ma**: *Xbarc218-3B* – 22 cM – **BR-B1** – 2 M – *Xwmc777-3B* [10280]. **tv**: Senatore Cappelli PI 342646[10242]; Sammartinara[10242]; others[10242].

The presence of **Br-B1** in some durums apparently does not lead to significant shattering under conditions of Mediterranean agriculture[10242].

Br-D1[10061] locus: 3DS[9970] syn: Br1[9970], Br[61] [10362]

v: KU510, KU511, KU515[10061]; R- 61[10362]; *T. aestivum* var. *tibetanum*[9970]. **dv**: *Ae. tauschii* KU2126[10227]. **ma**: In *Ae. tauschii*: *Br*[t] – 7 cM – *Xgdm72-3D* [10227].

Evidence for an orthologous series extending to many related species is discussed in [10061, 0130].

Br-S1[11080] locus: 3SS[11080]

v: Iranian spelts[11080]. **tv2**: *Triticum timopheevii*[11080]. **dv**: *Aegilops tauschii*[11080]. **ma**: *Xpsr1196-3S* – 32.3 cM – **BR-S1** – 1.5 cM – *Xabg471-3D* [11080].

BR-2

Br-D2[11080] locus: 3DL[11080]

v: Common wheat[11080]; European spelts[11080]. **dv**: AL8/78 (shattering)[11080]; TA1604 (non-shattering)[11080]. **ma**: *Xmwg2013-3D* – 1.5 cM – **BR-D2** – 2.9 cM – *Xpsr170-3D* [11080].

BR4

Br4[10082] locus: 2A[10082]

tv: *T. dicoccoides*[10082]. **ma**: 33 cM distal to *Xgwm294-2A* (LOD=6.3, R^2=14.4%)[10082].

1.15 Boron tolerance

Genes controlling tolerance to high concentrations of soil boron act additively.

Bo1[1111, 1113] locus: 7BL[10460] 7B[177] syn: Bot-B5b[11432]

v: Carnamah[10460]; Frame[10460]; Krichauff[10460]; Yitpi[10460]; Additional genotypes[10833, 10834]. **v2**: Halberd **Bo2 Bo3**. **tv**: Kalka[10834]; Linzhi[10834]; Niloticum[10834]; Additional genotypes[10834]. **ma**: **Bo1** co-segregated with several STS-PCR markers, including *Xaww11-7BL*, falling within a 1.8 cM interval[10460]; The AWW5L7 (*Xaww11*) PCR marker allele was a good predictor of boron tolerance[10460]; Co-dominant PCR marker AWW5L7 co-segregated with **Bo1** and was predictive of the response of 94 Australian wheat genotypes[10833]; *Xbarc32-7B* – 2.4 cM – *Xaww5L7* – 1.2 cM – *Xbarc182-7B*/**BO1** – 1.2 cM – *Xpsr680*/*Xmwg2062-7B* [10833]; *Xbarc32-7B* – 2.6 cM – *Xaww5L7*/**BO1** 10834}. **c**: Boron transporter-like gene[11432]. GenBank KF148625.

Bo1 functions as a boron transporter[11432].

Bo2[1111, 1113]

v2: (W1*MMC)/Warigal **Bo3**. Halberd **Bo1 Bo3**.

Bo3[1111, 1113] locus: 4A[0012]

v2: Warigal **Bo2**. Halberd **Bo1 Bo2**.

Bo4[11432] locus: 4AL[11431] syn: BOT(TP4A-B5C)[11432]

v: G61450[11431]. **c**: **Bo4** is a dispersed duplication of **Bo1**[11432].

A homoeologous nomenclature based on annotated boron transporters inferred from the IWGS CS sequence is provided in Extended Data Table 1 in [11432].

Very sensitive genotype: Kenya Farmer *bo1 bo2 bo3*.

Boron efficiency: In contrast to tolerance, boron efficiency was studied in [10135]. Monogenic segregation occured in Bonza (B inefficient)/SW41 (moderately B inefficient) and SW41/Fang60 (B efficient). Two genes, designated *Bod1* and *Bod2*, segregated in Bonza/Fang60.

QTL
Cranbrook (moderately tolerant) / Halberd (tolerant): DH population; QTLs for tolerance were identified on chromosomes 7B and 7D[10832].

For a review of boron tolerance in wheat, see [10835].

1.16 Cadmium Uptake

Low uptake is dominant.

Low cadmium uptake

CDU1

Cdu1[963] locus: Corrected to 5BL[10894] 5BL[10104] syn: Cdu[1128]

itv: Kyle*2/Biodur[10104]. **tv**: Biodur[1128]; Brigade[11044]; CDC Desire[11044]; CDC Verona[11044]; CDC Vivid[11044]; Enterprise[11044]; Eurostar[11044]; Fanfarran[10894]; Hercules[1128]; Napoleon[11044]; Nile[1128]; Transend[11044]; Strongfield[11044]. **bin**: 5BL9-0.76-0.79. **ma**: CDU1 – 4.6 cM – *OPC-20*[1128]; CDU1 – 21.2 cM – *UBC-180*[1128]; *Xfcp2-5B* – 12 cM – CDU1 – 3 cM – *ScOPC20*[10894]; *ScOPC20*/*Xrz575-5B*/*XBG608197* – 0.5 cM – **Cdu1**/*XbF293297*/*XBF474090*/*Os03g53590* (*Xusw15-5B*) – 0.2 cM – *XBF474164*[10895]; CDU1 is close to **VRN-B1**[10895].

cdu1[963] syn: cdu 1[1128]

itv: Kofa[10104]. **tv**: Kyle[1128]; DT369[10894].

1.17 Chlorophyll abnormalities

1.17.1 Virescent

V1 locus: 3BS[1423] 3B[122, 1294, 1311]

v: CS.

v1a syn: v[1294]

i: S-615*11/Neatby's Virescent[1500]. **s**: CS*9/Neatby's Virescent[1304]. **v**: Neatby's Virescent[1055].

v1b

i: CS*/Hermsen's Virescent ***v2b***[1304]. **v**: Hermsen's Virescent ***v2b***[1311].

V2 locus: 3A[1311, 1545]

v: CS.

v2a

v: Viridis 508[1545].

v2b

Expressed only when combined with ***v2b***

i: CS*/Hermsen's Virescent ***v1a***[1304]. **v**: Hermsen's Virescent ***v1a***[1311].

v1b and ***v2b*** are expressed only when both are present. Corresponding normal alleles are designated **V1** and **V2** following Sears[1295] demonstration of their effects on the expression of ***v1a***.

1.17.2 Chlorina

CN-1

Cn-A1 locus: 7AL[1131, 1304, 1311] 7°[1132]

v: CS.

cn-A1a syn: cn1a

i: ANK-32[10820]; Chlorina-1[1311].

cn-A1b syn: cn1b

i: Cornell Wheat Selection 507aB-2B-21/6*CS[1133].

cn-A1c syn: cn2

i: Chlorina-448. (CS background)[1545].

cn-A1d[665]

tv: *CDd6*[665, 666]. **itv**: ANW5A-7A[10820]. **ma**: Hexaploid wheat: *Xhbg234-7A* – 8.0 cM – **CN-A1** – 4.3 cM – *Xgwm282*/*Xgwm332-7A*[10820]; Tetraploid wheat: *Xbarc192-7A* – 19.5 cM – **CN-A1** – 11.4 cM – *Xgwm63-7A*[10820]; Diploid wheat: *Xgwm748-7A* – 29.2 cM – **CN-A1** – 33.3 cM – *Xhbg412-7A*[10820].

Cn-B1 locus: 7BL[1131]

v: Chinese Spring[1131].

cn-B1a[665]

tv: *CDd1*[665, 666]. **v**: CBC-CDd1[665].

cn-B1b[665]

tv: CDd2[665, 666].

Cn-D1 locus: 7D[1545]. 7DL[1131] syn: Cn3

v: Chinese Spring[1131].

cn-D1a syn: cn-D1, cn3

i: Chlorina-214[1545]. **v**: CD3[1583].

Two mutants in diploid wheat are reported in [10820].

1.17.3 Striato-virescens

A mutant of this type was described[376] but has been lost.

1.17.4 Yellow-green

yg locus: 2BS[11238] syn: y1718[11238]

Incompletely dominant

v: Xinong 1718 mutant[11238]. **ma**: *Be498358*– 4.0 cM – **yg** – 1.7 cM – *Xwmc25-2B*[11238].

The homozygous *ygyg* genotype is extremely yellow, stunted and sterile and the mutant is easily maintained as a heterozygote[11238].

1.18 Cleistogamous flowering

Cleisogamy in barley is controlled by the *Chy1* allele that encodes an AP2 protein. The *Cly* and *cly1* alleles differ by a single nucleotide within the miR172 binding site. Three wheat homologues of *Cly1, viz, TaAP-2A, TaAp-2B* and *TaAp-2D* were located in the terminal bins of chromosomes 2AL, 2BL and 2DL, respectively in Chinese

Spring and Shinchunaga[11013]. Cleistogamous flowering in durums Cleistogamy, a rare flowering habit in durum wheats, is controlled by a single recessive gene relative to chasmogamy[191].

ClCl

Chasmogamous genotypes

tv: IWP5308[191]; PWB34[191]; WH872[191].

clcl

Cleistogamous genotypes

tv: HI8332[191]; WH880[191].

1.19 Copper efficiency

Copper efficiency is a genetic attribute that enhances plant growth in copper deficient soil.

Ce[1276] locus: 4BL = T4BL5RL[1276]

v: Cornell Selection 82a1-2-4-7[462]; Backcross derivatives of Cornell Selection to Oxley, Timgalen, Warigal[464]; Hairy necked Viking[1276]. 5BS = T5BS.5RL. **ad**: CS+5R[463]. **su**: CS 5R {5D}[463]. **v**: Sears' stock HN-2[464]; Backcross derivatives to Warigal and Timgalen[464].

1.20 Corroded

co1 locus: 6BS[1293] syn: co[1297] wsl[11535].

v: Guomai Mutant[11535]; Sears' corroded mutant[1293, 1297, 11535]. **ma**: *Xgwm508-6B* – 5.1 cM – *Xgwm519-6B* – 8.2 cM – **CO1**[11535]; *Xgwm508-2* – 8.7 cM – **CO1** – *Xgpw7651-6B*[11534].

co2 locus: 6D[1570]

v: Kurrachee[1570]; Shannong 33 Mutant I30[11534]. **ma**: *Xcfd190-6D* – **CO2** – 9.1 cM – *6DS-5*[11534].

A gene(s) in chromosome 6A acts as an inhibitor of corroded[1039, 1570].

A gene(s) in chromosome 6A acted as an inhibitor of corroded[1039, 1570]. Corroded mutants are very frequent in EMS-treated populations[939].

1.21 Crossability with Rye and *Hordeum* and *Aegilops* Spp.

1.21.1 Common wheat

High crossability of some wheats, particularly those of Chinese origin, viz. Chinese 446[790], Chinese Spring[1216], and TH 3929[939], with cereal rye, weed rye (*S. segetale* L.)[1646], and other species, e.g., *Aegilops squarrosa*[691], *Hordeum bulbosum*[1387, 1397, 1469] and *H. vulgare*[349, 693], is determined by additive recessive genes. The *kr* genes influence crossability with *H. vulgare*. Allele **Kr1** is more potent in suppressing crossability than *Kr2*, which is stronger in effect than *Kr3*[1387]. According to Zheng et al.[1649], the effect of *Kr4* falls between **Kr1** and *Kr2*.

KR1

Kr1 locus: 5B[1216] 5BL[762]

ma: Mapped to a 2.0 cM region flanked by *Xw5145-5B* and *CA1500122/Xw9340-5B*[10922].

A second gene in 5BL distal to the **Ph1** locus and flanked by *Oshypl* and *Os09g36440*, but including *Xgwm371-5B*, affected the temperature sensitivity of seed-set in Kr1 genotypes in wide crosses[10922].

KR2

kr1 kr2

v: Chinese 446[790]; Chinese Spring[762, 1025, 1216]; Martonvarsari 9*4/CS[1016].

kr2 locus: 5A[1216] 5AL[1387]

KR3

kr3[11769] locus: 5DL[11769]

A very weak effect.

KR4

kr4 locus: 1A[1649]

KR5

Kr5[11387] locus: 5BS[11352, 11764] syn: skr[11352, 0134]

ma: Linked marker *Cfb306-5B*[11764].

kr5

su: Courtot (Fukuhokomugi 5B)[11352]. **v**: Balthazar-crossable[11352]; Deucendeu[11352]; MP98[11764]; Ornicar-crossable[11352].

ungrouped

Kr1 Kr2

v: Marquis[790]; Peragis[790].

Kr1 kr2

s: CS*6/Hope 5B[762, 1216]. **v**: Blausamtiger Kolben[790].

kr1 Kr2

s: CS*6/Hope 5A[1216].

kr1 kr2 kr3 kr4

v: J-11[1649].

Kr1 Kr2/Kr1 kr2

(heterogeneous).

v: Martonvarsari 9[1016].

Using the Chinese Spring/Cheyenne chromosome substitution series, Sasaki & Wada[1265] found significant differences in crossability for chromosome 5B, 7D, 1D and 4B. Differences between rye lines were also reported[1265, 1458]. Allelic variation in the potency of the dominant suppressor genes was reported[343, 1385]. Evidence for allelic variation in dominant supressors is reported in [1386]. Lists of wheat/rye crossabilities:[850, 858, 1383, 1642].

QTL

65% of the variability in a Courtot/CS population was associated with *Xfba-367-5A* (5AS), *Xwg583-5B* (5BL) and *Xtam51-7A*[0134]. Only the second QTL appeared to coincide with known locations of *Kr* genes. The former was *skr*.

1.21.2 Tetraploid wheat

The Chinese tetraploid, Ailanmai, possesses recessive crossability genes on chromosomes 1A, 6A and 7A with the 6A gene being the least effective[0017].

1.22 Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to pre-harvest sprouting (PHS). For a review of genes involved in preharvest sprouting see [11569].

Qphs.ocs-4A.1

May be the same as a QTL in AC Domain/Haruyutaka due to tight linkage with *Xcdo785-4A*[10245]. *QPhs.ocs.4B.1*, a CS allele contributing to dormancy, was located in the region of *Xgwm495-4B*[10245].

QPhs.sicau-3B.1

Distally located on chromosome 3B in *T. spelta* **CSSR6 (res) / Lang (sus)**; nearest marker *wPt-6157*; transferred to durum cv. Bellaroi using SCAR markers[11246].

1.22.1 Germination index

TASDR-1

Isolated using the seed dormancy related gene *OsSdr4*

TaSDR-A1[11199] locus: 2A[11199] syn: TaSdr-A1[11199]

ma: *Xgwm95-2A* – 1.4 cM – **TaSDR-A1** – 1.5 cM – *Xgwm372-2A*[11199].

TaSdr-A1a[11119]

This allele is associated with lower germination index

c: GenBank KF021988[11119].

TaSdr-A1b[11119]

c: GenBank KF021988[11119].

This allele is associated with higher germination index

TaSDR-B1[11119] locus: 2B[11119] syn: TaSdr-B1[11119]

TaSdr-B1a[11119]

This allele is associated with lower germination index

v: Yangxiaomai[11119]. **c**: GenBank KF021990[11119].

TaSdr-B1b[11119]

v: Zhongyou 9507[11119]. **c**: GenBank KF021991[11119].

This allele is associated with higher germination index.

1.22.2 Vivipary

Orthologues of maize viviparous 1 (*Vp-1*) are located in chromosomes 3AL, 3BL and 3DL[9961] approximately 30 cM distal to the *R* loci. Variability at one or more of these loci may be related to germination index and hence to PHS[10468]. Alleles at **VP-A1** were recognized using STS marker A17-19[10919].

Three sequence variants at **VP-B1** identified in [10468] were used to develop STS marker *Vp1B3* whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.

Alleles of **VP-B1** were recognised using STS marker *Vp1B3*[10615, 10621].

VP-1

Vp-A1[10919] locus: 3AL[10919]

Vp-A1a[10919]

v: Nongda 311[10919]. **c**: 599 bp[10919].

Higher germination index.

Vp-A1b[10919]

v: Wanxianbaimaizi[10919]; Yannong 15[10919]. **c**: 596 bp[10919].

Lower germination index.

Vp-A1c[10919]

v: Jing 411[10919]. **c**: 593 bp[10919].

Higher germination index.

Vp-A1d [10919]

v: Xiaoyan 6 [10919]. **c**: 590 bp [10919].

Lower germination index.

Vp-A1e [10919]

v: Zhengzhou 6 [10919]; Bainong 64 [10919]. **c**: 581 bp [10919].

Higher germination index.

Vp-A1f [10919]

v: Yumai 34 [10919]. **c**: 545 bp [10919].

Higher germination index.

Vp-A1g [11047] syn: Vp-1Ab [11047]

v: Kalyansona [11047]; Sonalika [11047]; Yaqui 50 [11047]; Yecora Rojo 76 [11047]. **c**: GenBank GU385899 [11047].

Vp-A1h [11047] syn: Vp-1Ad [11047]

v: Attila [11047]; Glenlea [11047]; Tanori F71 [11047]. **c**: GenBank GU385901 [11047].

Vp-A1i [11047] syn: Vp-1Af [11047]

v: Debeira [11047]; Kancahn [11047]; Rayon F89 [11047]. **c**: GenBank GU385903 [11047].

Vp-B1 locus: 3B [11047]

Vp-B1a [10615]

v: Charger [10616]; Zhongyou 9507 [10615]; 271 accessions [10616]. **c**: GenBank AJ400713 [10615].

Vp-B1b [10615]

v: Altria [10616]; Recital [10616]; Yongchuanbaimai [10615]; 2 accessions [10616]. **c**: 193 bp insertion in third intron relative to ***Vp-A1a***.

Vp-B1c [10615]

v: Scipion [10616]; Xinong 979 [10615]; 101 others [10616]. **c**: 83 bp deletion relative to ***Vp-B1a***.

Vp-B1d [10616]

c: 25 bp deletion relative to *Vp- A1a*.

Vp-B1e [10621] syn: Vp-1Be [10998]

v: Fulingkemai [10999]; Hongheshangtou [10621]; Hongmangchum [10998]; Wangshuibai [10999]. **c**: 83 bp deletion, 4 bp insertion and 2 SNPs relative to ***Vp-B1a*** [10621].

Vp-B1f [10998] syn: Vp-1Bf [10998]

v: Wanxanbaimaizi [10998].

Vp-B1g [11047] syn: Vp-1Bg [11047]

v: HD2939 [11047]; Pavon 76 [11047]; Sonora 64 [11047]. **c**: GenBank GU385904 [11047].

Vp-D1 [10919] locus: 3DL [10919]

c: AJ400714 [10919].

Vp-D1a [10919] locus: 3DL [10919]

v: 81 Chinese wheat cultivars [10919]. **c**: 5 pairs of primers [10919].

There was a suggestion of a relationship between alleles and PHS response [10615]

1.22.3 Pre-harvest sprouting

PHS1 syn: TaMKK3-A

c: Encodes a mitogen-activated protein kinase kinase (**TaMKK3-A**) [11737] and orthologue of **SD2** (*Qsd2-AK*) in barley [11737].

Phs1[10500] locus: 4AL[9960] syn: Phs[9960], Phs1-4AL, Phs-A1[11546], TaMKK-A[11546]

Semi-dominant[9960]

i: Haruyokoi*6/Leader[10500]; Haruyokoi*6/Os21-5[10500]. **v**: Chinese Spring[11737]; Leader[10500]; Os21-5[10500]; Soleil[9960]. **ma**: Associated with *Xpsr1327-4A*[10346]; *Xhbe03-4AL* – 0.5 cM – **Phs1** – 2.1 cM – *Xbarc170-4AL*[10500].

phs1

v: Haruyokoi[10500].

TaOsd1[11738]

CRISPR-Cas 9 knockout of *TaQsd1* homoeologues in chromosomes 5A, 5B and 5D led to a 3-4-fold increase in dormancy in Fielder wheat[11738]. *Qsd1* encoding an alanine amino transferase controls dormancy in barley.

Genotypes with and without favourable haplotypes are discussed in ▶[11546]. According to ▶[11547] red grain colour increases the time to dormancy release and has a cumulative effect when combined with other dormancy genes not associated with grain colour. For a review of Preharvest Sprouting[11595].

QTL

Several QTL for falling number and alpha-amylase activity, two indicators for pre-harvest sprouting resistance, were identified in ▶[0169]. The most significant were associated with *Xglk699-2A* and *Xsfr4(NBS)-2A*, *Xglk80-3A* and *Xpsr1054-3A*, *Xpsr1194-5A* and *Xpsr918-5A*, *Xpsr644-5A* and *Xpsr945-5A*, *Xpsr8(Cxp3)-6A* and *Xpsr563-6A*, and *Xpsr350-7B* and *Xbzh232(Tha)-7B*[0169].

AC Domain / Haruyutaka: one major QTL in chromosome 4AL and two lesser possibly homomeologous QTLs for dormancy in 4BL and 4DL[0226].

AC Domain (red seeded, PHS resistant) / RL4137 (white seeded, PHS moderately resistant): most measures of PHS occurred as clusters at the *R* loci. However, *QSi.crc-5D* for index, R^2=0.44, was independent of seed colour[10626].

Annong 0711 (res) / Henong 825 (sus): RIL population. Differences in germination index were attributed to a 33 bp insertion in the promoter (possibly the AP2 binding site) of *TaMFT-3A* in Annong 0711 relative to Henong 825. *TaMFt-3A* encodes a phosphatidyl ethanolamine-binding protein[11410].

Argent (non-dormant, white seeded) / W98616 (dormant, white seeded): 90 DH lines: Strong QTLs on chromosomes 1A, 3A, 4A and 7A and weaker QTLs on 2B, 5B, and 6B, all from W98616[10740].

CN10955 (PHS resistant white seeded) / Annuello (PHS susceptible, white seeded): F8 RIL population: *QPhs.dpivic-4A.2* in the *Xgwm637-4AS* – *Xgwm937*/*Xgwm894-4AL* region and *QPhs.dpivic- 4A.1* in the *Xwmc48-4AS* – *Xgwm397-4AS* region[10599].

SPR8198 (red seeded, PHS tolerant) / HD2329 (white seeded, PHS susceptible): Tolerance to preharvest sprouting (PHS) was associated with *Xwmc104-6B* and *Xmst101-7D*[0032]. In a further study 7 QTL were located on chromosomes 2AL, 2DL, 3AL and 3BL, the most important, on 2AL and 3AL[10670].

SPR 8198 (dormant) / HD2329: *QPhs.occsu-3A* was located in the *Xgwm155-3A* – *Xwmc153-3A* = 75% across 6 environments[10261].

Renan / Recital: QTL for preharverst sprouting were identified on chromosomes 3A (associated with *Xfbb293-3A* at P = 0.01), 3B (associated with *Xgwm403-3B* and *Xbcd131-3B* at P = 0.001), 3D (associated with *Xgwm3-3D* at P = 0.001) and 5A (associated with *Xbcd1871-5A* at P = 0.001) in the population[0347]. The resistant alleles on the group 3 chromosomes and on 5A were contributed by Renan and Recital, respectively. All QTL for preharvest sprouting co-located with QTL for grain colour[0347].

RL4452 (red seeded, low PHS tolerance) / AC Domain (red seeded, high PHS tolerance): DH lines: Genes associated with falling number, germination index and sprouting index contributing to PHS were located on chromosomes 3A, 4A (locus-2) and 4B in AC Domain and 3D, 4A (locus-1) and 7D in RL4452[10671].

Rio Blanco (white seeded, PHS resistant) / NW97S186 (white seeded, PHS susceptible): RIL population: *QPhs.pseru-3AS*, R^2=0.41, *Xgwm369-3A* – *Xbarc12-3A*, and one minor QTL[10634]. This major QTL was confirmed in a Blanco/NW98S079 RIL population, R^2up to 0.58[10634]. *Qphs.pseru- 3A* (*TaMFT*- 3A) was fine mapped to a 1.4 cM region flanked by two AFLP markers and was tightly linked to *Xbarc57-3A* and seven other AFLP markers[10893].

Sun325B (dormant white seeded) / QT7475 (semi-dormant white seeded): both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77-3B* – *Xwmc527-3B* = 0.19) in the approximate region of the **R-B1** locus[10669].

Totoumai (res) / Siyong (sus): RIL population: A QTL on chromosome 4AL was delimited to a 2.9 cM interval flanked by GBS109947 and GBS212432; nine and two SNP were associated with minor QTL on chromosomes 5A and 5B[11408], respectively.

Zenkoujikomugi / CS: *Qphs.ocs-3A.1* on chromosome 3AS was associated with *Xbcd1380-3A* and *Xfbb370-3A* accounting for 38% of the phenotypic variation[10195]. *QPhs.ocs.3A-1* was localized to a 4.6 cM interval flanked by *Xbarc310-3A* and *Xbcd907-3A*[10245]. A weaker QTL, *Qphs.ocs-3A.2* in 3AL, was not associated with *TaVp1*[10195], the wheat orthologue of the maize transcription factor Viviparous-1.

Zenkoujikomugi / Spica: White seeded wheats with the dormancy-related QTL, *QPhs-3AS* from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica[10377]. White seeded wheats with contrasting alleles of *QPhs-4AL* were not different[10377].

QTL analyses in several crosses[10275] indicated a common region in chromosome 4A associated with dormancy, dormant genotypes included AUS1408, SW95-50213 and Halberd. The location was consistent with Japanese and U.K. work even though different flanking markers were involved.

Association mapping of 198 winter wheat genotypes detected 8 QTLs on 7 chromosomes, viz. 1BS, 2BS, 2BL, 2DL, 4AL, 6DL, 7BS and 7DS[10959].

A GWAS identified 12 QTL for PBS resistance among which those on chromosomes 3AS and 4AL were most commonly detected[11409].

Diploid wheat QTL

T. monococcum **KT3-5 (non-dormant)** / *T. boeoticum* **KT1-1 (dormant)**: RIL population: QTL on chromosome 5A^{m}L, *Xcdo1236c-5A* – *Xabc302-5A*), R^2= 0.2-0.27. Weaker QTLs were found on 3A^m(*TmAB18* – *Xwmc102-3A* and *Xrz444-3A* – *TmABF*) and 4A^m(*Xrz261-4A* – *Xrz141-4A*)[0892]. The 3A^m

QTL co-located with *TmABF* and *TmAB18*[10417], derived from orthologous ABA signaling genes in *Arabidopsis*. The 5A QTL may be orthologous to the barley dormancy gene **SD1**[10417]. For a review of Preharvest sprouting see ▸[11595].

1.23 Ear emergence

QEet.inra-2B[10069] locus: 2B

ma: 2B linked to *Xgwm148* (LOD=5.7, R^2= 11.9%).

QEet.inra-2D[10069] locus: 2D

ma: 2D linked to *XksuE3* (LOD=2.7, R^2= 6.5%).

QEet.inra-7D[10069] locus: 7D

ma: 7D linked to **Pch1** (LOD=3.9, R^2= 7.3%).

QEet.ipk-2D[0255] locus: 2DS

QEet.ipk-2D coincides with a QTL for flowering time, *QFlt.ipk-2D*. Both QTLs may correspond to **Ppd-D1**[0255].

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Lateness was contributed by W-7984[0255]. **ma**: Associated with *Xfba400-2D* and *Xcdo1379-2D*[0255].

QEet.ipk-5D[0255] locus: 5DL

QEet.ipk-5D coincides with a QTL for flowering time, *QFlt.ipk-5D*. Both QTLs probably correspond to **Vrn-D1**[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Lateness was contributed by W-7984[0255]. **ma**: Associated with *Xbcd450-5D*[0255].

QEet.ocs-4A.1[0047] locus: 4AL[0047]

v: CS/CS(Kanto107 4A) mapping population. **ma**: Associated with **Wx-B1**[0047].

QEet.ocs-5A.1[0068] locus: 5AL[0068]

v: CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population[9903]. **ma**: Associated with *Xcdo584-5A* and morphological locus **Q**[0068].

QEet.ocs-5A.2[0026] locus: 5AL[0026]

ma: *Xcdo412-5A* – *Xbcd9-5A* region[0026].

1.24 Earliness per se

Genes for earliness *per se*[0023] affect aspects of developmental rate that are independent of responses to vernalization and photoperiod.

EPS-5

Eps-5BL.1[10075] locus: 5BL[10075]

ma: QTL mapped on chromosome 5BL, linked to *Xwmc73-5B* (this QTL explained 8% of the variance in flowering time, P < 0.03[10075]).

Eps-5BL.2[10075] locus: 5BL[10075]

ma: QTL mapped on chromosome 5BL, linked to *Xgwm499-5B* (this QTL explained 6% of the variance in flowering time)[10075]).

EPS-1

Eps-1A^{m}[0364] locus: 1AL[0364] syn: Eps-A^{m}1

dv: *T. monococcum* DV92 allele for late flowering, G3116 early flowering[0364]. **ma**: 0.8 cM distal to *Xwg241-1A*[0364]; within a 0.9 cM region within the *VAtpC* – *Smp* region[10246]; The circadian clock gene *Elf3* was identified as a candidate gene for *Eps- A* ^{m}1[11120].

Eps-A1a[0024] locus: 3AL[0024] 3A[0023]

v: Chinese Spring[0024].

Eps-A1b[0024]

v: Timstein[0024].

Eps-D1[11193, 11194] locus: 1DL[11193]

v: Earliness allele: Cadenza and Spark[11193]; Lateness allele: Avalon and Rialto[11193]. **ma**: The earliness allele was associated with a subtelomeric deletion containing three candidate genes one of which was *TaELF-D1*[11193].
A QTL for heading date co-segregated with *TaELF3-1DL* in a RIL population derived from **Gaocheng 8901** / **Zhoumai 16**[11194]; a deletion of the *Eps-1D* region was associated with earlier flowering.

ungrouped

epsCnn[0025]

v: Cheyenne[0025].

EpsWi[0025] locus: 3A[0025]

su: **Cheyenne*7 / Wichita 3A**[0025]. **ma**: Linked to QTLs for plant height, kernel number per spike, and 1,000-kernel weight in RSLs derived from CNN/CNN(WI3A)[0025].

QTL
CS / *T. spelta* var. *duhamelianum* **KT19-1**: RIL population: Two QTL for narrow-sense earliness were detected on chromosome 2B in a[10057]. These QTLs were associated with markers *Xpsr135-2B* and *Xabc451-2B*[10057]. For both QTLs, earliness was conferred by the CS allele.

Courtot / CS:[0132].

Cutler / AC Barrie: Three QTLs were mapped on chromosomes 1B (*QEps.dms-1B.1* and *QEps.dms- 1B.2*) and 5B *QEps.dms5B*)[11039].

Grandin / BR34: *QEet.fcu.5AL* identified in *Xfcp359-5A* – *Xfcp231-5A* interval (R^2= 0.38), at or near the **Q** locus in [10256]. Grandin was the earlier parent.

1.25 Embryo lethality

The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, R7) produced hybrid seeds with different proportions of differentiated embryos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74-100% differentiated embryos[10748]. A cross of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* on chromosome 6A[10748].

1.26 Flag leaf width

Two NILs in backgrounds of Mianyang 99-323 and PH691 possessing **Fhb5** in a *Xbarc303-5A* – *Xbarc100-5A* interval from Wangshuibai spanning the centromere had a narrow leaf phenotype. *QFlw.nau-5A*, re-designated as *TaFLW1*, was mapped to a 0.2 cM region, *Xwmc492-5A* – *Xwmc752-5A*: bin 5AL12-0.37-0.57, and was separated from **Fhb5**: bin 5AS3-C-0.75[10934]

1.27 Flowering time

The isolation of wheat genes orthologous to the Arabidopsis *Co* and rice *Hd1* genes was reported in [10054]. The genomic clones TaHd1-1, TaHd1-2 and TaHd1-3 originated from the long arms of chromosomes 6A, 6B and 6D, respectively. The orthology of the *TadHd1* genes with *Co/Hd1* was demonstrated by complementation of a rice line deficient in *Hd1* function with the TaHd1-1 genomic clone. The wheat *TaHd1* and rice *Hd1* genes were located in non-syntenic locations[10054]. To date, no variation for flowering time has been identified on wheat group 6 chromosomes.

QFlt.ipk-3A [0255] locus: 3AL[0255]

v: Opata/W-7984 (ITMI): RI mapping population[0255]; Lateness was contributed by W-7984[0255]. **ma**: Associated with *Xbcd451-3A* [255].

QFt.cri-3B.1 [10567]

Nearest marker *Xbarc164-3B*; identified in crosses of substitution lines of Ceska Presivka and Zlatka or Sandra[10567].

QTL

Arina (149 days) / Forno (150 days):winter wheat cross: Six QTL were detected over six environments. The 3 most important, all from Arina, were in chromosomes 6DL (R^2=16%), 3DL (R^2=14%) and 7BL (R^2=13%); 3 others in 2AL, 5BL and 6DL were from Forno[10172].

CI 13227 / Suwon 92: RIL population: Heading date: AFLP marker – 2.6 cM – *QHd.pser-2DS* – 121.1 cM – *Xgwm261-2D* [10269]. This QTL could be **Ppd-D1** [10269].

Ernie (early) / MO94-317 (late): winter wheat cross: days to anthesis (dta): *Qdta.umc-2D*, linked to *Xbarc95-2D*, R^2= 0.74[10456].

Karl 92*2 / TA 4152-4: F_2:F_4 population: Two QTLs, *QHd.ksu-2D*, associated with *Xgwm261-2D* (R^2=0.17), and *QHd.ksu-3D*, associated with *Xgwm161-2D* 9 (R^2)[10273].

Nanda 2419 / Wangshuibai: spring wheat cross: 7 QTL for flowering time identified with earlier alleles for five coming from Nanda 2419: *QFlt.nau-1B* (closest marker *Xbarc80-1B*, R^2=11 %), *QFlt.nau-1D* (*Xbarc62-1D*, *Xgwm232-1D*, R^2=6.13 %), *QFlt.nau-2B* (*Xwmc35-2B*, R^2=10 %), *XFlt.nau-2D* (*Xwmc601-2D*, R^2=10 %), *XFlt.nau-4A.1* (*Xcfd2-4A*, *Xmag1353-4A*, R^2=10 %), *XFlt.nau-4A.2* (*Xmag3386-4A*, *Xwmc161-4A*, R^2=18-19 %), *XFlt.nau7B* (*Xmag2110-7B*, *Xmag1231-7B*, *Xgwm537-7B*, *Xwmc218-7B*, R^2=18 %)[10566].

1.28 Flour colour

Loci controlling flour colour were identified and mapped in a recombinant inbred population derived from Schomburgk/Yarralinka[9936]. Regions in 3A and 7A accounted for 13% and 60% of the genetic variation, respectively, and *Xbcd828-3A*, *Xcdo347-7A* and *Xwg232-7A.1* were significantly associated with flour colour. The association was highly significant in all three replicates only for the 7A QTL. Symbols were not assigned to the flour colour loci. See also 29.2. Flour, semolina and pasta colour.

Lute[11189] locus: 7DS[11189]

High lutein ester.

bin: 7DS4-0.61-1.00. **v**: Indis[11189]; Sunco*2/Indus Der. DM5685*B12[11189]; Most bread wheat accessions. **ma**: *Xwmc438-7D* – 15.1 cM – *LUTE/XwPt-116/XwPt-3727* – 17.7 cM – *Xbarc154-7*[11189].

Sunco is low lutein but high ester, whereas Haruhikari is low lutein and zero ester.

lute[11189]

Low lutein ester.

v: Haruhikari[11189]. Lutein esters were not detected in durum[11189].

1.29 Free-threshing habit

QFt.mgb-5A[0046] locus: 5AL[0046]

tv: Messapia/*T. dicoccoides* MG4343 mapping population[0046]. **ma**: Associated with *XksuG44-5A*[0046].

QFt.mgb-6A[0046] locus: 6A[0046]

tv: Messapia/*T. dicoccoides* MG4343 mapping population[0046]. **ma**: Associated with *Xpsr312-6A*[0046].

1.30 Frost resistance

FR-1

Fr1[1446] locus: 5AL[1446]

v: Hobbit[1446]. **ma**: Mapped to the mid-region of 5AL, 2.1 cM distal from *Xcdo504-5A* and *Xwg644-5A* and proximal to *Xpsr426-5A*[419]; Mapped 2 cM proximal to *Xwg644-5A* and VRN-A1[0291]; and flanked by deletion points 0.67 and 0.68[0292].

Studies using induced and natural mutants of VRN-1 suggested that differences in frost tolerance previously attributed to **FR1** were pleiotropic effects of VRN-1[10708].

FR-2

Fr-A2[10079]

dv: *Triticum monococcum*. Frost tolerant parent G3116, frost susceptible parent DV92. **ma**: The QTL mapped on chromosome 5AL had a LOD score of 9 and explained 49% of the variation in frost tolerance. Closest markers: *Xbcd508-5A* and *Xucw90(Cbf3)-5A*. These markers are 30 cM proximal to *Xwg644-5A*, which is closely linked to frost tolerance locus FR-1. Eleven different *Cbf* transcription factors were identified at the **Fr-A2** locus[10302]; QTLs for frost tolerance in the **FR-A2** region were also identified in wheat chromosome 5B (**FR-B2**)[10079]) and in barley chromosome 5H (*FR-H2*)[10083].

Fr-B2 syn: Fr-Fr-B1[10075]

ma: QTL mapped on chromosome 5BL, linked to *Xgwm639-5B* (this QTL explained 12-31% of the variance in frost tolerance)[10075]. *Xgwm639-5B* mapped close to *Xmwg914-5B*, and to *Xbcd508-5B*, a marker located at the peak of the **Fr-A2** QTL[10075]. This data suggests that this locus is more likely orthologous to FR-2 than to FR-1.

Fr2[0291] locus: 5DL[0291]

s: CS*7/Cheyenne 5D[0291]. **ma**: **FR2** mapped 10 cM proximal to **VRN-D1**[0291].

Studies using induced and natural mutants of VRN-1 suggested that differences in frost tolerance previously attributed to **FR1** were pleiotropic effects of VRN-1[10708].

ungrouped

QWin.ipk-6A locus: 6AS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]. Winter hardiness was contributed by W-7984[0255]. **ma**: Associated with *Xfba85-6A* and *Xpsr10(Gli-2)-6A*[0255].

Responses to cold exposure and their genetics are reviewed in [0274, 0020].

QTL
Norstar (tolerant) / Winter Manitou (non-tolerant): DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the VRN-A1 locus (R^2=0.4); its peak co-incided with *Xwmc206-5A* and *Xcfd2-5A*, and expression of C-Repeat Binding Factor genes with strong homology to *Cfb14* and *Cfb15* located at the FR-2 locus in *T. monococcum* [10414].

1.31 Gametocidal genes and segregation distortion

1.31.1 Gametocidal activity

GC-1

GC1-B1

Gc1-B1a [1485] locus: 2B [1490] syn: Gc1a [1490], Gc1 [1487]

i: CS*8/*Aegilops speltoides* subsp. *aucheri* [1487].

Gc1-B1b [1485] locus: 2B [1490] syn: Gc1b [1490]

i: CS*8/*Aegilops speltoides* subsp. *aucheri* [1487].

Gc1-C1 [0188] locus: 2CL [0189]

ad: CS/2C [0189]. **su**: CS2C(2A), CS2C(2B), CS2C(2D) [0189].

Gc1-Sl1 [1485] locus: $2S^1$ [334] syn: Gc-$S^1$3 [1485]

ad: CS/*Ae. sharonensis* [334].

GC-2

GC2- S^l1

Gc2-S^l1a [1485] locus: $4S^1$ [866] syn: Gc-S^l1 [1485]

ad: CS/*Ae. longissima* [866].

Gc2-S^l1b [1485] locus: $4S^1$ [1013] syn: Gc-S^l2 [1485]

ad: S/*Ae. sharonensis* [1013]. **ma**: An EMS- induced *Gc-2* mutant was mapped to a wheat-*Aegilops sharonensis* T4B-$4S^{sh}$#1 translocation chromosome [10068].

GC-3

Gc3-C1 [1485] locus: 3C [333] syn: Gc-C [1485]

ad: CS/*Ae. triuncialis* [338].

Gc1-B1a, ***Gc1-B1b*** and *Gc1-S^1*, classified in the same functional group, are hypostatic to the genes *Gc2-$S^1$1a* and *Gc2-$S^1$1b*. **Gc3-C1** does not interact with the *Gc* genes in the other two groups.
In addition to these genes, chromosomes carrying gametocidal genes occur in *Ae. caudata* [337], *Ae. cylindrica* [336] and other strains of *Ae. longissima* and *Ae. sharonensis* [335, 1484].
Gametocidal genes in chromosomes in the same homoeologous group have the same gametocidal action [0190].
In monosomic additions of chromosomes with gametocidal effects, chromosome deletions and translocations are produced in gametes not having the gametocidal genes. This feature has been exploited to isolate genetic stocks suitable for physical mapping of wheat [0191] chromosomes, and of rye [0192] and barley [0193, 0194, 0195] chromosomes in a wheat background.
Genes with gametocidal activity (**Sd1** [1647] and **Sd2** [1161]) in wheat are present in homoeologous group 7 chromosomes of *Thinopyrum elongatum* [653, 1647]. A segment earlier believed to be derived from *Thin. distichum* [889, 892] is probably the same as that from *Thin. elongatum* [1162].

In the presence of both **Sd1** and **Sd2**, **Lr19** is transmitted preferentially in heterozygotes, the degree of distortion being determined by genetic background. In heterozygotes with the same background, and in the presence of only **Sd2**, **Lr19** shows strong self-elimination. Based on these results, it seems likely that the Sears' translocation 7D-7Ag#7 does not carry **Sd1** [939].
See also Pollen Killer.

1.31.2 Suppression of gametocidal genes

IGC1

Igc1[1489] locus: 3B

Causes suppression of the 3C chromosome gametocidal gene of *Ae. triuncialis*. This alien gametocidal factor also promotes chromosome breakage[1486]. 3B[1488]

v: Norin 26[1483, 1488]; Nineteen wheats listed in ▸[1483, 1488].

igc1

v: Chinese Spring[1483, 1488]; Forty wheats are listed in ▸[1483, 1488].

See also Pollen Killer

1.31.3 Segregation distortion

Sd1[1647] locus: 7D[1647]

v2: Agatha **Sd2**[1161, 1647]. **ma**: Proximal to **Lr19** and distal to *Xpsr165-7D*[10255].

Sd2[1161] locus: 7BL[1163]

v: 88M22-149[1161, 1163].

Zhang et al.[10255] question the existence of this gene and alternatively suggested a duplication or deletion event influencing the transmission.

1.32 Gibberellic acid response (insensitivity)

Gai1 locus: 4BS[980] 4B[406] syn: GAI1[565, 1246]

i: See ▸[408]. **v**: Norin 10 Der.[407, 565]. **ma**: *Xpsr622-4B* (distal) – 1.9 cM – **GAI1** – 8.3 cM – *Xbcd110-4B* (proximal)[9959]. **tv**: Messapia[9959].

Gai2 locus: 4D[411] 4DS[980] syn: GAI2[565, 1246]

i: See ▸[408]. **v**: Maris Hobbit[411]; Norin 10 Der.[565]; List in ▸[407].

Gai3 locus: 4B[413] 4BS[980] syn: GAI3[565, 1246]

i: See ▸[408]. **v**: Minister Dwarf[413]; Selection D6899[359]; Tom Thumb[405]; Tom Thumb Der.[565, 567]. In wheats with **Gai3**, the aleurone layer failed to respond to applied GA[405].

Two studies involving crosses between Tom Thumb derivatives and tall parents suggested that gibberellic acid insensitivity and reduced height were controlled by one gene, i.e., **Gai3**[359, 413]. In a third study involving a Tom Thumb derivative, recombinants were isolated, indicating separate but linked genes, i.e., **Gai3** and ***Rht-B1c***[565, 567]. Further evidence was obtained for linkage between genes for gibberellic acid insensitivity and Norin 10 genes for reduced height in hexaploid[568] and durum[720] wheats. Hu & Konzak[567] reported 27% recombination between **Gai1** and ***Rht-B1b*** and 10% recombination between **Gai2** and ***Rht-D1b*** in hexaploid wheats involving Norin 10 and Suwon 92 derivatives. In durum derived from crosses involving Norin 10, 15% recombination was obtained between one of the genes for reduced height and gibberellic acid insensitivity[1246, 1247]. Gale & Law[403] considered **Gai1** and ***Rht-B1b***, **Gai2** and ***Rht-D1b***, **Gai3**/ and ***Rht-B1c*** to be pleiotropic genes.

1.33 Glaucousness (Waxiness/Glossiness)

The W loci are complexes of closely linked genes involved in beta-diketone synthesis.

Glaucousness refers to the whitish, wax-like deposits that occur on the stem and leaf-sheath surfaces of many graminaceous species. The expression of glaucousness depends on the arrangement of wax deposits rather than the amount of wax[603]. Non-glaucous variants also occur and genetic studies indicate that non-glaucousness can be either recessive or dominant. Recessive forms of non-glaucousness are apparently mutants of the genes that produce the wax-like deposits. Dominant non-glaucous phenotypes (as assessed visually) appear to be due to mutations that affect the molecular structure, and reflectance, of the wax-like substances[10001]. The genes involved in wax production and the "inhibitors" are duplicated in chromosomes 2B and 2D. There appear to be independant genes for wax production and "inhibitors"[912, 1493, 10001]. In earlier issues of the gene catalogue the two

kinds of genes were treated as multiple alleles[1432]. All forms of wild and cultivated einkorn are non-glaucous[10001]. Orthologous loci occur in barley chromosome 2HS (*gs1*, *gs6*, *gs8*)[467], rye chromosome 7RL (*wa1*)[725] and maize (*gl2*)[211]. A gene for spike glaucousness, **Ws**, was mapped distally on chromosome 1BS in the cross *T. durum* cv. Langdon/*T. dicoccoides* acc. Hermon H52[0171].

1.33.1 Genes for glaucousness

W1

W1 locus: 2BS

i: Chinese Spring mono-2D/S615//10*wS615[10001]. **v**: Bethlehem[11458]; Chinese Spring[1493]; P86[11247]. **itv**: LD222*11/*T. turgidum* var. *pyramidale* recognitum[1546]. **v2**: S615 **W2**[10001]. **tv**: Kofa+**Lr19**[11458]; AUS2499[11458]. **c**: **W1** is a highly duplicated, variable gene cluster containing type III polyploid synthase, hydrolase and cytochrome P450 genes and is homologous to the *Cer-cqu* cluster in barley[11458].

w1 locus: 2BS[1432]

Recessive allele for reduced glaucousness

su: Bethlehem CASL*/*T. dicoccoides* TTD140 2BS(2B)[11458]. **v**: CS mono-4B mutant[1064]; J87[11247]; Mentana[1432]; Salmon[1493]. **tv**: AUS2499[11458].

W2

w1w2[10001]

i: w-S615 = S615*11/Salmon[10001]. **v**: Salmon[10001]; Mentana[1432]; CS mono-4B mutant[1064].

W2

i: Chinese Spring mono-2B/S615//11*w-S615[10001]. **v**: *T. compactum* cv. No 44[10001]. **v2**: S615 **W1**[10001].

W2a

dv: Glaucous forms of *Ae. tauschii*.

W2b

v: Chinese Spring - weak hypomorph recognized at increased dosage[1432].

A non-glaucous spike phenotype in line L-592, a 7S(7A) substitution line, is described in ▸[0113]

W3

W3[11456] locus: 3DL[11457]

dv: *Aegilops tauschii* KU-2126[11457]. **ma**: *Xgwm645-3DL* – 8.0 cM – **W3** – 8.9 cM – *Xbarc42-3DL*[11457].

W4

w4

dv: *Aegilops tauschii* KU-2104[11457]; KU-2105[11457].

Glaucous synthetics LDN/KU-2104 and LDN/KU-2105 are presumed to have genotype *W1W1W4W4*

1.33.2 Epistatic inhibitors of glaucousness

Each inhibitor inhibits all genes for glaucousness

Iw1[10001] locus: 2BS syn: W1^{I}[1493], I1-W[1493]

i: S615/Cornell 5075//10*S615[10001]. **v**: WE74[11094]; Shamrock[11090]. **tvsu**: $LDN_{DIC521\text{-}2B}$[11245]. **tv** *T. dicoccoides* PI 481521[11245]. **ma**: *JIC007* – 1.47 cM – **IW1** – 0.18 cM – *JIC010/JIC011*[11090]; Co-segregation with *BF474014*, *CJ876545* and CD927782 and flanked by *BE498358* and CA499581 within a 0.96 cM interval[11094]. **c**: **Iw1** encodes a long non-coding RNA (LncRNA) that putatively arose from an inverted repeat of a carboxylesterase gene (80% homology) in the **W1** cluster that consists of WI-COE (non-annotated carboxylesterase), WI-PKS (*Traes_2BS_9E10D26DB*, polykedide synthase) and WI-CYP (*Traes_2BS_163390FC4*, cytochrome P450-type hydroxylase)[11459]. GenBank C-DNA sequence, KX823910. The IR region has > 94% identity to an IR region in *Ae. tauschii* chromosome 2 that also produces MiRNA

and a marker-based location similar to that of **Iw2**[11459]. *Xgwm614-2B* – **IW1**/*Xbarc35-2B*/*CD893659/CD927782/BQ788707/CD938589* – *Be498111*[11245].

Iw2[10001] locus: 2DS[10001] syn: Iw3672[10510], I2-W[1493], IwT[11207]

bin: 2DS5-0.47- 1.00[10578]; 2DS5-0.84-1.00. **i**: S615/Golden Ball Synthetic//10*S615[10001]. **v**: Golden Ball Synthetic[10001]; Synthetic hexaploid line 3672[10510]; TA4152-60[11094]; Vernal Synthetic[10001]. **tv**: *T. dicoccoides* PI 481521[11245]. **dv**: Non-glaucous forms of *Ae. tauschii*[1493]. **ma**: In *Ae. tauschii*: **IW2** – 30.1 cM – *Xgdm35-2DS*[10227]; *Xbarc124-2D* – 0.9 cM – **IW2** – 1.4 cM – *Xwe6(AL731727)*[10510]; *Xcfd56-2D* – 6 cM – **IW2** – 10 cM – *Xcfd51-2D*[10578]; Co-segregation with *BF474014* and *CJ876545* and flanked by *CJ886319* and *CJ519831* within a 4.4 cM interval[11094]. *Xgwm614-2B* – **IW1**/*Xbarc35-2B*/*CD893659/CD927782/BQ788707/CD938589* – *Be498111*[11245].

Iw3[277] locus: 1BS[277] syn: IW3[277], I3-W[277]

sutv: Langdon*/*T. dicoccoides* 1B[11455]. **tv**: *T. turgidum* var. *dicoccoides*[277]. **ma**: *XWL1967*/*Xfcp168-1B* – 0.15 cM – *XWL3096* – 0.015 cM – **IW3** – 0.12 cM – *Xpsp3000-1B*[11455].

A non-glaucous spike phenotype in line L-592. A 7S(7A) substitution line, is described in ▶[0113]. A dominant gene (*Vir*) for non-glaucousness was located in chromosome 2BL of cv. Shamrock, a derivative of *T. dicoccoides*[10543]. This gene mapped 2 cM distal to *Xgwm614-2B*[10543] whereas the **W1**/**Iw1** locus was placed distal to *Xgwm614-2B* in ▶[10189]. Lines with *Vir* had delayed senescence ('staygreen') and an average yield advantage over their glaucous sibs[10543]. Although maps constructed from three tetraploid crosses suggested that **w1**, **W1** and **Iw1** DIC= *Vir* remain unresolved[10815].

1.33.3 Leaf glaucousness

QTL

RAC875 (non-glaucous leaf) / Kukri (glaucous leaf): *QW.aww-3A*, nearest marker *Xwmc264-3A*, accounted for 36-40% of the phenotypic variation; other QTL were located on chromosomes 1D, 2B (2 QTL), 4D, 5B and 2D[11131] =[11460].

GWAS of flag leaf glaucousness in a large panel of genotypes identified major QTL on chromosome 2B (**W1**/**IW1**) and 3A[11482].

1.33.4 Spike glaucousness

Spike glaucousness is recessive[10666].

WS

Ws[10666] locus: 1AS[10666]

bin: 1AS1-0.47-1.00[10666]. **v**: Svenno[10666]. **ma**: *BJ23702a* – 3.5 cM – *Tc95235* – 4.8 cM – **Bla**[10666].

ws[10666]

v: Ciccio[10666].

1.34 Glume colour and awn colour

Black glumes are now included in the following homoeologous series with red/brown/bronze glumes.

1.34.1 Red (brown/bronze/black) glumes

The majority of studies report a single dominant gene for red glume colour. A few papers report two factors[1009, 1477, 1520]. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes[1277] suggesting, because **Hg** is located in chromosome 1A, that a red glume factor different from **Rg1** is involved in the Swedish stocks. Nothing was known of the possible association of such a gene with ***Bg***, another glume colour gene on chromosome 1A. See ▶[1640] for review. A chromosome 1A gene, **Rg3**, was eventually identified by linkage with **Gli-A1**[1405] and shown to cosegregate with **Hg**[624].

RG-1

Rg-A1[10378] locus: 1AS[562, 923, 924, 9906] syn: Rg3[562, 923, 924]

Rg-A1a[10378]

v: TRI 542[10378]; White glumed genotypes. **dv**: DV92[282]; G2528[10378].

Rg-A1b[10378] syn: Rg3

i: Saratovskaya 29*3//F2 CS mono 1/Strela[924]. **v**: CS/Strela Seln[9906]; Iskra[9906]; L'goskaya-47[1405]; Zhnitsa[9906, 10378]. **v2**: Milturum 553 ***Rg-B1b***[9906]; Milturum 321 ***Rg-B1b***[9906]; Strela ***Rg-B1b***[924, 9906]; Sobko & Sozinov[1405, 1406]; reported a further group of 30 international wheats which, by inference from their **Gli-A1** alleles, probably carry ***Rg-A1b***. **ma**: A linkage order of ***Rg-A1b*** – **Hg** – cent – **Glu-A1**[1405]; *Xgwm1223-1A*/**Rg-A1**/**Hg** – 2.2 cM – *Xgwm136-1A* – 4.2 cM – *Xgwm33-1A*[10635].

Rg-A1c[10378] locus: 1A[282, 1304] syn: Bg[282, 1304], Bg(a)

i: ANK-22A[10378]; S29BgHg[10378]. **s**: CS*7/Indian 1A[1304]. **v**: TRI 14341[10638]. **v2**: Sears Synthetic ***Rg-D1c***[10638]. **dv**: G1777[282]; G3116[282]. **ma**: ***Rg-A1c*** (***Bg***) and *Nor9* co-segregated in *T. monococcum*; *Xutv1391-1A* (distal) – 3 cM – ***Rg-A1c***(***Bg***) – 1.6 cM – **Hg** – 2.4 cM – **Gli-A1** (proximal); *Xgwm1223-A1* – 0 & 0.6 cM – ***Rg-A1c*** – 4.7 & 4.6 cM – *Xgwm0136-1A*[10378]; Five of 6 wheats with ***Rg-A1c*** possessed a 264 bp allele at *Xgwm0136-1A*[10378]; ***Rg-A1c*** – 0.7 cM – *Xgwm1223-1A*[10638].

Rg-A1d syn: Bg(b)

dv: G3116[282].

At the diploid level ***Rg-A1c*** (*Bga*) and ***Rg-A1d*** (*Bgb*) were determinant and caused a solid black glume and a black line at the margins of the glume, respectively[282].
A single factor for black glumes was reported in diploid, tetraploid and hexaploid wheats[1347]. Linkage with **Hg** was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; ***Bg*** is epistatic to **Rg**.***1***

Rg-B1[10378] locus: 1B[1517] 1BS[369] syn: Rg1, Rg

TraesCS1B02G005200

Rg-B1a[10378]

v: TRI 542[10378]; White glumed genotypes, including Chinese Spring. **dv**: *T. turgidum* ssp. *dicoccoides* acc. MG4343[9959].

Rg-B1b[10378] syn: Rg1

s: CS*5/Red Egyptian 1B[1304]. **v**: Diamant I[9906]; Federation 41[1517]; Golubka[10635]; Highbury[1121]; Jagger[11538]; Norin 60[11538]; Red Egyptian[1304]; Red glume spelts[11538]; *T. petrapavlovsky*[9906]. **v2**: Milturum 321 ***Rg-A1b***[9906]; Milturum 553 ***Rg-A1b***[9906]; Strela ***Rg-A1b***[9906]. **tv**: Messapia[9959]; Ward[792]. **ma** *Xutv1518-1B* (distal) – 7.7 cM – **RG-B1** – 0.8 cM – **Gli-B1** (proximal)[9959]; *Xgwm1078-1B* – 1.5 cM – **RG-B1** – 3.1 cM – *Xgwm0550-B1*[10378]; *Xutv1518-1B* – (distal) – 7.7 cM – **RG-B1** – 0.8 cM – GLI-B1 (proximal); *Xgwm1078-1B* – 4.6 cM – **RG-B1** – 2.0 cM – *MW1B002*(**Gli-B1**) – 4.1 cM – *Xgwm550-1B*[10635]. **c**: Encodes an R2R3-MYB transcription factor[11538]. *TraesJAG1B01G000800* and *TraesNOR1B01G001100* in red glume Jagger and Norin 40, respectively, carried the same *Rg-B1b_h1* sequence; haplotype comparisons revealed that a specific group of MYB alleles was conserved in red glume genotypes[11538].

Rg-D1[10378] locus: 1DS 1DL[769, 1241] syn: Rg2

Rg-D1a[10378]

v: Novosibirskaya 67[10378]; L301[10378]; White glumed genotypes.

Rg-D1b[10378]

Derived from *Ae. tauschii*

i: Saratovskaya 29*5//*T. timopheevii* ssp. *timopheevii*/*T. tauschii*[9906]. **v**: ITMI Synthetic W7984[10635]; Synthetic Hexaploid-11[10218]; (*Triticum turgidum* ssp. *dicoccoides*/*Ae. tauschii*)[769]; (*Tetra Canthatch*/*Ae. tauschii* var. *strangulata* RL 5271); RL5404[1240]; (*Tetra Canthatch*/*Ae. tauschii* var. *meyeri* RL5289); RL5406[648, 1240]. **v2**: Sears Synthetic ***Rg-A1c***[10638]. **dv**: *Aegilops squarrosa* accessions.

Rg-D1c [10378] syn: Brg[729]

Brown or smokey-grey phenotype[729].

i: ANK-23 = Novosibirskaya 67*10/K-28535[729]. **v**: Golubka[10378]; K-28535[729]; K-40579[729]; *T. aestivum* botanical varieties cinereum, columbina and albiglaucum[10378]. **ma**: *Xgwm1223-1D* – 1.5 cM – **RG-D1** – 13.1 cM – *Xbarc152-1D* [10378]; *Xbarc149-1D* – 6.3 cM – **RG-D1** – 26.5 cM – *Xbarc152-1D* [10378].

QTL

Opata / W-7984 (ITMI) mapping population: *QRg.ipk-1D* was mapped in the[0255]; Linkage with GLI-D1 implied **RG-D1** (**Rg2**). This QTL coincided with a QTL for awn colour, *QRaw.ipk-1D* [0255]. ma: *Xpsp2000-1D* – 9.3 cM – **RG-D1** – 21.2 cM – *Xgwm106-1D* [10128]; *Xgwm1223-1D* – 6.6 cM – **RG-D1**/*Xksud14-1D* – 13.9 cM – *Xgwm33-D1* [10635]; **RG-A1** – 3.9 cM – *Xgwm1223-1D* [10638].

1.34.2 Pseudo-black chaff

This is a blackening condition transferred from Yaroslav emmer to Hope wheat by McFadden at the same time as stem-rust resistance was transferred. The association of this condition with mature-plant stem-rust reaction (**Sr2**) has been noted in a number of papers. According to [742], the condition is recessive. Pan[1102] considered linkage with stem-rust reaction could be broken, but this seems unlikely.

Pbc locus: 3B[742] 3BS

s: CS*6/Hope 3B[742]; CS*6/Ciano 5B[939].

1.34.3 Black-striped glumes

This phenotype was reported in group *dicoccon*. v: E4225[1417]

1.34.4 Inhibitor of glume pigment

An inhibitor of glume pigment was reported on chromosome 3A[106]

1.34.5 Chocolate chaff

cc[719] locus: 7B[719] 7BS[665]

tv: Langdon mutant[719]; PI 349056[665]. **dv**: CBC- CDd1[665].

The chocolate chaff phenotype was suppressed by a gene(s) in chromosome 7D[719]

1.34.6 Awn colour

The literature on awn colour is not clear. In general, awn colour is associated with glume colour[45]. Occasionally, however, awn colour and glume colour may be different. According to Panin & Netsvetaev[1103], black awns were determined by three complementary genes designated **BLA1**, *BLA2, BLA3*. **BLA1** was located in chromosome 1A and linked with **Gld 1A** (= GLI-A1) and **Hg**.

Bla1[10666] locus: 1AS[10666]

bin: 1AS1-0-0.47[10666]. **v**: Svenno[10666]. **ma**: *TC95235* – 4.8 cM – **BLA1**[10666].

QRaw.ipk-1A [0255] locus: 1AS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Awn colour was contributed by W-7984[0255]. **ma**: Associated with **Gli-A1**[0255].

QRaw.ipk-1D [0255] locus: 1DS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Awn colour was contributed by W-7984[0255]. **ma**: Associated with GLI-D1[0255].

1.35 Grain Hardness/Endosperm Texture

Grain hardness or endosperm texture significantly influences flour milling, flour properties and end-use. The difference in particle size index between a hard wheat (Falcon) and a soft wheat (Heron) was reported by Symes[1452] to be due to a single major gene. Symes[1452] also found evidence for "different major genes or alleles" which explained differences amongst the hard wheats Falcon, Gabo and Spica. Using Cheyenne (CNN)

substitution lines in CS and a Brabender laboratory mill, Mattern et al.[915] showed that the hard wheat milling and flour properties of Cheyenne were associated with 5D. Using Hope 5D substitution line in CS [CS(Hope 5D)] crossed to CS, and CS(Hope 5D) crossed to CS ditelosomic 5DL, Law et al.[777] showed that grain hardness was controlled by alleles at a single locus on 5DS. The dominant allele, **Ha**, controlling softness was present in Chinese Spring and the allele for hardness, **ha**, was present in the others. A similar study using CS (CNN5D)/CS recombinant inbred lines was reported by Morris et al.[03106].

A pleiotropic result of hardness is the decreased level of a 15 kD starch granule protein, friabilin, on the surface of water-isolated starch[470]. In endosperm, soft and hard wheats have similar amounts of friabilin, consequently the distinction between the two textural types depends upon the manner in which the friabilin co-purifies with starch. Friabilin is also referred to by the name 'Grain Softness Protein' (GSP)[0384], and was later shown to be comprised primarily of puroindoline a and puroindoline b[0295]. Grain hardness of reciprocal soft x hard F1 kernels was well correlated with friabilin occurrence on starch in triploid endosperm[0381]. See IV, Proteins: 5.8 Puroindoline. GSP-1 genes, which are closely related to puroindolines, are also listed in the Protein section.

HA

Ha[777] locus: 5DS[777]

Soft phenotype.

i: Falcon/7*Heron, Heron/7*Falcon[03109]; Paha*2//Early Blackhull/5*Paha[203, 298]; Early Blackhull Derivative/5*Nugaines[203, 298]. **v**: Chinese Spring[777, 03106]; Cappelle Desprez[470]; Heron[470, 1452]; Paha, Nugaines[203, 298]; NY6432-18[241].

ha[777]

Hard phenotype

i: Falcon/7*Heron, Heron/7*Falcon[03109]; Paha*2//Early Blackhull/5*Paha[203, 298]; Early Blackhull Derivative/5*Nugaines[203, 298]. **s**: CS*6/Cheyenne 5D[915]; CS*6/Hope 5D[777]; Capelle Desprez*7/Besostaya 5D[470]. **v**: Falcon[470, 1452]; Holdfast[470]; Early Blackhull, Early Blackhull Derivative[203, 298]; Cheyenne[03106]; Clark's Cream[241]. **ma**: **Ha** was closely linked to *Xmta9(Pui1)-5D*[1414].

QTL

ourtot / CS: DH population: a major locus in chromosome 5DS coincided with **Ha**; minor QTLs mapped in chromosomes 1A (associated with *Xfba92-1A*) and 6D (associated with *Xgwm55-6D*)[0141].

Forno / Oberkulmer: Ten QTLs for kernel hardness (54% of the variation) were mapped in spelt[0280].

Karl*2 / TA 4152-4: *QHa.ksu-3B*, associated with *Xksum9-3B* (R^2=0.09, and *QHa.ksu-5D* (**Ha**), associated with *Xcfd-5D* (R^2=0.3), were identified[10273].

Neixiang 188 (hard) / Yanshan 1 (medium hard): RIL population: *QGh.caas-1B.1* with hardness allele from Yanshan 1, R^2= 0.28, *Xwms153-1BL – Xbarc81-1BL*[10640].

Opata 85 / W-7984 Synthetic (ITMI population): RIL population: Two QTLs were detected[10051]. The QTL on the short arm of chromosome 5D was associated with *Xmta10-5D*, and increased hardness was contributed by Opata[10051]. The locus located proximally on the long arm of 5D was associated with *Xbcd450-5D* and increased hardness was contributed by the Synthetic allele[10051].

Using proteomic analysis of 2D-protein gels applied to 101 lines of the population, and after a preliminary study of a sub-group of these lines[10086], 446 amphiphilic protein spots were resolved, 170 specific to either of the two parents and 276 common to both[10087]. An important category of these proteins comprised the puroindolines. Seventy-two loci encoding amphiphilic proteins were conclusively assigned to 15 chromosomes. At least one Protein Quantity Locus (PQL) was associated with each of 96 spots among the 170 spots segregating; these PQL were distributed throughout the genome. The majority of the amphiphilic proteins were shown to be associated with plant membranes and/or play a role in plant defence against external invasions. Not only the puroindolines were associated with kernel hardness - a number of other amphiphilic proteins were also found to influence this trait.

1.36 Grain quality parameters

In the comprehensive study of 46 quality-related traits in a RL4452/AC Domain RIL population, 99 QTLs involving 41 traits were located in 18 chromosomes[10361]; 14 QTLs clustered in the *Glu-1B* region (50cM), 20 QTLs occurred in the *Xwmc617-4D - Xwmc48-4D* region (30cM), 10 QTLs mapped to the *Xgwm130-7D -*

Xwmc405-7D region (14cM) and 66 QTLs were dispersed[10361]. In a large study of 11 seed quality traits in a AC Karma/87E03-S2B1 DH population, 26 QTLs were detected in 7 chromosomes[10434]; 6 were clustered in the **Glu-D1** region and 5 were clustered in the **Rht-D1** region.

QTL analyses of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California) are reported in [10436].

Neixing 188/Yanshan 1 RIL population: 75 QTLs for 5 quality-related traits are reported in [10640].

1.36.1 Sedimentation value

Qsev.mgb-6A [9920] locus: 6AL [9920]

tv: Nessapia/*T. dicoccoides* MG4343 mapping population[9920]. **ma**: Associated with *Xrsq805-6A* [9920].

Qsev.mgb-7A [9920] locus: 7BS [9920]

tv: Messapia/*T. dicoccoides* MG4343 mapping population[9920]. **ma**: Associated with *Xpsr103-7A* [9920].

QTL

Cheyenne (high quality) / CS (low quality): RIL population: QTL were associated with Glu-1 on chromosome arms 1AL and 1DL and Gli-1/Glu-3 on 1BS[0251]. Cultivar Cheyenne contributed the higher SDS sedimentation values[0251]. The QTL on 1AL coincided with a QTL for bread loaf volume[0251]. The QTL on 1DL and 1BS coincided with QTL for bread mixing time[0251].

1.36.2 Flour, semolina and pasta colour

TaPod-A1

TaPod-A1 [11233]

TaPod-A1a [11233] locus: 3AL [11233]

v: Doumai[11233].

TaPod-A1b

v: Shi 4185[11233].

QTL

Huapei 3 / Yumai 57: DH lines: 18 additive QTLs and 24 pairs of epistatic QTLs affected flour colour parameters; *qa-1B*, closely linked with *Xbarc372-1B* was associated with variation of a*, R^2= 0.256[10625]. A further study confirmed major QTL on chromosome 1RS (R^2=0.319) and 7A (R^2= 0.339), minor QTL occurred on 1A and 4A[10716].

Omrabi 5 / *T. dicoccoides* 600545: A major QTL was detected in the distal region of chromosome 7BL. The QTL explained 53% of the variation and was completely linked to microsatellite marker *Xgwm344-7B*. Omrabi 5 contributed the allele for high yellow pigment level. Two additional small QTLs were detected on 7AL[0365].

PH82-2 (low) / Neixiang (high): RIL population: Analysis of yellow flour pigment revealed major QTL on chromosomes 7A co-segregating with marker *YP7A* (R^2= 0.2-0.28) (see Phytoene synthase 1), and 1B (R^2= 0.31-0.54) probably contributed by 1RS[10501].

Schomburgk / Yarralinka: A QTL was detected on chromosome 7A[9936]. Cultivar Schomburgk contributed the yellow colour allele[9936]. Markers *Xcdo347-7A* and *Xwg232-7A* accounted for 60% of the genetic variation[9936]. A Sequence Tagged Site PCR marker was developed[0180].

W9262-260D3 (low yellow colour) / Kofa (high colour): Four QTLs identified on chromosomes 2A (*Xgwm425-2A*), 4B (*Xgwm495-4B*), 6B (*Xgwm193-6B*) and **Psy-B1** (chromosome 7BL)[10230]. See also Enzymes Phytoene synthase.

Other references to flour colour are given under Flour Colour, **Lr19**, and **Sr25**.

Three QTL for peroxidase activity in the grain identified in a **Doumai (high POD activity) / Shi 4185 (low POD activity)** cross were named as *QPod.caas-3AL QPod.caas-4BS* and *QPod.caas-5AS* [11233]. Allelic variation was found at the *QPod.caas-3AL* locus[11233]

There was no apparent relationship to the Per- series identified by isozyme analyses and listed in the Protein section.

1.36.3 Amylose content

Amylose content has a significant effect on industrial quality; for example, reduced amylose wheats perform better in some types of noodles. The waxy protein genes have an important influence, but other genes are also involved.

QAmc.ocs-4A.1 [0047] locus: 4AS [0047]

v: CS/CS(Kanto107 4A) mapping population [0047]. **ma**: Associated with *Xbcd1738-4A* and *Xcdo1387-4A* [0047].

1.36.4 Milling yield

QTL

NY6432-18 / Clark's Cream: RIL population: A QTL associated with *Pinb* on chromosome arm 5DS was detected [0241]. Cultivar Clarks Cream contributed the higher flour yield allele [0241]. This QTL coincided with QTL for hardness, hydration traits (dough water absorption, damaged starch and alkaline water retention capacity (AWRC) and baked product traits (cookie diameter and cookie top grain) [0241].

Schomburgk / Yarralinka: A QTL was detected on chromosome 3A [0181]. Cultivar Schomburgk contributed an allele for the higher milling yield [0181]. RFLP markers *Xbcd115-3A* and *Xpsr754-3A* at LOD> 3 were associated with this QTL [0181].

1.36.5 Alveograph dough strength W

QTL

Courtot / Chinese Spring: QTLs for W were detected on chromosome arms 5DS (associated with *Xmta10-5D*), 1AS (associated with *Xfba92-1A*), and 3B (associated with *XksuE3-3B*) in cross [0141]. The first two QTLs coincided with those for hardness.

Forno / Oberkulmer spelt: Ten QTL for W (39% of the variation), nine QTL for P (48% of the variation) and seven QTL for P:L (38% of the variation) were mapped [0280].

1.36.6 Mixograph peak time

QTL

NY6432-18 / Clark's Cream: RIL population: A QTL associated with *Glu-Dy1* on chromosome arm 1DL was detected [0241]. Clark's Cream contributed the higher mixograph peak time allele [0241]. This QTL coincided with a QTL for bread mixing time [0241].

1.36.7 Starch characteristics

The Isoamylase-1 gene from *Ae. tauschii* (**Iso-1**) complemented the deficient rice sugary-1 mutant line [10295].

QTL

Cranbrook (*Wx-B1a*) / Halberd (null *Wx-B1b*): QTLs for starch viscosity and swelling were associated with the **WX-B1** locus. An additional QTL for starch viscosity was found on 7BL between markers *Xgwm344-7B* and *Xwg420-7B* in the first parent. This QTL disappeared when amylase activity was inhibited indicating that it was determined by the late maturing a-amylase activity contributed by Cranbrook. A QTL for starch viscosity was associated with the **WX-A1** locus in the cross CD87/Katepwa [0362].

1.36.8 Loaf volume

Lvl1 [10312] locus: 3A [10312] syn: Lvl 1 [10312]

s: Cappelle Desprez*7/Bezostaya 1 3A [10312]. **ma**: *Xgwm720-3A* – **Lvl1** appeared to be located in the *Xgwm2-3A* – *Xgwm720-3A* region [10312].

QTL

Renan / Recital: RIL population: Loaf volume score was consistent across three environments and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A*, *Xgwm666-3A*, positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A*, *Xbcd1930-7A*, positive effect from Recital) [10536].

Thirty QTLs were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTLs of largest effect were located on chromosomes 6B and 6D[10659].

1.36.9 Dough rheological properties

QTL

Cranbrook / Halberd: DH population: environmental factors were a major determinant of dough extensibility whereas additive effects of alleles at the high and low molecular weight glutenin loci determined dough strength[10247].

1.36.10 Grain fructan content

Fructans are non-digestible carbohydrates considered to have health benefits to consumers.

QTL

Berkut (high fructan concentration) / Krickauff (low fructan concentration): QTL detected on chromosomes 2B, 3B, 5A, 6D, and 7A of which *QGfc.aww-6D.2* (R^2= 0.17, nearest marker, *Xbarc54-6D*) and *QGfc.aww-7A.1* (R^2= 0.27, *Xgwm681-7A*) had the largest effects[10631].

1.36.11 Water absorption

QTL

Neixiang 188 / Yanshan 1: RIL population: *XAbs.caas-5D.1* with positive effects from Yanshan 1, R^2= 0.3, *Xcfd18-5DS – Xcfd189-5DS*[10640]

1.36.12 Chinese dry noodle quality

QTL

Chuan 35050 / Shannong 483: RIL population: 3 QTL for noodle palate, elasticity and smoothness were clustered near **Glu-D1** with beneficial effects associated with subunits 5+10 coming from Chuan 35050. A very significant taste QTL, *QStas.sdau-4A.1* and positive QTLs for stickiness and total score also on chromosome 4A came from Shannong 483[10647]

QTL Quality

AC Karma / 87E03-S2B1: DH population: 26 QTL were detected in 7 chromosomes in a large study of 11 seed quality traits[10434]; 6 were clustered in the **Glu-D1** region and 5 were clustered in the **Rht-D1** region.

Neixing 188 / Yanshan 1: RIL population: 75 QTLs for 5 quality-related traits are reported in [10640].

Opata 85 / W-7984 Synthetic (ITMI population): RIL population: QTL analyses was undertaken of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California)[10436].

1.36.13 Grain traits based on homology

Variation in grain traits based on gene homology with other species

TaBAS1

Tabas1-B1[11198] locus: 2BL[11198]

ma: *Xbarc167-2B* – 10.38 cM – **Tabas1** – 5.23 cM – *Xcfa2278-2B*[11198]. **c**: BAS1 is a type of 2-Cys peroxiredoxin in a large peroxidase family.

Tabas1-B1a[11198]

v: Jing 411[11198].

Associated with higher TGW.

Tabas1-B1b[11198]

v: Hongmanchun 21[11198].

Associated with lower TGW.

TaGASR

TaGASR7-A1[11115] locus: 7AL[11115]

Snakin/GASA gene family

ma: *Xwmc301-7A* – 17.9 cM – *TaGASR7* – 10.6 cM – *Xwmc9-7A*[11115]. **c**: GenBank KJ000052[11115].

Hap1c in Lumai 14 and Xiaoyan 81 conferred higher grain length and grain weight than *Hap1g* in Hanxuan 10 and Xinmai 10[11115]

TaGS1

TaGS-D1[11116] locus: 7DS[11116]

ma: **TaGs-D1** – 8.0 cM – *Xbarc184*[11116].

TaGs-D1a[11116]

v: Doumai[11116]; Jingdong 8[11116]. **c**: KF687956[11116].

Associated with higher TGW and grain length[11116]

TaGs-D1b[11116]

v: Shi4185[11116]; Yumai 21[11116]. **c**: KF687957[11116].

Associated with lower TGW and grain length[11116]

TaGW

TaGW-A2[11121, 11122] locus: 6A[11121]

Orthologous to the rice RING-type E3 ubiquitin ligase *OsGW2* that functions as a negative regulator of grain weight.

ma: *TaGW2* was mapped on the Spark x Rialto DH population to chromosome 6A and linked to markers *BS000072146, BS000105973* and *CA643341* at 46.8 cM[11121]. **c**: GenBank KP749901.1[11122].

A loss-of-function mutation in *TaGW2-A2* was associated with a 6.6 % increase in grain weight in tetraploid and hexaploid wheat[11122].

TaSAP1

TaSAP1-A1[11117] locus: 7A[11117]

Stress association protein gene family

ma: *Xwmc530-7A* – 2.1 cM – **TaSAP1-A1** – 13.9 cM – *Xbarc174-7A*[11117]. **c**: GenBank KC193579[11117].

Variation at this locus was associated with 1,000-grain weight, number of grains per spike, spike length, penuncle length and total number of spikelets per spike, but different haplotypes had different effects various traints[11117]

TaTGW-7A

TaTGW-7A[11197] locus: 7AS[11197]

ma: *SLAF49035* - 3.02 cM - *TaTGW7A*/TG - 9.19 cM - *Xbarc-7A*[11197]. **bin**: C-7AS8-0-0.45. **c**: Traes-7AS_378A12AA9.1. *GW2* in rice encodes an E3 ubiquitin ligase[11197].

TaTGW-7Aa[11197]

v: Jing 411[11197].

Associated with higher TGW.

TaTGW-7Ab[11197]

v: Hongmanchun 21[11197].

Associated with lower grain weight.

TaTGW-A1

TaTGW-A1

TaTGW-A1a [11196]

v: Doumai[11196]; Zhou 8425B[11196].

Associated with higher TKW.

TaTGW-A1b [11196]

v: Chinese Spring[11196].

Associated with lower TKW.

TaTGW6

TaTGW6-A1[11196] locus: 3AL[11196]

ma: *Gene-3665_61* – 2 cM – **TaTGW-A1** – 18 cM – *BobWhite_c47304_56*[11196]. **c**: TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase[11196].

TaTGW6-B1[11196] locus: 3BL[11196]

c: TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase[11196].

TaTGW6-D1[11196] locus: 3DL[11196]

c: TGW6 in rice encodes an indole-3-acetic acid-glucose hydrolase[11196].

QTL

Renan / Recital: *QGw1.inra-2B*[10071], favourable allele from Renan[10071]. (R^2= 10.7- 19.7%)[10071]. ma: *Xgwm374-2B* – *Xgwm388-2B*[10071]; *QGw1.inra-5B*[10071], Ranan/Recital, favourable allele from Recital[10071]. (R^2= 4.9-10.4%)[10071]. ma: *Xgwm639-5B* – *Xgwm604-5B*[10071]; *QGw1.inra-7A*[10071], favourable allele from Recital[10071]. (R^2=5.2-10.3%)[10071]. ma: *Xcfa2049-7A* – *Xbcd1930-7A*[10071].

RS111 / CS: RIL population: Variation at locus *QGw1.ccsu-1A* associated with *Xwmc333-1A*, accounted for 15% of the variation[0165].

Rye Selection 111 (high GW) / CS (low GW) RIL: two definitive QTLs *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1*, were detected by CIM analysis[10363]. The chromosome 7A QTL co-located with a QTL for early heading[10363].

1.37 Grain weight

QGw1.inra-2B[10071] syn: Renan / Recital

favourable allele from Renan[10071]. (R^2= 10.7 - 19.7%)[10071]

ma: *Xgwm374-2B* – *Xgwm388-2B*[10071]; *QGw1.inra-5B*[10071], Ranan/Recital, favourable allele from Recital[10071]. (R^2= 4.9-10.4%)[10071]; *Xgwm639-5B* – *Xgwm604-5B*[10071]; *QGw1.inra-7A*[10071], favourable allele from Recital[10071]. (R^2=5.2-10.3%)[10071]; *Xcfa2049-7A* – *Xbcd1930-7A*[10071].

QTL

RS111 / CS: RIL population: Variation at locus *QGw1.ccsu-1A* associated with *Xwmc333-1A*, accounted for 15% of the variation[0165].

Rye Selection 111 (high GW) / CS (low GW) RIL: two definitive QTLs *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1*, were detected by CIM analysis[10363]. The chromosome 7A QTL co-located with a QTL for early heading[10363].

1.38 Grass-clump dwarfness/Grass dwarfness

Complementary dominant genes. Genotypes producing dwarfness: *D1-D2-D3-, D1-D2D2, D1-D4-D3-, D1-D2-D4* and *D1-D4D4*

D1[534] locus: 2D[534, 939, 1595] 2DS[942] syn: G[972]

s: CS*7/Kenya Farmer 2D[1000]; CS*6/Timstein 2D[534]. **v**: Big Club[534]; Burt[1000]; Federation[942]; Mus[534]; Ramona 50[358]; Selection 1403[1000]. **v2**: Hermsen's pure-breeding dwarf **D2**[1000]; Falcon **D3**[1172]; Gabo **D3**[944]; Timstein **D3**[534]; Metzger's pure-breeding dwarf **D2 D3**[1000].

d1d2d3d4

v: Chinese Spring[534, 1000].

D2[534] locus: 4AL[939] 4A[534, 1595] syn: B I[972]

s: CS*7/Cheyenne 2B[1000]; CS*4/Red Egyptian 2B[1000]. **v**: Bezostaya 1[1595]; Crete-367[1029]; Desprez 80[1595]; Florence[1000]; Kenya W744[944]; Loro[1172]; Mara[1595]; Marquis[1000]; Poros[1595]; Redman[534, 574, 1001]; Riebesel[534]; Tobari 66[358]. **v2**: Hermsen's pure-breeding dwarf **D1**[534, 1000]; Amby **D3**[358]; Cedar **D3**[1000]; Mendel **D3**[534]; Plantahof **D3**[534]; Spica **D3**[944]; Cappelle-Desprez **D4**[1595]; Brevor **D4**[1000]; Cheyenne **D4**[1000]; Metzger's pure-breeding dwarf *D1D3*[1000].

D3[534] locus: 4AL[939] 4A[534, 1595] syn: A[972]

s: CS*6/Timstein 4A[534, 1000]; CS*7/Kenya Farmer 4A[534, 1000]. **v2**: Amby **D1**[358]; Falcon **D1**[1172]; Gabo **D1**[944]; Kenya Farmer **D1**[1000]; Timstein **D1**[534]; Metzger's pure-breeding dwarf **D1 D2**[1000].

D4[1000] locus: 2D[1000, 1595] 2DL[1598]

s: CS*7/Cheyenne 2D[1000]. **v2**: Cappelle-Desprez **D2**[1595]; Cheyenne **D2**[1000]; Brevor **D2**[1000].

Genotype lists in can be found in [358, 534, 972]. The effects of multiple allelism at **D2**, and possibly at **D1**, and modifying genes were demonstrated[1595].

Knott[683] described a lethal dwarf condition controlled by a dominant gene closely linked with **Sr30** (chromosome 5D) in Webster and a complementary recessive gene in LMPG.

Phenotypes resembling grass clump dwarfs in hybrids carrying a 2BL.2RS translocation were reported in [916]. The complementary gene {s} in wheat was not **D1**, **D2** or **D3**. The effect was suppressed at high temperature.

1.39 Growth rate and early vigour

QTL

Identified in *Ae. tauschii*: chromosomes 1D, 4D, and 7D carried QTLs for relative growth rate, biomass allocation, specific leaf area, leaf area ratio, and unit leaf rate. Chromosome 2D had QTLs for rate and duration of leaf elongation, cell production rate, and cell length. Chromosome 5D harbored QTLs for total leaf mass and area, number, and growth rate of leaves and tillers[10293].

1.40 Hairiness/Pubescence traits

1.40.1 Pubescent auricles

PA

Pa[42, 886] locus: 4BS[42, 886]

s: Saratovskaya 29*9/Yanetzkis Probat 4B[886]; Saratovskaya 29*5/Shabati Sonora 4B[886]; 29*4/Siete Cerros 4B[886]. **v**: Diamant 1[886]; Magali[886]; Pirotrix 28[886]; Shabati Sonora[886]; Siete Cerros[886]; Ulyanovka 9[886].

pa

v: Gabo[886]; Saratovskaya 29[886]. This phenotype was expressed in Diamant ditelo 4BL[886].

1.40.2 Hairy glumes

HG1

Hg1[1494] locus: 1A[1293] 1AS[947] syn: Hg[1494]

i: S-615*11/Jones Fife[1500]. **s**: CS*7/Indian 1A[1293]. **v**: A well-known, widespread and easily identified dominant marker - only a few examples will be listed. Indian[1293]; Jones Fife[1494]; Prelude[1494]. **itv**:

LD222*11/*T. turgidum* var. *durum melanops*[1546]. **tv**: Golden Ball[1342, 1494]. **dv**: *T. monococcum* lines[1494]. **ma**: *Xutv1391-1A* (distal) – 3 cM – ***Bg*** – 1.6 cM – **Hg** – 2.4 cM – **Gli-A1** (proximal)[9959]; Tel **Hg**/*BG605525* – 3.8 cM – *Xpsp2999(Glu3)-1A*[10193]. Mapped to region 1.337 – 2.162 Mb (CS Ref Seq v1)[11617].

A 1A gene controlling hairy glumes was mapped in a cross between durum cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343[9959].

hg1[1405]

v: Ulyanovka[1405]; Pionerskaya[715, 1405].

Evidence for multiple alleles in *T. monococcum* is given in [744]. The likelihood of three alleles, *hg* (hairless), **Hg1** (weakly hairy) and **Hg** (very hairy), with **hg1** being recessive to **Hg** and causing a short (weak) hairy phenotype, was mentioned in [1405]

HG2

Hg2[11508] locus: 2BS[11508]

v: CIGM86.944 [syn. Croc_1/*Ae. tauschii* 518][11508]. **tv**: Croc_1[11508]. **ma**: *XicsH020* – 1.18 cM – HG2 – 0.84 cM – *XicsHS358,* corresponding to physical interval 740.0-741.1 Mb in cv. Svevo[11508].

1.40.3 Hairy leaf

HL1

Hl1[0316] locus: 4BL[760] 4B[884] syn: Hl[884]

Weakly hairy.

v: Artemovka[925]; Caesium 111[925]; Lutescens 53/12[925]; Lutescens 62[925]; Milturum 321[884]; Poltavka[925]; Pyrothrix 28[925]; Saratov 321[884]; Saratovskaya 29[760, 884]; Sarrubra[925]. **ma**: *Xgwm375-4B* – 12.1 cM – **Hl1** – 2.1 cM[10516].

HL2

hl1 hl2

v: Chinese Spring[884].

Kuspira *et al.*[744] provided evidence for at least three alleles at an **Hl** locus in *T. monococcum*

Hl2[0316] locus: 7BS

v: Hong-mang-mai[0316].

The hairy leaf gene (**Hl** ^{Aesp}) in *Ae. speltoides* introgression line 102/00^{l}was allelic with **Hl2**[10516]

A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous to **Hl1**[10516]. Trichome number on leaf margins in *Ae. tauschii* was mapped to a 530 kb region in chromosome arm 4DL[11612].

1.40.4 Hairy leaf sheath

HS

Hs[795] syn: Hls[761]

v: Certain hexaploid derivatives of G25 produced in Israel[939]. **tv**: *T. dicoccoides* G25[761].

hs

v: Most hexaploid wheats[939]. **tv**: *T. dicoccoides* G7[761].

Levy & Feldman[795] concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides*

1.40.5 Hairy neck/Pubescent peduncle

Hp[275] locus: 4BL (T4B5R)[274, 275]

Derived from *Secale cereale*

i: S-615*11/CS Derivative[1500]. 5BS (T5B-5R)[1298]. **v**: HN-2 (CS type)[1298]. 6D (T6D-5R)[1298]; HN-1 (CS type)[1298]. 4BL (T4B.5R).[274, 275]; CS Derivative[1304].

1.40.6 Hairy node/Pubescent node

Inheritance of hairy (glabrous) node versus non-hairy node was attributed to a single, dominant gene difference[396, 837, 910, 914] and the **Hn**/**hn** locus was be linked with **B1** (awn inhibitor). Observations on 5A trisomics and telosomics of Chinese Spring confirmed this location. Love & Craig[837] studied a cross involving Velvet Node CI 5877 and Gaines & Carstens[396] studied an offtype single plant designated Velvet Node Wash. No. 1981.

HN

Hn locus: 5AL

v: Aurore[722]; Fylgia[722]; Extra-Kolben II[722]; Marquis[910]; Tammi[765]; *T. vulgare erythrospermum*[910]. **tv**: *T. polonicum vestitum*[910].

hn

v: Garnet[722]; Kimno[722]; Pika[722]; Timantii[722].

Multiple alleles were reported in *T. monococcum*[744]

1.41 Heat tolerance

QTL

Ventnor (tolerant) // Karl 92 (non-tolerant): QTLs contributing to grain-filling duration (GFD) under high temperatures were associated with *Xgwm11-1BS* (11% of variability) and *Xgwm293-5AS* (23% of variability) in [0327]

1.42 Reduced height

Ht is the general symbol.

1.42.1 Reduced height: GA-insensitive

RHT-1

RHT-A1

Rht-A1[11017] locus: 4A[11017]

v: Cadenza.

Rht-A1a[0019] locus: 4A[10923] 4AL[11017]

v: Chinese Spring[0019]. **ma**: *Xwmc48-4AS* – 2 cM – *Xgwm610-4A* – 1 cM – **Rht-A1** – 2 cM – *Xgpw4545-4AL*[11017]. **c**: GenBank KC767924.

All common wheats are assumed to be monomorphic. A functional ***Rht-A1a*** allele is expressed at a similar level to its orthologues[10923].
Haplotypes named as *Rht-A1b* to *Rht-A1g* are described in [11620].

RHT-B1

Rht-B1[116] locus: 4B, 4BS

Rht-B1a[116]

v: Tall wheats[116]; e.g. Chinese Spring[0019]. **c**: GenBank KC767925.

Rht-B1b[116] locus: 4B[109, 406, 1040] 4BS[89, 116] syn: Rht1[15], Sd1[15]

Partially recessive[24], recessive[357], semi-dominant[408]

v: Frontier[1597]; Guardian[1597]; Selection 14-53/Burt, 5[15]; Siete Cerros[407]; Wren[1174]; WW15[407]. **v2**: Norin 10-Brevor, 14 ***Rht-D1b***[15]; Oleson ***Rht-D1b***[357]; Selection D6301 ***Rht-D1b***[357]; Shortim ***Rht-D1b***[243]; See [407, 415, 1062, 1386]. **tv**: Cocorit 71[109, 416]; Creso[109, 416, 451]; Malavika[1442]; Mida[450]; Sansone[109]; Valgerado[109,

[416]; Valnova[450]; Valselva[450]. ma, **tv**: **Gai1**/***Rht-B1b*** – 1.8 cM – *Xpsr622-4B*[110]; Co-located with *Xbarc10-4B*[10189].

The development of allele-specific primers for ***Rht-B1b*** was reported in [0378].
An EcoTILLING study of > 1,500 Chinese wheat accessions identified 7 sequence variations in RHT-A1, 8 new variants in RHT-B1 and 4 new variants in RHT-D1[11697].

QTL
QTL for reduced plant height, peduncle length and coleoptile length contributed by Cranbrook were associated with *XcsMe1-4B* (up to 49% of variability for plant height and peduncle length and 27-45% of variability for coleoptile length) in the cross **Cranbrook (semidwarf) / Halberd (tall)**. The dwarfing effect underlying the QTL was caused by the ***Rht-B1b*** allele[0379].

Rht-B1c[116] syn: Sd3[565], Rht3[565]

Semi-dominant[1040]

i: Tom Thumb/7*Kharkov//Lancer[1040]; See [408]. **v**: Minister Dwarf[404]; Selection D6899 (Tom Thumb-Sonora 64/Tacuari)[357]; Tom Thumb[405]; Tom Pouce Blanc[407, 1634]; Tom Pouce Barba Rouge[407, 1634]; Topo; Tordo. **ma**: *Xmwg634-4B* (distal) – 30.6 cM – ***Rht-B1c*** – 11.9 cM – *Xpsr144-4B* (proximal)[117]; Allele-specific markers were designed from the gene sequence[10923]. **c**: The ***Rht-B1c*** transcript carries a 90 bp in-frame insertion within the region encoding the conserved N-terminal DELLA domain plus two SNPs upstream of the insertion. A much larger insertion occurs in the gDNA[10923].

Rht-B1d[116] syn: Rht1S[1599]

Semi-dominant[116, 1599]

Rht-B1e[116] syn: Rht11[718], Rht1(B-dw)[1600], RhtKrasnodari1[452]

v: Karlik 1 PI 504549[718, 10924]; Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezostaya 1)[1600]; Polukarlikovaya 49 and 11 derivatives[10924]. **ma**: A PCR marker distinguishes this allele from ***Rht-B1a*** and *Rht-* ***B1b***[10923]. **c**: A stop codon occurs three codons upstream of the ***Rht-B1b*** mutation[10923].

Rht-B1f[116] syn: RhtT. Aethiopicum[116]

Semi-dominant[116]

tv: *T. aethiopicum* accessions W6824D[116]; W6807C[116].

Rht-B1g[0019]

v: Highbury mutants M3 103-3 and M3 103-9[0019].

Allele ***Rht-B1g*** is a fast neutron-induced mutation of ***Rht-B1b*** and produces a tall gibberellin responsive phenotype[0019].
Haplotypes named *Rht-B1h* to *Rht-B1o* are described in [11620]

Rht-B1p[11621]

v: Chris Mutant CI 17241[1129]. **c**: Contains a C-to-T substitution at position 178 leading to a stop codon[11621]. GenBank KT013263.

Rht-B1^{IC2196}[10144]

tv: *T. turgidum* var. *polonicum* IC12195[10144].

RHT-D1

Rht-D1[116] locus: 4DS[116, 980, 1266] 4D[411, 583, 1544]

bin: 0.82-1.00[11017].

Rht-D1a[116]

v: Tall wheats[116]; e.g. Chinese Spring. **c**: KC767927.

Rht-D1b locus: 4D[411] 4DS[980] syn: Sd2[15], Rht2[15]

Partially recessive[24], recessive[357], semi-dominant[408]

i: Common wheat and durum NIL pairs are listed in [02102]. See [408, 414, 02102]. **v**: Biscay[10574]; Combe[567]; Era[407]; Gaines Sib 2[15]; Jaral[407]; Kite[1174]; Maris Hobbit[411]; Pirat[10574]; Pitic 62[567]; Rubens[10574]; Songlen[243]. **v2**: Oleson ***Rht-B1b***[357]; Norin 10-Brevor, 14 ***Rht-B1b***[15]; Selection D6301 ***Rht-B1b***[357]; List in [1386]. **ma**: *Xpsr1871(Pki)-4D* – 4 cM – **Rht-D1** – 6 cM – *Xubc821(PhyA)-4D*[410]; **Rht-D1** – 2.8 cM – *Xglk578-4D*[9966]; *Xpsr1871* – 1 cM – ***Rht-D1b*** – 4 cM – *Xpsr821* (PhyA)[0019].

The development of allele-specific primers for ***Rht-D1b*** was reported in [378]

Rht-D1c[116] syn: Rht10[1266]

Dominant[114]

v: Ai-bian[1266, 1544]. **ma**: *Xpsr921-4D* (4DS) – 0.8 cM – ***Rht-D1c*** - 28 cM – *Xgwm165-4D* (4DL)[117].

Rht-D1d[116] syn: RhtAi-bian 1a[115]

Semi-dominant[116]

v: Ai-bian 1a (spontaneous mutant of Ai-bian 1)[115].

Haplotypes named as *Rht-D1e* to *Rht-D1h* are described in [11620].

Line XN004, earlier considered to have **Rht21**[0230], was shown to carry an allele at the **Rht-D1** locus[0231].

Various common wheat and durum N1Ls differing at the RHT-B1 and RHT-D1 loci are listed in [02102]. Genotype lists in [402, 1382, 1612, 1613].

Rht-D1b, ***Rht-D1c*** and ***Rht-D1d*** are identical across the coding region, but ***Rht-D1c*** has a fourfold increase in copy number relative to ***Rht-D1b***; ***Rht-D1d*** has a reduced copy number relative to ***Rht-D1c***[10923, 11016].

ungrouped

RHT1[371, 0019] syn: Rht-1[371, 0019]

The *Rht-1* homoeoloci are orthologous with the *D8* locus in maize and the *GAI* locus in Arabidopsis. They encode proteins resembling nuclear transcription factors and are involved in sensing gibberellin levels[0019]. Those proteins are DELLA proteins that repress plant growth, but repression is relieved by GA-induced DELLA repression. Common wheat and durum NIL pairs are listed in [02102].

Genotypes of Indian semi-dwarf wheats based on the Ellis et al.[0378] markers are given in [10404] and those for U.S. eastern and central and winter wheat cultivars are given in [10868].

1.42.2 Reduced height: GA-sensitive

Borner *et al.*[116] found no evidence of orthologous GA-sensitive genes in rye, but reviewed evidence for orthologous GA-insensitive genes. The close linkage of **Rht8** and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of allelic variants at the **Rht8** locus[9962].

RHT4

Rht4[568] locus: 2BL[10249]

Recessive.

v: Burt *ert* 937, CI 15076[566, 717]. **ma**: Associated with *Xwmc317-2B*[10249].

RHT5

Traes3B02G025600 (predicted)

Rht5[717] locus: 3BS[10249]

v: Marfed *ert* 1, M1, CI 13988[717, 718, 1593]. **ma**: Approximately 10 cM from *Xbarc102-3B*[10249]. Located to an ~1 Mb interval flanked by *Kasp25* and *Kasp23* in the 0-30 Mb region[11625]. The predicted gene in Marfed M has a 30 bp deletion in the first intron[11625].

RHT6

Rht6[718]

Recessive.

v: Brevor[569]; Burt[569, 718]. **v2**: Norin 10-Brevor, 14 ***Rht-B1b Rht-D1b***[569].

RHT7

Rht7[1602] locus: 2A[1602]

v: Bersee Mutant A[1602]; Bersee Mutant C[1602].

RHT8

TraesCS6A02G221900; *TraesCSU03G0022100* (CS RefSeq v2.)

Rht8 locus: 2D[772, 1598, 1601] 2DS

s: Cappelle-Desprez*/Mara 2D[1601]. **v**: Chuan Mai 18[10249]; Novasadska Rana 1[1604]; Sava[414, 1601]; Yumai 8679[11624]. **v2**: Akakomugi **Rht9**[1191]; Mara **Rht9**[1191]. **ma**: *Xgwm484-2D* (proximal) – 19.9 cM – **Rht8** – 0.6 cM – *Xgwm261-2D* (distal)[727]; Close linkage with *Xgwm261-2D*[10249]; A survey of Chinese cultivars showed 13 alleles of *Xgwm261-2D*[10284]. **c**: RHT8 contains two ORF with near-identical sequences. Encodes an unknown 808 aa protein containing a zinc finger BED-type motif and predicted Ribonuclease H-like domain[11624, 11642]. CRISPR-Cas9 editing of the *RNHL-A1* (*Traes2A02G059900*) and *RNHL-B1* (*Traes2B02G073600*) homoeologous caused reduced height[11624].

Close linkage of **Rht8** and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of putative allelic variants at the **Rht8** locus[9962]. Allele sizes for *Xgwm261* in U.S. eastern and central wheat cultivars are given in [10868]. A series of ‘ alleles’ was based on variation in the closely linked marker *Xgwm261-2D*

Rht8a

Associated with a 165-bp fragment of WMS 261[9962]

v: Autonomia[9962]; Bobwhite[9962]; Brevor[9962]; Chaimite[9962]; Ciano 67[9962]; Chris[9962]; Dugoklasa[9964]; Federation[9962]; Frontana[9962]; Glennson 81[9962]; Hope[0243]; Jupateco 73[9962]; Kenya[9962]; Klein 32[9962]; Lerma Rojo[9962]; Lusitano[9962]; Maringa[9962]; Marquis[0243]; Mentana[9962]; Michigan Amber[0243]; Nainari 60[9962]; Newthatch[9962]; Opata 85[9962]; Othello[9962]; Penjamo 62[9962]; Quaderna[9962]; Rex[9962]; Riete[9962]; Saitama 27[9962]; Spica[9962]; Veery S[9962]; Victo[9962].

Rht8b

Associated with a 174-bp fragment of WMS 261[9962]

s: Cappelle Desprez*/Mara 2D[1601]. **v**: Arthur[0243]; Balkan[9962]; Bunyip[9962]; Cappelle-Desprez[9962]; Carstens[0243]; Diakovchanka[0243]; Eureka[9962]; Festival[9962]; Fronteira[9962]; Fultz[9962]; Gabo[9962]; Heine VII[9962]; Inallettabile 95[9962]; Jena[9962]; Klein Rendidor[9962]; Leonardo[9962]; Lutescens 17[9962]; Mironovskaya 808[9962]; Norin 10[9962]; Norin 10/Brevor 14[9962]; Oasis[243]; Odom[0243]; Podunavka[9962]; Purdue Abe[0243]; Record[9962]; Red Coat[9962]; Salzmunder Bartweizen 14/44[0243]; Soissons[9962]; Talent[9962]; Tevere[9962]; Timstein[9962]; Tp114/65[0243]; Wilhelmina[9962]; Wiskonsin 245 C/11226[0243].

Rht8c

Associated with a 192 bp fragment of WMS 261[9962]

v: Akakomugi[1191]; Alfa[9962]; Aquila[9962]; Ardito[9962]; Argelato[9962]; Avrora[9962]; Banija[9964]; Baranjka[9964]; Beauchamps[9962]; Bezostaya[9962]; Biserka[9962]; Campodoro[9962]; Centauro[9962]; Chikushi-Komugi (Norin 121)[9962]; Chuanmai 18[10512]; Damiano[9962]; Djerdanka[9964]; Dneprovskaya[9962]; Duga[9964]; Etoile-de-Choisy[9962]; Etruria[9962]; Fakuho- Komugi (Norin 124)[9962]; Farnese[9962]; Favorite[9962]; Fedorovka[0243]; Fiorello[9962]; Fortunato[9962]; Funo[9962]; Gala[9962]; Haya Komugi[9962]; Impeto[9962]; Irnerio[9962]; Jarka[9964]; Jugoslavia[9962]; Kavkas[9962]; Kalyan[0243]; Khar'kovskaya 50[0243]; Khar'kovskaya 93[0243]; Khersonskaya 86[0243]; Kolubara[9964]; Kosava[9964]; Libellula[9962]; Lonja[9964]; Lovrin 32[9962]; Macvanka-2[9964]; Mara[119, 9962]; Marzotto[9962]; Mv 03-89[0243]; Mv 06-88[0243]; Mv 17[0243]; Neretva[9962]; Nizija[9962]; Novasadska Rana 1[1604]; N.S. Rana 1[9962]; N.S. Rana 2[9962]; N.S. 649[9962]; N.S. 3014[9962]; Obrii[243]; Odesskaya 51[0243]; Odesskaya 117[0243]; Odesskaya 132[0243]; Odesskaya Krasnokolosaya[0243]; Odesskaya Polukarlikovaya[0243]; Orlandi[9962]; Osjecanka[9964]; OSK 5 5/15[9964]; OSK 4 57/8[9964]; OSK 3 68/2; Partizanka[9962]; Partizanka Niska[9962]; Poljarka[9964]; Posavka 1[9964]; Posavka 2[9962]; Pomoravka[9962]; Produttore[9962]; Radusa[9962]; Roazon[0243]; Salto[9962]; Sanja[9962]; San Pastore[9962]; Sava[414, 1601, 9962]; Siete Cerros[9962]; Sinvalocho[9962]; Simvol Odesskii[0243]; Sivka[0243]; Strumok[0243]; Skopjanka[9962]; Skorospelka 3B[9962]; Slavonija[9964]; Somorka[9964]; Sremica[9964]; Superzlatna[9962]; Svezda[9962]; Tira[0243]; Tisa[9964]; Transilvania[9962]; Ukrainka

Odesskaya[0243]; Una[9962]; Villa Glori[9962]; Vympel[0243]; Yubileinaya 75[0243]; Zagrebcanka[9964]; Zelengora[9964]; ZG 6103/84[9964]; ZG 7865/83[9964]; Zitarka[9964]; Zitnica[9962]; Zlatna Dolina[9964]; Zlatoklasa[9964]; Zolotava[0243].

Although CS carries a 192 bp fragment, sequencing showed it was a different allele than other genotypes with ***Rht8c***[02103].
Although the 'diagnostic' association of ***Rht8c*** and *Xgwm261* $_{192}$ applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives[10512]. The pedigrees of a number of Chinese wheats postulated to have ***Rht8c*** on the basis of the marker traced to Italian sources[10515].

Rht8d

Associated with a 201-bp fragment of WMS261[9962]

v: Pliska[9962]; Courtot[9962].

Rht8e

Associated with a 210-bp fragment of WMS261[9962]

v: Chino[9962]; Klein Esterello[9962]; Klein 157[9962].

Rht8f

Associated with a 215-bp fragment of WMS261[9962]

v: Klein 49[9962].

Rht8g

Associated with a 196-bp fragment of WMS261[0243]

v: Mirleben[0243].

Rht8h

Associated with a 206-bp fragment of WMS261[0243]

v: Weihenstephan M1[0243].

rht8 syn: RNHL-D1[11624]

Genotypes of Indian semi-dwarf wheats based on the Ellis et al.[0378] markers are listed in [10404] and those for U.S. eastern and central and winter wheat cultivars are listed in [10868].

RHT9

Rht9 locus: 5AL[10249] 7BS[772, 1601]

v: Acciao[718]; Forlani[718]; Mercia 12[10249]. **s**: Cappelle-Desprez*/Mara 5BS-7BS[1601]. **v2**: Akakomugi **Rht8**[1601]; Mara **Rht8**[1601]. **ma**: Close linkage with *Xwmc410-4A*[10249].

RHT10

See ***Rht-D1c***

RHT11

See ***Rht-B1e***

RHT12

TraesCS5A02G543100

Rht12[718] locus: 5A[1445, 1606]

Dominant

bin: 5AL-23, based on co-segregation with **B1**[1606]. **i**: N98-2105, Yangmai 5*5/Karcagi 522M7K[11428]. **v**: Karcagi 522M7K[721]; Mercia, Vigour 18 and Halberd derivatives[11622]. **ma**: **Rht12** is located distally on 5AL cosegregating with **B1** and closely linked to *b-Amy- A1*[1606]; *Xgwm291-5A* – 5.4 cM – **Rht12**[726]. The **Rht12** phenotype was due to deletion of a 10.73 Mb terminal deletion of chromosome 5AL[11428]. Reduced plant height might be due to activation of *TaGA2ox-A14*[11428]. **c**: Encodes a GA2oxA13 enzyme[11622] (previously predicted as GA2oxA14[11428]. **Rht12** delayed ear emergence by 6 days[1606].

Rht12 delayed ear emergence by 6 days[1606]

RHT13

Rht13[718] locus: 7BS

v: Magnif 41M1 CI 17689[718], **ma**: Associated with *Xwms577-7B*[10249]

Rht13a

v: Magnif 41 PI 34466. **c**: Encodes a nucleotide-binding site leucine repeat (NBS-LRR) protein[11626]. Greatest sequence similarity to contig TGAC_Cadenza_U_ctg7180000823280[11626].

***Rht13b*{M23019}** locus: 7BS[10249] syn: Rht13[718]

v: Magnif 41M1 CI 17689[718]. **ma**: Associated with *Xwms577* (*gwm577*)*-7B*[10249]. **c**: A serine-240-phenylalanine mutation caused autoactivation leading to transcriptional upregulation of pathogenesis-related genes including class III peroxidases associated with cell wall modelling[11626]. The same sequence was identified in TILLING line Cadenza0453[11626].

RHT14

Rht14[718] locus: 6AS[10767]

Allelic with *XRht16*, **Rht18** and **Rht24**[10767, 10818]

v: Cp B 132[123] = Castelporziano PI 347331[718]. **ma**: **Rht14** – 11.7 cM – *Xbarc3-6A*[10767]. Mapped to genomic region 383-422 Mb flanked by *GA20xA9* and *Xwmc753-6A*[11372]. *GA2oxA9* expression was higher in Castelporziano than in its tall parent Capelli – see **Rht18**[11301]. **c**: See RHT24.

[10818]

RHT15

Rht15[718]

tv: Durox[718].

RHT16

Rht16[718] locus: 6AS[10767]

Allelic with **Rht14** and **Rht18**[10767, 10818]

v: Edmore M1[718]. **ma**: **Rht16** – 28.0 cM – *Xbarc3-6A*[10767].

[10818]

RHT17

Rht17[718] syn: Rht-B1p {M23014}

v: Chris Mutant CI 17241[1129].

RHT18

Rht18[718] locus: 6AS[10767]

Allelic with **Rht14**, **Rht16** and **Rht24**[10767, 10818]

tv: Icaro[718]. **ma**: **Rht18** – 25.1 cM – *Xbarc3-6A*[10767]. Hexaploid derivatives in the backgrounds of Fengchan 3, Jinmai 47 **Rht8**, and Xifeng 20 are reported in [11096]. **matv**: *Xbarc118-6A* – 1.4 cM – RHT18/*TdGA2Ox-A9/S470865SSR4*/*Xbarc37-6A* – 0.4 cM – *IWA4371* – 0.4 cM – *Xgwm82.1-6A*[11295]. **c**: See **Rht24**.

Independent ‘ overgrowth’ mutants isolated from Icaris contained changes in the *GA2oxA9* coding region; this gene is predicted to encode GA2-oxidase that metabolizes GA biosynthetic intermediates into inactive products thus reducing bioactive GA1[11301].

RHT19

Rht19[718]

tv: Vic M1[718].

RHT20

Rht20[718]

v: Burt M860[718].

RHT21

Rht21[0230]

The existence of this gene was not confirmed[0231]

RHT22

Rht22[10857] locus: 7AS[10857]

tv: Aiganfanmai[10857]. Ailanmai[11587]. **ma**: *Xgwm471-7A* – 29.5 cM – **Rht22** – 20.1 cM – *Xgwm350-7A*[10857].

RHT23

Rht23[11077] locus: 5DL[11077]

v: NAUH164[11077]. **ma**: *Xgdm63-5D* – 4.7 cM – **Rht23** – 11.1 cM – *Xbarc110-5D*[11077].

NAUH164 is an EMS-derived mutant of Sumai 3[11077].

RHT24

Rht24 syn: QTL_height_6A_1[11183], QPH.caas-6A[11184], Rht24b[11293, 11294]

c: Encodes *TaGA2ox-A9* which is more highly expressed by the ***Rht24b*** allele[11623]. Same locus as **Rht14**, **Rht16**, and **Rht18**.

Rht24a[11183, 11184, 11185] locus: 6AL[11185] syn: Rht24[11185] QTL_height_6A_1[11183], QPH.caas-6A[11184], Rht24b[11293, 11294]

v: Aikang 58[11185]; Solotar[11294]. **ma**: *Xwmc256-6A* – 2.71 cM – *TaGa3* – 7.05 cM – *TaAP2* – 0.24 cM – **Rht24** – 1.61 cM – *TaFAR* – 13.87 cM – *Xbarc103-6A*[11185]. Excalibur_rep_c69275-346[11294].

Rht24 was identified in many Chinese cultivars and a low number of European wheats based on flanking markers designed from *TaAP2* and *TaFAR*[11185]

Rht24b

v: Chuanmai 107[11623]; Fan 6[11623]; Jinan 2[11623]; Jing 411[11623]; Taishan 1[11623]; Yannong 5[11623], Zhongmai 175[11623]. **tv**: Also identified in wild and cultivated emmer and durum accessions[11623].

RHT25

TraesCS6A02G156600

Significant differences in RHT25 haplotypes were reported in [11659]

Rht25

Rht25a syn: Platz-A1

c: Encodes a PLATZ transcription factor that interacts with DELLA (**RHT1**)[11659].

Rht25b[11300] locus: 6AS[11300] syn: QHt.ucw-6AS[11300].

v: Patwin-515HP[11659]; **U**C1110 *Rht- D1b*[11300]. **ma**: *QHt.ucw-6AS* was located in a 0.2 cM interval flanked by *6A13699/6A13791/6A14397* and *6A14825*[11300].

RHT26

Rht26

Rht26a[11739]

v2: Lunxuan 987 *RhtB1b*[11739].

Rht26b locus: 3DL[11739]

v: Jing 411[11739]. **v2**: Zhongmai 175 ***Rht-B1a***[11739]. **ma**: Delimited to a 1.4 Mb interval (517.1 – 518.5 CSRefSeqv.1) flanked by markers *KASP517* and *KASP518*[11739].

RHT27

Rht27[11740] locus: 3AL[11740]

GA sensitive.

dv: *T. urartu* G1812[11740]. **ma**: Flanked by *3T-387* and *3T-306*[11740]. Delimited to a 1.55 Mb region (517.5 – 528.6 Mb, CS RefSeq v1.0) containing 20 genes, 2 of which, or homoeologs of which, coded genes affecting plant height[11740].

1.42.3 Reduced height: temporary designations

Rht_NM9[11273] locus: 2A[11273]

v: Induced mutant NM9[11273]. **ma**: *Xgwm122-2A* – 1.7 cM – *SNP34* – 1.9 cM – **Rht_NM9** – 1.9 cM – *SNP41* – 14 .0 cM – *Xwmc261-2A*[11273].

1.42.4 Reduced height: QTL

in Grandin

QHt.fcu-4BL[10256]

ma: Associated with *Xbarc125-4B* (R^2= 0.57)[10256].

Reduced height allele[10256]

in BR 34

QHt.fcu-6AS[10256]

Reduced height allele[10256]

ma: Associated with *Xbarc23-6A - Xcp201-6A* (R^2= 0.07)[10256].

in RL4452 / AC Domain

QHt.crc-2D[10287] locus: 2D[10287]

ma: Linked to BE497718-260 (LOD 4.2).

QHt.crc-4B[10287] locus: 4B[10287]

ma: Linked to **Rht-B1** (LOD 7.7)[10287].

Associated with QTLs for lodging and 1000-grain weight.

QHt.crc-4D[10287] locus: 4D[10287]

ma: Linked to **Rht-D1** (LOD 30.9)[10287].

Associated with QTLs for lodging 1000-grain weight, yield, height, and test weight.

QHt.crc-5B[10287] locus: 5B[10287]

ma: Linked to *Xwmc640-5B* (LOD 6.1)[10287].

QHt.crc-7A[10287] locus: 7A[10287]

ma: Linked to *Xwmc139-7A* (LOD 3.3)[10287].

QHt.crc-7B[10287] locus: 7B[10287]

ma: Linked to *Xgwm333-7B* (LOD 3.3)[10287].

in Courtot / CS

QHt.fra-1A[9957]

ma: Linkage with *Xfba393-1A*[9957].

QHt.fra-1B [9957]

ma: Linkage with *Xcdo1188-1B.2* [9957].

QHt.fra-4B [9957]

ma: Linkage with *Xglk556-4B* [9957].

QHt.fra-7A [9957]

ma: Linkage with *Xglk478-7A* [9957].

QHt.fra-7B [9957]

ma: Linkage with *XksuD2-7B* [9957].

in Renan / Recital

QHt.inra-2B [10069]

ma: Associated with *Xgwm249-2B* (LOD=5.8, R^2=15.4%) [10069].

QHt.inra-4A [10069]

ma: Associated with *Xfba243-4A* (LOD=6.5, R^2=15.0%) [10069].

QHt.inra-5A [10069]

ma: Associated with *Xgwm639b-5A* (LOD=5.7, R^2=10.8% [10069].

QHt.inra-6D [10069]

ma: Associated with *Xcfd76-6D* (LOD=3.7, R^2=8.1% [10069].

QHt.inra-7A [10069]

ma: Associated with *Xcdo545-7A* (LOD=3.2, R^2=7.7%) [10069].

in Opata 85 / W-7984 (ITMI)

RIL mapping population

QHt.ipk-4A [0255] locus: 4AL [0255]

Tall allele contributed by Opata 85 [0255]

ma: Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A* [0255].

QHt.ipk-4A coincided with QTLs for ear length (*QEl.ipk-4A*), grain number (*QGnu.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) [0255].

QHt.ipk-6A [0255] locus: 6A [0255]

Tall allele contributed by Opata 85 [0255]

ma: Associated with *Xcdo29-6A* and *Xfba234-6A* [0255].

QHt.ipk-6A coincided with QTLs for peduncle length (*QPdl.ipk-6A*) and ear length (*QEl.ipk-6A*) [0255].

in CS / CS (Kanto107 4A)

mapping population

QHt.ocs-4A.1 [0047] locus: 4AL [0047]

ma: Associated with *Xpsr119-4A* and **Wx-B1** [0047].

QHt.ocs-4A.2 [0047] locus: 4AS [0047]

ma: Associated with *Xbcd1738-4A* and **Hd** [0047].

in CS (*T. spelta* 5A) / CS (Cappelle-Desprez 5A)

RI mapping population

QHt.ocs-5A.1 [0068] locus: 5AL [0068] syn: Qt.ocs-5A.1 [0068]

ma: Associated with the interval *Xcdo1088-5A* – *Xbcd9-5A* [0068].

This QTL coincided with a QTL for culm length, *QCl.ocs-5A.1* [0068].

in Sevannah / Senat

DH population

QHt.nau-2D[11463] locus: 2DS[11463]

Recessive. Gibberellin-sensitive.

bin: 2DS-0.47-1.00. **v**: EMS- Induced Dwarf Wangshuibai[11463]. **ma**: *Xbarc-2D* – 2.6 cM-*2D* – *QHt.nau-2D* – 0.3 cM-*2D* – *Xgpw361-2D*[11463].

QHt.riso-3A[10067]

ma: Mapped on the centromeric region between SSR markers *Xwmc505-3A* and *Xwmc264-3A* (LOD > 6)[10067].

Two QTLs for plant height were assigned to chromosome 3A in RSLs from Cheyenne*7/Wichita 3A substitution line[0025].

Seven QTLs on chromosomes 1A, 1D, 2B, 2D and 4B affected plant height among RILs of **CS** / *T. spelta duhamelianum*. Effects linked with the CS alleles of *Xbcd1160-1A*, *Xksu127-1D* and *XksuF11-2D* increased height whereas those CS alleles associated with *Xpsr131-2B*, *Xpsr125-2B*, *Xpsr934-2D* and *Xcs22.2-4B* reduced it[0196].

For review and identification of 65 QTL-rich clusters associated with plant height see ▸[11741].

1.43 Herbicide Response

1.43.1 Difenzoquat insensitivity

DFQ1

Dfq1[1396] locus: 2B[1396]

Insensitive.

v: CS[1396].

dfq1

Sensitive.

s: CS*6/Ciano 67 2B[1396]; CS*7/Marquis 2B[789]; CS*/Sicco 2B[1396]. **v**: Ciano 67[1396]; Sicco[1396].

Busch *et al.*[153] reported a single dominant gene for tolerance of Era and Marshall compared with the susceptibility of Eureka and Waldron, but its relationship to **Dfq1** is unknown.

1.43.2 2,4-D tolerance

Randhawa *et al.*[1190] reported a single dominant gene in each of WL711, CPAN1874 and CPAN1922 controlling tolerance. HD2009 and PBW94 were described as susceptible.

1.43.3 Chlortoluron insensitivity

SU1

Su1[1402] locus: 6B, 6BS

Insensitive.

v: Cappelle-Desprez[1402]. **tv**: B-35[735].

su1

Sensitive.

v: Chinese Spring[1402]; Poros[1402]. **tv**: B-7[735]. **ma**: *Xpsr312-6B* – 5.3 cM – **Su1** – 6.8 cM – *Xpsr477(Pgk2)-6B*[736]. ma, **tv**: **Nor2** (6BS) – 2.7 cM – **Su1**[1401]; **Su1** – 5.2 cM – *Xpsr371-6B* (6BL)[735].

Su1 also controls insensitivity to metoxuron[1402].

A single dominant gene for tolerance to isoproturon was found in tetraploid wheats derived from a tolerant *T. monococcum* source[1044]. This gene is presumably different from **Su1**.

1.43.4 Imidazolinone resistance

Resistance alleles found in mutagenized populations were incompletely dominant and additive in effect[10099]. Resistance is due to single base pair changes in acetohydroxyacid synthase.

Imi1[10099] locus: 6DL[10101] syn: Fs-4[10100], AhasL-D1[10101]

v: BW755 = Grandin*3/Fidel-FS- 4[10099]; CDS Teal IMI 1A[10099]; CDC Teal IMI 9A[10099]; CDC Teal IMI 10A = Fidel-FS- 2[10099]; Clearfield WHS Janz = Janz*4/Fidel-FS-2; Clearfield WHS Stiletto = Stiletto*3//Spear/Fidel-FS-3; Fidel-FS-2 = ATCC40997[10100]. **v2**: CDC Teal IMI 15A = PTA 3955 **Imi3**[10099].

Imi2[10099] locus: 6BL[10101] syn: AhasL-B1[10101]

v: CDC Teal IMI 11A = PTA 3953[10099].

Imi3[10099] locus: 6AL[10101] syn: AhasL-A1[10101]

v2: CDC Teal IMI 15A **Imi3**[10099]. **dv**: *T.monococcum* mutant EM2 (mutant of susceptible line TM23[10102]).

Mutant EM2 has a serine to asparagine substitution near the carboxyl end of the enzyme. The same change led to imidazolinone resistance in hexaploid wheat, rice and *Arabidopsis*[10102].

1.44 Hybrid Weakness

1.44.1 Hybrid necrosis

[Progressive lethal necrosis[155]; Firing[971]].

Complementary dominant genes. Descriptive alleles *w* (weak), *m* (medium) and *s* (strong) were allocated by Hermsen[532]. Phenotype is affected by modifying genes (and/or genetic background) and environment[566]. According to Dhaliwal *et al.*[257] progressive necrosis is suppressed at 28C.

NE1

Ne1[530] locus: 5B[1491] 5BL[1636] syn: Le[155, 550], F[971], Le1[1491]

ma: *Xbarc216-5B* – 8.3 cM – **Ne1** – 2 cM – *Xbarc74-5B*[10334]. **Ne1** – 11 cM – *Xgwm639-5B*[11343]. Mapped to a 4.06 Mb region (383.03 – 3.87.10 Mb) that was deleted in all tested non-**Ne1** carriers[11517]. Co-segregation with the null allele of indel marker *5B-InDel385*[11517]; Mapped to a 4.45 Mb interval represented by *Xwgrc3074-5B* – 0.07 cM – NE1/*5* markers – 0.12 cM – *Xwgrc3009-5B*[11518]. *Xbarc216-5B* – 3.8 cM – *Xwgrc3030* – 0.3 cM – NE1/*Xwgrc1426* 3009 – 4.8 cM – *Xbarc74 -5B*[11537]; *Xgwrc3030* – 1.4 cM – **Ne1**/*Xwgrc3146*/*3147*/*3150*/*Xmag1426* – 0.12 cM – *Xwgrc3150*[11537]; markers *Xwgrc3146*, *Xwgrc3147* and *Xwgrc3150* were dominant[11537]. *Nwu_5B-4137* – 0.2 cM – NE1 – 0.3 cM – *Nwu_5B_4114* at 383.30 – 388.01 Mb in CS RefSeq 1.0[11594].

Ne1m[530]

i: S-615*11/Prelude[1500]. **v**: Carpo[532]; Eskisehir 220-39[532]; Garnet[532]; Klein Aniversario[532]; Koga[532]; Mus XII/80/22[532]; Prelude[532, 1491].

Ne1s[530]

v: Big Club[155, 532, 550]; C306[1475]; Felix[531]; Gaza 141 PI 220429[532]; Luteseens 1163[1264]; Marquillo[115, 532, 550]; Ponca[532]; Spica[939]; Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60[10334]. **tv**: Gaza 1E PI 133460; Gaza PI 189262[532]; Iumillo[532]; Kubanka[532]; PI 94587[155, 532]; Quanah[532].

Ne1s is common in tetraploid wheats[1080]

Ne1w[530]

v: Bobin group[532]: Kenya Farmer[532]; The Bobin selection used in breeding Gabo[532] and its sister selection, Timstein[532, 1556] was in fact Gular. Hence Gular, not Steinwedel, is the presumed source. The Sydney University accession Bobin W39 was the parent of Gabo and Timstein, whereas "true" Bobin carried the accession number W360. The particular accession tested by Hermsen is not clear. According

to Metgzer[1000] Steinwedel is a non-carrier; Federation group[532]; Cadia[532]; Cleveland[971]; Minister group[532]; Rieti group[532]: Mentana[532]; Mara[532].

Unknown **Ne1** alleles. tv: HW75[697]; HW178[697].

Chinese Spring carries the weakest allele[532] and its effect can be observed in CS*7/Atlas 66 2B[939] relative to CS.

NE2

TraesCS2B01G182800[11530, 11531, 11532]; also predicted in [11529]

Ne2 locus: 2B[1491] 2BS[1085] syn: F[971], Le2[155, 550, 1491]

ma: *Xgwm148-2B* – 6.7 cM – **Ne2** – 3.2 cM – *Xbarc55-2B*[10334]. *Xbarc7-2B* – 3 cM – **Ne2** – 6 cM – *Xwmc344-2B*[11343]. *Xgwm148-2B* – 5.2 cM – *Xwgrc1713*/*Xwgrc1736-2B* – 1.3 cM – NE2/ 3 markers[11518]; *Xgwm148-2B* – 5.4 cM – **Ne2**/*Xwrgc1774*/*1775*/*1739* – 3.0 cM – *Xwmc474-2B*[11537].

Ne2m[530]

v: Alsen[10334]; Squarehead group[532]: European wheats[532]; Fronteira group[532]: Sonalika[1475]; South American wheats and derivatives, e.g. Atlas 40[532]: Wheats possessing **Lr13**[939], e.g. Manitou[939]; HD2329[10985]. **ma**: *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – **Lr13**/Ne2 – 5.8 cM; *Xgpw1109* – 3.7 cM – *Xbarc18-2B*[11068].

Ne2s[530]

i: S-615*11/Kharkov[1500]. **v**: Crimean group[532]: Blackhull[550]; Chiefkan[550]; Clarkan[550]; Kharkov[1491]; Liaochun 10[11530]; Zhoumai 22[11531]; Michigan Amber[532]; Minhardi[155]; Red Chief[550]; Stepnaja 135[1264]; Turkey[532]. **c**: Encodes a CC- NBS-LRR protein[11531, 11532, 11533]. One of two ***Ne2m*** haplotypes is **Lr13**[11531]. GenBank MW756036[11532]; Add: *N22m* is an allele of the YR27/LR13 locus (*M22053*).

Ne2w[530]

v: Vakka[532]; Varma[532].

Ne2ms[530]

v: Mediterranean group[532]: Dawson[155, 550]; Fultz[550]; Fulcaster[550]; Fulhard[550]; Honor[550]; Jones Fife[1491]; Shepherd[550, 971]; Trumbull[155]; Vermillion[530]; Wabash[155]. (Although placed in this group on basis of pedigree, the last three stocks, as well as Fultz selection of CI 19293, appear to have the stronger allele of the Crimean group[532]; Mironovskaya[10630]; Noe group[532]: Vilmorin 27[532].

Ne2m?[530]

v: Barleta group[532]: South American wheats, e.g. Klein Titan[532]; La Prevision 25[532]; Lin Calel[532].

However, **Ne2** was stated to be absent or rare in tetraploid wheats[1080]. The Chinese Spring 2BS telosome carries an **Ne2** allele that is not present in Chinese Spring[1085].

Ner

Rye line 1R136-2 carries **Ner1**[1210] that complements wheat gene **Ne2**[1210, 1289] and rye gene **Ne2**[1210] to produce necrosis. Rye lines L155 and L256 carry **Ne2**[1210] that complements **Ne1**[630, 1210] and **Ne1**[1210].

Ner1[1210] locus: 5RL[1211]

al: *S. cereale* 1R136-2[1210].

Ner2[1210] locus: 7RL[1211]

al: *S. cereale* L155, L256[1210].

ungrouped

ne1 ne2

v: Chancellor[531]; Elgin[1491]; Gladden[155]; Leap[155]; Purkof[155]; Red Bobs[1491]; Red Egyptian[1491]; Steinwedel[1000]; S-615[1491]; Wichita[531].

Genotype lists in [531, 532, 535, 640, 696, 698, 1093, 1135, 1264, 1381, 1473, 1474, 1475, 1492, 1496, 1497, 1502, 1503, 1505, 1506, 1507, 1508, 1509, 1510, 1512, 1630, 1631, 1632, 1633, 1637, 1638, 1639, 0112].

1.44.2 Hybrid chlorosis type 1

Chr1

A gene, **Chr1**, in rye produces chlorosis symptoms in hybrids with wheats such as C306, HD2939 and NI5439 possessing **Ch2**[1472]. Evidence for multiple alleles of **Chr1** was also presented[1472]

Chr1[1472]

dv: Cereal rye lines, EC179188 = WSP527A[1472]; EC143825 = WSP506A[1472]; EC338685 = Blanco[1472]; others[1472].

chr1[1472]

dv: EC179178[1472]; EC179185 = SAR/SWPY5[1472].

ungrouped

Ch1[535] locus: 2A[538, 939] syn: m^a[1245]

i: Steinwedel*2/Khapli[939]; *T. macha* var. *colchicum*[535]. **v**: *T. macha* var. *subletschumicum*[1245, 1493]. **tv**: Khapli[1080, 1549]; *T. dicoccoides* var. *kotschyanum*[535]; *T. dicoccoides* var. *straussianum*[535].

36 group dicoccon wheats are listed in ▸[697].

ch1 ch2

v: Albit[1000, 1509]; Burt[1000, 1509]; Chancellor[1000]; Garra[1549]; Kharkof[535]; Steinwedel[1549]. **su**: TAP 67 (= Pawnee 3Ag(3D))[1644].

Lists in ▸[535, 697, 1381, 1473, 1474, 1475, 1496, 1497, 1502, 1503, 1505, 1506, 1507, 1508, 1509, 1510, 1512]

Ch2[535] locus: 3DL[692, 939] 3D[1495, 1504] syn: Ne3[1504], m^b[1245]

v: Chinese Spring[535, 1504]; *T. vavilovi*.

Extremely widespread, very few wheats lack this gene.
Allelic variation at the **Ch2** locus was suggested[537, 1000]. Prelude, Reward and Red Bobs were exceptional in producing severe symptoms and death at an early stage. Konosu 25 may carry a weak allele[1000].
Different alleles in C306 (strong) and Sonalika (medium) were suggested in ▸[697].

1.44.3 Hybrid chlorosis type 2

Cs1[1511] locus: 5A[1498] syn: Chl^1

v: *T. dicoccum* cv. Hokudai[1511].

Occurs at high frequency in the *T. paleocolchicum* group of emmers.

Cs2[1511] locus: 4G[1498] syn: Chl^2[1501]

tv: Many accessions of *T. timopheevii* and *T. araraticum*[637, 1511].

Multiple allelism at the **Cs2** locus is discussed in ▸[637].

A gene named *NetJingW176* (after *Ae. tauschii* accession Jing Y176) was located in chromosome 2DS: *Xgwm-102*- 2D – 4.5 cM – *Nec2* – 3.8 cM – *Xgwm515-2D*[11307].

1.44.4 Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4-5 leaf stage. The lethal genotype was designated *apd1* **apd1 apd2** *apd2*[10492].

Apd1[10492]

v: WR95 = Kalyansona/Gigas//HD1999/Sonalika/3/*T. carthlicum*[10492].

Apd1 Apd2

v: Atila[10492]; Kalyansona[10492]; others[10492].

apd1 apd2

Lethal genotype.

Uniculm plants occured as heterozygous segregates among progenies, but homozygous uniculm lines could not be established[10492].

Apd2[10492]

v: HD2009[10492]; HW2041[10492]; Lok-1[10492]; others[10492].

1.44.5 Hybrid necrosis type 3

Nec1[11158] locus: 7DS[11158]

Although this form of hybrid necrosis is caused by complementary genes, mapping of **Nec1** was based on a cross of necrotic and non-necrotic Langdon x *Ae. tauschii* amphiploids. Consequently only **Nec1** was mapped[11158].

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1.45 Iron deficiency

Fe1[921] locus: 7DL[927]

v: Saratovskaya 29[921].

Fe2[921] locus: 7BS[927]

v: CS[927].

1.46 Lack of ligules

The liguleless character is controlled by complementary recessive genes in hexaploid wheat[77, 738, 942] and by a single recessive in tetraploid wheat[47, 50, 939, 10133]. One gene at the tetraploid level is allelic with one of those in the hexaploid[939, 10133]. Evidence for orthology of **lg1** and **lg2** with *lg* of rice[170], **lg1** of maize[4], *li* of barley[1155] and *al* of rye was presented in [725]. An Imperial rye chromosome 2R addition restored the liguled condition to a liguleless CS derivative[939]. An erect leaf mutant involving *TaSPL8* (SQUAMOSA promoter-binding protein-like transcription factor), a homolog of **LG1** in maize and rice and was located in chromosome 2D. Knockout mutants of *TaSPL8* orthologs led to a fully liguleless phenotype. The gene in 2D was identified as *TraesCS2D01G502900*. *TaSPL8* transcript was highly expressed in the laminar joint region and young spike. *TaSPL8*- 2D transcript was produced at much higher levels than *TaAPL-2B* whereas *TaSPL-2A* was produced at a minimal level[11401].

LG2

TraesCS2D01G502900

LG2

TraesCS2D01G502900

bin: C-2DL3-0.49. **ma**: *Xbarc228-2D* – 12.7 cM – **LG2**/*G3489_1DL12del/G3489_2DL11del* – 3.3 cM – *Xgdm6-2A* – 47.8 cM – *Xgwm301-2D*[11220].

lg2 locus: 2D[942]

i: ANK33 = Novosibirskaya 67*10/K59990. **v**: Eligulate W1342 **lg1 lg3**; Liguleless partial backcross derivative of CS[939].

A dominant mutant allele for liguleless phenotype is reported in *Ae. tauschii* – this locus is located in chromosome 2DL but is independent of **LG2**

ungrouped

lg1[47] locus: 2B[942] 2BS[10767]

i: ANK33 = Novosibirskaya 67*10/K59990[10061]. **v**: Eligulate W1342 **lg2 lg3**[942, 10133]; K31289[10133]; K59990[10061]; K53660[10133]; Liguleless partial backcross derivative of CS[939]; Partial backcross derivative of CS[939]. **tv**: K17769[10133]; K17784[10133].

Lg2^{t}

dv: Liguleless mutants of *Ae. tauschii* accession KU20-9[11220].

lg3[10133] locus: 2A[10133]

i: ANK33 = Novosibirskaya 67*10/K59990[10061]. **v**: Present in all hexaploid cultivars.

LG^{t} [11220]

bin: C-2DL9-0.75. **ma**: *Xgwm301-2DL* … … … *Xbarc159-2D* – 9.3 cM – **LG^{t}** [11220].

Genotypes of selected tetraploid wheat[10133]
Lg1Lg1 Lg3 Lg3: *T. turgidum* var. *durum* Ldn - dic DS 2A: *T. turgidum* var. dicoccum Khapli and Vernal; *T. turgidum* var. *dicoccoides* Israel A; MG4343.
Lg1Lg1 **lg3 lg3**: *T. turgidum* var. *durum*: Altaiskaya Niva; Castelpoziano; Langdon; Ldn-GB DS 2B; Golden Ball; Modoc; PI349056.
lg1lg1 Lg3Lg3: None identified.

1.47 Leaf characteristics

1.47.1 Leaf erectness

QLer.ipk-2A[0255] locus: 2AS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; The erect leaf phenotype was contributed by Opata[0255]. **ma**: Associated with *Xbcd348-2A*[0255]. Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants[0255].

Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants[0255].

1.47.2 Leaf tip necrosis

Ltn1[10281] locus: 7D[1361] syn: Ltn[1361]

v: with **Lr34**/**Yr18**[301, 1361]. **v2**: Parula **Ltn2**[10281]. **ma**: Associated with *Xgwm295-7D* and *Xgwm130-7D*[10281]. **c**: Putative ABC transporter[10648].

This gene is identical to **Lr34**, **Sr57**, **Yr18**, **Pm38**. **Ltn1** reportedly has effects on response to other diseases and pathogens including BYDV and *Bipolaris sorokiniana*.

Ltn2[10281] locus: 1B

v: Wheats with **Yr29**/**Lr46**[10281]; See **Yr29**, **Yr46**. **v2**: Parula **Ltn1**[10281]. **ma**: *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – **Ltn2** – 2.9 cM – *Xbac17R* ..... *gwm140-1B*[10281]; *Xgwm44-1B* – 3.6 cM – **Ltn2** – 2.1 cM – *XtG818/XBac17R.* .... *Xgwm140-1B*[10281].

According to Messmer et al.[0031] LTN may be caused by several QTLs and is affected by genetic background and environment.

Ltn3[11070]

i: RL6077[11070]. **v**: Chapingo 48[11070]. **c**: This multiple disease resistance/necrosis locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices[11070].

QLtn.sfr-1B[0050] locus: 1BS[0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0050]. **ma**: Associated with *Xgwm18-1B* and *Xglk483-1B*[0050].

QLtn.sfr-3A[0050] locus: 3A[0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0050]. **ma**: Associated with *Xpsr570-3A* and *Xpsr543-3A*[0050].

QLtn.sfr-4B.1 [0050] locus: 4B [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr921-4B* and *Xpsr593-4B* [0050].

QLtn.sfr-4B.2 [0050] locus: 4B [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr593-4B* and *Xpsr112-4B* [0050].

QLtn.sfr-4D [0050] locus: 4DL [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr302-4D* and *Xpsr1101-4D* [0050].

QLtn.sfr-5A [0050] locus: 5A [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr549-5A* and *Xglk163-5A* [0050].

QLtn.sfr-6A [0050] locus: 6A [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr563-6A* and *Xpsr966-6A* [0050].

QLtn.sfr-7B.1 [0050] locus: 7B [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr350* and *Xbzh232(Tha)-7B* [0050].

QLtn.sfr-7B.2 [0050] locus: 7B [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xglk750-7B* and *Xmwg710-7B* [0050].

QLtn.sfr-7D [0050] locus: 7DS [0050]

v: Forno/*T. spelta* var. Oberkulmer mapping population [0050]. **ma**: Associated with *Xpsr160-7D* and *Xgwm44-7D* [0050].

1.47.3 Seedling leaf chlorosis

sc [149] locus: 3BS [149]

s: CS*/Hope3B [149]. **v**: Hartog [149]; Suneca [149]; wheats with **Sr2** [149].

Leaf chlorosis is affected by temperature and light and is enhanced by infection with pathogens. The **sc** allele is completely linked with **Pbc** (pseudo-black chaff) and **Sr2** (reaction to *Puccinia graminis*).

1.47.4 Early leaf senescence

ELS3

ELS3

Candidate gene *CS2D02G332700*

ma: Located in a 2.52 Mb interval – *AX-109501942* – 2.0 cM – **Els3** – 1.4 cM – *AX109998182* [11772].

Els3 [11772]

v: Yanzhan 4110 [11772]. **c**: The candidate encodes an LRR-RLK -like gene located on the cell membrane [11772].

els3

v: **els3** mutant [11772].

The mutant was identified in an EMS-mutagenized population of Yanzhan 4110 [11772].

ungrouped

els1[11326] locus: 2BS[11326]

v: ZK331/Xiangmai 99171 // 2*Lumai 30 Line 114[11326]. **ma**: *WGGB305* – 0.3 cM – **els1**/*WGGB302* – 1.2 cM – *WGGB303/WGGB304/WGGB306* – 0.6 cM – *Xbarc92-2B*[11326].

The **els1** 'mutant' was detected in an F4 population. Since the parents had normal phenotype complementary genes were likely involved. The similar location of **ELS1** to the NE1 locus in chromosome 2BS and similar phenotype suggests that this gene may be **Ne2**. See 49, Hybrid Weakness; 49.1, Hybrid necrosis

Els2[11472] locus: 2BL[11472]

v: LF2099[11472]. **ma**: *Xgpw4043-2B* – 8.87 cM – **Els2** – 22.27 cM *Xwmc149-2B*[11472].

The incompletely dominant **Els2** mutant was found in an EMS-treated M_2 population of H261[11472].

1.48 Lesion Mimicry

Lesion mimic phenotypes are characterised by spontaneous hypersensitivity not unlike disease resistance. Lesions are often not produced when leaf sectors are protected from light, and disease levels on mutant individuals may be lower than on non-mutant sibs. Lesion mimics that resemble the response of plants to infection by pathogens occur in many species (10743 for examples).

LM1

LM1[11572] locus: 3BS[11572]

ma: *Xwmc674-3B* – 1.2 cM – **LM1** – 3.8 cM – *Xbarc133*/*Xbarc147* - 3B[11572].

lm1

v: Zaosui 30 *Lm2*[11572].

LM2

LM2[11573] locus: 3BL[11573]

ma: *Xgwm513-4B* – 1.5 cM – **LM2** – 2.9 cM – *Xksum154-4B*[11572].

lm2[11572]

v: Yanzhan 1 *Lm1*[11572].

LM3

LM3[11573] locus: 3BL[11573]

ma: Mapped to a 3 cM proximal region of chromosome 3BL[11573].

Lm3

Partially dominant.

v: Line **Lm3**[11573].

The mutant phenotype appeared in an F1 plant of cross Line 3-1/Jing 411. The plant was then backcrossed 6 times with Line3-1 and the selected line was named Lm3.

LM4

LM4[11577] locus: 2DS[11577]

ma: Fine mapped within a 8.06 cM interval flanked by *Xgwm210* -2D and *Xgwm455-2D* using specifically developed markers *m4_01_cib* and *lm4_02_cib*[11577].

Lm4

Wild type allele. Recessive.

lm4[11577]

The allele named lm4 and conferring the lesion phenotype was described as dominant[11577].

This lesion mutant appeared in a Yanzhan 1/Neixiang 188 RIL population in which the segregation of mutant versus normal phenotype was 1:1.

LM5

LM5 locus: 2AL[11576]

Semi-dominant.

Lm5[11576]

v: MC21, an EMS-induced mutant in Chuannong 16[11576]. **ma**: *KASP-4211* (630.3 Mbp) – 0.6 cM – **Lm5** – 3.7 cM – *KASP5353* (703.53 Mbp)[11576].

ungrouped

lm[10743] locus: 1BL[10743]

bin: C1BL6-0.32[10743]. **v**: Ning 7840[10743]. **ma**: Proximal to *Xgwm264.1-1B*[10743].

LM was positively associated with *QLr.pser.1BL*[10743].

1.49 Lodging

QLd.crc-3D[10287] locus: 3D[10287]

ma: Linked to *Xgwm191-3D* (LOD 3.7) in RL4452/AC Domain[10287].

QLd.sfr-1B[0052] locus: 1BS[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr949-1B* and *Xgwm18-1B*[0052].

This QTL coincided with QTL for reduced height, increased culm stiffness and broader leaf width[0052].

QLd.sfr-2A[0052] locus: 2AS[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr958-2A* and *Xpsr566-2A*[0052].

This QTL coincided with QTL for reduced height, increased culm stiffness, broader leaf width, more erect growth habit, later ear emergence and increased culm thickness[0052].

QLd.sfr-2D[0052] locus: 2D[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr933-2D* and *Xglk529-2D*[0052].

QLd.sfr-3A[0052] locus: 3AS[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr598-3A* and *Xpsr570-3A*[0052].

This QTL coincided with QTL for increased culm stiffness and reduced culm thickness[0052].

QLd.sfr-4A[0052] locus: 4AS[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xgwm397-4A* and *Xglk315-4A*[0052].

This QTL coincided with QTL for reduced height, increased culm stiffness and more erect growth habit[0052].

QLd.sfr-5A[0052] locus: 5AL[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr918-5A* and *Xpsr1201-5A*[0052].

This QTL coincided with QTL for reduced height, increased culm stiffness, reduced leaf width, more erect growth habit, later ear emergence and increased culm thickness[0052].

QLd.sfr-5B[0052] locus: 5BL[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr370-5B* and *Xpsr580-5B*[0052].

This QTL coincided with QTL for increased culm stiffness, broader leaf width and more erect growth habit[0052].

QLd.sfr-6B[0052] locus: 6BL[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr964-6B* and *Xpsr142-6B*[0052].

QLd.sfr-7B[0052] locus: 7BL[0052]

v: Forno/*T. spelta* var. Oberkulmer mapping population[0052]. **ma**: Associated with *Xpsr927-7B* and *Xpsr350-7B*[0052].

This QTL coincided with QTL for reduced height and later ear emergence[0052].

1.50 Male sterility

1.50.1 Chromosomal

MS1

MS1 locus: 4B[268] 4BS[64]

TraesCS4B02G017900

ma: Located in a 0.05 cM region between *X27140346* and *X12360198*[11269].

Ms1

c: Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is essential for pollen exine production[11269]. GenBank KX447407. **Ms1** is a phospholipid-binding protein[11421]. Sequence: SRP113340. Encodes a 219 amino acid polypeptide with similarity to a large family of GPI-anchored lipid transfer proteins affecting exine development[11269]. *Ms-A1* = *TraesCS4A02G295900*; *Ms-B1* = *TraesCS4B02G017900*.

ms1

Recessive alleles for sterility

ms1a[268]

v: Briggle's Chancellor Derivative[268]; Pugsley's Male Sterile[268]. **c**: Terminal deletion[11422].

ms1b[268]

v: Probus mutant[268]. **c**: Interstitial deletion[11269].

ms1c[64]

v: Cornerstone[64]. **c**: Terminal deletion[11269].

ms1d[619]

v: Mutant FS2[619]; Ningchen mutants *msd.1* and *msd.2*[11421]. **c**: G329A in exon 1[11269, 11421].

ms1e[619]

v: Mutant FS3[619]. **c**: G1431A del1432[11421]; C1435T + 16 bp del in exon 2[11269].

ms1f[619]

v: Mutant FS24[619]. **c**: G155A in exon 1[11269].

ms1g[10355, 11421] locus: 4BS[10354]

v: Lanzhou Mutant 257A[10354, 10355]; Male sterile line 257A[10546]. **c**: Deletion of entire sequence[11421].

ms1h[11421]

v: Ningchun 4 mutant[11421]. **c**: C1762T[11421].

ms1i[11421]

v: Ningchun 4 mutant[11421]. **c**: G1603A[11421].

ms1j[11421]

v: Ningchun 4 mutant[11421]. **c**: C1775A[11421].

ms1k[11421]

v: Ningchun 4 mutant[11421]. **c**: G1397A[11421].

ms1l[11421]

v: Ningchun 4 mutant[11421]. **c**: C226T[11421].

ms1m[11421]

v: Ningchun 4 mutant[11421]. **c**: C1472T[11421].

ms1n[11421]

v: Ningchun 4 mutant[11421]. **c**: T164A[11421].

ms1o[11421]

v: Ningchun 4 mutant[11421]. **c**: G281A[11421].

ms1p[11421]

v: Ningchun 4 mutant[11421]. **c**: G155A[11421].

ms1q[11421]

v: Ningchun 4 mutant[11421]. **c**: C148T[11421].

ms1r[11269] syn: Ms1h[11269]

v: Tilling mutant in Qual2000[11269]. **c**: G178A[11269].

Ms1376[10814]

Sterility is dominant

v: TR1376A[10814].

Male fertile counterpart: TR1376B[10814].
Ms1376 was discovered among progenies of a transgenic family of Xinong 1376 containing leaf senescence-inhibiting gene *P* SAG12-IPT[10814].

Ms1 orthologs in the A and D genomes are epigenetically silenced[11421].

MS2

ms2[806] locus: 4DS[806] syn: Ta1[240]

Dominant allele for sterility.

v: Taigu = Line 223[240, 806, 807]; **ms2** confers sterility when present in octaploid triticale[597]. **ma**: Mapped to a 0.05 cM region flanked by *Xsauw27-4D* and *Xsdauw29-4D*[11388]. **c**: **Ms2** has a long terminal-repeat in miniature (TRIM) transposon at position -314 to -310[11388]. Genbank KX585234[11388].
The TRIM element acts as an enhancer that activates anther-specific transcription of the **Ms2** allele[11388, 11389]. **Ms2** induced male sterility in barley and Brachypodium[11388] as well as triticale[597, 11388].

MS3

ms3[872] locus: 5AS[872]

Dominant allele for sterility.

i: Chris derivative[872]; KS87UP9[219]. **ma**: *Xwg341-5A* – 0.8 cM – **ms3** ... cent[0289]; *Xcdo-677-5A* and *Xbcd1130-5A* also cosegregated with *Xwg341-5A* but were located in a different region in the physical map[0289].

MS4

ms4[0293] locus: 4DS[0293]

Dominant allele for sterility, distinguished from **ms2** on the basis of different degrees of recombination with the 4D centromere.

v: Konzak's male sterile.

MS5

Ms5 locus: 3A[619], 3AL[11427]

Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is required for pollen exine development[11427]. *TraesCS3A02G217000*[11427]. GenBank MK577897.

ms5[0290] locus: 3A

v: Mutant FS20[619]; H45[11427].

Complete sterility conferred by **ms5** is dependent on the homoeologous *ms-D* genotype – Ecalibur, Gladius and RAC 875 have an *ms-D* allele that restores fertility to **ms5** genotypes[11427].

Two non-functional *ms-B* alleles (Chinese Spring and Synthetic W7984 types) were identified[11427].

Two non-functional *ms-B* alleles (Chinese Spring and Synthetic W7984 types) were identified[11427].

1.50.2 Sterility in hybrids with wheat

Shw[0331] syn: 1HL[331]

ad: Additions of 1H and 1HL to wheat and certain translocation lines[331]. **ma**: Located in a 16.4 cM interval flanked by *Xmwg800-1H* and *Xmwg943-1H*. A possible relationship with *Ncc* genes is discussed[331].

1.50.3 Photoperiod and/or temperature-sensitive male sterility (PTGMS)

tmsBS20T[11157] locus: 2BL[11157]

v: BS20-T[11157]. **ma**: *Xgwm403-2B* – 2.2 cM – **tmsBS20T** – 4.5 cM – *Xgwm374-2B*[11157].

wptms1[10333] locus: 5B[10333]

v: Line 337S **wptms2**[10333]. **ma**: *Xgwm335-5B* – 4.2 cM – **wptms1** – 24.4 cM – *Xgwm371-5B*[10333].

wptms1 produces sterility only in the presence of **wptms2**. Chromosome 5B was also implicated in spontaneous mutant line Xinong 291S: a second gene was not located[11143].

wptms2[10333] locus: 2B[10333]

v: Line 337S **wptms1**[10333]. **ma**: *Xgwm374-2B* – 6.9 cM – **wptms2** – 20.9 cM – *Xgwm120-2B*[10333].

wptms2 produces sterility only in the presence of **wptms1**. **wptms1** and **wptms2** were analysed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Although mapping data are different a possible relationship between **wtms1** and **wptms2** needs to be resolved.

wtms1[10332] locus: 2B[10332]

v: BNY-S[10332]. **ma**: E: AAG/M:CTA163 – 6.9 cM – **wtms1** – 4.8 cM – *Xgwm374-2B*[10332].

Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10C, but fertile at higher temperatures[10332].

1.51 Manganese efficiency

QTL

Stojocri 2 (Mn efficient) / Hazar (MN inefficient): durum cross: Variation associated with *Xcdo583-4B* explained 42% of the variation in Mn efficiency[0320].

1.52 Maturity time

RL4452 / AC Domain:

QMat.crc-3B[10287] locus: 3B[10287]

ma: Linked to *Xwmc231-3B* (LOD 3.0)[10287].

QMat.crc-4A[10287] locus: 4A[10287]

ma: Linked to **Wx-B1** (LOD 6.1)[10287].

QMat.crc-7D[10287] locus: 7D[10287]

ma: Linked to *Xgwm130-7D* (LOD 17.5)[10287].

1.53 Megasporogenesis

1.53.1 Control of megasporogenesis

Msg[625] locus: 7AS[625]

tv: Langdon[625].

1.54 Meiotic characters

1.54.1 Low-temperature pairing

ltp[527]

v: Chinese Spring[527].

Expressed in the absence of chromosomes 5D at 12ºC - 15ºC, but not at 20ºC. A contrasting allele, *Ltp*, for normal pairing at the lower temperature range was demonstrated in *T. dicoccum*.

1.54.2 Pairing homoeologous

PH1

Ph1[1537] locus: 5BL[1301] syn: Ta-Zip4-B2[11765]

v: Hexaploid wheat. **tv**: Tetraploid wheat. **ma**: PCR-based assays for presence and absence of **Ph1** were described[359, 9965, 0214, 0217]; The **Ph1** factor(s) was restricted to a region flanked by *Xrgc846-5B* and *Xpsr150-5B*[0219]; **Ph1** was physically mapped in 5BL to fraction length 0.55, bracketed by deletions 5BL-1 and ***ph1b***[446].

A complex **Ph1** candidate structure comprising at least one 5B-specific member of the *cdc2* complex multigenic cluster (involved in chromosome condensation), a unique repeat structure with similarities to repeats on chromosome 3B, and a heterochromatic sub-telomeric insertion from chromosome 3AL was identified[10240]. *Ta-Zip4-B2* is embedded within this complex[11765].
A set of homoeologous set of *Ta-Zip-1* genes (*Ta-Zip-A1*, *TaZip-B1* and *TaZip-D1* genes is present in Group 3 chromosomes but their expression levels are very low compared to *Ta-Zip-B2* {11765).

ph1b[1301]

v: Sears' high pairing mutant[1301]. **ma**: A PCR-based detection system for ***ph1b ph1b*** individuals is described in ▶[9965]. Dualplex marker *Xwgc2111* + *Xwgc2049* behaves like a co-dominant marker[11359]. The ***Ph1b*** deletion involves a region of at least 60,014,523 bp[11359].

ph1c[593]

tv: Cappelli *ph1* mutant[449, 593]; This mutant is deficient for a terminal portion of chromosome 5BL[449]. **ma**: Mutant lines with ***ph1b*** and ***ph1c*** carry deletions of the chromosome segment possessing **Ph1** in the respective parent lines[447, 593].

Several *ph1* mutants are described in ▶[0219].

PH2

TraesCS3D02G119400

Ph2[1302] locus: 3DS[1302]

TaMSH703D[11527]

ph2a[1302]

v: Sears' intermediate pairing mutant[1301, 1302]. **ma**: ***ph2a*** is a 120-125 Mb deletion[11526].

ph2b[1303, 1304] syn: ph1a[1537]

v: Chinese Spring mutant 10/13[1537]. **c**: Contains a G to A transition at position 74,359.312 in the *TaMSH7-3D* gene[11527]. *TaMSH7* is a plant-specific member of the DNA mismatch repair (MMR) family[11527].

Wide cross hybrids involving **ph2** mutants have a 5.5-fold increase in homoeologous pairing[11516].

1.54.3 Inhibitor of pairing homoeologous

Ph1^{I}

al: *Aegilops speltoides*[439, 1218].

1.54.4 Asynapsis/desynapsis

A putative gene for desynapsis designated *Ddes2* was placed between *Xwmc325-3B* and *wPt-8983* in deletion bin 3BL7-0.63-1.00 by mapping of deletion hybrids[11339]. There is no mutant stock to represent this gene first reported in CS nullisomic 3B by Sears[1293].

TAASY-1

TaASY-A1[11767]

TaASY-B1[11767]

TaASY-D1[11767]

TaASY1[11766]

Encodes an axial-element-associated protein that is essential for synapsis and cross- over formation in Arabidopsis and rice[11766]. Mutants affect synapsis and distribution of chiasmata along the chromosome[11767].

ungrouped

QTug.sau-3B[11471]

bin: 5BS5-0.07-0.03. **ma**: *Xgwm285-3B* – 1.0 cM – *Xcfp11012-3B*[11471].

Identified in *T. turgidum*/*Ae. tauschii* hybrids involving Langdon durum (high unreduced gamete formation) crossed with AS313 and AS2225 (low unreduced gamete formation) topcrossed with *Ae. tauschii* AS60. The QTL was located near *Ttam*, a homologue of the *TAM* (tardy asynchronous meiosis/CYCA1; 2) cyclin gene from Arabidopsis[11471].

1.55 Nitrate reductase activity

NRA

Nra[424]

v: UC44-111[424].

nra[424]

v: Anza[424].

1.56 Nuclear-cytoplasmic compatability enhancers

Scs[869] locus: 1AL[27, 870] syn: scs^{ti}[10878]

Derived from *T. timopheevii*[869].

v: *T. timopheevii*[869]. **ma**: A number of completely linked RAPD makers were identified[44]; *Xbcd1449.2-1A* – 0.6 cM – *SCS* – 2.3 cM – *Xbcd12-1A*[10878].

Asakura *et al*.[44] used the symbol *Ncc* as a synonymn for *scs* pointing out that the effects of the gene are not limited to a single species.

1.57 Nucleolus organizer regions

1.57.1 18S - 5.8S - 26S rRNA genes

NORs were observed as secondary constrictions associated with nucleoli on satellited chromosomes, e.g. ▸[221], and by *in situ* hybridization to chromosome spreads[39, 294, 1014] of 18S-5.8S-26S ribosomal-DNA probes[38, 433]. Allelic variation in gene number was demonstrated at all wheat *Nor* sites and at **Nor-R1** by filter[367] and *in situ* hybridization[1012]. Allelic variants of the *Nor* loci were detected by hybridization of rDNA probes to restriction endonuclease-treated DNA on Southern blots[37, 288, 917, 1399]. Alleles ***Nor-B2a*** to ***Nor-B2f*** were identified using *Taq1* digests of genomic DNAs hybridized to derivatives of the plasmid pTa250[433] containing spacer-DNA fragments pTa250.4[367, 917] and pTa250.15[288].

Other variants may have been isolated[1399] using *BamH1*/*EcoR1* double digests and pTa71[433]. The variants may or may not be equivalent to those described below. Other variants may have been isolated[1399] using *BamH1/EcoR1* double digests and pTa71[433]. The variants may or may not be equivalent to those described below.

NOR-1

Nor-A1 locus: 1AS[221, 367, 835, 1012]

v: *T. spelta*[221, 367, 835, 1012]. **dv**: *T. monococcum*[658].

Nor-Ag^{i}1[374] locus: 1Ag^{i}[374]

ad: Vilmorin27/*Ag. Intermedium*[374].

Nor-B1 locus: 1BS[221, 367, 835, 1041] 1B[37, 288] syn: Nor1[1120]

v: CS[288].

Deletion mapping divided the **Nor-B1** in a proximal subregion *Nor-B1p* (short repeat) and a distal subregion ***Nor-B1d*** (long repeat)[0275]

Nor-B1a[918]

v: Cheyenne, Chinese Spring, Hope, Kite, Oxley, Teal, Timstein[37, 288]; Vasco, 8 others[288].

Nor-B1b

v: Olympic, Robin, Shortim[917].

Nor-B1c[918]

v: Banks[917]; Corella[917]; Warigal[917]; 5 others[917].

Nor-B1d[918]

v: Maris Huntsman[918].

Nor-B1a-[918]

v: Cheyenne, Chinese Spring, Hope, Kite, Oxley, Teal, Timstein[37, 288]; Vasco, 8 others[288].

Nor-B1c-[918]

v: Rosella[918].

Nor-H1 locus: 1HS[794] syn: Nor-I1[794]

dv: Sultan barley[794].

Nor-R1 locus: 1RS[39]

ad: CS/Imperial[39].

Nor-S1 locus: 1SS[294]

al: *Ae. speltoides*[294].

Nor-U1 locus: 1U[906]

su: CS/*Ae. umbellulata*[906].

Nor-V1[241] locus: 1V[241]

ad: CS/*D. Villosum*[241].

More detailed listings for allelic variation at **Nor-B1** and **Nor-B2** are given in [917, 918].

NOR-2

Nor-B2 locus: 6BS[221, 366, 835, 1041] syn: Nor2[1120]

v: CS.

Nor-B2a[918] locus: 6B[288]

v: CS[37, 917].

Nor-B2b locus: T6B[288]

v: Banks, Oxley, Shortim, Timstein[37]; 12 others[917].

Nor-B2c

v: Corella, Robin, Teal, 1 other[917].

Nor-B2d[918] locus: H6B[288]

v: Hope[37]; Olympic[917]; Warigal[917].

Nor-B2e

v: Vasco[917].

Nor-B2f locus: Ch6B[288]

v: Cheyenne[37, 917].

Nor-B2g[918]

v: Falcon; Gluclub; La Prevision[918].

Nor-B2h[918]

v: Yaktana[918].

Nor-B2i[918]

v: Maris Huntsman; Thatcher[918].

Nor-B2a-[918]

v: Blueboy[918]; Sonora 64-1[918].

Nor-B2d-[918]

v: Harrier[918]; Kite[917, 918].

Nor-E2 locus: 6ES[294]

ad: CS/*E. elongata*[294].

Nor-G2 locus: 6G[578]

tv: *T. timopheevii* IPSR (PBI) No. 1[294].

Nor-H2 locus: 6H[39, 1070, 1248] 6HS[794] syn: Rnr1[1248]

al: Clipper barley[39]; Sultan barley[794].

Nor-S2 locus: 6SS[294]

al: *Ae. speltoides*[294].

More detailed listings for allelic variation at **Nor-B1** and **Nor-B2** are given in [917, 918].

NOR-3

Nor-A3 locus: 5AS[658, 1014]

dv: *T. monococcum*, *T. urartu* IPSR (PBI) Acc. A.

Nor-Ag^{i}3 locus: 5Ag^{i}[374]

ad: CS/*Ag. intermedium*[374].

Nor-D3 locus: 5DS[221, 835]

v: CS; most wheats[37, 288, 917].

Nor-E3 locus: 5ES[294]

ad: CS/*E. elongata*[294].

Nor-H3 locus: 5HS[794] 5H[39, 1070, 1248] syn: Rnr2[1248]

al: Clipper barley[39]; Sultan barley[794].

Nor-U3 locus: 5U[906]

ad, su: CS/*Ae umbellulata*[906].

NOR-4

Nor-D4[1042] locus: 7DL[1042]

v: CS[1042]. **dv**: *Ae squarrosa*[1042].

Nor-H4 locus: 7HS[793, 794] syn: Nor-I4[794]

al: Sultan barley[794].

NOR-5

Nor-H5 locus: 2HS[793, 794] syn: Nor-I5[794]

al: Sultan barley[794].

NOR-6

Nor-B6[601] locus: 1BL[601]

v: CS; Cheyenne, Wichita[601]. **tv**: Langdon[601].

NOR-7

Nor-A7[601] locus: 5AL[601]

v: CS; Cheyenne, Wichita[601]. **tv**: Langdon[601].

NOR-8

Nor-D8[601] locus: 3DS[601]

v: Witchita[601].

NOR-9

Nor-A9[00120] locus: 1AS[276, 282] syn: Nor-A1[221, 367, 835, 1012]

v: *T. spelta*[221, 367, 835, 1012].

NOR-10

Nor-A10[00120] locus: 5AS[276, 282] syn: Nor-A3[658, 1014]

dv: *T. monococcum*[276, 282]; *T.urartu* IPSR (PBI) Acc. A.

ungrouped

Nor1a and Nor2a

v: Maris Huntsman[1399].

Nor1b and Nor2b

v: Bezostaya 1[1399].

Nor1c and Nor2c

v: Cappelle-Desprez, Maris Ranger[1399].

Two sites designated temporarily as *Nor-Ax* and *Nor-Ay* were identified in *T. monococcum* ssp. *boeoticum*, but were absent in ssp. *urartu*.

1.58 Osmoregulation

Osmoregulation is a specific form of solute accumulation regulating turgor pressure and hydration during periods of stress with positive effects on growth. Wheat lines selected for higher osmoregulation in the greenhouse have greater growth and seed yields under water-limited conditions in the field.

OR

Or[1030]

Low osmoregulation.

s: CS (Red Egyptian 7A). **v**: Cappelle Desprez; Condor*4/3Ag14[1030]; Red Egyptian. **ma**: **Or** (proximal in 7AS) – 13 cM – *Xpsr119-7A*[1031].

or[1030] locus: 7AS[1031] 7A[1030]

High osmoregulation.

v: CS, Condor, Songlen, Takari[1030].

1.59 Phenol colour reaction of kernels

Wheat genotypes vary in response when caryopses are treated with weak solutions of phenol, a dark colour response being indicative of a positive response. This response is believed to be related to the action of tyrosinase. There seems to a genetic relationship with polyphenol oxidase activity which causes a darkening of flour, pasta and noodle products (see also Polyphenol Oxidase (PPO) activity).

TC

Tc1[10130] locus: 2AL[10130, 10131]

su: Various substitutions of chromosomes 2A into CS[10131]. **sutv**: Langdon*/dicoccoides 2A[10130]. **tv**: Golden Ball[10130].

Tc2[10130] locus: 2BL[10130]

sutv: Langdon*/Golden Ball 2B[10130]. **tv**: Golden Ball[10130].

Tc3[10131] locus: 2DL[10130] syn: Tc[10131]

v: Chinese Spring (intermediate response)[10130]. **v2**: Timstein **Tc1**[10131]. **su**: CS/*Timstein 2D[10131]. **tv**: Cocorit 71[10130]; Langdon[10130]. **sutv**: Langdon*/CS 2D(2A); Langdon*/CS 2B(2D)[10130]; *T. dicoccoides* Israel A[10130]. Lines with a negative phenol colour reaction.

1.60 Pollen killer

KI

Ki[1306] locus: 6BL

Killing allele is dominant.

v: Chinese Spring[1306]; Mentana[929].

ki

v: Probably the majority of wheats including Timstein, Gabo and Yalta[1306].

Modifiers also appear to be involved as Luig[840] found variation among *kiki* parents. Some F2 and F3 *Sr11sr11* plants from Yalta/Chinese Spring crosses segregated with less than 50% **Sr11**- phenotypes among the progeny indicating that killing extended to eggs as well as pollen. See also, Gametocidal Activity.

Kato & Maeda[10164] reported both partial pollen and seed sterility in crosses involving certain landraces and Chinese Spring. They attributed sterility to recessive alleles of three complementary genes. The genes were designated *Ki2, Ki3* and *Ki4*[10164], but the relationship of *Ki3* to the earlier designated **Ki** was not established. Some genotypes:

Ki2 Ki3 Ki4: v: Aka Kawa Aka[10165]; Hope[10165]; Marquis[10165]; Red Russian[10165]
ki2 Ki3 Ki4: v: Akadaruma[10165]; Canthatch[10165]; Norin 61[10165]; Pakistani Landrace IL159[10164]
Ki2 ki3 Ki4: v: Gabo[10165]; Thatcher[10165]; Timstein[10165]; Zlatiborka[10165] ***Ki2 Ki3 ki4***: v: Kagoshima[10165]; Komugi Jingoro[10165]; Sakobore[10165]
ki2 ki3 Ki4: v: Finnish Landrace WAG4339[10165]; Hungarian Landrace WAG4458[10165]; Novosadska Jara[10165]
ki2 Ki3 ki4: v: Chinese Spring[10165]; Eshima Shinriki[10165]; Ethiopian Landrace IL70[10164]; Norin 26[10165]
Ki2 ki3 ki4: v: Cadet[10165]; Iraqi Landrace IL171[10165]; Rex[10165] See Segregation distortion.

1.61 Polyphenol oxidase (PPO) activity

3,4 dihydroxyphenylalanine (L-DOPA) was used as a substrate in a non-destructive test of polyphenol oxidase activity in seeds. Chromosome 2D was shown to carry PPO gene(s) based on Langdon/Chinese Spring (2D) substitution lines and nullisomic-tetrasomic analysis[0342]. An orthologous series of genes affecting PPO activity in both common wheat and durum was proposed in [10149]. See also, Phenol colour reaction of kernels

QTL

Chara (mod high) / WW2449 (low): DH population: PPO activity Associated with *Xgwm294b-2A*(R^2=0.82), *Xwmc170-2A*, *Xgwm312-2A* and *Xwmc178-2A*(R^2> 0.7)[10410].

Chara (medium high PPO) / WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci *Xtc1* and *XPPO-LDOPA*. – 0.6 cM – *XPPO- LDOPA/XPPO18/BQ161439*[10484].

M6 (high activity) / Opata 85 (low activity): A QTL on 2D, associated with *Xfba314-2D* was identified using the L-DOPA assay[0344].

Y18 / Clark's Cream: Markers significantly associated with PPO activity were also detected on chromosomes 2A, 2B, 3B, 3D and 6B in the population[0344]. A multiplex of markers *PPO33* and *PPO16* was reliable for selecting genotypes with low PPO activity[10418].**Zhongyou 9507 / CA9632:** PPO18 explained 28-43% of the variation in PPO activity[10290].

Tetraploid wheat

Jennah Khetifa (high) / Cham 1 (low): Associated with *Xgwm312-2AL*[10411]. STS marker PPO18 based on a polyphenol oxidase (*PPO*) gene (GenBank *AY596268*) was closely linked to SSR markers *Xgwm312-2AL* and *Xgwm294-2AL*.

Messopia / *T. dicoccoides*: RIL population: Associated with RFLP *Xutv1427-2A*[10411].

1.62 Red grain colour

1.62.1 Red grain colour

Red colour is probably due to the polyphenol compounds phlobaphene or proanthocyanidin, synthesized through the flavanoid pathway. Himi & Noda[10107] provided evidence that the R genes were wheat forms of R2R3-type Myb-type transcription factors (*Tamyb10-3A, Tamyb10-3B, Tamyb10-3D*). Genetic evidence is provided in [10838].

Red colour is dominant to white. At each locus, the white allele is assigned *a* and the red allele, *b*. White-grained *T. aestivum* and amber-grained *T. durum* wheats carry recessive *a* alleles at each locus. White-grained CS*7/Kenya Farmer and CS*6/Timstein are considered near-isogenic to CS with ***R-D1b***.

R-1

R-A1[548] locus: 3AL[957, 1003] syn: R2[548]

v: Rio Blanco[10839]. **ma**: (Proximal) *Xpsr483(Cxp1)-3A* – 28 cM – **R-A1** – *Xpsr904-3A*[370] (distal); *Xwmc559-3A* – 16.3 cM – *R- A1*/*Xgwm155-3A* – 4.5 cM – *Xwmc153-3*^{a}[10839].

R-A1a

ma: Based on **Tamyb10-A1** sequences this allele in CS lacks the ability to bind DNA due to deletion of the first half of the R2 repeat of the MYB domain[10838]; the ***R-A1a*** allele in Norin 17 has a 2.2 bp insertion in the second intron that appears to prevent transcription[10838].

R-A1b syn: R2

Tamyb10-A1[10107].

i: Novosibirskaya 67*9/Solo[730]. **v**: Baron[370]; Diamant 2[14]; Hustler[370]; Norin 10- Brevor, 14[17]; Maris Widgeon[370]; Mercia;[370]; Motto[370]; Red Bobs[1003]; Sapphire[370]; Slejpner[370]; Talent[370]; Wembley[370]. **c**: GenBank AB191458.

R-B1[548] locus: 3BL[370, 1003] syn: R3[548]

ma: *Xbcd131-3B* – 5 cM – **R-B1** – 5 cM – *Xabc174-3B*[410]; *Xwmc29-3B* – 5 cM – **R-B1** – 5 cM – *Xbarc84-3B*[10280]; *Xgwm4010-3B* – 1.6 cM – **R-B1** – 4.6 cM – *Xgwm980-3B*[10839].

R-B1a

ma: Based on the **Tamyb10-B1** sequence this allele in CS has a 19 bp deletion of the CCG repeat region causing a frameshift mutation[10838].

R-B1b syn: R3

Tamyb-10-B1[10107]

i: Novosibirskaya 67*9/k-28536[730]. **v**: Canon[370]; Dollar[370]; Grana[370]; Supreme[370]. **c**: GenBank AB191459.

R-D1[549] locus: 3DL[1291, 1293] syn: R1[548]

v: CS. **ma**: *Xbcd131-3D*/**R-D1** – 15 cM – *Xabc174-3D*[410]; *Xgwm2-3D* – .4 cM – **R-D1** – 3.2 cM – *Xgwm4306-3D*[10839].

R-D1b syn: R1

Tamyb10-D1[10107]

i: Novosibirskaya 67*9/CS[730]. **v**: Alexandria[370]; Apollo[370]; Axona[370]; CS[1293]; Dwarf A[370]; Fortress[370]; Jerico[370]; Longbow[370]; Luna[370]; Mardler[370]; Maris Huntsman[370]; Minaret[370]; NFC 75/93/27A; Rapier[370]; Pawnee[549]; Voyage[370]; Vuka[370]. **c**: GenBank AB19160.

R-N1[1018] locus: 3N[1018]

su: CS/*Ae. Uniaristata*[1018].

R-R1[1011] locus: 6RL[1011]

ad: Holdfast/King II[1011].

R-V1[1518] locus: 3VL

ad: Creso/*D. villosum*[1518].

A *3Ag* chromosome from decaploid *Ag. elongatum* carries an allele for red grain colour which was transferred to Agent and the majority of Sears' 3D-3Ae#1 translocations[939].
Other studies have identified wheats carrying either one or two, unidentified R-1 alleles:[56, 370, 437, 549, 631, 654, 659, 1078, 1148, 1333, 1349, 1454].

See also Variegated Red Grain Colour.

ungrouped

R-A1a R-B1b R-D1b syn: R3, R1

v: Fenman[370]; Kharkov[1003]; Norman[370]; Pastiche[370]; Riband[370]; Sperber[370]; Squadron[370]; Urban[370].

R-A1b R-B1a R-D1b syn: R1, R2

v: Bezostaya 1[370]; Brigand[370]; Broom[370]; Brock[370]; Kronjuwel[370].

R-A1b R-B1b R-D1a syn: R2, R3

v: Red Chief[548]; Avalon[370]; Bersee; Cappelle Desprez; Feuvert; Mission; Parade; Rendezvous; Yuri[370].

R-A1b R-B1b R-D1b syn: R1,R2,R3

v: Bowie; Frondoso[1148]; Frontiera[437]; Hope[204, 206]; Japanese Bearded[1548]; Kanred[1078, 1426]; Lin Calel[1078].

Functional markers based on *Tamyb10* sequences are given in [10838].

A fourth QTL for red seed colour in hexaploid wheat was detected on chromosome 1B in a GWAS of U.S winter genotypes[11409].

1.62.2 Variegated red grain colour

Vg[498]

v: Line 10859[498].

vgvg genotypes in Line 10859 are variegated. The **Vg**/*vg* locus was independent of the single red gene locus in Line 10859. In a cross to Selkirk (***R-A1b***, ***R-B1b***, ***R-D1b***) *vgvg* was expressed only in plants with one *R* gene[498]. Variegated red pericarp was also studied in crosses of cv. Supreme. In this case, two red colour genes were present[0136].

1.63 Reaction to black-point of grain

Black-point, a common grain defect, is a dark discoloration of the embryo region of the kernels. Whereas black-point is often attributed to infection by a number of fungi, the presence of such fungi may be a consequence of saprophytic colonization of affected tissues rather than the cause (see [10148] for references). The condition may be triggered by high humidity[0845].

QTL
Batavia / Pelsart (resistant): DH population: Associated with markers *Xgwm319-2B* and *Xgwm048-4AS*[10494].

Cascades / AUS1408: DH population: QTL from Cascades located in chromosomes 2D (5 cM from *Xgwm484-2D*, 18% of phenotypic variation), 2A (13%), and 7AS (12%)[10148].

Sunco / Tasman: DH populaion: QTL located in chromosomes 2B (15% of phenotypic variation), 3D, 4A (from Sunco) and 1D, 5A and 7AS (from Tasman[10148]. The 2B gene was associated with the presence of **Sr36**[10148].

QTL

Batavia / Pelsart (resistant): DH population: Associated with markers *Xgwm319-2B* and *Xgwm048-4AS*[10494].

Cascades / AUS1408: DH population: QTL from Cascades located in chromosomes 2D (5 cM from *Xgwm484-2D*, 18% of phenotypic variation), 2A (13%), and 7AS (12%)[10148].

Sunco / Tasman: DH populaion: QTL located in chromosomes 2B (15% of phenotypic variation), 3D, 4A (from Sunco) and 1D, 5A and 7AS (from Tasman[10148]. The 2B gene was associated with the presence of **Sr36**[10148].

1.64 Response to photoperiod

One-gene[1169] and two-gene[638, 1137, 1170] differences were reported in inheritance studies. In Chinese Spring/Hope substitution lines for chromosomes 1A, 4B and 6B greater sensitivity to short photoperiod was found, whereas substitutions of 3B and 7D were less sensitive[487]. 'a' alleles are dominant.

There is an orthologous gene series on the short arms of homoeologous group 2. The "a" alleles confer the insensitive response[0063], the contrasting allele may be referred to as "b".

PPD-1

Ppd-A1[10612, 0063] locus: 2AL[1268] syn: Ppd3[1141]

v: C591[0057]. **tv**: GS100, Kofa (1027- bp deletion in the promoter)[10612]; GS105, Svevo (1117-bp deletion in the promoter)[10612]; A survey of **Ppd-A1** allele is reported in [10915]. **ma**: *Xwmc177-2A* – **Ppd-A1**, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively[10612].

GS100 and GS105 had different deletions relative to GS101 and GS104, respectively, and both were consistently a few days earlier flowering than their near-isogenic counterparts with ***Ppd-A1b***[10612].

Ppd-A1a[10612]

tv: GS100[10612]; GS105[10612].

Ppd-A1a was present in 39% of Chinese landraces and 97% of improved cultivars[10622]. GS100 and GS105 had different deletions relative to GS101 and GS104, respectively and both were consistently a few days earlier flowering than their near-isogenic counterparts with ***Ppd-A1b***[10612]

Ppd-A1b[10612]

tv: GS101[10612]; GS104[10612].

Ppd-A1b Ppd-B1b Ppd-D1b

v: Cheyenne[1141]; Diamont 1[887]; Lancer[638]; Saratovskaya 29[887]; Warrier[638].

Two genes controlled photoperiod response in *T. turgidum*[788].
Gene *Ppd-H2* on barley chromosome 2HS may be a member of the *Ppd-1* orthologous series[766].

Ppd-B1 locus: 2BS

ma: *Xwhs2002-2B*/*Xgwm257-2B* – *PpdB1* – *Xgwm148-2B*. Actual linkage value varied between crosses[10129]; *Xpsr666-2B* – 1.2 cM – *Xpsr109-2B* – 4.4 cM – **Ppd-B1** – 4.8 cM – *Xpsr804-2B* ...Cent[0062].

According to [10611] the **Ppd-B1** allele from Japanese wheats has a stronger effect than the allele from CS.

Ppd-B1a[0063] locus: 2BS syn: Ppd2[1566]

i: H(C) = Haruhikari*5/Fukuwasekomugi[10611]; H(D) = Haruhikari*/5/Fukuwasekomugi ***Ppd-D1a***[10611]. **s**: Cappelle-Desprez*/CS 2B[0058]. **v**: CS[1268]; Spica[557]; Timstein[1269]. **v2**: Fukuwasekomugi ***Ppd-D1a***[10611]; Sharbati Sonora ***Ppd-A1a***[887]. **c**: Varieties with the photoperiod insensitive allele have more than one **Ppd-B1** copy per chromosome 2B: two copies in Recital, three copies in Sonora 64, Timstein and C591, and 4 copies in Chinese Spring[10881].

Ppd-B1b[10611, 10881]

v: Beaver[10881]; Cappelle-Desprez[10881]; Cheyenne[10881]; Norstar[10881]; Paragon[10881]; Renan[10881]. **v2**: Haruhikari *Ppd-D1b*[10611]. **c**: Varieties with the photoperiod sensitive allele have a single **Ppd-B1** copy[10881].

Ppd-D1 locus: 2DS[1268]

Comparative mapping showed that **Ppd-D1** was co-linear with barley *Ppd-H1* - a member of the pseudo-response regulator (PRR) gene family[10466].

Jagger amplified the 414 bp band[10466] associated with daylength sensitivity whereas 2174 amplified the 288 bp band associated with insensitivity[10722].

Ppd-D1a[0063] syn: Ppd1[1566]

i: H(C) = Haruhikari*5/Fukuwasekomugi[10611]; Haruhikari*5/Saitama 27[10611]; H(D) Haruhikari*5/Fukuwasekomugi ***Ppd-B1a***[10611]. **s**: Capelle Desprez*/Ciano 2D[1598]; Capelle-Desprez*/Mara

2D[1598]; CS*/Ciano 2D ***Ppd-B1a***[1268]. **v**: Akakomugi[1604]; Bezostaya 1[1604]; Festival[10466]; Kavkaz; Mara[1604]; Orqual[10466]; Recital[10466]; Saitama 27[10466]; Sava[1604]; Sideral[10466]; Soissons[10466]; Sonora 64[1566]; Talent[10466]; Texel[10466]. **v2**: Sharbati Sonora ***Ppd-D1a***[887]; Fukuwasekomugi *Ppd- D1a*[10611]. **ma**: Stocks with ***Ppd-D1a*** had a 2,089-bp deletion upstream of the coding region leading to mis-expression of the 2D PRR gene[10466].

PPD-2

Ppd-B2[10628] locus: 7BS[10628]

su: Favorit (F26-70 7B)[10628]. **v**: F26-70[0093]. **ma**: *Xgwm255-7B* – 20.7 cM – **Ppd-B2** – 4.4 cM – *Xgwm537-7B*[10628].

This gene confers earlier flowering under long photoperiod conditions[10628].

CONSTANS

Wheat genes *CONSTANS1* and *CONSTANS2* interact with *PPD1* to regulate photoperiodic response[11495].

CONSTANS 1

CO-A1[11495] locus: 7A

v: Chinese Spring. **c**: *TraesCS7A02G211300*[11295], GenBank MT043302[11495]. **tv**: Kronos[11495].

CO-B1[11495] locus: 7B

v: Chinese Spring. **c** *TraesCS7B02G118300*[11495], GenBank MT043303[11495]. **tv**: Kronos[11495].

CO-D1[11495] locus: 7D

v: Chinese Spring. **c**: *TraesCS7D02G212900*[11495].

CONSTANS 2

CO-A2[11495] locus: 6A

v: Chinese Spring. **c**: *TraesCS6A02G289400*[11495], GenBank MT043304[11495]. **tv**: Kronos.

CO-B2[11495] locus: 6B

v: Chinese Spring. **c**: *TraesCS6B02G319500*[11495], GenBank MT043305[11495]. **tv**: Kronos.

CO-D2[11495] locus: 6D

v: Chinese Spring. **c**: *TraesCS6D02G269500*[11495].

Triticum turgidum ssp. *durum* cv. Kronos: accession numbers MT043302 (**CO-A2**) and MT043305 (**CO-B2**)[11495]

ungrouped

QPpd.zafu-4AL

tv: *T. dicoccoides* TTD140[11443]. **ma**: Flanked by *M576* and *Xwmc468-4AL* in a 1.2 cM region[11443].

Other publications reporting Ppd genes/QTL in the same region are reviewed in [11443].

QTL

Trident (early) / Molineux (late): In addition to an effect associated with chromosome 2B, three QTLs were designated as: *QPpd.agt-1AL* (*Xwmc304* – *Xgwm497* region), *QPpd.agt-7AS* (*Xbarc154* – *Xbarc108*) and *QPpd.agt-7BS* (*Xgwm46* – *Xgwm333*)[10382]. The QTL in chromosome 1A was possibly orthologous to *Ppd-H2* in barley.

A QTL was detected in chromosome 4BS in Courtot/CS[0132].

1.65 Response to salinity

1.65.1 K+/Na+ discrimination

Variation in K+/Na+ discrimination ratios correlates with salt tolerance, high ratios being indicative of higher tolerance.

KNA1

Kna1[290] locus: 4DL[290] 4BS-4BL-4DL[283] 4BS-4BL-4DL-4BL[849]

v: Hexaploid wheats[290]. **sutv**: Langdon 4D(4B)[283]. **trtv**: Various lines[290]; Selection 3*5-4[849]. **ma**: **Kna1** was completely linked with *Xabc305-4B*, *Xabc305-4D*, *Xbcd402-4B*, *Xbcd402-4D*, *Xpsr375-4D*, *Xpsr567-4B*, *Xpsr567-4D*, *Xwg199-4B* and *Xwg199-4D* in recombined *T. turgidum* 4B and *T. aestivum* 4D chromosomes[283, 849].

Kna1 is a possible orthologue of **Nax2** and is the Na+ transporter *TaHKT1;5-D*[10455].

Lophopyrum elongatum chromosome arms 1ES, 7ES, and 7EL enhance K^+/Na^+ selectivity in wheat under salt stress[0065].

1.65.2 Salt tolerance

QTL
Opata 85 / 7984: 77 QTLs effective at different growth stages were mapped to 16 chromosomes[10384].

1.65.3 Sodium exclusion

NAX1

Nax1[10452] locus: 2AL[10452]

itv: Tamaroi*6/Line 149 = P06306[10453]. **tv**: Line 149 **Nax2** = 126775b[10452]. **dv**: AUS 90382 **Nax2** = C68.101[10455] = JIC *T. aegilopoides* no. 3. **ma**: **Nax1** was mapped as a QTL in the region *Xpsr102-2A* – 5.4 cM – *Xwmc170-2A* – 0.9 cM – *Xksud22-2A*/*Xksu16-2A* – 0.8 cM – *Xgwm312-2A* with R^2 = 0.38 in Tamaroi/Line 149[10452]; *TmHKT7-A2* was identified as a putative candidate Na^+ transporter[10454].

Nax1 promotes withdrawal of Na^+ from xylem in leaf bases and roots[10453].

NAX2

Nax2[10453] locus: 5AL[10455]

itv: Tamaroi*6/Line 149 = P05603[10453]. **tv**: Line 149 **Nax1** = 126775b[10452, 10453]. **dv**: AUS 90382 **Nax1** = C68.101[10455] = JIC *T. aegilopoides* no. 3. **ma**: Co-segregation with *Xgwm291-5A*/*Xgwm140-5A*/*Xgpw2181-5A*[10455]; *TmHKT1;5-A* was identified as a candidate for **Nax2**[10455].

Nax2 is a likely orthologue of **Kna1**[10455].

QTL
Berkut / Krichauff: QTL for Na^+exclusion and seedling biomass under salt stress were detected in chromosomes 2A (**Nax1** region) and 6A (*Xcfd080-Xbarc171-6A*)[10917].

1.66 Response to tissue culture

QGpp.kvl-2A[0253] locus: 2AL[0253]

v: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano[0253]. **ma**: Associated with *Xpsp3045-2A*[0253].

QGpp.kvl-2B.1[0253] locus: 2BL[0253]

v: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano[0253]. **ma**: Associated with *Xgwm388-2B*[0253].

QGpp.kvl-2B.2[253, 0253] locus: 2BL[0253]

v: Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano[0253]. **ma**: Associated with AFLP markers[0253].

Qtcr.ipk-2B.1[84] syn: Tcr-B1[84]

ma: Weakly associated with *Xpsr102-2B*[84].

Qtcr.ipk-2B.2[84] syn: Tcr-B2[84]

ma: Closely linked and distal to **Ppd-B1**[84].

Qtcr.ipk-2B.3[84] syn: Tcr-B3[84]

ma: Linked with **Yr7**/***Sr9g***[84].

Qtcr:ipk-2B.3[84] syn: Tcr-B3

ma: Linked with**Yr7**/***Sr9g***[84]

1.67 Response to vernalization

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, vernalization requirement is controlled by four major genes designated VRN-1, VRN-2, VRN-3, and VRN-4. The first three genes were identified using map based cloning aproaches[10014, 10299, 10421]. The VRN-1 gene encodes a MADS-box transcription factor closely related to the Arabidopsis *AP1*/*FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat[10014].

Deletions in the promoter (***Vrn-A1a***, ***Vrn-A1b***)[10198] or the first intron of this gene (***Vrn-A1c***, ***Vrn-B1a***, ***Vrn-D1a***)[10202] are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide[10617, 10695, 10709]. The VRN-2 locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain[10299].

Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit[10299].

Among the cultivated tetraploid and hexaploid wheat species the **Vrn-B2** gene is generally functional whereas the *Vrn-A2* gene is not[10710]. At least one functional copy of **Vrn-2** combined with homozygous recessive alleles at all three **Vrn-1** loci is required to confer winter growth habit in hexaploid wheat. The *VRN-B3* locus (formerly known as *Vrn-5* or *Vrn-B4*) is homologous to the Arabidopsis *FT* gene[10421]. This dominant allele, found in the variety Hope, is associated with the insertion of a transposable element in the **Vrn-B3** promoter. Natural variation at the **VRN-A3** and *VRN-D3* loci has been also described in hexaploid wheat[10533]. VRN-3 promotes the transcription of **Vrn-1** and accelerates flowering[10421]. The *Vrn-D4* allele for early flowering was originally identified in the Australian cultivar Gabo[671] and was backcrossed into Triple Dirk to develop the isogenic line TDF[1172]. This locus was mapped on the centromeric region of chromosome 5D between markers *Xcfd78* and *Xbarc205*[10711]. Natural variation for flowering time at the centrometric region of homoeologous group5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of *Vrn-D4* but molecular markers are now available to separate the incorrect stocks[10711]. Using genetic analyses, Iwaki et al.[10003] found the *Vrn-D4* allele for spring growth habit occurred with a higher frequency in India and neighboring regions. The *VRN-D4* locus in TDF includes a duplication of a 290 kb region from chromosome arm 5AL inserted into the proximal region of chromosome arm 5DS. This translocated segment includes a functional copy of VRN-A1 that carries distinctive mutations in its coding and regulatory regions[11123].

VRN-1

VRN-A1

Dominant spring habit alleles at the **Vrn-A1** locus

Vrn-A1

ma: Xgwm271-5A - 6.5 cM - Vrn-A1 - Xbarc232-5A[10880]

Dominant spring habit alleles at the *Vrn-A1* locus

Vrn-A1a[1398] locus: 5AL[775, 883] syn: Vrn1[1172], Sk[2]

i: Triple Dirk D (GenBank AY616458 & AY616459). **s**: Kharkov 22MC*/Rescue 5A[358]; Winalta*8/Rescue 5A[876]; Rescue*/Cadet 5A ***Vrn-D1a Vrn-B1a***[1221]. **v**: Cadet[1221]; Conley[1171]; Diamant II[885]; Falcon[1172]; Koga II[1611]; Kolben[1, 1171, 1172]; Konosu 25[460]; Marquis[1]; Reward[1171]; Saitama 27[460].

Saratov 29[883]; Saratovskaya 29[885]; Saratovskaya 210[883]; Shabati Sonora[885]; Thatcher[1171]; WW15[1172]. v2: Shortandinka ***Vrn-B1a***[885]; Takari ***Vrn-B1a***[253]; Triple Dirk ***Vrn-B1a***[1173]; Hope ***Vrn-B4a***[1424]. ma: **Vrn-A1** – 7.5 cM – *Xwg644-5A*[726]; Located mid chromosome 5A cosegregating with *Xcdo504-5A*, *Xwg644-5A* and

Xpsr426-5A[419]; **Vrn-A1** – 0.8 cM – *Xbcd450-5A*/*Xrz395-5A* – 4.2 cM – *Xpsr426-5A*[9903]. *Xgwm271-5A* – 6.5 cM – **Vrn-A1** – *Xbarc232-5A*[10880];

Cultivars possessing ***Vrn-A1a*** are insensitive to vernalisation. ***Vrn-A1a*** is epistatic to other genes. According to [1221], ***Vrn-A1a*** is not always fully dominant and not always epistatic. Kuspira *et al.*[745] attributed single gene variation in *T. monococcum* to the ***Vrn-A1a*** locus. Multiple recessive alleles were suggested[745]. *Vrn-A*^{m}1 was mapped on the long arm of chromosome 5A^{m} closely linked to the same RFLP markers as **Vrn-A1**[279]. *Vrn-A*^{m}1 was mapped to the *Xcdo504-5A-Xpsr426-5A* region[0312]. In the opinion of the curators this location may not be correct

Multiple alleles also were reported in [9930], and the dominant allele of Novosibirskaya 67 and the weaker dominant allele of Pirotrix 28 were designated *Vrn1a* and *Vrn1b*, respectively.

Vrn-A1b[10198]

v: Marquis PI 94548 (GenBank AY616461)[10198]. **tv**: *T. turgidum* var. *durum* ST36[10198].

Vrn-A1c[10198]

This allele has a promoter similar to recessive ***vrn-A1a*** from Triple Dirk C[10198] and a large deletion in intron 1[10202].

v: IL162[10198]; IL369[10198] has a 5.5 kb deletion in **Vrn-A1** intron 1[10202]. **tv**: Aldura PI 486150[10202]; Leeds CI 13796[10202]; Mexicali 75 PI 433760[10202]; Minos CI 15161[10202]. Most durum genotypes have a 7.2 kb deletion in intron 1[10202].

Vrn-A1d[10198]

tv: *T. turgidum* var. *dicoccoides* Amrim 34[10198]; FA15 (GenBank AY616462)[10198]; Iraq 8736[10198]; Tabigha 15[10198].

Vrn-A1e[10198]

tv: *T. turgidum* var. *dicoccum* ST27 = Vernal (GenBank AY616463)[10198].

vrn-A1a[10198]

v: Claire[10880]; Triple Dirk C[10880]. **v2**: Chinese Spring ***Vrn-D1a***[10880].

c: GenBank AY616455[10198].

vrn-A1b[10881]

v: IL369[10202]; Malacca[10881]. **c**: GenBank JF965396[10881].

This allele has two copies of the gene, possibly arranged in tandem although the physical structure is unknown. Both copies are distinguished from Chinese Spring ***vrn-A1a*** by a SNP in exon 7 (T in Malacca, C in Chinese Spring). One copy also has a SNP in exon 4 (T in Malacca, C in Chinese Spring).

Sequenced cDNAs from Malacca show that both copies are expressed[10881].

vrn-A1c[10881]

v: Hereward[10881]. **c**: GenBank JF965397[10881].

A comparison of Claire (***vrn-A1a***), Malacca (***vrn-A1b***) and Hereward (***vrn-A1c***) indicated that increasing gene copy number is associated with lateness[10881]. Two winter alleles were identified based on an SNP in exon 4[10656].

vrn-A1v[10916]

v: Don Ernesto INTA[10916]; Jagger[10916]; Norin 61[10916]; Opal[10916].

vrn-A1w[10916]

v: Bezostaya[10916]; Bavicora M 92[10916]; Kavkaz[10916]; Gennson 81[10916]; Seri M 82[10916]; Wichita[10916].

vrn-A1

Copy number variation for **vrn-A1** was detected in IL369 (2 copies)[10202], Malacca (2 copies) and Hereward (3 copies). Higher copy number was associated with later flowering or with increasing requirement for vernalization (i.e. longer exposure to cold is needed to achieve full vernalization)[10881].

A polymorphism between Jagger and 2174 was associated with ***vrn-A1a***. A point mutation was present in exon 4[10695]; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele[10695].

All accessions of *T. aestivum* ssp. *petropavlovsky* shared the ***Vrn-A1a*** sequence (*Vrn-A1L*) of Langdon (7,222 bp deletion 391-7,612 bp) and some other tetraploid wheat accessions[11668].

VRN-B1

Vrn-B1

ma: **Tsn1** – 14.8 cM – **Vrn-B1** – 0.7 cM – *Xwmc75-5B*[10880].

Vrn-B1a[1398] locus: 5BL[885]. 5B[885, 920, 921]; 5BL or 7BL[282, 635]. 5D[635] syn: Vrn2a = Vrn2[920, 921], Vrn2[1172], Vrn4[1173],Vrn2b = Vrn2[920, 921], Ss[2]

i: Ank-18[920, 921]; Triple Dirk B[1172]. **s**: Diamant 1*8/Mironovskaya 5A[920]; Diamant 1*8/Skorospelka 35 5A[920]; Rescue*/Cadet 5A **Vrn-A1** ***Vrn-D1a***[885]; Saratovskaya 29*8/Mironovskaya 808 5A[920]; Saratovskaya 29*8/Odesskaya 51 5A[920]. **v**: Bersee[557]; Brown Schlanstedt[1, 2, 1171, 1172]; Cadet[1221]; Festiguay[1172]; Magali; Mara[1611]; Milturum 321[885, 920]; Milturum 885[885, 920]; Noe[2]; Pyrothrix 28[920]; Spica[557]; *T. spelta* var. *duhamelianum* KT19-1[10057]; Ulyanovka 9[920]. **v2**: Borsum *Vrn1-A1a*[1]; Dala *Vrn1-A1a*[1]; Diamant 1 **Vrn1**[1, 920]; Gabo **Vrn4**[1172]; Halland ***Vrn-A1a***[1]; Harukikari ***Vrn-A1a***[883]; Rubin ***Vrn-A1a***[1]; Saratovskaya 29 ***Vrn-A1a***[920]; Shortandinka ***Vrn-A1a***[1221]; Triple Dirk ***Vrn-A1a***[1173]. **ma**: A dCAPS marker derived from *Xwg644-5B* was 1.7 cM from **Vrn-B1**[10006]; ***Vrn-B1a*** – 1.6 cM – *Xwg644-5B* – 2.5 cM – *Xgwm408-5B*[10004]; Closely linked to *Xgwm408-5B* in Diamant I*/Mironovskaya 808 5A//Bezostaya 1[10007]; A close association of **Vrn-B1** with *Xcdo1326-5B* was reported in [10057]. When mapped as a QTL **Vrn-B1** showed closest association with *Xgwm408-5B*[10007]. **c**: GenBank AY74603.1[10695].

All common wheat genotypes carrying ***Vrn-B1a*** studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk B, Bersee, Festiguay, Mara, Milturum, Noe, Spica)[10202].

Two variants of ***Vrn-B1a*** were distinguished in [920, 921]. Carriers of an earlier designated *Vrn2b* (characterized by Diamant 1*8/Skorospelka 35 5A) showed accelerated flowering after 15 and 30 days of vernalization, whereas carriers of *Vrn-2a,* (characterized by Ank-18 and Saratovskaya 29*8/Mironovskaya 808 5A) did not respond to these periods of vernalization. This distinction was not made in the above list.

Vrn-B1b[10695]

v: Alpowa[10695]; Ciano 67[10991]; Polo[10991]; Yaktana 54[10991]. **c**: GenBank FJ766015. Relative to ***Vrn-B1a*** (Triple Dirk B), *Vrn-b1b* has a G-C SNP at position 1656 and a 36 bp deletion at 1661-1696[10695].

Vrn-B1c[10880]

tv: *T. turgidum* ssp. *carthlicum* PI 94749[10880]. Much more common in durum cultivars from Russia and Ukraine than from Europe[11771]. **c**: GenBank JN817430 contains a 5,463 retrotransposon insertion in the 5' UTR region[10880].

Vrn-B1d[11520] syn: Vrn-B1c[11520]

v: Paragon and 24 others[11521]; Saratovskaya 29 and 5 others[11521]. **c**: Carries a 0.8 kb deletion and 0.4 kb duplication in intron 1 relative to **vrn-B1**[11520, 11521].

Vrn-B1e[11522] syn: Vrn-B1d[11522]

v: Hongchunmai[11522]. **c**: Differs from **vrn-B1** by 2 deletions, a SNP and TTTT to ACAA change in in intron 1[11522]; GenBank HQ130482[11523]; HQ593668[11521].

Vrn-B1f[11523]

v: Barta[11523]. **c**: Has a partially duplicated 837 bp sequence in intron 1[11523].

vrn-B1

c: GenBank AY747604.1[10695].

VRN-D1

Vrn-D1 [775, 883, 1172, 1398, 11072] locus: *Vrn3* [1172]. 5DL [775, 883]

Vrn-D1a, *Vrn-d1b* and **Vrn-D1** were present in 27.3, 20.6 and 52.1% of 689 Chinese wheat accessions [11072].

Vrn-D1a [1398]

i: Triple Dirk E [1172]. **s**: Rescue*/Cadet 5A ***Vrn-A1a*** [1221]. **v**: Chinese Spring [1172]; Loro [1172]; Norin 61 [460]; Shinchunaga [460]; Shirasagi Komugi [460]; Ushio Komugi [460]. **v2**: Rescue ***Vrn-B1a*** [1221].

All the common wheat genotypes carrying ***Vrn-D1a*** studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk E, Chinese Spring, Norin 61, Shinchunaga, Shirasagi Komugi, Ushio Komugi) [10202].

Vrn-D1b [11072]

v: Additional Chinese germplasm [11072]. A **Vrn-D1** variant named *Vrn-D1s* contained a 844 bp TE insertion in the first intron of the wild type *vrn-D1* allele [11628]. GenBank KF800714. Identified in three *T. spelta* and one *T. compactum* accessions; *T. aestivum* ssp. *spelta* PI 348700 [11628].

Stock: Genotype: Vernalization Respons
Triple Dirk, Kolben: ***Vrn-A1a Vrn-B1b Vrn-D1b***: No
Triple Dirk B, Festiguay: ***Vrn-A1b Vrn-B1a Vrn-D1b***: Yes Gabo ***Vrn-A1b Vrn-B1a Vrn-D1b***: Yes
Triple Dirk E, Chinese Spring:***Vrn-A1b Vrn-B1b Vrn-D1a***: Yes
Triple Dirk F, ***Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5a***: Yes
Triple Dirk C, ***Vrn-A1b Vrn-B1b Vrn-D1b*** *Vrn-D5b*: Yes, winter type.

ungrouped

Vrn-1 [1398]

Synonymous with *TaVRT-1* [10019]

Orthologous series in long arms of chromosomes of homoeologous group 5. VRN-1 is a MADS-box gene similar to Arabidopsis *APETALA1* [10014]. Spring types are associated with mutations in the promoter or the first intron [10014, 10198, 10202, 10288]. Reduction of VRN-1 transcripts in transgenic hexaploid spring wheat delays flowering [10300].

Vrn1 [10014]

Spring type.

dv: G2528 [10014].

vrn1 [10014]

Winter type.

dv: DV92 [10014]; G1777 [10014]; G3116 [10014]. **c**: **Vrn1** was completely linked to MADS-box genes *AP1* and *AGLG1*. *AP1* was considered a better candidate than *AGLG1* and differences between winter and spring genotypes appeared to be related to differences in the promoter region of *AP1* [10014]; The involvement of *AP1* in vernalization response conditioned by **Vrn-1** was also reported in ▸ [10019].

VRN-2

Vrn-2 [1398]

[1398]

Vrn-A2a [279]

Winter habit, dominant in diploid wheat [279].

dv: G1777 [279]; G3116 [279].

Vrn-A2b [279]

Spring habit, recessive in diploid wheat.

dv: DV92 [279]; PI 355517 [10299]; PI 345242 [10299]; PI 352475 [10299]; PI 277137 [10299].

Contains a non-functional mutation in the CCT domain [10299].

Vrn-A2c [10299]

Spring habit, recessive in diploid wheat.

dv: PI 352484[10299]; PI 323437[10299]; PI 286068[10299]; PI 591871[10299]; PI 542474[10299]; PI 428175[10299]; PI 237659[10299]; PI 221329[10299]; PI 225164[10299]; PI 377662[10299]; PI 377648[10299]; PI 362610[10299].

Vrn-B2 [11163] locus: 4BL [11163]

A study of winter wheats 2174 and Jagger showed that 2174 has a tandem repeat of **Vrn-B2** whereas Jagger has a deletion of this gene[11163]. Identical apparently functional sequences of **Vrn-B2** were found in contig sequences of Chinese Spring obtained from chromosomes 4BS, 2BS and 5DL[11163].

Vrn-D2 [11163] locus: 4DL [11163]

VRN-3

Vrn-A3 locus: 7AS

Vrn-B3 [10421] locus: 7BS [768, 769, 771] syn: Vrn-4B[279], Vrn5, eHi[769, 771, 779]

s: CS(Hope 7B) ***Vrn-D1a*** [768]. **v2**: Hope ***Vrn-A1a*** [1424]. **tv**: Very common in durum cultivars from Russia and Ukraine[11771]. **ma**: **Vrn-B3** is completely linked to *TaFT* and 1 cM distal to *Xabc158-7B* on the region of 7BS proximal to the translocation with homoeologous group 5[10421].

The dominant **Vrn-B3** allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165)[10421]. Transformation of winter wheat Jagger with the dominant **Vrn-B3** significantly accelerated flowering[10421]. Different Hope seed sources were heterogeneous for this insertion[10421]. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B)[10421].

vrn-B3

v: Chinese Spring **Vrn-D1** (GenBank DQ890162)[10421].

TaFT are associated with variation of earliness components in hexaploid wheat[10533].

Vrn-H3 [10421] syn: Sh3

ma: Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage[1316, 1455].

Vrn3 [1398] syn: Vrn3 [1398]

Orthologous series in chromosomes of homoeologous group 1 predicted from orthology with **Vrn-H3** (**Sh3**) in barley chromosome 1H[1316, 1455]. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization[773].

In both wheat and barley VRN-3 is completely linked with a flowering promoter gene homologous to Arabidopsis *FLOWERING LOCUS (FT)* [10421]. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat[10533].

VRN-4

Vrn-4 [279]

To date, only *Vrn-B4* has been detected.

This is now re-named **Vrn-B3**; not the VRN-4 (**Vrn4**) of the text above

Vrn-B4a [279] locus: 7BS syn: *Vrn5*,*eHi*

The distal region of 7BS was translocated with a chromosome segment with homoeology to the distal region of 5AL. It is not known if **Vrn-4** is located in the region homoeologous to 5L or 7S.

s: CS*/Hope 7B ***Vrn-D1a***,**v**: Hope ***Vrn-A1a***

Vrn4 [279] locus: 5DL [10004]. 5D [10002] syn: Vrn5[769, 771], Vrn-D5[10004]

i: Triple Dirk F[10711]. **v**: Common in *T. sphaerococcum* accessions[11123]. **bin**: Centromeric region. **v2**: CS (Hope 7B) *VrnD1a* [768]; Gabo ***Vrn-B1a*** [1172]; IL47/***Vrn-A1a*** [10005]. **ma**: *Xgdm3-5D* – 11.5 & 4.5 cM – **Vrn4**[10004]; Located in a 1.8 cM interval flanked by markers *Xcfd78-5D* and *Xbarc205-5D* [10711]. **c**: **Vrn4** is located in a translocated segment from chromosome 5A containing a modified copy of **Vrn-A1** [11123].

VRN-5

Vrn-D5a [10004] locus: 5D [10002]. 5DL [10004] syn: Vrn4 [1172], Vrn-D5 [10004]

i: Triple Dirk F [1172]. **v2**: Gabo ***Vrn-B1a*** [1172]; IL47 ***Vrn-A1a*** [10005]. **ma**: *Xgdm3-5D* – 11.5 & 4.5 cM – ***Vrn-D5a*** [10004].

Eight landraces with only ***Vrn-D5a*** were detected in ▸[10003]; others combined ***Vrn-D5a*** with other *Vrn* genes. Stelmakh [1424] doubted the existence of ***Vrn-D5a***. Goncharov [10108] confirmed the existence of ***Vrn-D5a*** but failed to confirm its location on chromosome 5D. References to additional studies are given in ▸[1424].

VIL

Three genes up-regulated by vernalization were cloned from *T. monococcum* [10531]. These were VIN3-like genes similar to Arabidopsis VIN3.

Vil-1 [10531]

GenBank DQ886919 [10531].

ma: *T. monococcum* chromosome $5A^m$ [10531].

Vil-2 [10531]

GenBank DQ886917 [10531].

ma: *T. monococcum* chromosome $6A^m$ [10531].

Vil-3 [10531]

GenBank DQ886918 [10531].

ma: *T. monococcum* chromosome $1A^m$ [10531]. A QTL analysis of Courtot/CS is reported in ▸[0132].

A QTL on chromosome 5BL was linked to *Xgwm604-5B* (this QTL explained 11% of the variance in flowering time) [10075]

Allelic variations at the **Vrn-1** and **Vrn-B3** loci in Chinese wheat cultivars are summarized in ▸[10617]. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization [773].

Stem-elongation in winter wheat: In regions where wheat is used as a dual purpose crop for grazing and grain production a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).

In a Jagger/2174 RIL population, QTL for stem elongation included *Qste.ocs-5A* (associated with the **Vrn-A1** locus), *Qste.ocs-1BL*, *Qste.ocs-2D* (associated with the **Ppd-D1** locus) and *Qste.ocs-6A* [1010]. In 2007 the respective R^2 values were 0.289, 0.155, 0.067 and 0.058. Jagger alleles on chromosome 5A, 1B and 6A promoted stem elongation whereas the allele on chromosome 2D had a delaying effect [10722].

1.68 Restorers for cytoplasmic male sterility

1.68.1 Restorers for *T. timopheevi* cytoplasm

RF1

Rf1 [823] locus: 1A [873, 1224, 1619]. 1AS [868]

v: L22 [868]; (*T. timopheevii*/*Aegilops squarrosa*)//3*Dirk [1619]. **v2**: *T. timopheevii*/3*Marquis **Rf2** [823]; R113 **Rf4** [873].

The second gene referred to as **Rf4** [1619] in the last stock was located in chromosome 7D, but its relationship to **Rf2** in ▸[823] was unknown.

RF2

Rf2 [823] locus: 7D [871]

v: *T. timopheevii*/3*Marquis **Rf1** [823].

RF3

Rf3[1453] locus: 1BS. 1B[1453]

v: R18[10222]; R9034[10222]; *T. spelta* var. *duhamelianum*[1453]. **v2**: Primepi **Rf7**[11476]. **ma**: *Xcdo388-1B* – 1.2 cM – *Xabc156-1B*[9934]; RFLP markers *Xcdo442-1B* and *Xbcd249-1B* were found to be associated with **Rf3** on 1BS[860]; Mapped as a QTL in the region *Xbarc207-1BS* – *Xgwm131-1BL* – *Xbarc61-1BL* in crosses R18/ND36 and R9034/ND36[10222]; *Xbarc128-1Bs* – 5.3 cM – *IWB14060* – 2.0 cM – **Rf3**/*IWB72107*/*IWB73447* – 14.5 cM – *Xwmc406-1B*[11476].

RF4

Rf4[1619] locus: 1BS[868]. 6B[873, 1619] syn: Rf2[1619]

v: L3[868]; (*T. timopheevii*/*Aegilops squarrosa*)/3*Canthatch **Rf5**[1619]; R113 **Rf1**[873].

RF5

Rf5[1619] locus: 6D[1619] syn: Rf3[1619]

v: (*T. timopheevii*/*Aegilops squarrosa*)/3*Canthatch **Rf4**[1619].

RF6

Rf6[859, 865] locus: 6BS [T6BL.6BS-6U][865]. 6AS [T6AL.6AS-6U][865]

tr: Line 2114[865]; Lines 040-5; 061-1[865]; 061-4[865].

Genes *Rfc3* in chromosome 6RL and *Rfc4* in chromosome 4RL were reported in ▶[225]. Novel *Rf* genes were identified on 5AL linked to *Xcdo786-5A* and *XksuH1-5A*[860].

RF7

Rf7[11473] locus: 5DS[11473] syn: Rf6[11473]

v2: Primepi **Rf3**[11474].

RF8

Rf8[11474] locus: 2DS[11474]

v: PWR4099[11474]. **ma**: *Xwmc503-2D* – 3.3 cM – **Rf8** – 5.8 cM – *Xgwm296-2D* – 0.9 cM – *Xwmc112-2D*[11474].

RF9

Rf9[11475] locus: 6AS[11475]

v: Gerek 79[11475]. **ma**: *IWB72413-6A* – 4.3 cM – **Rf9** – 4.7 cM – *IWB1550*-6A[11475].

Minor restorer effects were associated with *Xbarc330-5A* in R18 and *Xgdm130-7D* in R9034[10222]. The relationships of these QTL with previously located restorers in chromosomes 5A[860] and 7D (**Rf2**) are unknown.

Minor restorer effects were associated with *Xbarc330-5A* in R18 and *Xgdm130-7D* in R9034[10222]. The relationships of these QTL with previously located restorers in chromosomes 5A[860] and 7D (**Rf2**) are unknown.

1.68.2 Restorers for *Aegilops longissima* cytoplasm

Vi[867] locus: 1B[870]. 1BS[27]

v: *T. turgidum*[867].

Probably derived from a cv. Selkirk (*T. aestivum*) line with *Ae. cylindrica* cytoplasm[867].

1.68.3 Restorers for photoperiod-sensitive*Aegilops crassa* cytoplasm

Morai & Tsunewaki[1047] described photoperiod sensitive CMS caused by *Ae. crassa* cytoplasm in wheat cv. Norin 26. Almost complete sterility occurred when plants were grown in photoperiods of 15 h or longer.

Rfd1 [1047] locus: 7BL [1047]

v: Chinese Spring [1047].

A different system of restoration occurs in cv. Norin 61 where at least four chromosomes, 4A, 1D, 3D and 5D, appear to be involved [1046]. Several Japanese wheats carry a similar or equally effective gene combination [0335].

1.68.4 Restorers for temperature-sensitive*Aegilops kotchyi* cytoplasm

Two recessive genes for temperature-sensitive sterility as follows.

rfv_1^{sp} [11151] locus: 1BS [11151]

v2: MS line KTP116A *rfv_2* [11151]. **ma**: *Xgwm413-1B* – 8.9 cM – *rfv_1^{sp}* – 12 cM – *Xgwm11-1B* [11151].

rfv_2 [11151] locus: 2A [11151]

v: MS line KTP116A *rfv_1^{sp}* [11151]. **ma**: *Xwmc474-2A* – 23.9 cM – *rfv_2* – 13.7 cM – *Xwmc644-2A* [11151].

1.68.5 Restorers for multi-species cytoplasm

Restorer of *Ae. kotschyi*, *Ae. uniaristata* and *Ae. mutica* cytoplasmic male sterility.

Rf^{multi} [11477] locus: 1BS [11477]

v: All common wheat genotypes except *T. spelta* var. *duhamelianum* [11477]. **ma**: All common wheat genotypes except *T. spelta* var. *duhamelianum* [11477].

rf^{multi}

v: *T. spelta* var. *duhamelianum* [11477].

Sterility in the same plasmons is also found in lines with the 1BL.1RS translocation. Hohn & Lukaszewski [11478] produced a chromosome $1B_{1:6}$ translocation with a short rye insert replacing the **Rf^{multi}** region (**rf^{multi}** equivalent) causing partial sterility that can be restored by most common wheat genotypes.

1.69a Ribosomal RNA

The *5S-Rrna-1* loci were physically mapped in 1AS, 1BS, and 1DS and the *5S-Rrna-2* loci were physically mapped in 5AS, 5BS and 5DS of Chinese Spring using deletion lines [1043].

Table 1 in ▸[276] lists the chromosome or chromosome arm locations of rRNA loci in 12 Triticeae species.

1.69a.1 5S rRNA genes

Within the Triticeae there are basically two sets of 5S rRNA loci. One set, identified by repetitive units 320-468 bp in length, is located on group 1 chromosomes. The other set, identified by repetitive units 469-500 bp in length, is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

5S-RRNA-1

5S-Rrna-A1 locus: 1AS [295, 658] syn: 5SDna-A1 [295]

v: CS [1043].

5S-Rrna-B1 locus: 1BS [39, 295] syn: 5SDna-B1 [295]

dv: *T. monococcum*. **ma**: A PCR marker specific.

5S-Rrna-B1 was developed [9974].

5S-Rrna-D1 locus: 1DS [295]. 1D [295, 758] syn: 5SDna-D1 [295]

v: CS [295, 758]. **dv**: *Ae. tauschii* [758]. **ma**: A PCR marker specific for **5S-Rrna-D1** was developed in ▸[9974].

5S-Rrna-E1 locus: 1E [1290] syn: 5SDna-E1 [960]

dv: *L. elongatum*.

5S-Rrna-R1 locus: 1RS [39, 1206] syn: 5SDna-R1 [1206]

al: *S. cereale*. **ma**: A PCR marker specific for **5S-Rrna-R1** was developed in ▸[9974].

5S-Rrna-Sc1 locus: 1S^{c} [1290] syn: 5SDna-Sc1[960]

al: *Elymus ciliaris*.

5S-Rrna-S^{t}1 locus: 1S^{t} [1290] syn: 5SDna-S^{t}1[960]

al: *E. trachycaulus*.

5S-Rrna-Y1 locus: 1^{Y} [1290] syn: 5SDna-Y1[960]

al: *E. ciliaris*.

5S-RRNA-2

5S-Rrna-A2 locus: 5AS[295, 658] syn: 5SDna-A2[295]

v: CS[295]. **dv**: *T. monococcum*[295, 658].

5S-Rrna-B2 locus: 5BS[295] syn: 5SDna-B2[295]

v: CS.

5S-Rrna-D2 locus: 5DS[758]. 5D[295, 758] syn: 5SDna-D2[295]

v: CS[295, 758]. **dv**: *Ae. Tauschii*[758].

5S-Rrna-H^{t}2 locus: 5H^{t} [1290] syn: 5SDna-H^{t}2[960]

al: *E. trachycaulus*.

5S-Rrna-R2 locus: 5RS[1206] syn: 5SDna-R2[1206]

al: *S. cereale*.

5S-Rrna-U2 locus: 5U[295] syn: 5SDna-U2[295]

al: *Ae. umbellulata*.

5S-Rrna-V2 locus: 5V[1290] syn: 5SDna-V2[960]

al: *D. villosa*.

5S-RRNA-3

5S-Rrna-H3 locus: 2H[710]. 2HL[793] syn: 5SDNA-H3[793]

al: Betzes Barley; Sultan barley.

5S-RRNA-4

5S-Rrna-H4 locus: 3HL[793] syn: 5SDNA-H4[793]

al: Betzes barley; Sultan barley.

5S-RRNA-5

5S-Rrna-H5 locus: 4HL[793] syn: 5SDNA-H5[793]

al: Betzes barley; Sultan barley.

5S-RRNA-6

5S-Rrna-H6 locus: 4HS[793] syn: 5SDNA-H6[793]

al: Betzes barley; Sultan barley.

1.69b Segregation distortion

See also, Gametocidal Genes.

QSd.ksu-1D[9931] locus: 1DL[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704[9925]. **ma**: Association with *Xcmwg706-1D*[9931].

QSd.ksu-3D[9931] locus: 3DS[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc TA1704[9925]. **ma**: Association with *Xwg177-3D*[9931].

QSd.ksu-4D[9931] locus: 4DS[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704[9925]. **ma**: Association with *XksuF8-4D*[9931].

QSd.ksu-5D.1[9931] locus: 5D[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704[9925]. **ma**: Association with *Xcdo677-5D*[9931].

QSd.ksu-5D.2[9931] locus: 5DL[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704[9925]. **ma**: Association with *Xglk614-5D* (synonym '*Xtag614-5D*')[9931].

QSd.ksu-5D.3[9931] locus: 5DL[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704[9925]. **ma**: Association with *Xwg1026-5D*[9931].

QSd.ksu-7D[9931] locus: 7DS[9931]

dv: *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704[9925]. **ma**: Association with *Xglk439-7D* (synonym '*Xtag439-7D*')[9931].

1.70 Short roots

A 'very short root' phenotype was produced by heterozygous genotypes from selected crosses between Chinese Spring and certain synthetics. The **Vsr1** locus was localized to a 3.8 cM interval on chromosome 5DL[11014].

Vsr1[11014] locus: 5DL[11014]

ma: *Xwmc765-5D* – 7.7 cM – **Vsr1** – 1.1 cM – *Xbarc144-5D*[11014]; *Xwmc765-5D* – 1.9 cM – *XWL938* – 3.3 cM – *XWL2506* – 3.3 cM – **Vsr1** – 0.5 cM – *XWL954* – 0.5 cM – *Xbarc144-5D*[11014].

Vsr1a[11014]

v: Chinese Spring[11014].

Vsr1b[11014]

v: TA4152-71[11014].

1.71 Soft glumes

SOG was considered to be an homologue of TG1 and TG2. See Tenaceous glumes. The Soft Glume locus was not considered to be an orthologue of Tenacious Glumes[10769].

SOG

Sog[10555]

dv: *T. monococcum* ssp. *boeoticum* ID49[10555]; *T. monococcum* ssp. *aegilopoides*. TA4342-96[10769].

sog[10555] locus: 2AS[10555]

bin: C-2AS5-0.78. **dv**: *T. monococcum* ssp. *monococcum* var. *sinskajae* (syn. *aegilopoides*) UD69[10555]; Tm-9, a mutant of TA4342-96[10769]. **ma**: Co-segregation with AFLP loci *Xe4232041* and *Xe373311*[10555]; *Xgwm71-2A* – 3.3 cM – **sog** – 3.5 cM – *Xbcd120-2A*[10769].

1.72 Sterol esterification in kernels - Synthesis of b-sitosterol esters

Two sterol-ester phenotypes, p-L (palmitate + linoleate) and L (linoleate) are inherited as alleles at a single locus.

Pln[428] locus: 7DS[1476] syn: P-L[428]

v: Aradi[428]; Aragon 03[428].

pln[428] locus: L syn: L[428]

v: Mara[428]; Pane 247[428].

1.73 Stem solidness

Solid stem, caused by increased pith in normally hollow stem regions, is associated with resistance to wheat stem sawfly, *Cephus cinctus*. Solid stem confers resistance to wheat stem sawfly. See also Reaction to *Cephus* spp.

Qsf.spa-3B[10351]

tv: Kyle*2/Biodur (solid stem)//Kofa (hollow) DH population: *Qsf.spa-3BL* was located to a 21.3cM interval flanked by *Xgwm247-3B* and *Xgwm114-3B*[10351]. Mapped as a single gene, *Xgwm247-3B* – 6.9cM – *Qsf.spa-3B* – .4cM – *Xgwm114-3B*[10351]. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents[10351].

Qsst.msub-3BL locus: 3BL[10206]

bin: 3BL11-0.81-1.00. **v**: Fortuna[11230]; Genou[11230]; Judee[11230]; Rampart PI 59388[10206]; Rescue[11230]; S-615[11230]; Vida[11230]. **ma**: Linked to microsatellite markers *Xgwm247-3B*, *Xgwm340-3B*, and *Xgwm547-3B*. These markers explained 76% of the total variation for stem solidness in Rampart/Jerry[10206].

Haplotype analyses in a range of hexaploid and tetraploid accessions suggested the possibility of multiple alleles or loci in the QTL region[11230, 11239]. Conan with an intermediate level of stem solidness represents a different haplotype from other North American cultivars[11230].

Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines[10730].

Qsst.msub-3DL locus: 3DL[10395] syn: Qss.msub-3DL[10395]

Associated with *Xgwm645-3DL* (R^2=0.31), *Xwmc656-3DL* (R^2=0.1), and *Xcfd9-3DL* (R^2=0.13)[10395].

This gene acted as an enhancer of *Qsst.msub-3BL*[10395].

1.74 Temperature-sensitive winter variegation

This phenotype involves reduced vigour and chlorotic patches on leaves of certain genotypes in *Ae. umbellulata* cytoplasm when grown at low temperatures[1596].

Vgw locus: 5BL[1021] syn: Vg[1021]

Variegation is dominant[1596].

v: Bersee[1596]; Cappelle-Desprez[1596]; Hobbit Sib[1596]; Mara[1596].

vgw[1021]

v: Besostaya I[1596]; CS[1596]; Poros[1596]; Sava[1596]; *T. spelta*[1596].

1.75 Tenacious glumes

TG1

Tg1[1240] locus: 2DS[1240] syn: Tg[1240]

Derived from *Ae. tauschii*. Dominant.

bin: 2BS-3 1.00-0.84. **v**: Synthetic ABD wheats[652]. **ma**: Placed in a 12 cM interval between *Xwmc112-2D* and *Xbarc168-2D*[10497].

TG2

Tg2[0046] locus: 2BS

Derived from *T. dicoccoides* 2BS[0046].

v: TA 3419 = *Tetra Canthatch*/*Ae. tauschii* ssp. *meyeri* TA1599[10769]. **ma**: **Tg2** is associated with *Xrsq805(Embp)-2B* and *Xpsr899-2B*[0046]; *Xgwm261*/*Xwmc503-2D* – 2.3 cM – **Tg2** – 5.9 cM – *Xfba88*/*Xfbc400-2D*[10769].

Soft Glume locus is not an orthologue of Tenacious Glumes[10769].

A QTL analysis of the relationship of glume tenacity (*Gt*) with threshability (*Ft*) and the size of the glume base scar (**Gba**) after glume detachment in two crosses, viz. the ITMI population and CS*/CS (*Ae. tauschii* 2D), was undertaken[10497]. In the first cross *QFt.orst-2D.1* and *QGt.orst-2D.1* were closely associated with *Xgwm261-2D*, and *XFt.orst-2D.2* and *XGt.orst-2D* were associated with *Xgwm455-2D*, in the second population only the first pair along with *Xba.orst-2D* were detected; these appeared to correspond with **Tg1**[10497].

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1.76 Tiller inhibition / Tiller number

TIN1

Tin1 locus: 1A[10193]. 1AS[1212] syn: Tin[1212]

tin1[1212] locus: 1AS, 1A syn: Tin

Restricted tiller number is recessive[1212]

v: Israel Uniculm 494[1212]; Banks + *tin*[10193]; Oligoculm 390[10193]; Uniculm 492[10193]. **ma**: *Xpsp2999(Glu3)-1A* – 3.9 cM – **tin1**/*Xgwm136-1A* – 2.4 cM – *Xwhs179-1A*[10193]; the 350 bp allele of *Xgwm136-1A* was diagnostic of **tin1**[10193]. **c**: A candidate gene identified by map-based cloning was predicted to encode a cellulose synthase-like (Csl) protein with homology to members of the CslA clade; allelic variation was attributed to dinucleotide repeat-length polymorphism in the 5´UTR region of the *Csl* gene[11657].

A near recessive gene, *ftin*, was located proximal to the TIN1 locus in putative *Agropyron cristatum* derivative Pubing3558[11462]: *Xgwm136-1A* – 4.3 cM – *Xpsp2999-1A* – 0.7 cM – *Xcfa2153-1A* – 1.0 cM – *FTIN*[11462].

TIN2

TIN2 2A[9909].

Tin2

Tiller-reducing affect of this allele was dominant[9909].

tin2[1212] locus: 2A syn: Tin[9909]

v: 88 F2 185[9909].

TIN3

TIN3 $A^{m}L$[10329].

tin3[10329] locus: $3A^{m}L$

dv: *T. monococcum* TA4443 = TA4342-96 mutant[10329]. **ma**: *Xbcd131*/*Xbcd1431-3A* – 9.6 cM – **tin3**/*Xpsr1205-3A* – 4.7 cM – *Xcfa2076-3A*[10329].

TIN4

Tin4[11575] locus: 2DL[11574, 11575] syn: QLtn.sicau-2D[11574]

Low tillering.

i: H461/Chuannong 16 NIL7A[11575]. **v**: H461[11574, 11575].

tin4

High tillering.

i: H461/Chuannong 16 NIL7A[11575]. **v**: Chuannong 16[11574, 11575].

An EMS-derived, reduced tiller number mutant allele identified in YZ4110 was named *tn1*[11650]. The *TN1* allele in YZ4110 encoded a transmembrane ankyrin (ANK) repeat protein and the *TN1* locus was identified as *TraesCS6B02G013100* (CS REFSeq 1.0)[11650]. *Tn1* likely promoted tillering by inhibiting ABA biosynthesis and signalling[11650].

Three QTL were located on chromosomes 2DL (*Qltn.siau-2D*), 2BL and 5AL in a RIL population from H461 (low tillering)/CN16 (high tillering), but only the 2DL QTL was confirmed in H461/CM107 and H461/MM37 RIL populations[11465].

QTL

Fukuho-Komugi / Oligoculm: DH population: A QTL of large effect on spike number per plant in a DH population of mapping to the **Hg** – *Xpsp2999(Glu3)-1A* region[10218] probably corresponds to **Tin1**.

1.77 Uniculm stunt

Stunting is favoured by a combination of long days and low night temperatures[581]. Caused by duplicate recessive genes, *us1* and *us2*, located in chromosomes 4A and 5B, respectively[200]. Genotypes: Normal: v: *Us1 us2*: Alfa[581]; Jaral[581].

Normal: v: *us1 Us2*: Mabruk[581]. Stunted: v: *us1 us2*: Line 492[581].

1.78 Yield and yield components

1.78.1 Grain number per spike

QGnu.ipk-4A[0255] locus: 4AL[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Higher grain number was contributed by Opata[0255]. **ma**: Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A*[255].

QGnu.ipk-4A coincides with QTL for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*)[0255].

QKps.unl-3A.1[10044] locus: 3AS[10044]

v: Cheyenne/Cheyenne(Wichita 3A) RI mapping population[10044]; a higher kernel number of 0.3 kernels was contributed by Wichita and the QTL explained 15.5% of the phenotypic variation[10044]; The QTL coincided with QTLs for grain yield, kernel number per square metre and 1000-kernel weight[10044]. **ma**: Associated with *Xbarc12-3A*[10044].

Qkps.unl-3A.2[10044]

v: Cheyenne/Cheyenne(Wichita 3A) RI mapping population[10044]; a higher kernel number of 0.3 kernels was contributed by Cheyenne and the QTL explained 9.5% of the phenotypic variation[10044]. **ma**: Associated with *Xbcd141-3A*[10044].

Three QTL for kernel number per spike were assigned to chromosome 3A in RSLs from Cheyene*7/Wichita[0025].

1.78.2 Grain volume weight

QGvwt.unl-3A.1[10044] locus: 3A[10044]

v: Cheyenne/Cheyenne(Wichita 3A) RI mapping population[10044]; higher grain volume weight (+23 kg/hL) was contributed by Wichita and the QTL explained 43.1% of the phenotypic variataion[10044]; the QTL coincided with a QTL for spikes per square metre[10044]. **ma**: Associated with *Xbcd1380-3A*[10044].

1.78.3 Grain weight

1000-grain weight

QTL: Two QTLs for 1,000-kernel weight were assigned to chromosome 3A in RSLs from Cheyenne*7/Wichita 3A[0025]. QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL in a RIL population from RS111/CS[0236]. Eight QTLs for 1,000-kernel weight (54 % of the variation) were mapped in Forno/Oberkulmer spelt[0280].

TaCwi-A1[10812]

ma: *Xbarc15-2A* – 10.9 cM – **TaCwi-A1** – STS markers *Cwi21* and *Cwi22* – 17.6 cM – *Xgwm71-2AL*[10812].

TaCwi-A1 was cloned based on the rice *GIF1* gene encoding a cell wall invertase (GenBank accession EU095553), and STS markers *Cwi21* and *Cwi22* were developed from the polymorphisms between two allelic variants. On average, *TaCwi-A1a* had 1,000 grain weights 2.4 g higher than *TaCwi-A1b*[10812].

TaGW2-6A[10781]

ma: *Xcfd80-6AS.2* – 0.6 cM – *TaGW2-CAPS* – 0.5 cM – *Xbarc146-6A.1*/*Xwms132.4-6A*[10781].

QGw1.ccsu-1A[0165] locus: 1AS[0165]

Population: RS111/CS.

ma: Associated with *Xwmc333-1A*[0165].

QGwt.crc-3D[10287] locus: 3D[10287]

Population: RL4452/AC Domain.

ma: Flanked by *Xgwm341-3D* – *Xwmc552-3D* (LOD 4.3)[10287].

QGwt.crc-4A[10287] locus: 4A[10287]

Population: RL4452/AC Domain.

ma: Flanked by *Xgwm494-4A* – *Xgwm162-4A* (LOD 6.7)[10287].

QGwt.crc-6D[10287] locus: 6D[10287]

Population: RL4452/AC Domain.

ma: Flanked by *Xgwm325-6D* – *Xgwm55-6D* (LOD 3.9)[10287].

QTgw.ipk-5A[255, 0255] locus: 5AL[255]

Population: Opata/W-7984 (ITMI).

v: }; The higher yielding allele was contributed by W-7984[255]. **ma**: Associated with *Xfba351-5A* and *Xcdo1312-5A*[255].

QTkwt.unl-3A.1[10044] locus: 3AS[10044]

Population: Cheyenne/Cheyenne(Wichita 3A).

Higher kernel weight of 0.27% was contributed by Cheyenne and the QTL explained 12.7% of the phenotypic variation[10044]; The QTL coincided with QTLs for grain yield, kernel number per square metre and kernels per spike[10044].

ma: Associated with *Xbarc12-3A* and *Xtam55-3A*[10044].

50-grain weight

QFgw.ocs-4A.1[0047] locus: 4A[0047]

v: CS/CS(Kanto107 4A) mapping population[0047]. **ma**: Associated with *Xbcd265-4A* and *Xbcd1738-4A*[0047].

ungrouped

gw-A1

A TILLING mutation (mutant T4-2235; G2373A) in

tv: Kronos backcrossed to Kronos and. **v**: Paragon caused increased TGW, grain length and grain width; the increased grain size was attributed to larger carpel size[11690].

TaCKX6-D1[11407] locus: 3D[11407]

Encodes a cytokinin oxidase/dehydrogenase.

v: Hap a associated with high TKW has an 18 bp deletion relative to hap b: Wenmai 6, Yanzhan 1, Lumai 14[11407]; Hap b: Bainong 321, Chinese Spring, Hanxuan 10, Neixiang 188[11407]. **ma**: *Xcfd70-3D* – 3.7 cM – **TaCKX6-D1** – 2.0 cm – *Xwmc533-3D*[11407].

TaGW2-A1 locus: 6AS, a homolog of *OsGw2* [11690]

Based on its *OsGW2* orthologue in rice this gene was characterized and mapped as a CAPS marker in wheat[10781]. SNPs in the promoter region allowed distinction of two haplotypes. Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average Hap-6A-A had 1,000 grain weights more than 3g higher than Hap-6A-G[10781]. Encodes an E3 RING ligase[11122].

QTL

Cheyenne / Cheyenne(Wichita 3A): RI mapping population. *QTkwt.unl-3A.1*.

Cheyenne*7 / Wichita 3A: RSL population: Two QTL for 1,000-kernel weight were assigned to chromosome 3A[0025].

Forno / Oberkulmer spelt: Eight QTLs for 1,000-kernel weight accounted for 54% of the variatio) were mapped in [0280].

Opata / W-7984 (ITMI): RI mapping population. *QTgw.ipk-5A*.

RS111 / CS: mapping population. *QGw1.ccsu-1A*.

RS111 / CS: RIL population[0236]: QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL.

RL4452 / AC Domain. *QGwt.crc-3D*, *QGwt.crc-4A*, *QGwt.crc-6D*.

1.78.4 Test weight

QTwt.crc-1B[10287] locus: 1B[10287]

ma: Linked to *Xgwm374.1-1B* (LOD 3.9)[10287].

QTwt.crc-1D[10287] locus: 1D[10287]

ma: Linked to *Xgdm126-1D* (LOD 5.8)[10287].

QTwt.crc-2D[10287] locus: 2D[10287]

ma: Linked to *Xgwm349-2D* – *Xbarc59-2D* (LOD 5.2)[10287].

QTwt.crc-3B[10287] locus: 3B[10287]

ma: Linked to *Xwmc625-3B* – *Xbarc164-3B* (LOD 15.4)[10287].

QTwt.crc-3D[10287] locus: 3D[10287]

ma: Linked to *Xbarc71-3D* (LOD 5.2)[10287].

QTwt.crc-5D[10287] locus: 5D[10287]

ma: Linked to *Xgdm63-5D* – *Xwmc765-5D* (LOD 5.3)[10287].

In **RL4452 / AC Domain**[10287].

1.78.5 Grain weight/ear

In **Opata / W-7984 (ITMI)**: RI mapping population:

QGwe.ipk-2D[0255] locus: 2DS[0255]

Higher grain weight was contributed by Opata[0255].

ma: Associated with *Xcdo1379-2D* and *Xbcd1970-2D*[0255].

QGwe.ipk-4A [0255] locus: 4AL [0255]

Higher grain weight was contributed by Opata [0255].

ma: Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A* [0255].

QGwe.ipk-4A coincided with QTLs for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain number (*QGnu.ipk-4A*) [0255].

QGwe.ocs-4A.1 [0047] locus: 4AS [0047]

Population: CS/CS(Kanto107 4A).

ma: Associated with *Xbcd1738-4A* [0047].

QTL
CS / CS(Kanto107 4A): mapping population. *QGwe.ocs-4A.1*.

1.78.6 Grain yield

QGyld.unl-3A.1 [10044] locus: 3AS [10044]

Population: Cheyenne/Cheyenne(Wichita 3A).

Higher grain yield of 32 kg/ha was contributed by Wichita and the QTL explained 6.6% of the phenotypic variation [10044]; The QTL coincided with QTLs for kernel number per square metre, 1000-kernel weight and kernels per spike [10044];

QGyld.unl-3A.2 [10044] locus: 3A [10044]

Population: Cheyenne/Cheyenne(Wichita 3A).

Higher grain yield of 82 kg/ha was contributed by Wichita and the QTL explained 28.1% of the phenotypic variation [10044]; The QTL coincided with a QTL for kernel number per square metre [10044].

ma: Associated with *Xbarc67-3A* and *Xbcd366-3A* [10044].

QYld.crc-2A [10287] locus: 2A

Population: RL4452/AC Domain.

ma: Linked to *Xgwm339-2A* (LOD 3.0) [10287].

QYld.crc-2B [10287] locus: 2B

Population: RL4452/AC Domain.

ma: Linked to *Xgwm257-2B* (LOD 9.4) [10287].

QYld.crc-4A [10287] locus: 4A

Population: RL4452/AC Domain.

ma: Linked to *Xgwm130-4A* (LOD 4.4) [10287].

QYld.inra-7D [10071]

Population: Renan/Recital.

ma: *Xcdf69-7D* (R^2=3.7-15.7%) [10071].

QYld.ndsu-5B [10161] syn: QGy.ndsu-5B [10161]

Population: Langdon(DIC5B)/Langdon.

Higher yield contributed by contributed by Langdon [10161].

ma: Mapped to the *Xbcd1030-5B-Xgwm604-5B* interval [10161].

QYld.ocs-4A.1 [0047] locus: 4AS [0047]

Population: CS/CS(Kanto107 4A).

ma: Associated with *Xbcd1738-4A* [0047].

QTL
CS / CS(Kanto107 4A): mapping population: *QYld.ocs-4A.1*.

Cheyenne / Cheyenne(Wichita 3A): RI mapping population. *QGyld.unl-3A.1*, *QGyld.unl-3A.2*.

Renan / Recital: *QYld.inra-7D*.

RL4452 / AC Domain: *QYld.crc-2A*, *QYld.crc-2B*, *QYld.crc-4A*.

Shamrock / Shango: DH population: Non-glaucous (virescent) lines had higher yields than glaucous sibs[10543]; see Glaucousness, subsection Epistatic inhibitors of glaucousness. Tetrapoloid wheat

Langdon(DIC5B) / Langdon: *QYld.ndsu-5B*.

Dharwar Dry (drought tolerant) / Sitta: SSR locus *Xwmc89-4AL* was the most closely associated marker with a QTL for grain yield, grain fill rate, spike density, grains/m^2, biomass and drought susceptibility index covering a genetic distance of 7.7 cM[10488].

1.78.7 Kernel number per square metre

QKpsm.unl-3A.1[10044] locus: 3AS[10044]

Population: Cheyenne/Cheyenne(Wichita 3A).

Higher kernel number (170 kernels) was contributed by Wichita and the QTL explained 14.6% of the phenotypic variation[10044]; The QTL coincided with a QTL for grain yield[10044].

ma: Associated with *Xbarc12-3A*[10044].

QKpsm.unl-3A.2[10044] locus: 3A[10044]

Population: Cheyenne/Cheyenne(Wichita 3A).

ma: Associated with *Xbarc67-3A*[10044].

QTL
Cheyenne / Cheyenne(Wichita 3A): RI mapping population. *QKpsm.unl-3A.1*, *QKpsm.unl-3A.2*.

1.78.8a Spikelet number/spike

FUL2

Ful2[11384]

Loss of function mutation in gene *FUL-A2* (Kronos mutant T4-837) and *FUL-B2* (Kronos mutant T4-2911) resulted in significant increases in spikelet number[11384].

ungrouped

FT-A2 locus: *TraesCS3A02G143100*. 3AL[11605]

A natural mutation causing an aspartic acid (v: Pavon; tv: Kronos) to alanine (v: Chinese Spring; Berkut) change at position 10 (D10A) in **FT-A2** was associated with significant increases in SNS and grain number per spike with no negative effect on fertility[11605].

WAPO-A1 locus: *TraesCS7A02G481600* [11383]. 7AL[11383]

WAPO-A1 is the causal gene for *QSNS.ucw-7A*[11383] that also affects grain number per spike and spike yield[11603].

WAPO-A1a[11383]

Associated with low SNS; has a 115-bp promoter deletion and a D384N amino acid change[11383].

v: RAC875, Clark, Lancer, CDC Lanmark, Julius, Arina, Jagger, Cadenza, Robigus, and SY_Mattis[11383]. **tv**: Kronos, Ben[11383]. Most frequent allele in durum[11383].

WAPO-A1b[11383]

Associated with high SNS; has a C47F amino acid change and no promoter deletion[11383].

v: Berkut, Ning7840, PI 41025, MPV57, Platte[11383]. Most frequent allele in *T. aestivum*. **tv**: Rare in durum[11383].

WAPO-A1c[11383]

Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion[11383].

v: *T. dicoccoides* PI 471033 and PI 355455; *T. dicoccum* CItr 14135, PI 94638, and PI 298586; *T. durum* PI 286539[11383].

WAPO-A1d[11383]

Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion but differs from ***WAPO-A1c*** by a C667 and G764A DNA changes[11383].

tv: *T. durum* Rusty and Lang; *T. dicoccum* CItr14919, PI 193877, PI 193882, PI 217640, PI 221400, PI 225332, PI 273980, and PI 94657[11383].

QSns.sau-2DS[11424] locus: 2DS[11424]

v: RIL populations from Line 20828/Chuanong 16, Line 20828/Shumai 51 and Line 20828/Sy95-71; LOD score 3.47 – 38.24, PV 10 – 46% in 8 environments. Located in a 2 cM interval flanked by *Ax-109836946* (32.8 Mb) and *AX-111956072* (34.43 Mb)[11424].

QSns.ucw-7AL[11383] locus: 7AL[11383]

v: Underlying gene: *WAPO1*.

QSpn.ocs-4A.1[0047] locus: 4AS[0047]

Population: CS/CS(Kanto107 4A).

v:[0047]. **ma**: Associated with *Xbcd1738-4A*[0047].

Loss-of-function mutations in *FT2* increased spikelet number per spike but reduced but reduced fertility[11604].

Loss-of-function mutations of both homoeologs in *SVP1* (*TraesCS6A02G313800* and *TraesCS6B02G343900*) and *VRT2* (*TraesCS7A02G175200* and *TraesCS7B02G080300*) in tetraploid wheat increase number of spikelets per spike, delay heading time and reduce plant height[11607].

QTL
CS / CS(Kanto107 4A): mapping population: *QSpn.ocs-4A.1*.

1.78.8b Spike number per plant

QSn.sdau-4BL[10784]

Population: Line 05210/Laizhou 953.

ma: *Xwmc657-4B* – 4.6 cM – *QSn.sdau-4B* – 1.6 cM – *Xgwm495-4B*[10784].

QSn.sdau-4BL was resolved as a single gene in [10784]. It was associated with decreased spike length and grain number per spike.

QTL
Line 05210 / Laizhou 953: *QSn.sdau-4BL*.

1.78.9 Spikelet number per square metre

QTL
Cheyenne*7 / Wichita 3A: RSL: A QTL for spike number per square metre was assigned to chromosome 3A[0025].

1.78.10 Spike length

QEl.ipk-1B[0255] locus: 1BL[0255]

Population: Opata/W-7984.

Longer ear was contributed by Opata[0255].

ma: Associated with *Xbcd388-1B* and *Xwg605-1B*[0255].

QEl.ipk-4A[0255] locus: 4AL[0255]

Population: Opata/W-7984.

Longer ear was contributed by Opata[0255].

ma: Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A* [0255]. This QTL is likely to be a pleiotropic effect of the gene underlying the height QTL, *QHt.ipk-4A* [0255].

QEl.ipk-5A [0255] locus: 5AL [0255]

Population: Opata/W-7984.

Longer ear was contributed by W-7984 [0255].

ma: Associated with *Xmwg522-5A* [0255].

QTL
Courtot / Chinese Spring: Five QTL for spike length were detected in [0114] but only one on chromosome arm 5AL was consistent for at least two years.

Opata / W-7984: (ITMI) RI mapping population: *QEl.ipk-1B*, *QEl.ipk-4A*, *QEl.ipk-5A*.

1.78.11 Tiller number/plant

QTn.ocs-4A.1 [0047] locus: 4AS [0047]

Population: CS/CS(Kanto107 4A).

ma: Associated with *Xpsr163-4A* [0047].

QTL
CS / CS(Kanto107 4A): mapping population: *QTn.ocs-4A.1*.

1.79 Yellow berry tolerance

QTL
RS111 / CS: A QTL for yellow berry tolerance, contributed by RS111, was associated with *Xgwm190-5D* and *Xgwm174-5D* in a RIL population from [0237]. A tolerance QTL contributed by CS, the susceptible parent, was detected on 6B [0237].

2.1 Grain protein content

Thirteen QTLs for grain protein content were identified in a RI population from the cross WL711 (low protein content)/PH132 (high grain content)[10055]. The QTLs that were identified using more than one method or in more than one environment are listed below. Also listed is a QTL that was identified in the mean over the four environments and was therefore deemed important[10055]. QTLs for grain protein content were detected on chromosome arms 6AS (associated AFLP marker, *XE38M90v200v*) and 1BL (associated RFLP marker, *Xcdo1188*) in Courtot/Chinese Spring[0141].

GPC-1

Gpc-B1

Gpc-B1a syn: QGpc.ndsu-6Ba[623]

This allele, fixed in cultivated durum, is a non-functional frame-shift mutation[10438]. A similar non-functional allele, or a complete deletion of **GPC-B1**, is fixed in hexaploid wheat[10438].

Gpc-B1b[10296] locus: 6BS syn: QGpc.ndsu-6Bb[623, 10071], Gpc-6B1[10299], NAM-B1[10995]

i: Yecora Rojo NIL PI 638740[10138]. **v**: As II[10995]; Burnside[11044]; Diamant[10995]; Glencross[11044]; Glupro[10138]; Lilian[11044]; Prins[10995]; Somerset[11044]; Stanley[10995]; *T. spelta* Altgold[10995]. **tv**: *T. dicoccoides* FA-15[10138]. **ma**: Mapped to a 0.3 cM interval flanked by *Xucw79-6B* and *Xucw71-6B*[10229]; *Xcdo365-6B* – 1.5 cM – **Gpc-B1** – 1.2 cM – *Xucw67-6B* {10296. A high-throughput codominant marker, *Xuhw89-6B*, was then mapped less than 0.1 cM from **Gpc-B1**[10297].

Gpc-B1b, the functional allele[10438] in *T. dicoccoides*, affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity[10298]. **Gpc-B1** is a NAC transcription factor designated **Nam-B1**[10438]. A paralogous copy of this gene is present in homologous group 2 (*Nam2*).

This allele was relatively frequent in Scandinavian and Finnish common wheats, landraces and spelts[10995].

ungrouped

Pro1[777] locus: 5DL[777]

s: CS*6/Hope 5D[777].

May be identical to **VRN-D1**.

Pro2[777] locus: 5DL[777]

s: CS*6/Hope 5D[777].

QGpc.ccsu-2B.1[10055] locus: 2BL[10055]

v: WL711/PH132 RI mapping population[10055]; higher protein content was contributed by PH132 and the QTL explained 13.4% of the phenotypic variation[10055]. **ma**: Associated with *Xgwm1249-2B*[10055].

QGpc.ccsu-2D.1[10055, 0015] locus: 2DL[10055, 0015]

v: WL711/PH132 RI mapping population[10055, 0015]; higher protein was contributed by PH132 and the QTL explained 19%[0015] and 14%[10055] of the phenotypic variation. **ma**: Associated with *Xgwm1264-2D*[10055].

QGpc.ccsu-3D.1[10055] locus: 3DS[10055]

v: WL711/PH132 RI mapping population[10055]; higher protein content was contributed by PH132 and the QTL explained 16.3% of the phenotypic variation[10055]. **ma**: Associated with *Xgwm456-3D*[10055].

QGpc.ccsu-3D.2[10055] locus: 3DS[10055]

v: WL711/PH132 RI mapping population[10055]; higher protein content was contributed by PH132 and the QTL explained 14% of the phenotypic variation[10055]. **ma**: Associated with *Xgwm892-3D*[10055].

QGpc.ccsu-7A.1[10055] locus: 7AS[10055]

v: WL711/PH132 RI mapping population[10055]; higher protein content was contributed by PH132 and the QTL explained 32.4% of the phenotypic variation[10055]. **ma**: Associated with *Xgwm1171-7A*[10055].

QGpc.ndsu-5B.1[10161] locus: 5B[10161]

v: LDN (DIC5B)/LDN, contributed by DIC5B[10161]. **ma**: Nearest marker, *Xgwm604-5B*[10161].

QGpc.ndsu-5B.2 [10161] locus: 5B [10161]

v: LDN (DIC5B)/LDN, contributed by DIC5B [10161]. **ma**: Nearest marker, *Xabc310-5B* [10161].

QGpc.ndsu-5B.3 [10161] locus: 5B [10161]

v: LDN (DIC5B)/LDN, contributed by DIC5B [10161]. **ma**: Nearest marker, *Xwg909-5B* [10161].

QPro.inra-2A [10071] locus: 2A [10071]

v: Renan/Recital [10071]. **ma**: *XksuD18-2A* – *Xgwm614-2A* (R^2 = 4.4-8.9%) [10071].

QPro.inra-3A [10071] locus: 3A [10071]

v: Renan/Recital [10071]. **ma**: *Xcfd79-3A* – *Xfbb250-3A* (R^2 = 4.1-8.3%) [10071].

QPro.inra-4D [10071] locus: 4D [10071]

v: Renan/Recital [10071]. **ma**: Linked to *Xcfd71-4D* (R^2 = 4.6-10.3%) [10071].

QPro.inra-7D [10071] locus: 7D [10071]

v: Renan/Recital [10071]. **ma**: *Xcfd69-7D* – **Pch1** (R^2=6.4-10.4%) [10071].

QPro.mgb-4B

Associated with **Gai1** and *Xpsr622-4B* [110 2].

QPro.mgb-5A

Associated with *Xpsr911-5A* [110 2] and *Xcdo412-5A* [0343 *].

QPro.mgb-6A.1

Associated with *Xpsr167-6A* and *XksuG8-6A* [110 2].

QPro.mgb-6A.2

Associated with *Xmgb56-6A* [110 2] and *Xpsr627-6A* [0343 *].

QPro.mgb-6B

Associated with *Gli-B2-6B* [110 2] and *Nor-2* [0343 *].

ma: *QGpc.ndsu-6B* was associated (LOD score =18.9) with the interval *Xmwg79-6B* – *Xabg387-6B*. These loci were mapped in 6BS: *Xmwg79-6B* – 5.9 cM – *Xabg387-6B* – 9.0 cM – centromere [623].

QPro.mgb-7A

Associated at P<=0.01 with **Pan2** [0343 *].

QPro.mgb-7B

Associated with *Xpsr490(Ss1)-7B*, **Pc** [110 2] and *Xutv913-7B* [0343 *].

QTL

Forno / Oberkulmer spelt: Nine QTLs (51% of the variation) were mapped in cross [0280]. **Cheyenne (high quality wheat) / CS (low quality wheat):** RSL population: A QTL for grain and flour protein content, contributed by CS, was associated with *XTri-1D*/Centromere [0251].

Renan / Recital: Four QTL conferring grain protein content [10071]; only QTL stable over at least 4 of 6 locations were presented. Renan contributed the four alleles for high grain protein content. **Ning 7840 / Clark:** RIL population: QTL from Ning 7840 were detected on chromosomes 3AS (*Xwmc749-3AS* – *Xgwm369-3AS*; R^2= 0.09-0.11) and 4B (*Xgwm368-4B* – *Xwmc617-4B*, R^2= 0.08-0.11) [10702].

Tetraploid wheat

T. dicoccoides / **Latino:** In line 3BIL-85 high grain protein was detected in chromosomes 2AS (associated with *Xcfa2164-2A*, R^2= 17%), 6AS (*Xp39M37* 250-6A, R^2= 17%) and 7BL (*Xgwm577-7B*, R^2= 9%) [10338]

2.2 Enzymes

2.2.1 Acid phosphatase

ACPH-1

Acph-A1[504] locus: 4AS[504, 516] syn: Acph-B1[936], Acph3[516], Acph2[516]

v: CS.

Acph-B1[504] locus: 4BL[504, 516] syn: Acph8[516], Acph4[516], Acph-A1[936]

v: CS.

Acph-D1[504] locus: 4DL[504, 516] syn: Acph5[516], Acph6[516]

v: CS.

Acph-H1[1153] locus: 4H[1153]

ad: CS/Betzes.

Acph-M^{v}1[237] locus: 4M^{v} [237] syn: Acph-M^{v}1[985], Aph-v[237]

tr: H-93-33[984].

Acph-R1 locus: 7R[1457]. 7RS[506]

ad: CS/Imperial.

Acph-S^{s}1[1140] locus: 4S^{s} [1140]

ad: CS/*T. searsii*.

ACPH-2

Acph-D2[10309, 10407] locus: 2DL[10309] syn: Acph1[10309]

dv: **Acph-D2**$_{100}$ and **Acph-D2**$_{95}$ alleles distinguished accessions of *Ae. tauschii* ssp. *tauschii* and *strangulata*, respectively[1030]. **tv**: *Ae. tauschii*[10407]. **ma**: Cent … **Acph-D2** – 4 cM – *Xgwm157-2D*[10309].

2.2.2 Alcohol dehydrogenase (Aliphatic)

ADH-1

Adh-A1[502] locus: 4A[502]. 4AL[504, 516] syn: Adh-B1[504], Adh$_{B}$[502]

v: CS.

Adh-Ag^{i}1[374, 560] locus: 4Ag^{i} [560] syn: Adh-X1[361]

ad: Vilmorin 27/*Th. intermedium*; Caribo/*Th. intermedium*.

Adh-B1[501, 502] locus: 4B[502]. 4BS[504, 516] syn: Adh$_{1}$[501], Adh$_{A}$[502], Adh-A1[504]

v: CS.

Adh-B1a[1442] syn: Adh$_{11}$[501], Adh-A1a[1442]

v: CS. **tv**: PI 226951[501]; Malavika[1442].

Adh-B1b[1442] syn: Adh$_{12}$[501], Adh-A1b[1442]

v: Rageni derivative[1443]. **tv**: CI 4013[501]; Bijaga Yellow[1442].

Adh-B1b was the only variant ADH-1 allele detected in study of a large number of *T. aestivum* and *T. turgidum* accessions[503].

Adh-C1[1278] syn: G[1278]

ad: *T. aestivum* cv. Alcedo/*Ae. caudata* line G.

Adh-D1[504] locus: 4D[502]. 4DS[504, 516] syn: Adh_D[502]

v: CS. **ma**: **Adh-D1** [**Adh1**, *Adh2*] was mapped 4 cM distal to *Xpsr163-4D* and closely proximal to *Xcsiha114-4D.1*. [*XcsIHA114-1a*']][757].

Adh-E1[518] locus: 4ES[518]

ad: CS/*E. elongata*.

Adh-H1[520] locus: 4H

ad: CS/Betzes

Adh-M^{v}1[984] locus: 4M^{v} [984] syn: ADHmu[984], Adh-M^{v}1[985]

v: H-93-33.

Adh-R1[1457] locus: 4R[582, 1457]. 4RS[506] syn: AdhR2[582]

ad: CS/Imperial[506, 1457]; FEC28/Petkus[43]; Holdfast/King II[582].

Adh-V1[242, 1026] locus: 4V[1026]

ad: CS/*D. villosum*.

ADHG-H1[520] locus: 4H[520]

ad: CS/Betzes.

Three *Adh* genes were identified in *Hordeum vulgare* and *H. spontaneum*[144, 490, 493, 520]. Two of these were tightly linked at the **Adh-H1** locus[144]. The third gene was tentatively located in 5H[490].

A low-level of aliphatic alcohol dehydrogenase activity is commonly observed on zymograms in the absence of added substrate[513]; this may account for the observation of wheat lactate dehydrogenase that was reported in [1465].

The gene series formerly designated *Adh-2* and *Adh-3* appear under Aromatic Alcohol Dehydrogenase

2.2.3 Aminopeptidase

AMP-1

Amp-A1[504] locus: 6AS[504, 516]

v: CS.

Amp-A1a

v: CS[1533].

Amp-A1b

v: Vitka[1533].

Amp-Ag^{e}1[1575] locus: 6Ag^{e} [1575]

su: Rescue/*Th. elongatum*.

Amp-Ag^{i}1[703] locus: 6Ag^{i} [703]

ad: Vilmorin 27/*Th. intermedium*.

Amp-B1[504] locus: 6BS[504, 516]

v: CS.

Amp-B1a

v: CS[1533].

Amp-B1b

v: Iskra[1533].

Amp-B1c[703, 1244] locus: Null allele

v: *T. spelta* IPSR 1220017[703]; Sinvalocho M.A[1244].

Amp-C1[1278] locus: 6D[1278]

ad: Alcedo/*Ae. caudata* line D.

Amp-D1[504] locus: 6DS[504, 516]

v: CS.

Amp-D1a[703]

v: CS.

Amp-D1b[703]

v: Sears' Synthetic IPSR1190903.

Amp-E1[518] locus: 6E[518]

ad: CS/*E. elongata*.

Amp-H1[520] locus: 6H[520]

ad: CS/Betzes.

AMPp-R1[1457] locus: 6R[1280, 1457]

ad: CS/Imperial[1457]; Holdfast/King II[1280].

AMP-2

Amp-A2[703] locus: 4AL[703]

v: CS.

Amp-A2a[703]

v: CS.

Amp-A2b[703]

v: *T. spelta* IPSR 1220017.

Amp-Ag^{i}2[703] locus: 4Ag^{i}[703]

ad: Vilmorin27/*Th. intermedium*.

Amp-B2[703] locus: 4BS[703]

v: CS.

Amp-B2a[703]

v: CS.

Amp-B2b[703]

v: Timstein.

Amp-B2c[703]

v: Hope.

Amp-D2[703] locus: 4DS[703]

v: CS.

Amp-D2a[703]

v: CS.

Amp-D2b[703]

v: Sears' Synthetic IPSR 1190903.

Amp-D2c[703]

v: Bersee.

Amp-E2[703] locus: 4E[703]

ad: CS/*E. elongata*.

Amp-H2[703] locus: 4H[703]

ad: CS/Betzes.

Amp-H^{ch}2[703] locus: 4H^{ch} [703]

ad: CS/*H. chilense*.

Amp-J2[703] locus: 4J[703]

ad: CS/*Th. junceum*.

Amp-M^{v}2[235] locus: 4M^{v} [235]

su: H-93-33[235].

Amp-R2[703] locus: 4RS[93, 702]. 4R[703]

ad: CS/Imperial.

Amp-S^{l}2[703] locus: 4S^{l}L[703]

ad: CS/*Ae. sharonensis*[180]. **tr**: 4DS.4DL-4S^{l}L[660].

Amp-V2[703] locus: 4V[703]

ad: CS/*D. villosum*.

AMP-3

Amp-A3[703] locus: 7AS[703]

v: CS.

Amp-A3a[703]

v: CS.

Amp-A3b[703]

v: Timstein.

Amp-H3[703] locus: 7H[703]

ad: CS/Betzes.

2.2.4 Alpha-amylase

α-AMY-1

a-Amy-A1[7, 7] locus: 6AL[412, 1082] syn: Amy6$_A$[1082]

v: CS.

a-Amy-A1a[7, 7] syn: Amy 6A1[1084]

v: CS.

a-Amy-A1b^{5}[7, 7]

v: Bezostaya 1; Kavkaz.

a-Amy-A1c^{5} syn: Amy 6A1^{m} [1084]

v: Aka.

a-Amy-Ag^{i}1[374] locus: 6Ag^{i} [374]

ad: Vilmorin 27/*Th. intermedium*.

a-Amy-B1[7] locus: 6BL syn: Amy6B

v: CS

a-Amy-B1a[7, 7] syn: Amy 4[1084], Amy 6B2^{o} [1084], Amy 6B1[1084]

v: CS[7]; Rare.

a-Amy-B1b[7, 7] syn: Amy 4^{m} [1084], Amy 6B1^{o} [1084], Amy 6B2[1084]

v: Mara[7].

a-Amy-B1c[7, 7] syn: Amy 6B1[1084], Amy 6B2[1084], Amy 4[1084]

v: Sava[7]; Rare.

a-Amy-B1d[7, 7] syn: Amy 4^{m} [1084], Amy6B2^{o} [1084], Amy 6B1^{o} [1084]

v: Sicco[7]; Rare.

a-Amy-B1e[7, 7] syn: Amy 6B2^{o} [1084], Amy 6B1$^{4'}$ [1084], Amy 4^{m} [1084], Amy 6B1$^{4'}$

v: Cappelle-Desprez[7].

a-Amy-B1f[7, 7] syn: Amy 6B1^{4} [1084], Amy 6B2^{o} [1084], Amy4^{m} [1084]

v: Sappo[7].

a-Amy-B1g[7, 7] syn: Amy 4[1084], Amy 6B2^{o} [1084], Amy 6B1^{4} [1084]

v: Cheyenne[7].

a-Amy-B1h[7, 7] syn: Amy 6B2^{o} [1084], Amy 6B1^{o} [1084], Amy 4[1084]

v: *T. macha* Line 1[7]; Rare.

a-Amy-D1[7, 7] locus: 6DL[412, 1082] syn: Amy6D[1082]

v: CS.

a-Amy-D1a[7, 7] syn: Amy6D1[1084], Amy 6D2[1084]

v: CS.

a-Amy-D1b[7, 7] syn: Amy 6D2[1084], Amy6D1[1084]

v: Prelude[1082]; Cappelle-Desprez[7].

a-Amy-D1c syn: Amy6D1^{m} [1084], Amy 6D2[1084]

v: *T. spelta* var. *duhamelianum*.

a-Amy-E1[13] locus: 6E[13]

ad: CS/*E. elongata*.

a-Amy-H1 locus: 6H {146, 1 051} syn: a-Amy1[146]

ad: CS/Betzes.

a-Amy-R1[13] locus: 6RL[13]

ad, su: CS/Imperial; CS/King II; Holdfast/King II.

a-Amy-R^{m}1[13] locus: 6R^{m}L[13]

ad: CS/*S. montanum*.

a-Amy-S1[598] locus: 6SS[598]

v: Wembley derivative 31. **al**: *Ae. speltoides*.

a-Amy1[1083, 1084] locus: 6BL syn: Amy 6B2,Amy-B2

v: CS

a-Amy1a[1083] syn: a-Amy-B1a

v: CS.

a-Amy1b[1083] syn: a-Amy-B1b

v: CS.

a-Amy1c [1083] syn: a-Amy-B4

tv: *T. durum* ssp. *georgicum*.

α-AMY-2

a-Amy-A2 [7, 7] locus: 7AL [412, 1082] syn: Amy_{7A} [1082]

v: CS

a-Amy-Ag^{i}2 [374] locus: 7Ag^{i} [374]

ad: Vilmorin 27/*Th. intermedium*.

a-Amy-B2 [7, 7] locus: 7BL [412, 1082] syn: Amy_{7B} [1082]

v: CS; CS.

a-Amy-B2a [412] syn: Amy 7B 1 [1084], Amy 7B2 [1084]

v: CS.

a-Amy-B2b [412] syn: Amy 7B1 [1084], Amy 7B2^{m} [1084]

v: Hope.

The alternative states of ***Amy 7B2***, namely, ***Amy 7B2*** and ***Amy 7B2***^{m} [1084], are identical to the variation in band 2 [412]. The complete description of the **a-Amy-B2** variation also includes variation in band 11 [412].

a-Amy-D2 locus: 7DL [412, 1082] syn: Amy_{7D} [1082]

v: CS.

a-Amy-D2a [412] syn: Amy 7D1 [1084]

v: CS.

a-Amy-D2b [417] syn: Amy 7D1^{o} [1084]

v: Largo [7]; Sears' Synthetic [7]; VPM1 [417].

It was estimated [902] that there are two *a-Amy-1* genes in chromosome 6A and five or six in both 6B and 6D, and three or four *a-Amy-2* genes at each of the 7A, 7B, and 7D loci.

a-Amy-E2 [13] locus: 7EL [13]

ad: CS/*E. elongata*.

a-Amy-H2 locus: 7HL [146, 793, 1051] syn: a-Amy2 [146]

ad: CS/Betzes.

a-Amy-H^{ch}2 [1015] locus: 7H^{ch}beta [1015]

ad, su: CS/*H. chilense*.

a-Amy-R2 [13] locus: 7RL [13]

ad, su: CS/Imperial; CS/King II; Holdfast/King II.

a-Amy-S^{b}2 [13] locus: 7S^{b} [13]

ad: Holdfast/*Ae. bicornis*.

a-Amy-U2 [13] locus: 7U [13]

ad: CS/*Ae. umbellulata*.

2.2.5 Beta-amylase

β-AMY-1

b-Amy-A1 [8, 8, 227] locus: 5AL [8, 227] syn: b-Amy-A2 [8], b-Amy-B1 [1331]

v: CS [8]. **s**: CS/Federation [227].

b-Amy-A1a[8, 8] syn: b-Amy-A2a[8], b-B1a[936]

v: CS.

b-Amy-A1b[8, 8] syn: b-B1b[936], b-Amy-A2b[8]

v: Koga II.

b-Amy-A1c[8, 8] syn: b-B1c[936], b-Amy-A2c[8]

v: *T. macha* IPSR 1240005.

b-Amy-A1d[8, 8] syn: b-Amy-A2d[8], b-B1d[936]

v: Holdfast.

b-Amy-A1e[8, 8] locus: *[b-Amy-A2e* [8], *b-B1e* [936]] syn: b-Amy-A2e,b-B1e

v: Bezostaya I.

b-Amy-Ag^{i}1[13, 168] locus: 4Ag^{i} [168]

ad: Vilmorin27/*Th. intermedium*.

b-Amy-B1[628] locus: 4BL {628,[8] syn: b-Amy-A1[8]

v: CS.

b-Amy-B1a[1330] syn: b-Amy-A1a[1330]},[8], b-Amy-A1a

v: CS.

b-Amy-B1b[1330] syn: b-Amy-A1b[8, 1330]

v: Sears' Synthetic IPSR 1190903.

b-Amy-B1c[1330] syn: b-Amy-A1c[1330], b-Amy-A1b[8]

v: Ciano 67.

b-Amy-B1d[1330] syn: b-Amy-A1c[400, 1330]

v: Manella.

b-Amy-C1[1278] locus: *B* [1278]

ad: *Aestivum* cv. Alcedo/*Ae. caudata* line B.

b-Amy-D1[8, 8] locus: 4DL[8, 628]

v: CS.

b-Amy-D1a[8, 8]

v: CS.

b-Amy-D1b[8, 8]

v: Bersee.

b-Amy-D1c[8, 8]

v: Sears' Synthetic. Rare.

Previously listed alleles *b-Amy-D1d* and-*D1e* were found to be **b-Amy-B1** alleles[400]. Two *b-Amy-D*^{t}1 alleles were predominant in 60 accessions of *T. tauschii* [1578].

b-Amy-E^{b}1[661] locus: 5E^{b}L[661]

tr: 5AS.5E^{b}L.

b-Amy-H1 locus: 4H[1153]

ad: CS/Betzes.

b-Amy-H^{ch}1[13] locus: 4H^{ch} [13]

ad: CS/*H. chilense*.

b-Amy-R1 locus: 5R[103, 1280]. 5RL[43] syn: b-AmyR1[43], b-Amy-R2[13]

ad: FEC 28/Petkus[43]; Holdfast/King II[43, 1280]. **tr**: CS/Imperial 5BL-5RL[43].

b-Amy-S^{l}1[13] locus: *D* [13]. 4S^{l} [13]

ad: CS/*Ae. sharonensis* D[13]. **su**: CS/*Ae. sharonensis*. **ad**: CS/*Ae. longissima*.

b-Amy-U1[13] locus: 5U[13] syn: b-Amy-U2[13]

su: CS/*Ae. umbellulata*.

2.2.6 Endopeptidase

EP-1

Ep-A1[516] locus: 7AL[516]

v: CS.

Ep-A1a[516, 708]

v: CS.

An EP isozyme encoded by ***Ep-A1a*** of CS is visible on zymograms following starch gel electrophoresis[516]. The product of this allele is not observable, however, on zymograms following isoelectric focusing[708].

Ep-A1b[708]

v: Cappelle-Desprez[708]; Hobbit[704]; Rendezvous[1603].

Ep-A1c[708]

v: Sears' Synthetic.

Ep-A1d[894] locus: Isozyme 6

v: PI 294994[894].

Ep-B1[516] locus: 7BL[516] syn: Ep1[516]

v: CS.

Ep-B1a[708]

v: CS.

Ep-B1b[708]

v: Cappelle-Desprez.

Ep-B1c[708]

v: Ciano 67.

Ep-B1d[708]

v: Bersee.

Ep-B1e[708]

v: Sears' Synthetic.

Ep-D1[516] locus: 7DL[516]

v: CS.

Ep-D1a[708]

v: CS.

Ep-D1b syn: EP-V1[973]

v: 5L 219[1521]; H-93-70[1521]; Hyak[21]; Madsen[20]; Rendezvous[708]; VPM1[973].

Assuming that **Ep-D1** encoded an oligopeptidase G, comparative genetics were applied to develop a STS marker for identifying resistance gene **Pch1**[10513] (see Reaction to *Tapesia yallundae*.

Ep-D1c[708]

v: Sears' Synthetic.

Ep-D1d[1587] locus: Null allele

v: Wheats with **Lr19**[1587].

Ep-D1e[894] locus: Isozyme 5

v: PI 294994[894].

Ep-E1[518] locus: 7EL[518]

al: CS/*E. elongata*.

Ep-H1[520] locus: 7HL[520]

al: CS/Betzes.

Ep-H^{ch}1[708] locus: 7H^{ch} [708]

su: CS/*H. chilense*.

Ep-H^{t}1[1037] locus: 7H^{t}S[1037]

ad: CS/*E. trachycaulus*.

Ep-M^{v}1[985] locus: 7M^{v}L syn: Ep-M^{v}1[985]

su: 7M^{v}.

Ep-R1[92, 266, 708] locus: 6RL[92]

ad: CS/Imperial.

Ep-S^{b}1[708] locus: 7S^{b} [708]

su: Holdfast/*Ae. bicornis*.

Ep-S^{l}1[517] locus: 4S^{l} [517]

ad: CS/*Ae. longissima*.

Ep-S^{s}1[1140] locus: 7S^{s} [1140]

ad: CS/*T. searsii*.

Ep-U1[708] locus: 7U[708]

su: CS/*Ae. umbellulata*.

Ep-V1[708] locus: 7V[708]

ad: CS/*D. villosum*.

EP-2

Ep-B2[599] locus: 6BS[599]

An *Ep* locus was located in 4RS in King II[1280], using Holdfast/King II addition lines and in 4R in Imperial[266] using Chinese Spring/Imperial addition lines.

2.2.7 Esterase

Genetic control of esterases [carboxylic ester hydrolases (E.C.3.1.1.1)] was the subject of a comparative study[814].

EST-2, EST-5 and EST-8 are controlled by genes on 3L and where a recombination test was possible between **EST-D5** and **EST-D8**, no segregation was observed. The different gene symbols were retained because of the different tissue specificities and polymerisation profiles of the enzymes. The same arguments surround the EST-1 and EST-6 genes located in the 3S arms[814].

The EST-6 gene of rye was mapped[249]. The EST-6 genes of wheat were mapped comparatively in the proximal regions of chromosomes 2S[256]. The EST-2, EST-5 and EST-8 were mapped to the extreme distal regions in the 3L arms[247].

EST-1

EST-1 is a dimeric enzyme that electrofocuses around pH4.0 and is expressed in all tissues except endosperm[814].

Est-A1 locus: 3AS[60] syn: Est_A[61]

v: CS.

Est-B1 locus: 3BS[100]. 3B[60] syn: Est_B[61]

v: CS.

Est-D1 locus: 3D[60]. 3DS[100] syn: Est_D[61]

v: CS.

Each of 208 hexaploid accessions carried the same Est-1 allele except accessions of *T. compactum* var. *rubriceps*, each of which carried an **Est-B1** or **Est-D1** electrophoretic mobility variant[585].

Est-E1[518] locus: 3ES[518]

ad: CS/*E. elongata*.

Est-H1[814] locus: 3H[814]

ad: CS/Betzes.

Est-R1 locus: 3R[60, 1254] syn: Est_R[61]

ad: CS/Imperial[60]; Holdfast/King II[100]; Kharkov/Dakold[100].

Est-S^{1}1[814] locus: 3S^1 [814]

ad: CS/*Ae. longissima*.

EST-2

EST-2 is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.

Est-A2 locus: 3A[585] syn: Est-2_A[585]

v: CS.

Est-B2 locus: 3BL[585] syn: Est-2_B[585]

v: CS.

Among 208 hexaploid accessions, an apparent **Est-B2** null allele occurred frequently in accessions of *T. macha* and *T. sphaerococcum* and occasionally in accessions of *T. compactum*. The allele was not observed in *T. aestivum* and *T. spelta* accessions[585].

Est-D2 locus: 3DL[585] syn: Est-2_D[585]

v: CS.

EST-3

EST-3 is a monomeric enzyme that is expressed in young seedlings (this enzyme was not observed in [814]).

Est-B3 locus: 7BS[585] syn: Est-3_B[585]

v: CS.

Est-D3 locus: 7DS[585] syn: Est-3_D[585]

v: CS.

Est-H3[520] locus: 7H[520]

ad: CS/Betzes.

One accession carrying an apparent **Est-B3** null allele and one carrying an apparent **Est-D3** null allele were found among 208 hexaploid accessions[585].

A 7AS locus encodes three esterase isozymes in immature grains[9].

EST-4

EST-4 is a monomeric, leaf-specific enzyme that electrofocuses around pH 4.5.

Est-A4 locus: 6AL[585, 919] syn: Est-4_A[585]

v: CS.

Est-B4 locus: 6BL[585, 919] syn: Est-4_B[585]

v: CS.

Est-D4 locus: 6DL[585, 919] syn: Est-4_D[585]

v: CS.

Probable **Est-A4** and **Est-D4** null alleles were detected in several accessions of *T. compactum* var. *rubriceps*[585]; otherwise, no Est-4 variant occurred among 208 hexaploid accessions[585]. An esterase gene was located in chromosome L7 (= $6Ag^i$) of *Th. intermedium*[361].

EST-5

EST-5 consists of 20 or more monomeric, grain-specific isozymes that electrofocus between pH 5.6 and 7.0.

Est-A5[9, 9] locus: 3AL

v: CS

Est-A5a[9, 9] locus: 3AL[9]

v: CS.

Est-A5b[9, 9]

v: Kalyansona[9]; *T. compactum* AUS12084[756].

Est-Ag^i5[374] locus: $3Ag^i$[374]

ad: Vilmorin 27/*Th. intermedium*.

Est-B5[9, 9] locus: 3BL[9]

v: CS.

Est-B5a[9, 9]

v: CS.

Est-B5b[9, 9]

v: Big Club.

Est-B5c[9, 9]

v: Timstein.

Est-B5d[9, 9]

v: Sears' Synthetic.

Est-D5[9, 9] locus: 3DL[9]

v: CS.

Est-D5a[9, 9]

v: CS.

Est-D5b[9, 9]

v: *T. macha*.

Est-D5c[9, 9]

v: Hobbit 'S'.

Est-D5d [9, 9]

v: *T. macha* Line 1.

Est-D5e [756]

v: *T. macha* WJR 38548.

Sixty *Ae. tauschii* lines revealed six *Est-D*^{t}5 alleles [1578].

Encoding of the endosperm esterases of hexaploid wheat by 12-15 genes in five compound loci located in 3AL, 3BL, 3DL, 3AS and 3DS was postulated in [1204].

Three and six alleles at *Est-D*^{t}5 (in *Ae. tauschii*) were reported in [756, 1578], respectively.

In *S. cereale*, in addition to **EST-R1**, genes encoding leaf esterases were located in three chromosomes [1561]. These included a gene designated *EST8* in 6R in cvs. Imperial and King II, a gene designated *EST2* and two genes, designated *EST6* and *EST7*, which are part of a separate compound locus [1560], in 5RL in Imperial, and a gene designaged *EST10* in 4R of King II and 4RL of Imperial. In *Hordeum vulgare*, genes encoding leaf esterases were in 3H [1071]; see also [520, 580] and 7H [520].

Est-H5 [10] locus: 3H [10]

ad: CS/Betzes.

Est-H^{ch}5 [10] locus: 3H^{ch} [10]

ad: CS/*H. chilense*.

Est-R5 [10] locus: 6R [43, 1280] syn: EstA [737]

ad: CS/Imperial [10, 43]; Kharkov/Dakold 6RL [10, 1280]; CS/King II [10]; Holdfast/King II [43, 1280].

A second *S. cereale* gene encoding grain esterases, designated *EstB*, was located in 4RL in King II and Petkus and in 7RS in Imperial [737].

Est-R^{m}5 [10] locus: 6R^{m}L [737]. 6R^{m} [10] syn: EstB [737]

ad: CS/*S. montanum*.

Est-S^{b}5 [10] locus: 3S^{b} [10]

ad, su: CS/*Ae. bicornis*.

Est-S^{l}5 [10] locus: 3S^{l} [10]

ad: CS/*Ae. longissima*.

EST-6

EST-6 is a dimeric enzyme that electrofocuses around pH 7.6 and is specific to endosperm.

Est-A6 [1130] locus: 2AS [1130]

v: CS.

Est-A6a [1130]

v: CS.

Est-A6b [1130]

v: Ceska Previvka.

Est-B6 [1130] locus: 2BS [1130]

v: CS.

Est-B6a [1130]

v: CS.

Est-B6b [1130]

v: Hope.

Est-D6[1130] locus: 2DS[1130]

v: CS.

Est-D6a[1130]

v: CS.

Est-D6b[1130]

v: Sears' Synthetic IPSR 1190903.

Est-M6[1130] locus: 2MS[1130]

su: CS/*Ae. comosa*.

Est-R6[370] locus: 2RS[370]

al: DS2 x RxL10 rye popn.

A group of leaf esterase isozymes controlled by the long arms of the homoeologous group 3 chromosomes were reported[919]. The relationship of these esterases to EST-2 and to the leaf esterase designed EST-6 reported in [629] was not determined.

EST-7

EST-7 is a monomeric enzyme that electrofocuses in the same region as EST-6 but is specific to green tissues.

Est-A7[812] locus: 2AL[812]

v: CS.

Est-B7[812] locus: 2BL[812]

v: CS.

Est-D7[812] locus: 2DL[812]

v: CS.

Est-D7a[812]

v: CS.

Est-D7b[812]

v: Synthetic (IPSR 1190903).

Est-E7[812] locus: 2^{E} [812]

ad: CS/*E. elongata*.

Est-H7[812] locus: 2HL[812]

ad: CS/Betzes.

Est-R7[812] locus: 2RL[812]

ad: CS/Imperial. **su**: Holdfast/KingII.

Est-R^{m}7[812] locus: $2R^{m}$alpha[812]

ad: CS/*S. montanum*.

Est-U7[812] locus: 2U[812]

ad: CS/*Ae. umbellulata*.

Est-V7[812] locus: 2V[812]

ad: CS/*D. villosum*.

EST-8

EST-8 consists of about 10 isozymes that electrofocus between pH 4.5 and 6.5 and are expressed only in vegetative tissues. EST-8 is likely to be the enzyme previously described in [629, 919].

Est-A8[629, 814] locus: 3AL[629] syn: Est-A6[629]

v: CS.

Est-B8[613, 814] locus: 3BL[629] syn: Est-B6[629]

v: CS.

Est-D8[629, 814] locus: 3DL[629] syn: Est-D6[629]

v: CS.

Est-R8[613, 814] locus: 6RL[629]

ad: CS/Imperial, CS/King II.

EST-9

EST-9 is a monomeric enzyme that electrofocuses around pH 5.0 and is expressed only in embryos.

Est-A9[814] locus: 3AS[814]

v: CS.

Est-B9[814] locus: 3BS[814]

v: CS.

Est-D9[814] locus: 3DS[814]

v: CS.

2.2.8 Glucosephosphate isomerase

Varietal differences in GPI zymograms were noted in [1127].

GPI zymogram phenotypes observed in *Triticum* and *Aegilops* species are reported in [456, 457].

GPI-1

Gpi-A1[507] locus: 1AS[195, 507]

v: CS.

Gpi-Ag^{i}1[361, 374] locus: 1Ag^{i}[361] syn: Gpi-X1[361]

ad: Vilmorin 27/*Th. intermedium*.

Gpi-B1[507] locus: 1BS[195, 507]

v: CS.

Gpi-D1[507] locus: 1DS[195, 507]

v: CS.

Gpi-D1a[195]

v: CS.

Gpi-D1b[195]

v: CS variant and certain CS aneuploids. Rare.

No allelic variation at *Gpi-D*^{t}1 was found in 60 accessions of *Ae. tauschii*[1578].

Gpi-E1[518] locus: 1ES[518]

ad: CS/*E. elongata*.

Gpi-H1[1153] locus: 1HS[1153]

ad: CS/Betzes.

Gpi-H^{ch}1[195] locus: 1H^{ch}[195]

ad: CS/*H. chilense*.

Gpi-R1[195] locus: 1R[195].1RS[779]

ad: CS/King II[195]. **al**: 2a, 2b, and R14[779].

Gpi-R^{m}1[195] locus: 1R[195]

ad: CS/*S. montanum*.

Gpi-S^{l}1[1228] locus: 1S^{1}S[1228].1S^{1} [517]

ma: In *Ae. longissima 2 x Ae. longissima 10, GPI-S^{l}1*, two glutenin loci, and three gliadin loci were mapped relative to one another as follows: *GLU-S^{l}1* – 15.9 cM – *GPI-S^{l}1* – 38 cM – *GLI-S^{l}4* – 7.1 cM – *GLU-S^{l}3* – 0.9 cM – *GLU-S^{l}1* – 5.6 cM – *GLI-S^{l}5*[1228]; *GLU-S^{l}1* is located in 1S^{l}L and the other loci are in 1S^{l}S.

Gpi-S^{s}1[1140] locus: 1S^{s} [1140]

ad: CS/*Ae. searsii*.

Gpi-U1[195] locus: 1U[195]

ad: CS/*Ae. umbellulata*.

Gpi-V1[1026] locus: 1V[241, 1026]

ad: CS/*D. villosum*.

2.2.9 Glutamic oxaloacetic transaminase

GOT-1

Got-A1[505] locus: 6AS[505]

v: CS.

Got-B1[505] locus: 6BS[505]

v: CS.

Got-D1[505] locus: 6DS[505]

v: CS.

GOT-2

Got-A2[505] locus: 6AL[505]

v: CS.

Got-Ag^{e}2[1575] locus: 6Ag^{e} [1575]

ad, su: Rescue/*Th. elongatum*.

Got-B2[505] locus: 6BL[505]

v: CS.

Got-D2[505] locus: 6DL[505]

v: CS. **ma**: Cent – **Got-D2** – 2 cM – *Xpsr154-6D*[757].

Got-E2[518] locus: 6EBeta[518]

ad: CS/*E. elongata*.

Got-H2[520] locus: 6H[520]

ad: CS/Betzes.

Got-H^{t}2[1037] locus: 6H^{t} [1037]

ad: CS/*E. trachycaulus*.

Got-R2[1457] locus: 6R[1457]; 6RL[1280] syn: Got3[1559]

ad: CS/Imperial 6R[1457]; Holdfast/King II 6RL[1280].

Got-V2[242, 1026] locus: 6V[1026]

ad: Creso/*D. villosum*.

GOT-3

Got-A3[505] locus: 3AL[505]

v: CS.

Got-Ag^{e}3[521] locus: 3Ag^{e}L[521]

ad: CS/TAP 67. **su**: CS/TAP 67. **tr**: Certain CS 3D/Ag lines.

Got-B3[505] locus: 3BL[505]

v: CS.

Got-C3[1278] locus: *F* [1278]

ad: *T. aestivum* cv. Alcedo/*Ae. caudata* line C.

Got-D3[505] locus: 3DL[505]

v: CS.

Got-E3[518] locus: 3EL[518]

ad: CS/*E. elongata*.

Got-H3 locus: 3H[90] syn: Got-b3[90]

ad: CS/Betzes.

Got-H^{ch}3[351] locus: 3H^{ch} [351]

ad: MA/*H. chilense*.

Got-R3[1457] locus: 3R[1457] syn: Got3[1559]

ad: CS/Imperial[1457]; Holdfast/King II[1253]; Kharkov/Dakold[1253].

Got-S^{s}3[1140] locus: 3S^{s} [1140]

ad: CS/*Ae. searsii*.

Got-V3[242, 1518] locus: 3VL[1518]

ad: Creso/*D. villosum*.

GOT-4

Got-R4 locus: 7RL[1203] syn: Got1/7R[1203], Got2[1559]

al: *S. cereale*.

Wehling[1559] identified a GOT locus designated *Got1* in 4RL of *S. cereale*.

2.2.10 Hexokinase

HK-1

Hk-B1[6, 6] locus: 1BS[6]

v: CS.

Hk-D1[6, 6] locus: 1DS[6]

v: CS.

HK-2

Hk-A2[810] locus: 3A[810]

v: CS.

Hk-A2a[810]

v: CS.

Hk-A2b[810]

s: CS*/Sears' Synthetic 3A. **v**: Sears' Synthetic IPSR 1190903.

Hk-B2[6, 6] locus: 3BS[6, 810]

v: CS.

Hk-D2[810] locus: 3DS[810]

v: CS.

Hk-D2a[810]

v: CS.

Hk-D2b[810]

v: Sears' Synthetic IPSR 1190903.

Hk-E2[6, 6] locus: 3ES[6]

ad: CS/*E. elongata*.

Allelic variation was observed in three of 55 hexaploid accessions[6].

2.2.11 Lipoxygenase

The LPX-1 gene in wheat corresponds to barley *LoxA* (GenBank L35931). The **LPX-B1** locus is duplicated, with the **LPX-B1.1** and **LPX-B1.2** loci corresponding to GenBank sequences DQ474240 and DQ474241, respectively. The ***Lpx-B1b*** allele corresponds to a deletion associated with a 4.5-fold reduction in lipoxygenase activity. The LPX-2 gene in wheat corresponds to the barley *LoxC* gene (GenBank L37358) whereas the LPX-3 gene in wheat corresponds to the barley *LoxB* gene (GenBank L37359).

LPX-1

Lpx-A1[516] locus: 4AL[516] syn: Lpx-B1[516]

v: CS[516]. **ma**: *Xksu919(Lpx-1)-4A*[0091].

Lpx-B1[516] locus: 4BS[516] syn: Lpx-A1[516]

v: CS[516]. **ma**: *Xcn110(Lpx-1)-4B*[0269, 0367].

Lpx-B1a[1533] syn: Lpx-A1a[936]

v: CS.

Lpx-B1b[1533] syn: Lpx-A1b[936]

v: Bosanka[1533].

Lpx-D1[516] locus: 4DS[516]

v: CS.

Lpx-E1[518] locus: 4ES[518]

ad: CS/*E. elongata*.

Lpx-H1[716] locus: 4H[716]

ad: CS/Betzes.

LPX-2

Lpx-A2[516] locus: 5AL[516, 10303]

v: CS. **ma**: *Xksu919(Lpx-2)-5A*[91].

Lpx-B2[516] locus: 5BL[516, 10303]

v: CS. **ma**: *Xksu919(Lpx-2)-5B*[91]; *Xcn111(Lpx-2)-5B*[269].

Lpx-D2[516] locus: 5DL[516]

v: CS.

Lpx-E2[518] locus: 5EL[518]

ad: CS/*E. elongata*.

Lpx-H2[716] locus: 5H[716]

ad: CS/Betzes.

Lpx-S^{s}2[1140] locus: 5S^{s} [1140]

ad: CS/*Ae. searsii*.

Lpx-V2[242] locus: 5V

ad: CS/*D. villosum*.

LPX-3

Lpx-A3[10303] locus: 4AL[10303]

tv: UC1113 (GenBank DQ474244) and Kofa (GenBank DQ474242)[10303]. **ma**: *Xwmc617a-4A* – 10 cM – **Lpx-A3** – 15 cM – *Xgwm192b-4A*[10303].

Lpx-B3[10303] locus: 4B[10303]

tv: UC1113 and Kofa (GenBank DQ474243)[10303].

ungrouped

Lpx-B1.1[10303] locus: 4BS[10303]

ma: *Xksm62-4B* – 8 cM – *LpxB1.1* – 13 cM – *Xwmc617b-4B*[10303].

Lpx-B1.1a[10303]

tv: UC1113[10303].

Lpx-B1.1b[10303]

tv: Kofa, deletion[10303].

Lpx-B1.2[10303] locus: 4B[10303]

v: CS.

2.2.12 Malate dehydrogenase

MDH-1

Mdh-A1 locus: 1AL[87] syn: Mdh2A[87]

v: CS.

Mdh-B1 locus: 1BL[87, 101] syn: Mdh2B[87]

v: CS.

Mdh-D1 locus: 1DL[87] syn: Mdh2D[87]

v: CS.

Mdh-H1[1153] locus: 1HL[1153]

ad: CS/Betzes.

Mdh-H^{ch}1[352] locus: 1H^{ch} [352]

ad: MA/*H. chilense*.

Mdh-R1 locus: 1RL[1252] syn: Mdh2-1[1252]

ad: CS/Imperial 1R; Kharkov/Dakold 1R; Holdfast/King II 1RL.

Mdh-S^{s}1[1140] locus: 1S^{s}[1140]

ad: CS/*T. searsii*.

MDH-2

Mdh-H2 locus: 3H[90] syn: Mdh2-b2[90]

Mdh-R2 locus: 3R[1252] syn: Mdh2-2[1252]

ad: CS/Imperial.

MDH-3

Mdh-A3[811] locus: 5AS

v: CS.

Mdh-A3a[811]

v: CS.

Mdh-A3b[811]

v: Bersee.

Mdh-B3[811] locus: 5BS

v: CS.

Mdh-B3a[811]

v: CS.

Mdh-B3b[811]

v: Hope.

Mdh-D3[811] locus: 5DS

v: CS.

Mdh-D3a[811]

v: CS.

Mdh-D3b[811]

v: Sears' Synthetic.

Mdh-E3[811] locus: 5ES

ad: CS/*E. elongata*.

Mdh-H3[811] locus: 5H

ad: CS/Betzes.

Mdh-U3[811] locus: 5U

ad: CS/*Ae. umbellulata*.

MDH-4

Mdh-R4[360] locus: 1RL[360]

v: Various crosses.

2.2.13 Peroxidase

Peroxidase (EC1.11.1.7) isozymes have high tissue specificity. Staining and electrophoretic systems are reviewed in ▶[118]. PER-1,-2,-3,-4 and-5 are all reported in ▶[816].

PER-1

PER-1 is expressed in leaf[12] and coleoptile[816] tissues.

Per-B1[12] locus: 1BS[12, 919]

v: CS.

Per-D1[12] locus: 1DS[12, 919]

v: CS.

Per-D1a[12]

v: CS.

Per-D1b[12]

v: Sears' Synthetic.

Per-H^{ch}1[12] locus: 1H^{ch}[12]

ad: CS/*H. chilense*.

Per-R1[12] locus: 1RS[12, 1561] syn: Prx[1561]

ad: CS/King II[12]; Holdfast/King II[1561]. **tr**: Veery 'S'[12].

Per-V1[241] locus: 1V[241]

ad: Creso/*D. villosum*.

PER-2

PER-2 is expressed in young leaf[118], coleoptile and root[816] tissues.

Per-A2 locus: 2AS

v: CS.

Per-A2a[816]

v: CS.

Per-A2b[816]

v: Timstein.

Per-B2[118] locus: 2BS[118]

v: CS.

Per-B2a[816]

v: CS.

Per-B2b[816]

v: Sears' Synthetic IPSR1190903.

Per-D2[118] locus: 2DS[118]

v: CS.

Per-H2[118] locus: 2H[118] syn: Per-5[95]

ad: CS/Betzes.

Per-R2[118] locus: 2RS[118]

ad: CS/Imperial; Kharkov/Dakold.

PER-3

PER-3 is expressed in embryo[119, 816] and scuteller[119] tissues.

Per-A3[119] locus: 3AL[119]

v: CS.

Per-A3a[816]

v: CS.

Per-A3b[816]

v: Timstein.

Per-A3c[816]

v: Hobbit 'S'.

Per-B3[86, 119] locus: 3BL[86, 119] syn: Per4[961]

v: CS.

Per-B3a[816]

v: CS.

Per-B3b[816]

v: Hope.

Per-B3c[816]

v: *T. macha* IPSR1240005.

Per-B3d[816]

v: Timstein.

Per-B3e[816]

v: Sears' Synthetic IPSR1190903.

Per-D3[86, 119] locus: 3DL[86, 119] syn: Per5[961]

v: CS.

Per-D3a[816]

v: CS.

Per-D3b[816]

v: Hope.

Per-D3c[816]

v: Timstein.

Per-D3d[816]

v: *T. macha* IPSR 142005.

Per-D3e[816]

v: Sava.

Per-D3f[816]

v: Cheyenne.

Per-D3g[816]

v: Sears' Synthetic IPSR 1190903. Varietal variation for PER-3 was reported in [94].

PER-4

PER-4 is expressed in endosperm tissue[86, 119].

Per-A4[119, 695] locus: 7A[695]. 7AS[86, 119, 694] syn: Per3[961]

v: CS.

Per-A4a[816]

v: CS.

Per-A4b[816]

v: Hope.

Per-A4c[816]

v: Sicco.

Per-Ag^{e}4 locus: 7Ag^{e}S[694]

tr: Certain CS 7D/*Ag*^{e} lines.

Per-Ag^{i}4 locus: 7Ag^{i} [168] syn: Per-Ag^{i}3[374]

ad: Vilmorin 27/*Th. intermedium*. Cultivar variation for Per-4 was reported in [94].

Per-B4[119, 695] locus: 4A[695]. 4AL[86, 119, 694] syn: Per2[961]

v: CS.

Per-B4a[816]

v: CS.

Per-B4b[816]

v: Hope.

Per-B4c[816]

v: Thatcher.

Per-D4[119, 695] locus: 7D[695], 7DS[86, 119, 694] syn: Per1[961]

v: CS.

Per-D4a[816]

v: CS.

Per-D4b[816]

v: Thatcher.

PER-5

PER-5 is expressed in roots[816].

Per-D5[816] locus: 2DS[816]

v: CS.

Per-S^{l}5[816] locus: 2S^{l} [816]

ad: CS/*Ae. longissima*.

2.2.14 Phosphodiesterase

PDE-1

Pde-A1 locus: 3AS[1589].3A[1590] syn: Pde-A3[1590]

v: CS.

Pde-B1 locus: 3BS[1589].3B[1590] syn: Pde-B3[1590]

v: CS.

Pde-D1 locus: 3DS[1590] syn: Pde-D3[1590]

v: CS.

Pde-S^{l}1 locus: 3S^{l}S[172]

ad: CS/*Ae. longissima*.

Pde-V1[1518] locus: 3VS[1518]

ad: CS/*D. villosum*.

2.2.15 Phosphogluconate dehydrogenase

Pgd1[282] locus: 7A^{m}S[282] syn: Pgd-A3[963], Pgd3[282]

v: *T. monococcum*[664].

PgdR1 locus: 4RL[1191]

ad: CS/Imperial; Holdfast/King II.

PgdR2 locus: 6RL[1191]

ad: CS/Imperial; Holdfast/King II.

Loci were also identified in 6B[1435], 1EL[1435], 1HL[147, 1072], 1H^{ch} [352] and 1RL[779].

2.2.16 Phosphoglucomutase

PGM-1

Pgm-A1[88] locus: 4AL[88] syn: Pgm-B1[88]

v: CS.

Pgm-Ag^{i}1[361, 374] locus: 4Ag^{i} [361] syn: Pgm-X1[361]

ad: Vilmorin 27/*Th. intermedium*.

Pgm-D1[88] locus: 4DS[88]

v: CS.

Pgm-H1 locus: 4H[90] syn: Pgm-b1[90]

ad: CS/Betzes.

Pgm-H^{ch}1[351] locus: 4H^{ch} [351]

ad: MA/*H. chilense*.

Pgm-R1 locus: 4RS[1253, 1561]

ad: CS/Imperial 4RS[1253, 1561]; Kharkov/Dakold 4R[1253]; Holdfast/King II 4RS[1253, 1561].

2.2.17 Shikimate dehydrogenase

SKDH-1

KDH-D1[706, 1065] locus: 5DS[706, 1065]

v: CS.

Skdh-A1[706, 1065] locus: 5AS[706, 1065]

v: CS.

Skdh-B1[706, 1065] locus: 5BS[706, 1065]

v: CS.

Skdh-H1[85] locus: 5H[85]

ad: CS/Betzes.

Skdh-H^{t}1[1037] locus: 5H^{t} [1037]

ad: CS/*E. trachycaulus*.

Skdh-M^{v}1[985] locus: 5M^{v} syn: Skdh-M^{v}1[985]

su: 5M^{v}(5A), 5M^{v}(5D).

Skdh-R1[706] locus: 5RS[706]. 5R[85]

ad: CS/King II[85]; CS/Imperial[706]; Kharkov/Dakold[85]. **tr**: CS 4AS-5RL; CS 5BL-5RL.

Skdh-S^{l}1[85] locus: 5S^{l}S[85]

ad: CS/*Ae. longissima*.

Skdh-S^{s}1[1140] locus: 5S^{s} [1140]

ad: CS/*Ae. searsii*.

Skdh-U1 locus: 5U[706]

ad, su: CS/*Ae. umbellulata*..

Skdh-V1[85] locus: 5V[85]

ad: CS/*D. villosum*.

2.2.18 Superoxide dismutase

SOD-1

Sod-A1[1066] locus: 2AL[1066]

v: CS.

Sod-B1[1066] locus: 2BL[1066]

v: CS.

Sod-D1[1066] locus: 2DL[1066]

v: CS.

Sod-E1[808] locus: VI E[808]

ad: CS/*E. elongata*.

Sod-H1[716] locus: 2H[716]

ad: CS/Betzes.

Sod-R1[1066] locus: 2R[1066] syn: Sod-3[586]

ad: CS/Imperial.

Sod-S^{s}1[1140] locus: 2S^{s} [1140]

ad: CS/*Ae. searsii*.

ungrouped

Sod-VI[1026] locus: 7V[1026]

ad: CS/*D. villosum*.

2.2.19 Triosephosphate isomerase

TPI-1

Tpi-A1[1139] locus: 3AS[1139]

v: CS.

Tpi-B1[1139] locus: 3BS[1139]

v: CS.

Tpi-D1[1139] locus: 3DS[1139]

v: CS.

Tpi-E1[1139] locus: 3E[1139]

ad: CS/*E. elongata*.

Tpi-H1[1139] locus: 3H[1139]

ad: CS/Betzes.

Tpi-R1[1139] locus: 3R[1139]

ad: CS/Imperial; Kharkov/Dakold.

Tpi-S^{l}1[1139] locus: 3S^{l}[1139]

ad: CS/*Ae. longissima*.

TPI-2

Tpi-A2[1139] locus: 5AL[1139]

v: CS.

Tpi-Ag^{i}2[374] locus: 5Ag^{i}[374]

ad: Vilmorin 27/*Th. intermedium*.

Tpi-B2[1139] locus: 5BL[1139]

v: CS.

Tpi-D2[1139] locus: 5DL[1139]

v: CS.

Tpi-H2[1139] locus: 5H[1139]

ad: CS/Betzes.

Tpi-R2[1139] locus: 5R[1139]

ad: CS/Imperial; Kharkov/Dakold.

Tpi-S^{l}2[1139] locus: 5S^{l}[1139]

ad: CS/*Ae. longissima*.

Tpi-U2[1139] locus: 5U[1139]

ad: CS/*Ae. umbellulata*.

2.2.20 Aromatic alcohol dehydrogenase

AADH-1

Aadh-A1 locus: 5AL[584] syn: Adh-A2[584]

v: CS. **ma**: *XksuG44-5A*(proximal)-6.9 cM-*AADH-A1*-24.7 cM-*Xcdo412-5* (distal)[9959].

Aadh-A1a

v: CS; 133 other accessions[584].

Aadh-A1b

v: *T. spelta*; K-24696; other accessions[584].

Aadh-B1 locus: 5BL[584] syn: Adh-B2[584]

v: CS.

Aadh-B1a

v: CS[1533].

Aadh-B1b

v: Drina[1533].

Aadh-C1[1278] locus: *C*[1278]

ad: Alcedo/*Ae. caudata* line C.

Aadh-D1 locus: 5DL[584] syn: Adh-D2[584]

v: CS.

Aadh-E1 locus: 5EL[518] syn: Adh-E2[518]

ad: CS/*E. elongata*.

Aadh-R1 locus: 5RL[1280]

ad: Holdfast/King II.

AADH-2

Aadh-A2 locus: 6A[1279].6AL[513, 587] syn: Adh-A3[508]

v: CS[513]; Carola[1279].

Aadh-Ag^{e}2[1575] locus: 6Ag^{e} [1575]

ad, su: Rescue/*Th. elongatum*.

Aadh-B2 locus: 6B[1279].6BL[513] syn: Adh-B3[508]

v: CS[513]; Carola[1279].

Aadh-D2 locus: 6DL[513].6D[1279] syn: Adh-D3[508]

v: CS[513]; Carola[1279].

Aadh-E2 locus: 6EBeta[518] syn: Adh-E3[518]

ad: CS/*E. elongata*.

Aadh-R2 locus: 6RL[1280]

ad: Holdfast/King II.

Aadh-V2[241] locus: 6V[241]

ad: CS/*D. villosum*.

The *Aadh-1* and *Aadh-2* loci were designated with the synonyms *Adh-2* and *Adh-3*, respectively, in a number of publications in addition to [508, 518, 584]. These include:[509, 510, 511, 517, 519, 587, 1066, 1139].

2.2.21 Aconitase

ACO-1

Aco-A1[189] locus: 6AL[189]

v: CS.

Aco-A1a

v: CS[1533].

Aco-A1b

v: Dubravka[1533].

Aco-Ag^{e}1[1575] locus: 6Ag^{e} [1575]

ad, su: Rescue/*Th. elongatum*.

Aco-B1[189] locus: 6BL[189]

v: CS.

Aco-B1a

v: CS[1533].

Aco-B1b

v: Dubravka[1533].

Aco-B1c

v: Slavonka[1533].

Aco-D1[189] locus: 6DL[189]

v: CS.

Further alleles at **Aco-A1** and **Aco-B1** are listed in [1127]; these have not been tested against those found in [1533].

Aco-E1[189] locus: 6Ebeta[189]

ad: CS/*E. elongata*.

Aco-H1[147, 189] locus: 6HL[189].6H[147] syn: Aco-1[147]

ad: CS/Betzes.

Aco-R1[189] locus: 6RL[189]

ad: Sturdy/PI 252003.

Aco-S^{l}1[189] locus: 6S^{l}[189]

ad: CS/*Ae. longissima*.

Aco-S^{s}1[1140] locus: 6S^{s}[1140]

ad: CS/*Ae. searsii*.

Aco-U1[189] locus: CSU-31[189]

ad: CS/*Ae. umbellulata*.

ACO-2

ACO-B2

Aco-B2[189] locus: 4BL[1513]

v: CS.

Aco-B2a[1513]

v: CS.

Aco-B2b[1513]

v: PI 278437.

Aco-B2c[1513]

v: PI 182575.

Aco-B2d[1513]

v: PI 157589.

ungrouped

Aco-A2[189] locus: 5AL[189]

v: CS.

Aco-D2[189] locus: 4DL[1513]

v: CS.

Aco-E2[189] locus: 4EL[189]

ad: CS/*E. elongata*.

Aco-M^{v}2[1341] locus: 5M^{v} syn: Aco-M^{v}2[985]

ad: 5M^{v}(5A),5M^{v}(5D).

Aco-R2[189] locus: 5RL[189]

ad: CS/King II 5R; Holdfast/King II 5RL.

Aco-S^{s}2[1140] locus: 4S^{s} [1140]

ad: CS/*Ae. searsii*.

2.2.22 NADH dehydrogenase

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *NDH1* (NADH dehydrogenase) and *DIA3* (diaphorase) represent the same locus[0356].

NDH-1

Ndh-A1[513, 1037] locus: 4AL[513] syn: Ndh-B1[513]

v: CS.

Ndh-A1a[1533] syn: Ndh-B1a[936]

v: CS.

Ndh-A1b[1533] syn: Ndh-B1b[936]

v: Sutjeska.

Ndh-A1c[1533] syn: Ndh-B1c[936]

v: Fruskogorka.

Ndh-A1d[1037] syn: Ndh-A1b[1037]

v: Hope, Timgalen.

Ndh-B1[513] locus: 4BS[513] syn: Ndh-A1[513]

v: CS.

Ndh-D1[513] locus: 4DS[513]

v: CS.

Ndh-E1[362] locus: 4E[362]

ad: CS/*E. elongata*.

Ndh-H1[147, 513] locus: 4H[147].4HS[813] syn: Nadhd-1[147]

ad: CS/Betzes.

Ndh-H^{ch}1[813] locus: 4H^{ch} [813]

ad: CS/*H. chilense*.

Ndh-R1[813] locus: 4RS[813].4R[362]

ad: CS/Imperial, CS/King II[362, 813]; CS/Dakold[362].

Ndh-S^{l}1[813] locus:[813]. 4S^{l} [813]

ad: CS/*Ae. longissima*.

Ndh-U1[362] locus: *A* [362]

ad: CS/*Ae. umbellulata*.

Ndh-V1[241] locus: 4V[241]

ad: CS/*D. villosum*.

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh1* (NADH dehydrogenase) and *Dia3* (diaphorase) represent the same locus[0356].

NDH-2

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the NDH-2 (NADH dehydrogenase) and *DIA2* (diaphorase) represent the same locus[0356].

Ndh-A2[813] locus: 7A[813]

v: Hope.

Ndh-D2[813] locus: 7DS[813]

v: CS.

Ndh-R2[813] locus: 7RS[813]

ad: CS/Imperial, CS/King II, Holdfast/King II (7R).

NDH-3

Ndh-A3[813] locus: 3AL[813]

v: CS.

Ndh-B3[813] locus: 3BL[813]

v: CS.

Ndh-B3a[813]

v: CS.

Ndh-B3b[813]

v: Carmen.

Ndh-D3[813] locus: 3DL[813]

v: CS.

A *NDH* locus, designated *NADHD2*, was mapped 27 cM from *Est-D10* in an *Ae. tauschii* F_2 population derived from VIR-1954/VIR-1345[10046]. This locus may be homologous to **NDH-D3**.

Ndh-H3[813] locus: 3HL[813]

ad: CS/Betzes.

Ndh-R3[813] locus: 6RL[813]

ad: Holdfast/King II, CS/Imperial (6R), CS/King II (6R).

Ndh-S^{l}3[813] locus: 3S^{l}L[813]

ad: CS/*Ae. longissima*; CS/*Ae. sharonensis* (3S^l).

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that NDH-3 (NADH dehydrogenase), *DIA1* (diaphorase) and *MNR1* (menadione reductase) represent the same locus[0356].

NDH-4

Ndh-A4[813] locus: 3AS[813]

v: CS.

Ndh-B4[813] locus: 3BS[813]

v: CS.

Ndh-E4[813] locus: 3ES[813]

ad: CS/*E. elongata*.

Ndh-H4[813] locus: 3HS[813]

ad: CS/Betzes.

Ndh-R4[813] locus: 3RS[813]

ad: CS/King II, CS/Imperial (3R).

2.2.23 Dipeptidase

DIP-1

Dip-A1[454, 700] locus: 6AL[454, 700] syn: Pept-A1[454]

v: CS.

Dip-A1a[700]

v: CS.

Dip-A1b[700]

v: Cheyenne.

Dip-B1[454, 700] locus: 6BL[454, 700] syn: Pept-B1[1533]

v: CS.

Dip-B1a[700]

v: CS.

Dip-B1b[700]

v: Cappelle-Desprez.

Dip-D1[700] locus: 6DL[700]

v: CS.

Dip-H1[147, 700] locus: 6H[145, 147, 700] syn: Pept-1[147], Dip 1[145]

ad: CS/Betzes.

Dip-J1[700] locus: 6J[700]

ad: CS/*Th. junceum*.

Dip-V1[700] locus: 6V[700]

ad: CS/*D. villosum*.

2.2.24 Malic enzyme

A dimeric enzyme extractable from mature grains.

MAL-1

Mal-A1[809] locus: 3AL

v: CS.

Mal-B1[809] locus: 3BL

v: CS.

Mal-B1a[809]

v: CS.

Mal-B1b[809]

v: *T. spelta* IPSR line 1.

Mal-B1c[809]

v: Sears' Synthetic.

Mal-D1[809] locus: 3DL

v: CS.

Mal-E1[809] locus: 3E

ad: CS/*E. elongata*.

Mal-H1[809] locus: 3H

ad: CS/Betzes.

Mal-R1[809] locus: 3R

ad: CS/Imperial.

2.2.25 Adenylate kinase

ADK-1

Adk-A1[91] locus: 7AL[91] syn: Adk-a[91]

v: CS.

Adk-Ag^{i}1[91] locus: 7Ag^{i}[91]

ad: CS/*Th. intermedium*.

Adk-B1[91] locus: 7BL[91] syn: Adk-b[91]

v: CS.

Adk-D1[91] locus: 7DL[91] syn: Adk-d[91]

v: CS.

Adk-E1[91] locus: 7E[91].7E[1435]

ad: CS/*E. elongata*.

Adk-H1[91] locus: 7HS[1435].7H[91]

ad: CS/Betzes.

Adk-M^{v}1[985] locus: 7M^{v}L syn: Adk-M^{v}1[985]

su: 7M^{v}(7D).

Adk-R1[91] locus: 7RL[91]

ad: CS/Imperial; Holdfast/King II.

Adk-U1[91] locus: *E* [91]

ad: CS/*Ae. umbellulata*.

ADK-2

Adk-H2 locus: 6HL[1435]

ad: CS/Betzes.

2.2.26 Glutamate-pyruvate transaminase

GPT-1

Gpt-A1[1435] locus: 1AS[1435]

v: CS.

Gpt-B1[1435] locus: 1BS[1435]

v: CS.

Gpt-D1[1435] locus: 1DS[1435]

v: CS.

Gpt-E1[1435] locus: 1ES[1435]

ad: CS/*E. elongata* 1E.

Gpt-H1[1435] locus: 1H[1435]

dv: *H. vulgare* cv. Betzes.

2.2.27 Catalase

CAT-1

Cat-B1[1466] locus: 4BL[1466] syn: Cat-A1[1466]

v: CS.

A catalase locus, designated *CAT2*, was mapped 6 cM proximal to **ACO-D2** in an *Ae. tauschii* F_2 population derived from VIR-1954/VIR-1345 cross[10046]. This locus may be orthologous to **CAT-B1**[10046].

2.2.28 Beta-glucosidase

b-Gls[282] locus: $2A^mL$[282]

dv: DV92.

b-Glsa[282]

dv: DV92.

b-Glsb[282] locus: Null allele

dv: G3116.

2.2.29 Starch branching enzyme I

SBEI

SbeI1[9937] locus: 1DL[9937]

v: CS[9937].

SbeI2[9937] locus: 7BL[9937]

v: CS[9937].

2.2.30 Starch branching enzyme II

SbeII

Suppression of SBEIIb expression alone had no effect on amylose contents, however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose[10534].

Suppression of SBEIIb expression alone had no effect on amylose contents; however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose[10534]. Combined loss-of-function mutations in *SbeIIa-A, SbeIIa-B, SbeIIb-A*, and *SbeIIb-B* (PI 670160) increased amylose content by 66% and resistant starch by 753% relative to the control in tetraploid wheat cv. Kronos[11125]. Combination of these four mutations with mutations of *SbeIIa-D* in hexaploid wheat (PI 670160) increased amylose content by 63% and resistant starch by 1,057% in field experiments relative to the control[11126]

2.2.31 Benzoxinones

The putative role of benzoxinones sets *BX-1* to *BX-5* is to catalyze the pathway Indole-3-glycerol phosphate to DIBOA. Primers designated from maize sequences were used to generate RT-PCR products utilised to screen a cDNA library from CS seedlings. Full-length cDNAs were heterologously expressed in yeast and the *Bx* gene products had enzymatic action. The *BX* genes located by Southern analysis of CS deletion stocks occurred as clustered groups in homoeologous groups 4 (*BX-1, BX-2*) and 5 (*BX-3.1, .2, BX-4, BX-5*)[10103].

2.2.32 Acetohydroxyacid synthase (EC 4.1.3.18)

An orthologous series was mapped as the active target sites of imidazolinone herbicides. See section 1: Herbicide Response: Imidazolinone resistance.

AHASL-1

AhasL-A1[10101] locus: 6AL[10101] syn: Imi3[10099]

v2: CDC Teal IMI 15A **Imi3**[10099]. **dv**: *T. monococcum* mutant EM2 (mutant of susceptible line TM23[10102].

AhasL-B1[10101] locus: 6BL[10101] syn: Imi2[10099]

v: CDC Teal IMI 11A = PTA3953[10099].

AhasL-D1[10101] locus: 6DL[10101] syn: Imi1[10099]

v: BW755 = Grandin*3/Fidel-Fs-4[10099].

2.2.33 Phytoene synthase

Phytoene synthase, which condenses two molecules of geranyl geranyl diphosphate to produce phytoene, is the first of the specific enzyme necessary for carotene biosysthesis in plants.

Homology with the same gene in rice (*Psy1*)[10230].

Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Section 1: Flour colour and Grain quality parameters: Flour, semolina and pasta colour). Gene **Psy-A1** was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents[10501]. Most hexaploid wheat cultivars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The ***Psy-B1b*** allele from tetraploid wheat Kofa is the result of a B-A intergenomic conversion event that probably occurred in Cappelli ***ph1c*** mutant 1[10530]. An EMS mutation in the **Psy-E1** gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

PSY1-1

Psy1-A1[10230] locus: 7AL[10230]

tv: Kofa[10230]. **ma**: *Xwmc809-7A* – 5.8 cM – *Yp7A*[10501].

Psy1-A1a[10230, 10501] syn: Psy-A1a

tv: Kofa[10230]. **ma**: *Xwmc809-7A* – 5.8 cM – *Yp7A*[10501].

Psy1-A1b syn: Psy-A1b

v: Chinese common wheats with low yellow pigment content[10501]; PH82-2[10501]; Shaan 9314[10501]; Xinong 336[10501]. **c**: GenBank EF600064[10501]. 37-bp insertion in intron 2 (231 bp fragment for marker *Yp7A*)[10501]. 676-bp insertion in intron 4[10530].

Psy1-A1c[10530] syn: Psy-A1c

v: M564[10650]. **c**: GenBank EU650391[10650]; No 37-bp insertion in intron 2 and no 676-bp insertion in intron 4[10530]; High yellow pigment cultivars: Aroona (PI 464647)[10530]; Dundee (PI 89424, PI 106125)[10530]; Raven (PI 303633, PI 330959)[10530].

Psy1-A1d[10651]

tv: Langdon[10651]; *T. dicoccum* DM28[10652]. **c**: GenBank EU263018[10651]; FJ393515[10652].

Psy1-A1e[10651]

v: Sunco[10654]. **tv**: DR8[10651]. **c**: EU649791[10654]; EU263019[10651].

Psy1-A1f[10652]

dv: *T. urartu* PI 428326[10652]. **c**: FJ393516[10652].

Psy1-A1g[10652]

dv: *T. urartu* UR1[10652]. **c**: FJ393517[10652].

Psy1-A1h[10652]

dv: *T. boeoticum* BO1[10652]; *T. monococcum* MO5[10652]. **c**: FJ393518[10652]; FJ393519[10652].

Psy1-A1i[10652]

dv: *T. monococcum* MO1[10652]. **c**: FJ393520[10652].

Psy1-A1j[10652]

dv: *T. monococcum* MO2[10652]. **c**: FJ393521[10652].

Psy1-A1k[10652]

v: Spelt 167[10652]. **tv**: *T. dicoccoides* DS3[10652]; *T. dicoccum* DM37[10652]. **c**: FJ293527[10652]; FJ293522[10652]; FJ293523[10652].

Psy1-A1l[10652]

tv: Kofa[10230, 10530]; Strongfield[10653]; *T. dicoccoides* DS6[10652]. **c**: EU096090[10230, 10530]; FJ393524[10652].

Psy1-A1m[10652]

tv: *T. dicoccum* DM26[10652]. **c**: FJ393525[10652].

Psy1-A1n[10652]

v: Spelt SP9[10652]. **c**: FJ393526[10652].

Psy1-A1o[10653]

tv: Commander[10653]. **c**: FJ234424[10653].

Psy1-A1p[10654]

v: Tasman[10654]. **c**: EU649792[10654].

Psy1-A1q[10654]

v: Cranbrook[10654]. **c**: EU649793[10654].

Psy1-A1r[10654]

v: Halberd[10654]. **c**: EU649794[10654].

Psy1-A1s[10654]

v: Schomburgk[10654]. **c**: EU649795[10654].

Psy1-A1t[10920]

v: WAWHT2074[10920]. **ma**: *Xgwm344-7A* – 3.9 cM – ***Psy1-A1t*** – 9.9 cM – *Ccfa2257a-7A*[10920]. **c**: GenBank HM006895[10920].

Psy1-B1[10230] locus: 7BL[10230]

tv: Kofa[10230]. **ma**: *Xcfa2040-7B* – 12 cM – **PSY1-B1** – 5 cM – *gwm146-7B*[10230].

Psy1-B1a[10650] syn:[10530]

GenBank EU096093[10530].

v: Chinese Spring[10530, 10650, 10654]; Spelt SP9[10652]. **tv**: *T. dicoccoides* DS4[10652]. **c**: FJ393529[10652]; FJ393528[10652]; EU650392[10650]; EU096094[10530]; EU649789[10654].

Psy1-B1b[10650]

v: Neixiang 188[10650]. **c**: EU650393[10650].

Psy1-B1c[10650]

v: CA 9648[10650]. **c**: EU650394[10650].

Psy1-B1d[10650]

v: Ning 98084[10650]. **c**: EU650395[10650].

Psy1-B1e[10650]

v: M484[10650]. **tv**: DR8[10650]; *T. dicoccum* DM28[10652]. **c**: EU263021[10650]; FJ393541[10652].

Psy1-B1f[10651]

tv: Langdon[10651]. **c**: EU263020[10651].

Psy1-B1g[10651]

tv: DR1[10651]; *T. dicoccoides* DS6[10652]. **c**: EU650396[10651]; FJ393530[10652].

Psy1-B1h[10652]

tv: *T. dicoccoides* DS3[10652]. **c**: FJ393531[10652].

Psy1-B1i[10652]

tv: *T. dicoccoides* DS8[10652]. **c**: FJ393532[10652].

Psy1-B1j[10652]

tv: *T. dicoccum* DM26[10652]. **c**: FJ393533[10652].

Psy1-B1k[10652]

tv: *T. dicoccum* DM33[10652]. **c**: FJ393534[10652].

Psy1-B1l[10652]

tv: *T. dicoccum* DM37[10652]. **c**: FJ393535[10652].

Psy1-B1m[10652]

v: Spelt 167[10652]. **tv**: *T. dicoccum* DM47[10652]. **c**: FJ393540[10652]; FJ393539[10652].

Psy1-B1n[10530]

Previously designated ***Psy1-B1b***[10656].

tv: Kofa. **c**: EU096092[10530]; DQ642439[10230].

Psy1-B1o[10530]

Previously designated ***Psy1-B1a***[10656].

tv: UC1113[10530]; W9262-260D3[10230]. **c**: EU096093[10530]; DQ642440[10230].

Psy1-D1[10652] locus: 7DL[10652]

Psy1-D1a[10652]

v: Chinese Spring[10652]. **c**: EU650397[10652]; EU649790[10654].

Psy1-D1b[10652]

dv: *Ae. tauschii* Ae34[10652]. **c**: FJ393542[10652].

Psy1-D1c[10652]

dv: *Ae. tauschii* Ae46[10652]. **c**: FJ393543[10652].

Psy1-D1d[10652]

dv: *Ae. tauschii* Y99[10652]. **c**: FJ393544[10652].

Psy1-D1e[10652]

v: Spelt SP9[10652]. **c**: FJ393545[10652].

Psy1-D1f[10652]

v: Spelt 217[10652]. **c**: FJ393546[10652].

Psy1-D1g[10652]

v: Zhonliang 88375[10652]. **c**: FJ807498[10652].

Psy1-D1h[10652]

dv: *Ae. tauschii* Ae37[10652]. **c**: FJ807499[10652].

Psy1-D1i [10652]

dv: *Ae. tauschii* Ae38 [10652]. **c**: FJ807500 [10652].

Psy1-D1j [10652]

dv: *Ae. tauschii* Ae42 [10652]. **c**: FJ807501 [10652].

Psy1-D1k [10655]

v: Nongda 3291 [10655]. **c**: FJ807495 [10655].

Psy1-D1l [10655]

v: E 86642 [10655]. **c**: FJ807496 [10655].

Psy1-D1m [10655]

v: Ning 97-18 [10655]. **c**: FJ807497 [10655].

Psy1-E1 syn: Psy-E1

Psy1-E1a [10530] syn: Psy-E1a [10530]

GenBank EU096095 [10530].

v: Agatha (7EL translocation) [10530].

Psy1-E1b [10530] syn: Psy-E1b [10530]

Similar to EU096095, but with P to L substitution at amino acid 422 [10530].

v: EMS mutant Agatha 28-4 [10530]; Wheatear [10530].

Psy1-S1 [10652]

al: *Ae. speltoides* Ae48 [10652].

Psy1-S1a [10652]

al: *Ae. speltoides* Ae48 [10652]. **c**: FJ393536 [10652].

Psy1-S1b [10652]

al: *Ae. speltoides* Ae49 [10652]. **c**: FJ393537 [10652].

Psy1-S1c [10652]

al: *Ae. speltoides* Y162 [10652]. **c**: FJ393538 [10652].

PSY2-1

Psy2-A1 [10230] locus: 5A [10230]

tv: Kofa [10230].

Psy2-B1 [10230] locus: 5B [10230]

tv: Kofa [10230]. **ma**: *Xgwm191-5B* – 17 cM – *PSY-B2* [10230].

2.2.34 Polyphenol oxidase

High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.

Primers different from those in ▶ [10386] were developed in ▶ [10504], but their ability to distinguish phenotypic groupings (alleles) was similar. A null allele of **Ppo-D1** was identified for this locus using primer pair WP3-2 [10504].

PPO-1

Ppo-A1 [10386] locus: 2AL [10385] syn: PPO-2A [10385]

ma: Detected with STS markers PPO18 [10385] and *PPO33* [10386]; *Xgwm321-2A* – 1.4 cM – **PPO-A1** – 5.8 cM – *Xgwm294-2* [10385]; *Xcfa2058-2A* – 0.4 cM – **PPO-A2** – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – **PPO-A1** – 11.0 cM – *Xwmc181-2* [10931].

Ppo-A1a[10386] syn: PPO-2Aa[10385]

v: Nongda 139[10386]; Zhongyou 9507[10385, 10386, 10504]; others[10386, 10504]. **c**: EF070147[10386].

Wheats with this allele tend to have lower PPO activity[10385, 10386].

Ppo-A1b[10386] syn: PPO-2Ab[10385]

v: Chinese Spring[10386]; CA 9632[10385, 10386]; Nongda 183[10504]; others[10386, 10504]. **tv**: *T. dicoccoides* DS4[10386]. **c**: EF070148[10386].

Ppo-A1c[10657]

dv: *T. urartu* UR1[10657]. **c**: EU371651[10657].

Ppo-A1d[10657]

dv: *T. boeoticum* BO1[10657]. **c**: EU371652[10657].

Ppo-A1e[10657]

tv: DR8[10657]. **dv**: *T. monococcum* MO1[10657]. **c**: EU371653[10657].

Ppo-A1f[10657]

v: Penawawa[10931]. **tv**: *T. dicoccoides* DS3[10657]. **c**: EU371654[10657].

Ppo-A1g[10657]

tv: Langdon[10657]. **c**: EU371655[10657].

Ppo-A1h[10931]

v: Louise[10931]. **c**: GenBank JN632506[10931].

Ppo-B1[10658]

v: Chinese Spring[10658].

Ppo-B1a[10658]

v: Chinese Spring[10658]. **c**: GQ303713[10658].

Ppo-D1[10386]

ma: Detected with primers *PPO16* and PPO29. *Xwmc41-2D* – 2.0 cM – **PPO-D1**[10386]; *Xcfd62-2D* – 0.2 cM – **PPO-D2** – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – **PPO-D1** – 0.9 cM – *Xbarc349-2D*[10931].

Ppo-D1a[10386]

v: Chinese Spring[10386]; Louise[10931]; Zhonghou 9507[10386, 10504]; others[10386, 10504]. **c**: EF070149[10386]. Wheats with this allele tend to have lower PPO activity[10386].

Ppo-D1b[10386] locus: EF070150[10386]

v: CA 9632[10386]; CA 9719[10386]; Nongda 183[10504]; others[10386, 10504]. **c**: EF070150[10386].

Wheats with this allele tend to have higher PPO activity[10386].

Ppo-D1c[10657]

dv: *Ae. tauschii* Ae38[10657]. **c**: EU371656[10657].

Ppo-D1d[10657]

dv: *Ae. tauschii* Y59[10657]. **c**: EU371657[10657].

Ppo-D1e[10504] syn: Ppo-D1null[10504], Ppo-D1c[10656]

v: Gaiyuerui[10504]; Zm2851[10504]; XM2855[10504]; 9114[10504].

PPO-2

Ppo-A2[10930, 10931] locus: 2AL[10930] syn: PPO-A2[10931]

ma: *Xcfa2058-2A* – 0.4 cM – **PPO-A2** – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – **PPO-A1** – 11.0 cM – *Xwmc181-2*[10931].

Ppo-A2a [10930]

v: Alpowa[10930]. **c**: GenBank HQ228148[10930].

Ppo-A2b [10930, 10931]

v: Panawawa[10931]. **c**: GenBank HQ228149[10930].

Ppo-A2c [10931]

v: Louise[10931]. **c**: JN632507[10931].

Ppo-B2 [10930, 10931] locus: 2B[10930] syn: PPO-B2[10930]

ma: *Xiwa175*/*Xiwa4866-2B* – 0.7 cM – **PPO-B2** – 2.3 cM – *Xiwa7593-2B*[10931].

Ppo-B2a [10930, 10931]

v: Penawawa[10931]. **c**: GenBank HQ228150[10930].

Ppo-B2b [10930]

v: Alpowa[10930]. **c**: GenBank HQ228151[10930].

Ppo-B2c [1211, 10930]

v: Louise[1211]. **c**: GenBank JN632508[10930].

Ppo-D2 [10930, 10931] locus: 2DL[10930] syn: PPO-D2[10930]

ma: *Xcfd62-2D* – 0.2 cM – **PPO-D2** – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – **PPO-D1** – 0.9 cM – *Xbarc349-2D*[10931].

Ppo-D2a [10930, 10931]

v: Louise[10931]. **c**: GenBank HQ228152[10931].

Ppo-D2b [10930]

v: Penawawa[10930]. **c**: HQ228153[10930].

2.2.35 Protein disulfide isomerase (EC 5.3.4.1)

PDI-1

Pdi-A1 [10422] locus: 4AL[10422]

v: CS[10422].

Pdi-B1 [10422] locus: 4DS[10422]

v: CS[10422].

Pdi-D1 [10422] locus: 4BS[10422]

v: CS[10422].

The genes for PDI and their promoters were sequenced in [10423]. A related sequence on 1BS was shown to be a partial, non-expressed copy in [10424], but not detected in [10409]. PCR-RFLP markers for [*TaPDI-4A*] and [*TaPDI-4B*] were designated [*Xvut(PDI)-4A*] and [*Xvut(PDI)-4B*] in [10409]. These were also closely associated with Germin (oxalate oxidase[10441]) genes[10409].

2.2.36 Isoamylase 1

ISO-1

Iso-1 [10295] syn: ISA-1[10295]

dv: *Ae. tauschii*[10295].

2.2.37 Polygalacturonase-inhibiting proteins

PGIPs are leucine-rich repeat (LRR) proteins involved in plant defence.

PGIP-1

Pgip-A1 [10608]

Tapgip3, AM180658 [10608].

dv: *T. monococcum* PI 538722 [10608].

Not expressed in *T. urartu* PI 428315 (AM884191) [10608] or in polyploid wheat because of inactivation by an inserted copia transposon in the fourth LRR [10608].

Pgip-B1 [10608] locus: 7BS [10608, 10610] syn: Tapgip1 [10610]

ma: *XS13M50-7B*-5 cM-*PGIP-B1*-11.7 cM-*Xmgb105s-7B* [10608].

Pgip-B1a [10608] syn: Tapgip1a [10608]

tv: Messapia [10608].

Pgip-B1b [10608]

Tapgip1b, AM884195 [10608].

tv: *T. turgidum* ssp. *dicoccoides* MG4343 [10608].

This non-expressed allele produces a large amplicon in southern blots using the Pgip sequence as probe, due to an insertion of a Vacuna mutator element [10608].

Pgip-D1 [10608] locus: 7DS [10610] syn: Tapgip2 [10610]

tv: Langdon 7D(7A) [10610]; Langdon 7D(7B) [10610].

Pgip1 [10390] locus: 7BS [10390]

v: CS ditelo 7BL [10390]. **v2**: Chinese Spring **Pgip2** [10390]. **tv**: Langdon [10390].

ungrouped

Pgip2 [10390] locus: 7DS [10390]

v: CS ditelo 7DL [10390]. **v2**: Chinese Spring **Pgip1** [10390].

2.2.38 Flavone 3-hydroxylase (EC 1.14.11.9)

F3H-1

F3h-A1 [10823] locus: 2AL [10823]

v: CS [10823]. **ma**: *Xgwm1067-2A* – 2.1 cM – **F3H-A1** – 11.4 cM – *Xgwm1070-2*^{a} [10823]. ALLELIC VARIATION.

F3h-B1 [10823] locus: 2BL [10823]

v: CS [10823]. **ma**: **F3H-B1**/*Xgwm1067-2B* – 11.4 cM – *Xgwm1070-2B* [10823]. ALLELIC VARIATION.

F3h-D1 [10823] locus: 2DL [10823]

v: CS [10823]. **ma**: *Xgwm877-2D* – 1.8 cM – **F3H-D1**/*Xgwm1264-2D* – 22.7 cM – *Xgwm301-2D* [10823]. ALLELIC VARIATION.

F3H-2

F3h-B2 [10823] locus: 2BL [10823]

v: CS [10823]. **ma**: *Xgwm1070-2B* – 30.1 cM – **F3H-B2** [10823].

Located in the terminal region near *Xgwm1027-2B* [10823]. ALLELIC VARIATION

2.2.39 Zeta-carotene desaturase

ZDS-1

Zds-A1 [10905] locus: 2A [10905]

tv: Langdon [10905].

Zds-B1[10905] locus: 2B[10905]

tv: Langdon[10905].

Zds-D1[10906] locus: 2DL[10906]

v: CS[10906].

Zds-D1a[10906] syn: TaZDS-D1a[10906]

v: CA9632[10906]; Many Chinese wheats and 80 CIMMYT lines[10906].

Zds-D1b[10906] syn: TaZDS-D1b[10906]

v: Ning 99415-8[10906]; Zhengzhou 9023[10906]; Zhongyou 9507[10906]; Zhoumai 13[10906].

Cv. Zhongyou 9507 has lower yellow flour pigment content, preferred for Chinese steamed bread and dry Chinese noodles. A QTL in the ***Zds-D1a*** region explained 18.4 % of the variation in yellow pigment content in Zhongyou 9507/CA 9632[10906].

2.2.40 Carotenoid beta-hydroxylase (non-heme di-iron type)

HYD are non-heme di-iron b-hydroxilases that act primarily on b-carotene.

HYD-1

Hyd-A1[10913] locus: 2AL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

Hyd-B1[10913] locus: 2BL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

Hyd-D1[10913] locus: 2DL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

HYD-2

Hyd-A2[10913] locus: 5AL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

Hyd-B2[10913] locus: 4BL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

Hyd-D2[10913] locus: 4DL[10913]

tv: Kronos[10913]. **v**: UC1041[10913].

2.2.41 Lycopene-zeta-cyclase

Catalyzes the conversion of lycopene to zeta-carotene, a step in the lutein pathway that leads to yellow flour colour.

e-LCY-A1[10654] locus: 3A[10654] syn: E-LCY3A[10654]

eLCY-A1a[11713]

v: Chinese Spring (11713{; WAWHT2074[11713]. GenBank EU649785.

eLCY-A1b[11713]

v: Ajana[11713]. GenBank JX288762.

Alleles *a* and *b* were distinguished by a CAPS marker based on a SNP at position 2,028 bp. This difference was associated with differences in b flour colour in some Australian accessions[11713].

e-LCY-B1[10654] locus: 3B[10654] syn: E-LCY3B[10654]

GenBank EU649786.

e-LCY-D1[10654] locus: 3D[10654] syn: E-LCY3A[10654]

GenBank EU649787.

2.2.42 Dehydration-responsive element (DREB) proteins; Dehydration response factors (DRF)

2.2.43 Starch synthase

SSI-1

SsI-A1[0041] locus: 7A[0041]

SsI-B1[0041] locus: 7B[0041]

SsI-D1[0041] locus: 7D[0041]

Starch synthase I proteins are identical to the starch granule proteins SGP-3[0041].

SSII-1

SsII-A1[0042] locus: 7A[0042]

SsII-B1[0042] locus: 7B[0042]. ***SsII-D1*** [0042]. 7D[0042]

SsII-D1[0042] locus: 7D

Starch synthase II proteins are identical to the starch granule proteins SGP-1[0042].

2.3 Endosperm storage proteins

2.3.1 Glutenins

These are heterogeneous mixtures of proteins comprising subunits linked by disulfide bonds. ‘A’ are high-molecular-weight (HMW) and ‘B’, ‘C’ and ‘D’ are low-molecular-weight (LMW) subunits.

Using proteomic analysis of 2D gels of seed storage proteins in 39 ditelocentric lines of cv. CS, 105 protein spots were resolved[03129]. Locations of structural genes controlling 26 spots were identified in 10 chromosomal arms (4 on 1BL, 5 on 1BS, 4 on 1DL, 4 on 1DS, 2 on 6AS, 3 on 6BS, 1 on 6DL, 1 on 6DS, 1 on 3BS and 1 on 3BL). Multiple regulators of the same protein located on various chromosome arms were observed. Two novel subunits, named 1Bz and 1Dz, were found to have very similar structures to HMW glutenin subunit 12 (encoded by *Glu-D1-2a*-see the relevant list below) and were located to chromosome arms 1BL and 1DL, respectively.

PCR amplification of genomic DNA was used to isolate three LMW glutenin genes in cultivar Chinese Spring, named LMWG-MB1, LMWG-MB2 and LMWG-MB3[01101]. The deduced amino-acid sequences showed a high similarity between these ORFs and with those of other LMW glutenin genes. The authors state that the study provided direct evidence that insertions and/or deletions provide a mechanistic explanation for the allelic variation, and hence the resultant evolution, of prolamin genes, and comment on relationships with gamma-secalins and beta-hordein families. Single-base substitutions at identical sites generate premature stop codons in both LMWG-MB2 and LMWG-MB3, indicating that these clones are pseudogenes.

GLU-1

The GLU-1 loci, all of which are compound, encode HMW glutenin subunits.

Each GLU-1 locus in hexaploid wheat contains two genes, the products of which were described as 'x- type' and 'y-type' based on differences in molecular weight and isoelectric point[1118]. Other evidence has shown that these gene products differ in electrophoretic fingerprint pattern[1124] and cysteine content[1028], and the genes themselves differ in nucleotide sequence[373, 1433, 1470]. Although early evidence suggested up to 6 genes in total at each locus[373, 1471], it appears likely that only a single copy of each gene is present at the 1AL, 1BL, and 1DL loci[495].

No 'y-type' protein from the GLU-A1 locus has been demonstrated in hexaploid wheat[1118], although they are found in diploid wheats[798, 1535], and sequencing experiments have shown the presence of two stop codons

in the transcribed portion of the gene[10088]. Definitive evidence that subunit 21* [602], which has a mobility close to that of subunit 21, is a 'x-type' protein rather than a 'y-type' protein has not been obtained. The gene coding for 'x-type' proteins within GLU-A1 is also often silent[420, 1118].

The symbols for the genes within the GLU-1 loci coding for 'x-type' and 'y-type' proteins will be *GLU-1-1* and *GLU-1-2*, respectively, rather than *GLU-1x* and *GLU-1y*[1470]. The genes are closely linked but recombination has been observed between GLU-B1-1 and GLU-B1-2 with a frequency of 3 in 3,450[1117]. The gene order, relative to the centromere, has not been ascertained.

The subunit nomenclature used is that devised in ▶[1116]; however, an alternative system based upon molecular weight was proposed in ▶[1068]. A system of naming the GLU-A1-1, GLU-A1-2, GLU-B1-1 and GLU-B1-2 alleles in *T. turgidum* var. *dicoccoides* is given in ▶[796].

In[00116], a comparison between spelt wheats (*T. spelta*) and bread wheat was carried out for the glutenins using a nomenclature system described in ▶[00117].

The GLU-1 loci may be recognised by the DNA probe pTag1290[1471] and probes pWHE3 (Ax2*), γ WHE4 (Ay), γ WHE5 (Bx7), γ WHE6 (By9), pWHE2 (Dx5) and pWHE1 (Dy10)[3144]. Individual *GLU-1-1* loci on 1A, 1B and 1D and the *GLU-1-2* loci may be recognised by specific primers[263]. In ▶[00105], the evolution of the high molecular weight glutenin loci of the A, B, D and G genomes of wheat was explored; 30 partial allele sequences were compared, designated by Greek letters (alpha, beta, gamma, etc.) (5 of which were cited as Schlumbaum, pers. comm.; the remaining 25 were deposited as GenBank, accession nos. X98583-X98592, X98711-X98715 and Y12401-Y12410). These partial alleles derive from all six *GLU-1-1* and *GLU-1-2* loci in current-day samples taken from seven species of wheat, as well as from DNA extracted from charred grain of two samples from archaeological excavations, dated 3000 and 5000 years old, respectively.

Following the first listing which considers the GLU-1 set for hexaploid wheat as a single locus, there is a provisional listing based on x- and y- type glutenins. These are not referenced.

A nomenclature system for prolamin banding patterns of triticale was proposed in ▶[03139]. Extensive allelic variation in triticale at GLU-A1, GLU-B1, GLU-R1 and GLI-R2 loci was reported in ▶[03121].

GLU-A1

Glu-A1[780, 1125] locus: 1AL[781, 1125]. 1A[780] syn: Glt-A1[420], Glu 1A[1415], Glt-A2[420]

s: CS*/Hope 1A[1125]. **v**: CS[780, 781]; various[420].

Primers were designated that enabled Ax2* to be distinguished from Ax1 or Ax-null[10641].

Glu-A1a[1116] locus: 1[1116]

v: Hope.

Glu-A1b[1116] locus: 2*[1116]

v: Bezostaya 1.

Glu-A1c[1116] locus: Null allele[1116]

v: CS.

Glu-A1d[1535]

v: V74, Spain[1115].

Glu-A1e[1535]

v: 132c, Poland[1115].

Glu-A1f[1535]

v: 112-29, Sudan[1115].

Glu-A1g[1535]

v: Landrace 1600.

Glu-A1h[1527] syn: GLU-A1-l[1527]

tv: PI 94683, USSR, *T. dicoccum*.

Glu-A1i[1527] syn: GLU-A1-II[1527]

tv: CI 12213, India, *T. dicoccum*; Lambro[1523].

Glu-A1j[1527] locus: 1'[125] syn: GLU-A1-III[1527]

tv: PI 352359, Germany, *T. dicoccum*.

Glu-A1k[478] locus: 26[478]

v: BT-2288[478].

Glu-A1l[847]

tv: Chinook, Canada.

Glu-A1m[1069]

tv: Nugget Biotype 1, Canada, *T. durum*.

Glu-A1n[1526] locus: 1'[125] syn: Glu-A1m[959], Glu A1-IV[1526]

tv: Corado, Portugal[1526].

Glu-A1o[125, 1526] locus: 2** [125] syn: Glu A1-V[125, 1526], Glu-A1n[959]

tv: Aric 581/1[125].

PI 61189[1525]; USSR.

Glu-A1p[1146] locus: 3* [1146]

v: David 1.

Glu-A1q[125] locus: 2*** [125] syn: Glu A1VI[125]

tv: Melianopus 1528.

Glu-A1r[1232] locus: 39+40[1232]

i: *T. thaoudar* IPSR 1020006/6*Sicco.

Glu-A1s[1231] locus: 41+42[1231]

i: *T. thaoudar* G3152/6*Sicco.

Glu-A1t[602] locus: 21* [602]

v: W29323, W3879, W31169.

Glu-A1u[02106] locus: 2^{*B} [02106]

v: Bankuti 1201.

The allele designated ***Glu-A1u*** and ***Glu-A1-1u*** in the appropriate list below encodes a high molecular weight glutenin subunit (denominated 2^{*B}) that is identical to subunit 2* apart from one amino acid difference involving the exchange of serine for cysteine (which itself is due to a C to G point mutation at the 1181 bp point of the coding region of 2*). The authors of ▶[02106] suggest that the additional cysteine residue facilitates the formation of further disulphide bonds (cf. the 1Dx5 subunit) which might lead to an improvement in gluten quality characters.

Glu-A1v[10327, 03137] locus: VII[03137] syn: Glu-A1-VII[03137]

v: Emmer accession PI 308879[03137].

Glu-A1w[10327] locus: 2.1*[10327]

v: KU-1094, KU-1026, KU-1086, Grado, KU-1139[10327].

Glu-A1x[10327] locus: 2'[10327]

v: TRI14165/91[10327].

The alleles formerly designated *t* to *x* in ▶[959] were renamed *x* to *ab* because allele *t* in ▶[847] and alleles *u, v* and *w* in ▶[1069] had precedence.

Glu-A1y [10535] syn: 2" [10535], 2"

v: 211.12014 [10535].

Glu-A1z [10805] syn: Glu-A1^{m}a [10805]

dv: PI 191146, *T. monococcum* ssp. *monococcum* [10805].

Glu-A1aa [10805] syn: Glu-A1^{m}b [10805]

dv: PI 190946, *T. monococcum* L. ssp. *monococcum* [10805].

Glu-A1ab [10805] syn: Glu-A1^{m}c [10805]

dv: PI 191098, *T. monococcum* ssp. *monococcum* [10805].

Glu-A1ac [10806] syn: Glu-A^{u}1-I [10806]

dv: PI 428319 [10806].

Glu-A1ad [10806] syn: Glu-A^{u}1-II [10806]

dv: PI 428232 [10806].

Glu-A1ae [10806] syn: Glu-A^{u}1-III [10806]

dv: PI 428240 [10806].

Glu-A1af [10806] syn: Glu-A^{u}1-IV [10806]

dv: PI 428335 [10806].

Glu-A1ag [10806] syn: Glu-A^{u}1-V [10806]

dv: PI 538741 [10806].

Glu-A1ah [10806] syn: Glu-A^{u}1-VI [10806]

dv: PI 428230 [10806].

Glu-A1ai [10806] syn: Glu-A^{u}1-VII [10806]

dv: PI 428253 [10806].

Glu-A1aj [10806] syn: Glu-A^{u}1-VIII [10806]

dv: PI 427328 [10806].

Glu-A1ak [10806] syn: Glu-A^{u}1-IX [10806]

dv: PI 428327 [10806].

Glu-A1al [10806] syn: Glu-A^{u}1-X [10806]

dv: PI 428256 [10806].

Glu-A1am [10806] syn: Glu-A^{u}1-XI [10806]

dv: PI 428224 [10806].

Glu-A1an [10806] syn: Glu-A^{u}1-XII [10806]

dv: PI 428228 [10806].

Glu-A1ao [10806] syn: Glu-A^{u}1-XIII [10806]

dv: PI 538724 [10806].

Glu-A1ap [10806] syn: Glu-A^{u}1-XIV [10806]

dv: TRI 6734 [10806].

Glu-A1aq [10806] syn: Glu-A^{u}1-XV [10806]

dv: TRI 11494 [10806].

Glu-A1ar [10806] syn: Glu-A^{u}1-XVI [10806]

dv: TRI 11495 [10806].

Glu-A1as[10806] syn: Glu-A^{u}1-XVII[10806]

dv: PI 428217[10806].

Glu-A1at[10806] syn: Glu-A^{u}3-XVIII[10806]

dv: PI 428225[10806].

Glu-A1au[10806] syn: Glu-A^{u}3-XIX[10806]

dv: PI 538733[10806].

Glu-A1av[10806] syn: Glu-A^{u}3-XX[10806]

dv: PI 428196[10806].

Glu-A1aw[10806] syn: Glu-A^{u}3-XXI[10806]

dv: PI 538724[10806].

Glu-A1ax[10806] syn: Glu-A^{u}3-XXII[10806]

dv: PI 428191[10806].

Glu-A1ay[10806] syn: Glu-A^{u}3-XXIII[10806]

dv: TRI 6734[10806].

Glu-A1az[10806] syn: Glu-A^{u}3-XXIV[10806]

dv: TRI 11496[10806].

Glu-A1ba[11106, 11107] locus: 1.1[11106] syn: Glu-A1g[11106]

v: Barbela 28[11106].

The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other GLU-A1 alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1[11107].

Glu-A1bb[11540]

tv: *T. turgidum* ssp. *turgidum* BGE019307[11540].

The importance of the HMW glutenin subunits for bread-making quality was first noted from observations in wheat cultivars of related pedigree on the effects of the presence of subunit 1 encoded by ***Glu-A1a***[0197], effects that have repeatedly been confirmed since (for example[0198, 0199, 01100]). There is a possibility that GLU-A1 alleles *i, j*[1527] and *k*[478] correspond to alleles *d, e, f* or *g*[1535] that were published shortly earlier. ***Glu-A1m*** [1526] was changed to *n*, because the *m* allele in ▶[1069] has precedence. Allele *n* [1526] was changed to *o*. An earlier reference to an allele designated ***Glu-A1d***[1411] was withdrawn[1114]. There appears to be a minor band associated with subunit 2 encoded by ***Glu-A1b***[1516]; this may be the same as a band named A5 in ▶[420].

Six combinations involving 5 HMW subunits [1A (u-z)] are listed in ▶[420], from a study of 109 genotypes including representatives of botanical varieties. Numerous alleles in *T. turgidum* var. *dicoccoides* populations, 12 at GLU-A1-1 and 3 at GLU-A1-2, were described in ▶[798]. In a further study using different germplasm of this species[205], 14 alleles at GLU-A1 were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at GLU-A1-1 (with up to 10 not previously observed), and 5 alleles at GLU-A1-2 (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.

In a study including emmer accessions (*T. dicoccum*)[00115], new subunits named 1^{+} and 2^{-} were found in accessions MG4378/1 and MG5380/1, respectively, and provisionally assigned to GLU-A1. Until confirmed, they are not included in the GLU-A1 list.

GLU-B1

Glu-B1[107, 1125] locus: 1BL[107, 780, 1125] syn: Glt-B1[420], Glu 1B[1415], Glt-B3[420], Glt-B2[420]

v: CS.

Glu-B1a[1116] locus: 7[1116]

v: Flinor.

Glu-B1b[1116] locus: 7+8[1116]

v: CS.

Subunit 8 of ***Glu-B1b*** (7+8) is more acidic in isoelectric focusing than subunit 8 of ***Glu-B1d*** (6+8)[555]. Variation in the mobility of subunits designated 7 was observed[1118], according with later observations[714, 1069]. The subunit encoded by ***Glu-B1v***[1069] has the same mobility as subunit 7 of ***Glu-B1c*** (7+9); it could be the same subunit as 7' encoded by ***Glu-B1ai*** [714]. Variation in the staining intensity of subunit 7 in different lines was observed[1069]; a duplication of the gene encoding subunit 7 probably occurred in cultivar 'Red River 68', as evidenced by increased intensity of the subunit in SDS-PAGE and by approximately doubled intensity of restriction fragments carrying the gene in Southern blotting[9989].

Glu-B1c[1116] locus: 7+9[1116]

v: Bezostaya 1.

Glu-B1d[1116] locus: 6+8[1116]

v: Hope. **tv**: Kronos[11497].

Simultaneous and individual truncation mutations were found in ***Glu-B1x*** and ***Glu-B1y*** subunits in Kronos mutant lines[11497]. Germplasm was accessioned as PI 692251 (T4-0865, *Bx6* single mutant), PI 692253 (T4-2197, *By8* single mutant) and PI 692252 (T4-1280, *Bx6* + *By8* combined mutant).

Glu-B1e[1116] locus: 20[1116].20x+20y[03133]

v: Federation.

Glu-B1f[1116] locus: 13+16[1116]

v: Lancota (rare).

Primers were designed to distinguish subunit By8 from By8*, for distinguishing subunit By9-containing alleles from non-By9 alleles, and for diagnosing the presence of ***Glu-B1f***.

Glu-B1g[1116] locus: 13+19[1116]

v: NS 335 (rare).

Glu-B1h[1116] locus: 14+15[1116]

v: Sappo (rare).

Glu-B1i[1116] locus: 17+18[1116]

v: Gabo.

Although alleles ***Glu-B1i*** encoding subunits 17+18, and ***Glu-B1bc*** encoding subunit 6+17, apparently share a common subunit (Ax17 and By17, respectively) it is not clear that this is in fact true.

Glu-B1j[1116] locus: 21[1116].21x+21y[03116]

v: Dunav (rare); Foison[03116].

Glu-B1k[1116] locus: 22[1116]

v: Serbian (rare).

Glu-B1l[778] locus: 23+24[778]

v: Spica D.

Glu-B1m[1527] syn: GLU-B1-l[1527]

tv: PI 94640, Iran, *T. dicoccum*.

Glu-B1n[1527] syn: GLU-B1-II[1527]

tv: PI 355505, Germany, *T. dicoccum*.

Glu-B1o[1527] syn: GLU-B1-III[1527]

tv: PI 352354, Ethiopia, *T. dicoccum*.

Glu-B1p[1527] locus: 23+18[125] syn: GLU-B1-IV[1527]

tv: Dritto[1523]; Ethiopia, PI 94655, *T. dicoccum*[1527].

Subunit 23 of ***Glu-B1p*** (23+18) and ***Glu-B1ad*** (23+22)[125] may not be the same subunit as that numbered 23 of ***Glu-B1l*** (23+24)[778].

Glu-B1q[1527] syn: GLU-B1-V[1527]

tv: PI 94633, Morocco, *T. dicoccum*.

Glu-B1r[1527] locus: 19[125] syn: GLU-B1-VI[1527]

tv: PI 946669, Bulgaria, *T. dicoccum*[1527]; Lambro[1523].

Glu-B1s[478] locus: 7+11[478]

v: BT-2288.

Subunit 11 of ***Glu-B1s*** (7+11) was so numbered in ▶[478] because its mobility is the same as one of the subunits encoded by a GLU-D1 allele (2+11) described in ▶[755].

Glu-B1t[847]

v: Supreza, Canada.

Glu-B1u[1069] locus: 7*+8[1146]

v: Owens[1069]; Fiorello[1146].

Glu-B1v[1069]

v: Mondor.

Glu-B1w[1069] locus: 6*+8*[1146]

v: Dawbull[1069]; Sieve[1146].

Possible low gene expression at **Glu-B1** was noted for ***Glu-B1w***, where subunits 6*+8* stain very faintly[1146].

Glu-B1x[1526] syn: Glu-B1-VII[1526], Glu-B1t[959]

tv: Canoco de Grao Escuro, Portugal, *T. turgidum*.

Glu-B1y[1526] syn: Glu-B1-VIII[1526], Glu-B1u[959]

tv: Tremez Mollez, Portugal, *T. durum*.

Glu-B1z[1524] locus: 7+15[125] syn: Glu-B1-IX[1524], Glu-B1v[959]

tv: Roccia, Italy, *T. durum*[125, 1523].

Glu-B1z carried by Roccia was numbered (7+15) and named *Glu-B1-XII* in ▶[125]; however, the earlier name, ***Glu-B1-IX***[1523], has precedence; also,[1523] states that the ***Glu-B1-IX*** subunit of faster mobility is slightly slower than subunit 15.

Glu-B1aa[1524] syn: Glu-B1w[959], Glu-B1-X[1524]

tv: Quaduro, Italy, *T. durum*.

Glu-B1ab[1523] syn: Glu-B1x[959], Glu-B1-XI[1523]

tv: Athena, Italy, *T. durum*.

Glu-B1ac[125] locus: 6+16[125] syn: Glu B1XIII[125]

tv: Espa l8914, *T. durum*.

Glu-B1ad[125] locus: 23+22[125] syn: Glu B1XIV[125]

tv: Greece 20, *T. durum*.

Glu-B1ae[1146] locus: 18*[1146]

v: David.

Glu-B1af[1146] locus: 26+27[1146]

v: Cologna 1.

One of the ***Glu-B1af*** subunits was numbered 26 in [1146]; 26 was previously used to number the subunit encoded by ***Glu-A1k***[478].

Glu-B1ag[1146] locus: 28+29[1146]

v: Forlani.

Subunit 28 of ***Glu-B1ag*** (28+29)[1146] is referred to as subunit 19* in [1068].

Glu-B1ah[782] locus: Null allele[782]

v: Olympic mutant.

Glu-B1ai[714] locus: 7'[714]

v: Adonis.

Glu-B1aj[759] locus: 8[759]

v: AUS 14444, Afghanistan.

Glu-B1ak[899] locus: 7*+8*[899]

v: Norstar.

Glu-B1al[899] locus: 7^{OE}+7^{OE}+8*[899]

v: Benkuti 1201; Glenlea[899]; Klein Universal II[10196].

Tezanos Pintos Precoz[10196]; Tobari 66[10196]. Other genotypes are listed in [10196].

Many of the cultivars carrying the over-expressed subunit 7 encoded by ***Glu-B1al*** show %UPP values that transcend the normal range observed for cultivars that lack this subunit[10089], which presumably is associated in some way with its unusually high amount in the grain. The underlying cause of the increased amount may be due to an increased transcriptional rate compared to other alleles, for which a known difference in promoter sequence compared to other alleles expressing normal levels of this subunit[10090] may be responsible.

However, there is evidence that over-expression is due to duplication of subunit 7[10196]. Regarding to subunit 8*, evidence was presented to indicate that in Glenlea, one of the standard cultivars for the allele, this subunit is the same as subunit 8[10808].

Glu-B1am[1229] locus: 18[1229]

v: Royo.

Glu-B1an[1229] locus: 6[1229]

v: BG-2013.

Glu-B1ao[1229] locus: 7+16[1229]

v: BG-3545.

Glu-B1ap[1229] locus: 30+31[1229]

v: Marinar.

Glu-B1aq[1229] locus: 32+33[1229]

v: BG-1943.

Glu-B1ar[1229] locus: 34+35[1229]

v: Jeja Almendros.

Glu-B1as[1229] locus: 13[1229]

v: PI 348435.

Glu-B1at[1229] locus: 13+18[1229]

v: PI 348449.

Glu-B1au[1032] locus: 37[1032]

v: Shedraya Polesja.

Glu-B1av[03116] locus: 7-18[03116] syn: Glu-B1r[03116]

v: Triticor hexaploid *triticale*[03116].

Glu-B1aw[03116] locus: 6.8-20y[03116] syn: Glu-B1s[03116]

v: Carnac hexaploid *triticale*[03116].

Glu-B1ax[03137] locus: *XV* [03137] syn: Glu-B1-XV[03137]

tv: PI-190922, BG-012302 emmer[03137].

Glu-B1ay[03137] locus: *XVI* [03137] syn: Glu-B1-XVI[03137]

tv: PI 277681 emmer[03137].

Glu-B1az[03137] locus: *XVII* [03137] syn: Glu-B1-XVII[03137]

tv: PI 348620 emmer[03137].

Glu-B1ba[03122] locus: 13*+16[03122] syn: Glu-B1-XVIII[03122]

v: PI 348767 spelt[03122].

Glu-B1bb[03122] locus: 6+18'[03122] syn: Glu-B1-XLX[03122]

v: PI 348631 spelt[03122].

Glu-B1bc[03138] locus: 6+17[03138]

v: ICDW 20975[03138].

Glu-B1bd[03140] locus: 20+8[03140]

v: Abadja[03140].

Glu-B1be[10186]

tv: *T. dicoccoides* Israel-A[10186].

Glu-B1bf[10186]

tv: *T. dicoccoides* PI 481521[10186].

Glu-B1bg[10186]

tv: *T. dicoccoides* PI 478742[10186].

Glu-B1bh[10327] locus: 13+22[10327]

v: Grado[10327]; KU-1026[10327]; KU-1086[10327]; KU-1094[10327]; KU-1139[10327].

Glu-B1bi[10327] locus: 13+22.1[10327]

v: KU-1135[10327].

Glu-B1bj[10327] locus: 14*+15*[10327]

v: TRI11553/92[10327].

Glu-B1bk[10327] locus: 6.1+22.1[10327] syn: Glu-B1be[10327]

v: Hercule[10327]; Rouguin[10327]; Schwabenkorn[10327]; SP3[10327]; Steiners Roter Tiroler[10327].

Glu-B1bl[10327] locus: 6.1[10327] syn: Glu-B1bf[10327]

v: KU-3418[10327]; KU-3446[10327]; TRI4613/75[10327].

Glu-B1bm [10327] locus: 13*+19* [10327] syn: Glu-B1bg [10327]

v: KU-3410 [10327]; Renval [10327]; Rechenbergs Fruher Dinkel [10327]; Schlegel [10327]; SP1 [10327]; TRI9885/74 [10327]; Zeiners WeiSer [10327].

Glu-B1bn [10425] locus: 7+19 [10425]

v: Triticales: Lasko, Dagno, Tewo, Vision, Dato [10425].

Glu-B1bo [10425] locus: 7+26 [10425]

v: Triticales: Presto, Modus [10425]. The number 26 was also used to designate a subunit encoded by ***Glu-A1k*** and ***Glu-A1-1k***.

Glu-B1bp [10643] locus: 7**+8 [10643]

v: XM1368-2 [10643]; XM1404-2 [10643].

Glu-B1bq [10643] locus: 7+8** [10643]

7+8** [10643].

Glu-B1br [10807] locus: 7.1+7.2+8* [10807]

v: H45 [10807].

Glu-B1bs [10807] locus: 7.3+7^{OE}+8* [10807]

v: VQ0437 [10807].

Glu-B1bt [10809] locus: 17'+18' [10809]

tv: TGR-214 [10809].

Glu-B1bu [10809] locus: 17'+18* [10809]

tv: TGR-2246 [10809].

Glu-B1bv [10809] locus: 13**+8* [10809]

tv: TGR-003 [10809].

Glu-B1bw [10809] locus: 8' [10809]

tv: TGR-244 [10809].

Glu-B1bx [10810] locus: 7+17 [10810]

v: CWI-59797, *T. aestivum* var. *ferrugineum* [10810].

Glu-B1by [10808] locus: 7b*+8 [10808]

v: Eshimashinriki [10808].

Glu-B1bz [10808] locus: 7^{OE} [10808]

v: Attila [10808]; Darius [10808]; Cappelle-Desprez [10808]; Festin [10808]; Petrel [10808].

Glu-B1ca [10808] locus: 6+8b* [10808]

v: Appolo [10808]; Brimstone [10808]; Clement [10808]; Nidera Baguette 10 [10808]; Ruso [10808]; Pepital [10808]; Thesee [10808].

Glu-B1cb [10808] locus: 7^{OE}+8 [10808]

v: ACA 303 [10808]; Courtot [10808]; Demai 3 [10808]; Shinchunaga [10808].

Glu-B1cc [10808] locus: 7^{OE}+8a* [10808]

v: Klein Jabal 1 [10808]; Pioneer [10808]; ProINTA [10808].

Redemon [10808].

Glu-B1cd [10808] locus: 7^{OE}+8b* [10808]

v: ACA 601 [10808].

Glu-B1ce[10808] locus: 7+8a*[10808]

v: Jing 411[10808]; Tasman[10808].

In a study including emmer wheats (*T. dicoccon*)[00115], new subunits named 7^{+} (in accessions MG5400/5 and MG30835/1), 8^{-} (in accessions MG5400/5, MG30835/1, MG5333/1 and MG5507) and 13^{-} (in accession MG5282/2) were found and provisionally assigned to **Glu-B1**. Until confirmed, they are not included in the **Glu-B1** list.

Glu-B1cf[11490] locus: 20*+33*[11490]

tv: *T. turgidum* ssp. *durum* Mexican landrace accession 22 (CWI52215)[11490].

Glu-B1cg[11490] locus: 13+16*[11490]

tv: *T. turgidum* ssp. *durum* Mexican landrace accession 19 (CWI52200)[11490].

Glu-B1ch[11490] locus: 7+22[11490]

v: *T. aestivum* ssp. *aestivum* cv. Wilbur (CW13735)[11490].

Glu-B1ci[11490] locus: 7+22*[11490]

tv: *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280) {11490.

Glu-B1cj[11490] locus: 13*+15*[11490]

tv: *T. turgidum* ssp. *durum* Iranian landrace accession 46 (CWI56913)[11490].

Glu-B1ck[11491] locus: 15[11491]

v: *T. aestivum* ssp. *compactum* PI 157920[11491].

Glu-B1cl[11491] locus: 14+8[11491]

v: *T. aestivum* ssp. *macha* PI 272554, PI 278660, PI 290507[11491].

Glu-B1cm[11491] locus: 6+8*[11491]

v: *T. aestivum* ssp. *macha* PI 428177[11491].

Glu-B1cn[11491] locus: 17[11491]

v: *T. aestivum* ssp. *sphaerococcum* CItr 4531, PI 272581, PI 282452[11491].

Glu-B1co[11493] locus: 20+22*[11493]

tv: *T. turgidum* ssp. *durum* Moroccan landraces MGB-2963, MGB-3152[11493].

Glu-B1cp[11493] locus: 20*[11493]

tv: *T. turgidum* ssp. *durum* North American cv. MGB-66023[11493].

Glu-B1cq[11492] locus: 7+8*[11492]

tv: *T. turgidum* ssp. *turgidum* BGE048494[11492].

Glu-B1cr[11492] locus: 8*.1+20y[11492]

tv: *T. turgidum* ssp. *durum* BGE045649[11492], BGE047535[11492].

Glu-B1cs[11492] locus: 20x[11492]

tv: *T. turgidum* ssp. *durum* BGE045673[11492].

Glu-B1ct[11540] locus: 6+(8)[11540]

tv: *T. turgidum* ssp. *durum* Langdon[11540].

GLU-D1

Glu-D1[1100, 1125] locus: 1DL[107, 150, 780, 1100, 1125] syn: Glt-D2[420], Glu 1D[1415], Glt-D1[420]

v: CS.

Five combinations involving 6 HMW subunits [1D (p-t)] are listed in ▶[420]. Eleven additional GLU-D1 alleles in *T. tauschii* were described[755]. Seven transfers of ***Glu-D1a*** and 10 of ***Glu-D1d*** (5+10) from chromosome 1D to chromosome 1A in triticale were described[846]. The subunit 2.2* encoded by

Glu-D1al and ***Glu-D1-1m*** in the appropriate list below has an unusually high Mr. Comparison of its N-terminal sequence and amino acid composition with those of subunit 2 (encoded by ***Glu-D1-1a***) indicated that its greater Mr could be due to the presence of a larger central repetitive domain, although further evidence suggested that this does not affect the conformational properties of the subunit[02107]. The alleles originally designated ***Glu-D1w*** (encoding 'subunits' 2 (or 2^t denoting its origin in the *Ae. tauschii* genome) +T1+T2), ***Glu-D1af*** (encoding 3 (or 3^t)+T1+T2) and ***Glu-D1ag*** (encoding 1.5 (or1.5^t)+T1+T2) share the component T1 that was originally classified as a HMW glutenin. However, it has since been shown[02108] that this protein is soluble in aqueous ethanol, casting doubt upon this classification.

More recently, it was shown[02109], from one- and two-dimensional gel electrophoresis based upon SDS-PAGE and A-PAGE, and from N-terminal sequencing, that this protein is an omega-gliadin of unusually low electrophoretic mobility in SDS-PAGE, encoded by a locus located on the short arm of chromosome 1D, though distant (13.18 cM) from the principle gliadin-encoding locus on 1D, **Gli-D1**, and 40.20 cM from the high molecular weight encoding locus, **Glu-D1**. The authors named the locus **Gli-DT1** (see Gliadins). Reference to T1 was consequently removed from the GLU-D1 list. As a consequence of this finding, allele ***Glu-D1w*** was reused for a distinct allele, and ***Glu-D1af*** was omitted and will be reused for a future allele, since the combinations of subunits that these alleles originally represented are no longer unique. In ▸[03124], null alleles were observed for both GLU-D1-1 and GLU-D1-2, which, naturally, are not necessarily the same as those previously reported for this locus, meaning that composite alleles involving them in this study and corresponding to combinations apparently already listed in the Catalogue, may, in fact, represent novel alleles. It was also found that certain subunits of apparently identical relative mobility in SDS-PAGE showed different surface hydrophobocities in RP-HPLC; and the reverse situation was also observed (the same hydrophobicity, but different electrophoretic mobilities). It was shown[03126] that the relatively small size of a y-type HMW glutenin subunit, named 12.4^t (encoded by ***Glu-D1-1t***[03124] – see below) and carried by accession CPI 110750 of *Ae. tauschii*, is due to the deletion of blocks of repetitive motifs, amounting to approximately 200 amino acids, probably caused by unequal crossing-over

Glu-D1a[1116] locus: 2+12[1116]

v: CS.

Primers were designated that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12[10641].

Glu-D1b[1116] locus: 3+12[1116]

v: Hobbit.

Glu-D1c[1116] locus: 4+12[1116]

v: Champlein.

Glu-D1d[1116] locus: 5+10[1116]

v: Hope.

Glu-D1e[1116] locus: 2+10[1116]

v: Flinor (rare).

Glu-D1f[1116] locus: 2.2+12[1116]

v: Danchi (rare).

Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality[10573].

Glu-D1g[478] locus: 5+9[478]

v: BT-2288.

Subunit 9 of ***Glu-D1g*** (5+9) was so numbered in ▸[478] because its mobility is the same as one of the subunits encoded by ***Glu-B1c*** (7+9).

Glu-D1h[1145] locus: 5+12[1145]

v: Fiorello, Italy.

Cultivar Fiorello is given as a standard for ***Glu-D1h*** encoding subunits 5+12 and for ***Glu-D1w*** encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1i[107] locus: Null[107]

v: Nap Hal, Nepal.

Glu-D1j[1146] locus: 2+12* [1146]

v: Tudest.

Glu-D1k[421] locus: 2[421]

s: CS/Timstein 1D.

Glu-D1k[421] appears to have arisen as the result of a deficiency of subunit 12 from ***Glu-D1a*** (2+12); subunits 2 and 12 are referred to as D1 and D5 in [421].

Glu-D1l[759] locus: 12[759]

v: AUS 10037, Afghanistan.

Glu-D1m[759] locus: 10[759]

v: AUS 13673, Afghanistan.

Glu-D1n[759] locus: 2.1+10[759]

v: AUS 14653, Afghanistan.

Glu-D1o[755] locus: 2.1+13[755]

v: AUS 14519, *T. macha*.

One of the ***Glu-D1o*** subunits was numbered 13 in [755]; 13 was previously used to number a subunit encoded by ***Glu-B1f*** (13+16) and ***Glu-B1g*** (13+19)[1116].

Glu-D1p[1233] locus: 36[1233]

i: Iranian landrace accession 3048/5* Sicco.

Glu-D1q[124] locus: 2+11[124]

v: Flinor.

Glu-D1r[1229] locus: 2.3+12[1229]

v: PI 348465.

Glu-D1s[1032] locus: 38[1032]

v: Leningradka.

Glu-D1t[668] locus: 43+44[668]

dv: *Ae. tauschii* accession TA2450/2*.

Glu-D1u[836] locus: 2+10'[836]

v: Coker 68-15.

Glu-D1v[755] locus: 2.1+10.1[755]

dv: *Ae. tauschii*.

Glu-D1w[03124] locus: 5*+10[03124]

v: Fiorello[03124].

Note that the cultivar Fiorello is given as a standard for ***Glu-D1h*** encoding subunits 5+12 and for ***Glu-D1w*** encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1x[755] locus: 2+T2[755].2^{t}+12.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1y[755] locus: 3[t]+12.2[t][03124]. 3+T2[755]

dv: *Ae. tauschii*.

Glu-D1z[755] locus: 3+10[755]

dv: *Ae. tauschii*.

Glu-D1aa[755] locus: 3+10.3[755]

dv: *Ae. tauschii*.

Glu-D1ab[755] locus: 4.1+10[755]

dv: *Ae. tauschii*.

Glu-D1ac[755] locus: 4+10[755]

dv: *Ae. tauschii*.

Glu-D1ad[755] locus: 5.1+10.2[755]

dv: *Ae. tauschii*.

Glu-D1ae[1578] locus: 2.1[t]+12.2[t][03124]. 2.1+T2[1578]

dv: *Ae. tauschii*.

Glu-D1af[1578] locus: 3+T1+T2

Currently undesignated for reasons given in the preamble to this section.

Glu-D1ag[1578] locus: 1.5+T2[1578]. 1.5[t]+12.2[t][03124]

dv: *Ae. tauschii*.

Glu-D1ah[1578] locus: 1.5+10[1578]

dv: *Ae. tauschii*.

Glu-D1ai[1578] locus: 2.1+10.5[1578]

dv: *Ae. tauschii*.

Glu-D1aj[1578] locus: 1.5+12[1578]

dv: *Ae. tauschii*.

Glu-D1ak[1578] locus: 3+10.5[1578]

dv: *Ae. tauschii*.

Glu-D1al[02107] locus: 2.2[*][02107]

v: MG315.

Glu-D1am[03122] locus: 2+12'[03122] syn: Glu-D1-I[03122]

v: PI 348495 spelt[03122].

Glu-D1an[03122] locus: 2+12[*][03122] syn: Glu-D1-II[03122]

v: PI 348672 spelt[03122].

Glu-D1ao[03122] locus: 2.4+12[03122] syn: Glu-D1-III[03122]

v: PI 348473 spelt[03122].

Glu-D1ap[03122] locus: 2.5+12[03122] syn: Glu-D1-IV[03122]

v: PI 348572 spelt[03122].

Glu-D1aq[03124] locus: 1.5[t]+10.1[t][03124]

dv: *Ae. tauschii*.

Glu-D1ar[03124] locus: 2[t]+10.1[t][03124]

dv: *Ae. tauschii*.

Glu-D1as [03124] locus: 1.5^{t}+10.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1at [03124] locus: 3^{t}+10.1^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1au [03124] locus: 2.1^{t}+10.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1av [03124] locus: 2^{t}+12.3^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1aw [03124] locus: 1^{t}+10^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1ax [03124] locus: 1^{t}+12^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1ay [03124] locus: 1^{t}+10.1^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1az [03124] locus: 4^{t}+12.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1ba [03124] locus: 1^{t}+12.3^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bb [03124] locus: 1.5^{t}+11^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bc [03124] locus: 1.5^{t}+10.3^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bd [03124] locus: 1^{t}+11^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1be [03124] locus: 2.1^{t}+12.4^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bf [03124] locus: 2^{t}+12.1^{t} [03124]

dv: *Ae. tauschii* [03124].

Glu-D1bg [03124] locus: 3^{t}+10.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bh [03124] locus: 4^{t}+10.1^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bi [03124] locus: 4^{t}+10.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bj [03124] locus: 5^{t}+11^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bk [03124] locus: 5^{t}+10.1^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bl [03124] locus: 5^{t}+12.2^{t} [03124]

dv: *Ae. tauschii*.

Glu-D1bm [03124] locus: 5*t+null [03124]

dv: *Ae. tauschii*.

Glu-D1bn [03124] locus: 5*t+12 [03124]

dv: *Ae. tauschii*.

Glu-D1bo [10091] locus: 5'+12 [10091]

v: W958 [10091].

This putative new allele encodes two subunits that have very similar electrophoretic mobilities compared to subunits 5+12 encoded by ***Glu-D1h***, but analysis using the specific PCR primers for Dx5 described in [10092, 10093] shows that the x-type subunit of ***Glu-D1bo***, provisionally denominated 5' [10091], does not appear to be the same protein as subunit 5 [10091]. Definitive evidence awaits sequencing information (See note to allele ***Glu-D1-1s***).

Glu-D1bp [10327] locus: 2.1'+12 [10327]

v: KU-1034 [10327].

Glu-D1bq [10304] locus: 2.6+12 [10304] syn: Glu-D1bp(t) [10304]

v: Baidongmai [10304]; Hongdongmai [10304]; Hongkedongmai [10304]; Jinbaojin [10304].

The complete sequence of this subunit was determined [10319].

Glu-D1br [10426] locus: 5*t+10.1^{t} [10426]

tv: *Ae. tauschii* TD81 [10426].

Subunit 10.1^{t} possesses a mobility slightly lower than subunit 10 in SDS-PAGE and its deduced amino acid sequence is similar to subunit 12 (8 amino acid differences) [10426]; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that a Glu-1 gene duplication event occurred about 16.83 million years ago.

Glu-D1bs [10642] locus: 1.6^{t}+12.3^{t} [10642]

dv: *Ae. tauschii* TD16 [10642].

Glu-D1bt [10568] locus: 2.1^{t}+12^{t} [10568]

v: Syn 396 [10568].

Glu-D1bu [10810] locus: 2'+12 [10810]

v: CWI-64806, *T. aestivum* var. *aestivum* [10810].

Glu-D1bv [10810] locus: 2''+10 [10810]

v: CWI-65297, *T. aestivum* var. *erythroleucon* [10810].

Glu-D1bw [10810] locus: 2''+12 [10810]

v: CWI-60509, *T. aestivum* var. *graecum* [10810].

GLU-E1

Glu-E1 [781] locus: 1ES [781]

ad: CS/*E. elongata*.

HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced [10439] and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intra-molecular disulphide bond formation.

Four [10660, 10661] and 11 [10662] alleles were observed in *Agropyron elongatum* (E^{e} genome, 2n = 10X = 70) and named *Aex1* to *Aex5* (producing x-type subunits) and *Aey1* to *Aey10* (producing y-type subunits). *Aex4, Aey7* and *Aey9* were very similar to three alleles in the diploid progenitor *Lophopyrum elongatum* [10439, 10663]. The C-terminal regions of three of the y-type subunits (products of *Aey8, Aey9*

and 11[10662] alleles were observed in *Agropyron elongatum* (E^e genome, 2n = 10X = 70) and named *Aex1* to *Aex5* (producing x-type subunits) and *Aey1* to *Aey10* (producing y-type subunits). *Aex4, Aey7* and *Aey9* were very similar to three alleles in the diploid progenitor *Lophopyrum elongatum*[10439, 10663]. The C-terminal regions of three of the y-type subunits (products of *Aey8, Aey9* and *Aey10*) were more similar to x-type subunits than to other y-type subunits[10662]. The subunit from *Aex4* contained an additional cysteine residue, which may be associated with good processing quality in wheat introgression lines[10662]. Allele *Aey-4* was a chimeric gene formed by recombination of two other genes[10662].

Chinese *T. aestivum* cultivar Xiaoyanmai carries a subunit with electrophoretic mobility in 10% SDS-PAGE well beyond that of subunits so far observed in *T. aestivum*. It may derive from *Agropyron elongatum*, which was used in the breeding program that led to the variety[1538]. It has not been given a subunit number or allelic designation, because its genetic control has not been elucidated.

Glu-E1a[781]

ad: CS/*L. elongatum* W0622[781].

Glu-E1b[10644]

ad: Langdon/*L. elongatum* DGE-1[10644]. **al**: *L. elongatum* PI 531719[10644].

Glu-H1

Glu-H1[781] locus: 1HL[1337].1H[781] syn: Hor 3[1337]

ad: CS/Betzes[781]. **al**: Various barley cultivars[1337].

Glu-H^{ch}1 locus: $1H^{ch}$ [1123]

ad: CS/*H. chilense*.

38 accessions (natural populations) of *Hordeum chilense* carrying the following 10 subunits were used as the maternal parents of 121 lines of primary tritordeum, and evaluations for associations with bread-making quality initiated[03114]. Subunits 1^{Hch}, 2^{Hch} and 3^{Hch} were previously referred to as H^{ch}a, H^{ch}b and H^{ch}c[03112].

Glu-H^{ch}1a[03114] locus: 1^{Hch} [03114]

al: *H. chilense* accession H1[03114].

Glu-H^{ch}1b[03114] locus: 2^{Hch} [03114]

al: *H. chilense* accession H11[03114].

Glu-H^{ch}1c[03114] locus: 3^{Hch} [03114]

al: *H. chilense* accession H7[03114].

Glu-H^{ch}1d[03114] locus: 4^{Hch} [03114]

al: *H. chilense* accesion H16[03114].

Glu-H^{ch}1e[03114] locus: 5^{Hch} [03114]

al: *H. chilense* accession H47[03114].

Glu-H^{ch}1f[03114] locus: 6^{Hch} [03114]

al: *H. chilense* accession H220[03114].

Glu-H^{ch}1g[03114] locus: 7^{Hch} [03114]

al: *H. chilense* accession H293[03114].

Glu-H^{ch}1h[03114] locus: 8^{Hch} [03114]

al: *H. chilense* accession H297[03114].

Glu-H^{ch}1i[03114] locus: 9^{Hch} [03114]

al: *H. chilense* accession H252[03114].

Glu-H^{ch}1j[03114] locus: 10^{Hch} [03114]

al: *H. chilense* accession H210[03114].

Glu-H^{t}1[1037] locus: 1H^{t}L[1037]

ad: CS/*E. trachycaulum*.

GLU-R1

Glu-R1[781, 1356] locus: 1RL[1340, 1356].1R[781, 1336] syn: Sec 3[1336]

ad: CS/Imperial; Holdfast/King II[1340]. **tr**: CS Imperial 1DS.1RL[1356].

Glu-R1a[03116] locus: 1^{r}-4^{r} [03116]

v: Indiana hexaploid triticale[03116].

Glu-R1b[03116] locus: 2^{r}-6.5^{r} [03116]

v: Graal hexaploid triticale[03116].

Glu-R1c[03116] locus: 6^{r}-13^{r} [03116]

v: Almao hexaploid triticale[03116].

Glu-R1d[03116] locus: 2^{r}-9^{r} [03116]

v: Olympus hexaploid triticale[03116].

Glu-R1e[03116] locus: 6.5^{r} [03116]

v: Clercal hexaploid triticale[03116].

Glu-R1f[03115] locus: 0.8^{r}-6^{r} [03115]

v: Carmara hexaploid triticale[03115].

Glu-R1g[03115] locus: 5.8^{r} [03115]

v: Arrayan hexaploid triticale[03115].

From study of chromosome substitutions in bread wheat[03117], it was found that a chromosome 1R carrying HMW secalin subunit 6.5^{r} (***Glu-R1e***), originally derived from the 'Petkus' rye population, was associated with bread making quality (i) intermediate between chromosome 1A carrying the null allele ***Glu-A1c*** and chromosome 1A carrying HMW glutenin subunit 2* encoded by ***Glu-A1b***; (ii) equivalent to a chromosome carrying HMW glutenin subunit 7 encoded by ***Glu-B1a***; and (iii) inferior to chromosomes 1D with distinct alleles.

There is a difficulty in the assignment of subunit 6^{r} in the **GLU-R1-1** and **GLU-R1-2** lists, since it appears as an x-type subunit in allele ***Glu-R1c*** and as a y-type subunit in allele ***Glu-R1f***. It is currently provisionally assigned to the **GLU-R1-1** list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

Five new x-type subunits (plus the null allele) and four y-type subunits were reported in [10094]. They vary principally through duplications and deletions of the tri-, hexa- and nona-peptide motifs found in the central repetitive region of the subunits. Orthologous genes were found to be more closely related than paralogous genes, supporting the hypothesis that gene duplication occurred before Triticeae speciation[10094, 10095].

Glu-R1-2 locus: 1R, 1RL

Glu-R1-2a[03116] locus: 4^{r} [03116]

v: Indiana hexaploid triticale[03116].

Glu-R1-2b[03116] locus: 6.5^{r} [03116]

v: Graal hexaploid triticale[03116].

Glu-R1-2c[03116] locus: 13^{r} [03116]

v: Alamo hexaploid triticale[03116].

Glu-R1-2d[03116] locus: 9^{r} [03116]

v: Olympus hexaploid triticale[03116].

Glu-R^{m}1[1339] locus: $1R^{m}L$ [1339, 1340]

ad: CS/*S. montanum* [1339, 1340].

GLU-S^{l}1

Glu-S^{l}1[1228] locus: $1S^{l}L$ [1228]

ma: In *Ae. longissima 2*/*Ae. longissima 10, GLU-S*^{l}1, G*LU-S*^{l}*3*, one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one and other[1228] as follows: *GLU-S*^{l}1 – 15.9 cM – *GPI-S*^{l}1 – 38 cM – *GLI-S*^{l}4 – 7.1 cM – *GLU-S*^{l}3 – 0.9 cM – *GLI-S*^{l}1 – 5.6 cM – *GLI-S*^{l}5. *GLU-S*^{l}1 is located in $1S^{l}L$ and the other loci are in $1S^{l}S$.

GLU-Ta1

Glu-Ta1[10449]

al: *Taeniatherum crinitum* PI 204577[10449].

GLU-A1-1

Glu-A1-1

Glu-A1-1a locus: Null

v: CS.

Glu-A1-1b locus: 1

v: Hope.

Glu-A1-1c locus: 2^{*}

v: Bezostaya 1.

A PCR marker specific for the ***Glu-A1-1c*** (Ax2^{*}) allele was developed in [0147].

Glu-A1-1d

v: V74, Spain.

Glu-A1-1e

v: 132c, Poland.

Glu-A1-1f

v: 112-29, Sudan.

Glu-A1-1g

v: Landrace 1600.

Glu-A1-1h

tv: PI 94683, USSR, *T. dicoccum*.

Glu-A1-1i

tv: CI 12213, India, *T. dicoccum*.

Glu-A1-1j locus: 1’

tv: PI 352359, Germany, *T. dicoccum*; Lambro.

Glu-A1-1k locus: 26

v: BT-2288.

Glu-A1-1l

tv: Chinook, Canada.

Glu-A1-1m

tv: Nugget Biotype 1, Canada.

Glu-A1-1n locus: 1”

tv: Corado, Portugal.

Glu-A1-1o locus: 2**

tv: PI 61189, USSR, Aric 581/1.

Glu-A1-1p locus: 3*

v: David 1.

Glu-A1-1q locus: 2***

tv: Melianopus 1528.

Glu-A1-1r locus: 39

i: *T. thaoudar* IPSR 1020006/6* Sicco.

Glu-A1-1s locus: 41

i: *T. thaoudar* G3152/6*Sicco.

Glu-A1-1t[602] locus: 21* [602]

v: W29323, W 3879, W 31169.

Glu-A1-1t is a provisional designation; definitive evidence that subunit 21*, which has a mobility similar to that of subunit 21, is a ‘x-type’ and not a ‘y-type’ protein has not been obtained.

Glu-A1-1u[02106] locus: 2*B [02106]

v: Bankuti 1201.

Glu-A1-1v[10327] locus: 2.1*[10327]

v: Grado[10327]; KU-1026[10327]; KU-1086[10327]; KU-1094[10327]; KU-1139[10327].

Glu-A1-1w[10327] locus: 2’[10327]

v: TRI14165/91[10327].

Glu-A1-1x[10535] locus: 2”[10535]

v: 211.12014[10535].

Glu-A1-1y[11540]

tv: *T. turgidum* ssp. *turgidum* BGE019307[11540].

Glu-A1-1z[11106] locus: 1.1[11106] syn: Glu-A1g[11106]

v: Barbela 28[11106].

The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other GLU-A1 alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1[11107].

GLU-A1-2

Glu-A1-2

Glu-A1-2a locus: Null

v: CS.

Glu-A1-2b locus: 40

i: *T. thaoudar* IPSR1020006/6* Sicco.

Glu-A1-2c locus: 42

i: *T. thaoudar* G3152/6*Sicco.

GLU-B1-1

Glu-B1-1

Glu-B1-1a locus: 7

v: CS.

A PCR marker (2373 bp) for the ***Glu-B1-1a*** (Bx7) allele was developed in 0145.

Glu-B1-1b locus: 7, 7*

v: Flinor, Bezostaya 1, Owens, Norstar.

Glu-B1-1c locus: 7'

v: Adonis.

Glu-B1-1d locus: 6

v: Hope.

Glu-B1-1e locus: 20

v: Federation.

Glu-B1-1f locus: 13

v: Lancota.

Glu-B1-1g locus: 14

v: Sappo.

Glu-B1-1h locus: 17

v: Gabo.

Glu-B1-1i locus: 21.21x03116

v: Dunav; Foison03116.

Glu-B1-1j locus: 23

v: Spica D.

Glu-B1-1k

tv: PI 94640, Iran, *T. dicoccum*.

Glu-B1-1l

tv: PI 355505, Germany, *T. dicoccum*.

Glu-B1-1m

tv: PI 352354, Ethiopia, *T. dicoccum*.

Glu-B1-1n

tv: PI 94633, Morocco, *T. dicoccum*.

Glu-B1-1o

v: Supreza, Canada.

Glu-B1-1p

v: Mondor.

Glu-B1-1q

tv: Canoco de Grao Escuro, Portugal.

Glu-B1-1r

tv: Tremez Mollez, Portugal.

Glu-B1-1s

tv: Quaduro, Italy.

Glu-B1-1t

tv: Athena, Italy.

Glu-B1-1u locus: 26

v: Cologna 1.

Glu-B1-1v locus: 28

v: Forlani.

Glu-B1-1w locus: Null

v: Olympic mutant.

Glu-B1-1x locus: 30

v: Marinar.

Glu-B1-1y locus: 32

v: BG-1943.

Glu-B1-1z locus: 34

v: Jeja Almendros.

Glu-B1-1aa locus: 37

v: Shedraya Polesja.

Glu-B1-1ab locus: 6*

v: Dawbill.

Glu-B1-1ac[03116] locus: 6.8[03116]

v: Carnac hexaploid triticale[03116].

Glu-B1-1ad[03122] locus: 13* [03122]

v: PI 348767 spelt[03122].

Glu-B1-1ae[10327] locus: 14*[10327]

v: TRI11553/92[10327].

Glu-B1-1af[10327] locus: 6.1[10327]

v: Hercule[10327]; KU-3418[10327]; KU-3446[10327]; Rouguin[10327]; Schwabenkorn[10327]; SP3[10327]; Steiners Roter Tiroler[10327]; TRI4613/75[10327].

Glu-B1-1ag[10643] locus: 7** [10643]

v: XM1368-2[10643].

Glu-B1-1ah[899] locus: 7OE [899]

v: Benkuti 1201[10196, 10197]; Glenlea[899]; Klein Universal II[10196]; Tezanos Pintos Precoz[10196]; Tobari[10196].

Glu-B1-1ai[10807] locus: 7.1[10807]

v: H45[10807].

Glu-B1-1aj[10807] locus: 10807}. 7.2[10807]

v: H45[10807].

Glu-B1-1ak[10807] locus: 7.3[10807]

v: VQ0437[10807].

Glu-B1-1al [10809] locus: 17' [10809]

tv: TGR-214 [10809]; TGR-2246 [10809].

Glu-B1-1am [10809] locus: 13** [10809]

tv: TGR-003 [10809].

Glu-B1-1an [10808] locus: 7b* [10808]

v: Eshimashinriki [10808].

Glu-B1-1ao [11490] locus: 20* [11490]

tv: *T. turgidum* ssp. *durum* Mexican landrace accession 22 (CWI52215) [11490].

GLU-B1-2

Glu-B1-2

Glu-B1-2a locus: 8

v: CS.

Glu-B1-2b locus: 9

v: Bezostaya 1.

Glu-B1-2c locus: 16

v: Lancota.

Glu-B1-2d locus: 19

v: NS 335.

Glu-B1-2e locus: 15

v: Sappo.

Glu-B1-2f locus: 18

v: Gabo.

Glu-B1-2g locus: 22

v: Serbian.

Glu-B1-2h locus: 24

v: Spica D.

Glu-B1-2i

tv: PI 355505, Germany, *T. dicoccum*.

Glu-B1-2j

tv: PI 352354, Ethiopia, *T. dicoccum*.

Glu-B1-2k

tv: PI 94633, Morocco, *T. dicoccum*.

Glu-B1-2l locus: 11

v: BT-2288.

Glu-B1-2m

v: Supreza, Canada.

Glu-B1-2n

v: Mondor.

Glu-B1-2o locus: 8*

v: Dawbull.

Glu-B1-2p

tv: Canoco de Grao Escuro, Portugal.

Glu-B1-2q

tv: Tremez Mollez, Portugal, *T. durum*.

Glu-B1-2s locus: 18*

v: David.

Glu-B1-2t locus: 27

v: Cologna 1.

Glu-B1-2u locus: 29

v: Forlani.

Glu-B1-2v locus: Null

v: Olympic mutant.

Glu-B1-2w locus: 31

v: Marinar.

Glu-B1-2x locus: 33

v: BG-1943.

Glu-B1-2y locus: 35

v: Jeja Almendros.

Glu-B1-2z[03116] locus: 20y[03116]

v: Carnac hexaploid triticale[03116].

Glu-B1-2aa[03122] locus: 18'[03122]

v: PI 348631 spelt[03122].

Glu-B1-2ab[03116] locus: 21y[03116]

v: Foison[03116].

Glu-B1-2ac[10327] locus: 22*[10327]

v: Grado[10327]; KU-1026[10327]; KU-1086[10327]; KU-1094[10327]; KU-1139[10327].

Glu-B1-2ad[10327] locus: 22.1[10327]

v: Hercule[10327]; KU-1135[10327]; Rouguin[10327]; Schwabenkorn[10327]; SP3[10327]; Steiners Roter Tiroler[10327].

Glu-B1-2ae[10327] locus: 15*[10327]

v: TRI11553/92[10327].

Glu-B1-2af[10327] locus: 19*[10327]

v: KU-3410[10327]; Rechenbergs Fruher Dinkel[10327]; Renval[10327]; SP1[10327]; TRI9885/74[10327]; Zeiners Weiser Schlegel[10327].

Glu-B1-2ag[10643] syn: 8**[10643]

v: XM1404-2[10643].

Glu-B1-2ah

Currently undesignated.

Glu-B1-2ai[10809] locus: 8'[10809]

tv: TGR-244[10809].

Glu-B1-2aj[10808] locus: 8a*[10808]

v: Jing 411[10808]; Pioneer[10808]; Tasman[10808].

Glu-B1-2ak[10808] locus: 8b*[10808]

v: ACA 601[10808]; Nidera Baguette 10 {10808.

Glu-B1-2al[11490] locus: 33*[11490]

tv: *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280)[11490].

Glu-B1-2am[11490] locus: 22*[11490]

tv: *T. turgidum* ssp. *durum* Iranian landrace accession 51 (CWI57280)[11490].

Glu-B1-2an[11492] locus: 8*.1[11492]

tv: *T. turgidum* ssp. *durum* BGE045649[11492], BGE047535[11492].

Glu-B1-2ao[11540] locus: (8)[11540]

tv: *T. turgidum* ssp. *durum* Langdon[11540].

Eight alleles at GLU-B1-1 and 10 alleles at GLU-B1-2 in *T. turgidum* var. *dicoccoides* populations were described in [798]. In a further study using different germplasm of this species[205], 19 alleles at GLU-B1 were observed, including 15 not previously observed; the 19 alleles included 11 alleles at GLU-B1-1 and 14 alleles (including the null allele) at GLU-B1-2, although, as the authors pointed out, it was not conclusively clear how many of these alleles were distinct from each other, or from others previously observed.

GLU-D1-1

Glu-D1-1

Glu-D1-1a locus: 2

v: CS.

Glu-D1-1b locus: 3

v: Hobbit.

Glu-D1-1c locus: 4

v: Champlein.

Glu-D1-1d locus: 5

v: Hope.

PCR markers specific for the ***Glu-D1-1d*** (Dx5) allele were developed in [0145, 0147].

Glu-D1-1e locus: 2.2

v: Danchi.

Glu-D1-1f locus: Null

v: Nap Hal, Nepal.

Glu-D1-1g locus: 2.1

v: AUS 14653, Afghanistan.

Glu-D1-1h locus: 2.3

v: PI 348465.

Glu-D1-1i locus: 38

v: Leningradka.

Glu-D1-1j[668] locus: 43[668]

i: *Ae. tauschii* accession TA2450/2*.

Glu-D1-1k[755] locus: 4.1[755]

dv: *Ae. tauschii*.

Glu-D1-1l [1578] locus: 1.5[1578]. D^tx1.5[10306]

dv: *Ae. tauschii* accession SQ-214[10306].

A restriction enzyme-based method named the 'restricted deletion method' was used to characterize the ORF of this subunit[10306] (as in the case of subunit D^ty10 encoded by ***Glu-D1-2u***[10306]. Allele-specific PCR markers were developed based upon SNPs located at the non-repetitive N-terminal[10320].

Glu-D1-1m [02107] locus: 2.2* [02107]

v: MG315.

Glu-D1-1n [03122] locus: 2.4[03122]

v: PI 348473 spelt[03122].

Glu-D1-1o [03122] locus: 2.5[03122]

v: PI 3484572 spelt[03122].

Glu-D1-1p [03124] locus: 1^t [03124]

dv: *Ae. tauschii*[03124].

Glu-D1-1q [03124] locus: 5^{*t} [03124]

dv: *Ae. tauschii*[03124].

Glu-D1-1r [755] locus: 5.1[755]

dv: *Ae. tauschii*.

This allele was designated ***Glu-D1-1j*** in the 1998 Catalogue edition.

Glu-D1-1s [10091] locus: 5'[10091]

v: W958[10091].

This putative allele encodes a subunit, provisionally denominated 5'[10091], that has a very similar electrophoretic mobility compared to subunit 5 encoded by ***Glu-D1-1d***, but analysis using the specific PCR primers for Dx5 described in ▸[10092, 10093] shows that it does not appear to be the same protein as subunit 5[10091]. Definitive evidence awaits sequencing information (See note to allele ***Glu-D1bo***).

Glu-D1-1t [10304] locus: 2.6[10304]

v: Baidongmai[10305]; Jinbaojin[10305]; Hongdongmai[10305]; Hongkedongmai[10305].

Glu-D1-1u [10327] locus: 2.1'[10327]

v: KU-1034[10327].

Glu-D1-1v [10642] syn: 1.6^t [10642]

dv: *Ae. tauschii* TD16[10642].

GLU-D1-2

Glu-D1-2

Glu-D1-2a locus: 12

v: CS.

A PCR marker (612 bp) for the ***Glu-D1-2a*** (Dy12) allele was developed in ▸[0145].

Glu-D1-2b locus: 10

v: Hope.

PCR markers (576 bp and 2176 bp) for the ***Glu-D1-2b*** (Dy10) allele were developed in ▸[0145, 0147], respectively.

Glu-D1-2c locus: 9

v: BT-2288.

Glu-D1-2d locus: Null

v: Nap Hal, Nepal.

Glu-D1-2e locus: 12*

v: Tudest.

Glu-D1-2f locus: 13

v: AUS 14519, *T. macha*.

Glu-D1-2g locus: 36

i: Iranian landrace 3048/5* Sicco.

Glu-D1-2h locus: 11

v: Flinor.

Glu-D1-2i[668] locus: 44[668]

i: *Ae. tauschii* TA2450/2*.

Glu-D1-2j[836] locus: 10'[836]

v: Coker 68-15.

Glu-D1-2k[755] locus: T1[755]

dv: *Ae. tauschii*.

Glu-D1-2l[755] locus: T2[755]

dv: *Ae. tauschii*.

Glu-D1-2m[755] locus: 10.1[755]

dv: *Ae. tauschii*.

Glu-D1-2n[755] locus: 10.2[755]

dv: *Ae. tauschii*.

Glu-D1-2o[755] locus: 10.3[755]

dv: *Ae. tauschii*.

Glu-D1-2p[1578] locus: 10.5[1578]

dv: *Ae. tauschii*.

Glu-D1-2q[03122] locus: 12'[03122]

v: PI-348495 spelt wheat accession[03122].

Glu-D1-2r[03124] locus: 12.1^{t}[03124]

dv: *Ae. tauschii*.

Glu-D1-2s[03124] locus: 12.3^{t}[03124]

dv: *Ae. tauschii*.

Glu-D1-2t[03124] locus: 12.4^{t}[03124]

dv: *Ae. tauschii*.

Glu-D1-2u[10306] locus: D^{t}y10[10306]

v: *Ae. tauschii* accession SQ-214[10306].

A restriction enzyme-based method named the 'restricted deletion method' was used to characterize the ORF of this subunit[10306] (as in the case of subunit 1.5 (or D^{t}x1.5[10306]) encoded by ***Glu-D1-1l***[10306]. This subunit was first recognized as being different from subunit 1- encoded by ***Glu-D1-2b*** in hexaploid wheat in ▸[10307].Six combinations involving 5 HMW subunits [1A (u-z)] are listed in ▸[420], from a study of 109 genotypes including representatives of botanical varieties. Alleles in *T. turgidum* var. *dicoccoides* populations, 12 at GLU-A1-1 and 3 at GLU-A1-2, were described in ▸[798]. In a further study using different

germplasm of this species[205], 14 alleles at GLU-A1 were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at GLU-A1-1 (with up to 10 not previously observed), and 5 alleles at GLU-A1-2 (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously.

In a study including emmers (*T. dicoccum*)[00115], new subunits named 1^+ and 2^- were found in accessions MG4378/1 and MG5380/1, respectively, and provisionally assigned to GLU-A1. Until confirmed, they are not included in the GLU-A1 list.

Glu-R1-1

Glu-R1-1

Glu-R1-1a[03116] locus: 1^r[03116]

v: Indiana hexaploid triticale[03116].

Glu-R1-1b[03116] locus: 2^r[03116]

v: Graal hexaploid triticale[03116].

Glu-R1-1c[03116] locus: 6^r[03116]

v: Alamo hexaploid triticale[03116].

Glu-R1-1d[03115] locus: 0.8^r[03115]

v: Carmara hexaploid triticale[03115].

Glu-R1-1e[03115] locus: 5.8^r[03115]

v: Arrayan hexaploid triticale[03115].

There was difficulty in assigning subunit 6^r in the **GLU-R1-1** and **GLU-R1-2** lists, since it appeared as an x-type subunit in allele ***Glu-R1c*** and as a y-type subunit in allele ***Glu-R1f***. It is currently provisionally assigned to the **GLU-R1-1** list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

GLU-V1-1

Alleles and subunits at GLU-V1-1 and GLU-V1-2: The following is analogous to the *GLU-1-1* and *GLU-1-2* lists given earlier to identify x-type and y-type subunits in wheat. It was assumed that where an allele at **GLU-V1** produces only a single subunit, it is an x-type subunit and so encoded by GLU-V1-1 rather than by GLU-V1-2; the electrophoretic mobilities of the subunits are all greater, though some only marginally so, than subunit 7 encoded by ***Glu-B1-1a*** (an x-type subunit), and extend beyond the mobility of subunit 12 encoded by ***Glu-D1-2a*** (a y-type subunit)[1651]; therefore, it is quite possible that any one of the subunits designated as encoded by GLU-V1-1 is, in fact, encoded by GLU-V1-2. The designation given here is intended to be the most practically useful until the identities of the genes encoding the alleles are directly established.

Glu-V1-1

Glu-V1-1a[1651] locus: 71[1651]

al: *D. villosum*.

Glu-V1-1b[1651] locus: 72[1651]

al: *D. villosum*.

Glu-V1-1c[1651] locus: 73[1651]

al: *D. villosum*.

Glu-V1-1d[1651] locus: 74[1651]

al: *D. villosum*.

Glu-V1-1e[1651] locus: 75[1651]

al: *D. villosum*.

Glu-V1-1f[1651] locus: 76[1651]

al: *D. villosum*.

Glu-V1-1g[1651] locus: 77[1651]

al: *D. villosum*.

Glu-V1-1h[1651] locus: 78[1651]

al: *D. villosum*.

Glu-V1-1i[1651] locus: 79[1651]

al: *D. villosum*.

Glu-V1-1j[1651] locus: 80[1651]

al: *D. villosum*.

Glu-V1-1k[1651] locus: Null[1651]

al: *D. villosum*.

Glu-V1-1l[1651] locus: 81[1651]

al: *D. villosum*.

Glu-V1-1m[1651] locus: 83[1651]

al: *D. villosum*.

Glu-V1-1n[1651] locus: 85[1651]

al: *D. villosum*.

GLU-V1-2

Glu-V1-2

Glu-V1-2a[1651] locus: Null[1651]

al: *D. villosum*.

Glu-V1-2b[1651] locus: 82[1651]

al: *D. villosum*.

Glu-V1-2c[1651] locus: 84[1651]

al: *D. villosum*.

Glu-V1-2d[1651] locus: 86[1651]

al: *D. villosum*.

ungrouped

Glu-Ag^{i}1[374] locus: 1Ag^{i}[374]

ad: Vilmorin 27/*Th. intermedium*.

Glu1-2r

tv: Quaduro, Italy, *T. durum*.

GLU-2

Glu-B2[277, 819] locus: 1BS syn: XGlu-B2[277]

s: CS*/Cheyenne 1B[277]. stv: Langdon*/*T. turgidum* var. *dicoccoides* 1B[277].

Glu-B2a[00114] locus: 12[00114]

tv: Mexicali.

Glu-B2b[00114] locus: Null[00114]

tv: Langdon.

GLI-B3 was designated **GLU-B2**[589] until the name of the locus was changed in [1119].

Glu-B2c[10215] locus: 12*[10215]

tv: Alcala la Real[10215].

Glu-B2d[11493] locus: 12.1[11493]

tv: *T. turgidum* ssp. *durum* Moroccan landrace MGB-3125[11493].

GLU-3

The GLU-3 loci are defined as the cluster of LMW glutenin genes previously considered a component of the compound GLI-1 loci.

More than 30 LMW glutenin complete genes, partial genes or pseudogenes have been sequenced from *Triticum* species (reviewed in [0245]).

In *T. aestivum*, only GLU-B3 was shown to recombine with the gliadin genes (1.7 +/- 0.8)[1355, 1358]. However, in *T. durum*, recombination was observed for both GLU-A3 and GLU-B3 with their respective GLI-1 loci: the map distance between GLU-A3 and GLI-A1 has been estimated as 1.3 +/- 0.4 cM[1242], and that between GLU-B3 and GLI-B1 as 2.0 +/- 0.8 in [1144] and as 2.0 +/- 0.4 in [1242]. It appears that GLU-B3 is proximal to GLI-B1, and there is some evidence that GLU-A3 is proximal to GLI-A1[1242].

Whereas hitherto it was widely thought that all LMW glutenin subunits were encoded by genes located on the chromosomes of homoeologous group 1, it has been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of the C subunits must be controlled by loci elsewhere in the genome[482].

A novel type of polymeric protein (M_r approx. 71,000) was reported in the Australian advanced breeding line DD118[03125]. It participates in the polymeric structure of glutenin (possibly as a chain terminator), and has an M_r of approximately 71,000, could be considered as a D-subunit of LMW glutenin. However, N-terminal sequencing suggests it to be a **Gli-B1** type omega-gliadin that has acquired a cysteine residue through mutation.

In an electrophoretic survey of 51 primary tritordeums[03113], 20 distinct whole banding patterns (a-t), each consisting of between one and three bands, were observed for D-zone prolamins exhibiting glutenin- like solubility characteristics.

In 85 Japanese common wheat cultivars and 61 elite F_6 breeding lines, 3 alleles were observed at each of GLU-A3 and GLU-B3, and 2 alleles at GLU-D3 were named according to their parental origins in three doubled haploid mapping populations[03135].

C-type LMW glutenin subunits in CS were assigned to chromosome groups 1 and 6, and shown to have sequences very similar to those of alpha- and gamma-gliadins[03134]. The authors suggest that they may be encoded by novel genes at loci tightly linked or present within the GLI-1 and GLI-2 loci, unlike other LMW glutenin subunits encoded by the GLU-3 loci.

The HMW and LMW glutenin subunits carried by chromosome $1A^m$of *T. monococcum* accession G1777 were characterised electrophoretically and evaluated for quality characteristics using recombinant chromosome substitution lines with chromosome 1A of CS[03142]. The HMW subunits from G1777 are promising for bread-making quality, whereas its LMW subunits are promising for biscuit-making quality. The bread wheat cv. Salmone was shown to carry two DNA fragments designated as SF720 and SF750 located on the chromosome 1B satellite and associated with the presence of two LMW glutenin subunits[03143]. However, the authors suggest that they occur at a locus other than GLU-B3 due to their relatively high frequency of recombination with **GLI-B3**.

A naming system in which Roman numerals are assigned to whole banding patterns for the LMW glutenin subunit is given in [03131] as an alternative to the LMW-1/-2 system described in [03136]. A further system naming whole banding patterns from LMW-1 to LMW-23 in emmer wheat is described in [03137]. In [00111], in a study of common and durum wheats from Portugal, the authors used the nomenclature system described in [00113] for the LMW subunits in common wheat, and that described in [00114] for the LMW subunits in durum wheat. The latter system was updated according to [02110] but has been changed herein to new

alleles with the earlier durum designation[00114] given as synonyms. In [03116], it was suggested that ***Glu-B3d*** (common wheat standard genetic stock) is equivalent to ***Glu-B3r*** (durum wheat standard genetic stock), and that (referring to article[03127]) LMW subunits observed in some Portugese triticales could be of the durum type.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated **Ch1** to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the GLI-1 and GLU-3 loci. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated[10307]. Characterization of near isogenic lines for the different GLU-3 alleles provides a useful quantification of their contribution to bread making quality[11129].

GLU-A3

Glu-A3[1358] locus: 1AS[1358]

v: CS.

The first 7 alleles were distinguished using 5 allele-specific primer sets[10185]. Further mainly Australian genotypes with alleles *a* to *f* are listed in [10185].

In 112 common wheat cultivars from Argentina, 11 microsatellite alleles plus a null allele were found at the GLU-A3 locus[03123].

Glu-A3a[481]

v: CS.

Glu-A3b[481]

v: Gabo.

Glu-A3c[481]

v: Cheyenne.

Glu-A3d[481]

v: Cappelle Desprez, Orca; Suneca[10185].

Glu-A3e[481]

v: Halberd[10185]; Hope, Insignia.

Glu-A3f[481]

v: Rescue.

Glu-A3g[00113]

v: Glenlea[10185].

Glu-A3h[03116, 00114] locus: Null[00114] syn: Glu-A3d'[03116], Glu-A3d'

v: Magistral hexaploid triticale[03116].

Glu-A3i[02110] locus: 8*+11[02110]

tv: Mourisco Fino.

Glu-A3j[00114] locus: 6[00114] syn: Glu-A3a[00114]

tv: Mexicali.

Glu-A3k[00114] locus: 5[00114] syn: Glu-A3b[00114]

tv: Langdon.

Glu-A3l[00114] locus: 6+10[00114] syn:[00114], Glu-A3c

tv: Cocorit.

Glu-A3m[00114] locus: 6+11[00114] syn: Glu-A3d[00114]

tv: Alaga.

Glu-A3n[00114] locus: 11[00114] syn: Glu-A3e[00114]

tv: Blatfort.

Glu-A3o[00114] locus: 6+11+20[114] syn: Glu-A3f[00114]

tv: Clarofino.

Glu-A3p[00114] locus: Null[00114] syn: Glu-A3h[00114]

tv: Jiloca.

Glu-A3q[10215] locus: 5+20[10215] syn: Glu-A3i[10215]

tv: Fanfarron[10215].

Glu-A3r[03116] syn: Glu-A3d'[03116], Glu-A3d'

v: Magistral hexaploid triticale[03116].

Glu-A3s[00114] locus: 6+10+20[00114] syn: Glu-A3g[00114]

tv: Claro de Balazote[00114].

Glu-A3t[10805] syn: Glu-A3^{m}a[10805]

dv: PI 190947, *T. monococcum* ssp. *monococcum*[10805].

Glu-A3u[10805] syn: Glu-A3^{m}b[10805]

dv: PI 190946, *T. monococcum* ssp. *monococcum*[10805].

Glu-A3v[10805] syn: Glu-A3^{m}c[10805]

dv: BGE-020466, *T. monococcum* ssp. *monococcum*[10805].

Glu-A3w[10805] syn: Glu-A3^{m}d[10805]

dv: PI 191097, *T. monococcum* ssp. *monococcum*[10805].

Glu-A3x[10805] syn: Glu-A3^{m}e[10805]

dv: BGE-013624, *T. monococcum* ssp. *Monococcum*[10805].

Glu-A3y[10805] syn: Glu-A3^{m}f[10805]

dv: PI 191094, *T. monococcum* ssp. *monococcum*[10805].

Glu-A3z[10806] syn: Glu-A^{u}3-I[10806]

dv: PI 428139, *T. urartu*[10806].

Glu-A3aa[10806] syn: Glu-A^{u}3-II[10806]

dv: PI 428327, *T. urartu*[10806].

Glu-A3ab[10806] syn: Glu-A^{u}3-III[10806]

dv: PI 428340, *T. urartu*[10806].

Glu-A3ac[10806] syn: Glu-A^{u}3-IV[10806]

dv: PI 428322, *T. urartu*[10806].

Glu-A3ad[10806] syn: Glu-A^{u}3-V[10806]

dv: PI 428188, *T. urartu*[10806].

Glu-A3ae[10806] syn: Glu-A^{u}3-VI[10806]

dv: PI 428203, *T. urartu*[10806].

Glu-A3af[10806] syn: Glu-A^{u}3-VII[10806]

dv: PI 428255, *T. urartu*[10806].

Glu-A3ag [10806] syn: Glu-A^{u}3-VIII [10806]

dv: PI 428328, *T. urartu* [10806].

Glu-A3ah [10806] syn: Glu-A^{u}3-IX [10806]

dv: PI 428256, *T. urartu* [10806].

Glu-A3ai [10806] syn: Glu-A^{u}3-X [10806]

dv: PI 428217, *T. urartu* [10806].

Glu-A3aj [10806] syn: Glu-A^{u}3-XI [10806]

dv: PI 428335, *T. urartu* [10806].

Glu-A3ak [10806] syn: Glu-A^{u}3-XII [10806]

dv: PI 428186, *T. urartu* [10806].

Glu-A3al [10806] syn: Glu-A^{u}3-XIII [10806]

dv: PI 428183, *T. urartu* [10806].

Glu-A3am [10806] syn: Glu-A^{u}3-XIV [10806]

dv: TRI 11563, *T. urartu* [10806].

Glu-A3an [10806] syn: Glu-A^{u}3-XV [10806]

dv: PI 427328, *T. urartu* [10806].

Glu-A3ao [10806] syn: Glu-A^{u}3-XVI [10806]

dv: PI 428253, *T. urartu* [10806].

Glu-A3ap [10806] syn: Glu-A^{u}3-XVII [10806]

dv: PI 538735, *T. urartu* [10806].

Glu-A3aq [10806] syn: Glu-A^{u}3-XVIII [10806]

dv: PI 428225, *T. urartu* [10806].

Glu-A3ar [10806] syn: Glu-A^{u}3-XIX [10806]

dv: PI 538733, *T. urartu* [10806].

Glu-A3as [10806] syn: Glu-A^{u}3-XX [10806]

dv: PI 428196, *T. urartu* [10806].

Glu-A3at [10806] syn: Glu-A^{u}3-XXI [10806]

dv: PI 538724, *T. urartu* [10806].

Glu-A3au [10806] syn: Glu-A^{u}3-XXII [10806]

dv: PI 428191, *T. urartu* [10806].

Glu-A3av [10806] syn: Glu-A^{u}3-XXIII [10806]

dv: TRI 6734, *T. urartu* [10806].

Glu-A3aw [10806] syn: Glu-A^{u}3-XXIV [10806]

dv: TRI 11496, *T. urartu* [10806].

Glu-A3ax [10116] locus: 6.1 [10116]

tv: Buck Cristal [10116].

The designation of this protein (subunit 6.1) as encoded by GLU-A3, previously deduced from its electrophoretic mobility [10116], was confirmed through mapping studies [11492]. According to ▸ [11492], this subunit is equivalent to that designated 7* in ▸ [11539].

Glu-A3ay[11490] locus: 6+20[11492]

tv: *T. turgidum* ssp. *durum* landraces BGE047515 and BGE047516[11492]; Mexican durum landrace accession 10 (CWI52016)[11490].

Glu-A3az[11490] locus: 6+10+11*[11490]

tv: *T. turgidum* ssp. *durum* Mexican landrace accession 3 (CWI51941)[11490].

Glu-A3ba[11490] locus: 5+11[11492]

tv: *T. turgidum* ssp. *turgidum* landrace BGE047535[11492].

Iranian landrace accession 77 (CWI73342)[11490].

Glu-A3bb[11493] locus: 20[11492]

tv: *T. turgidum* ssp. *dicoccon* landrace BGE047498[11492]; *T. turgidum* ssp. *turgidum* landrace BGE047531[11492]; *T. turgidum* ssp. *durum* Moroccan landrace MGB-16563[11493].

Glu-A3bc[11493] locus: 5**[11493]

tv: *T. turgidum* ssp. *durum* Moroccan cv. MGB-20[11493].

Glu-A3bd[11492] locus: 5+22[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047532[11492].

Glu-A3be[11492] locus: 5*[11492]

tv: *T. turgidum* ssp. *turgidum* BGE048495[11492].

Glu-A3bf[11492]

5*+20[11492]. tv: *T. turgidum* ssp. *turgidum* BGE048498[11492].

Glu-A3bg[11539] locus: 5*+11+20[11539]

tv: *T. turgidum* ssp. *turgidum* BGE018646[11539].

Glu-A3bh[11539] locus: 10[11539]

tv: *T. turgidum* ssp. *durum* BGE013622[11539].

Glu-A3bi[11539] locus: 5*+11+22[11539]

tv: *T. turgidum* ssp. *turgidum* BGE013089[11539].

Glu-A3bj[11540] locus: 5*[11540]

tv: *T. turgidum* ssp. *durum* Fanfarron[11540].

Glu-A3bk[11540] locus: 8*[11540]

tv: *T. turgidum* ssp. *durum* BGE019300[11540].

Glu-A3bl[11540] locus: 5+8*[11540]

tv: *T. turgidum* ssp. *durum* BGE013718[11540].

GLU-B3

Three different approaches were employed to identify putative SNPs used to design gene-specific primers for LMW-GS genes, and six functional STS markers, three for GLU-B3 and three for GLU-D3[10664]. These markers distiguished cultivars with different haplotypes at the GLU-B3 and GLU-D3 loci, but there was no clear correlation between the alleles of cultivars defined by protein electrophoretic mobility and the separation patterns of the DNA markers, since all three GLU-3 loci were multiple copies and each protein electrophoretic mobility allele was controlled by 3-6 coding genes[10665].

Glu-B3[1358] locus: 1BS[1358]

v: CS.

***Glu-B3a*{481,}**

v: CS.

Glu-B3b[481]

v: Gabo, Timstein, Hope.

Glu-B3c[481]

v: Insignia, Halberd.

Glu-B3d[481]

v: Orca.

Glu-B3e[481]

v: Cheyenne.

Glu-B3f[481]

v: Radja.

Glu-B3g[481]

v: Kharkov, Bungulla.

Glu-B3h[481]

v: Thatcher, Rescue.

Glu-B3i[481]

v: Norin-61.

Glu-B3j[476, 02110] locus: 4+6*+15+19

v: Kavkaz.

Null allele carried by the 1BL.1RS translocation. This allelic designation was originally incorrectly used in the catalogue to name an allele from *T. turgidum* ssp. *durum* that was subsequently redesignated as ***Glu-B3ce***, since the Kavkaz allele had precedence.

Glu-B3k[476, 02110] locus: 8+9+13+16+19[02110]

tv: ALP-153, Dural, Durati, Edmore; Faisca.

Glu-B3l[476]

tv: Gionp-1954.

Glu-B3m[03120] syn: Glu-B3b'[03120], Glu-B3b'

v: Soissons[03120].

Glu-B3n[03120] syn: Glu-B3c'[03120], Glu-B3c'

v: Courtot[03120].

Glu-B3o[03116] syn: Glu-B3i'[03116], Glu-B3i'

v: Olympus hexaploid triticale[03116].

Glu-B3p[03116] syn: Glu-B3k[03116]

v: Alamo hexaploid triticale[03116].

Glu-B3q[03115] syn: Glu-B3h'[03115], Glu-B3h'

v: Torote hexaploid triticale[03115].

Glu-B3r[00114] locus: 2+4+15+19[00114] syn: Glu-B3a[00114]

tv: Mexicali.

Glu-B3s[00114] locus: 8+9+13+16[00114] syn: Glu-B3b[00114]

tv: Langdon.

Glu-B3t[00114] locus: 2+4+14+15+19[00114] syn: Glu-B3c[00114]

tv: Jiloca.

Glu-B3u[00114] locus: 2+4+15+17+19[00114] syn: Glu-B3d[00114]

tv: Mundial.

Glu-B3v[00114] locus: 2+4+15+16+18[00114] syn: Glu-B3e[00114]

tv: Granja Badajoz.

Glu-B3w[00114] locus: 2+4+15+17[00114] syn: Glu-B3f[00114]

tv: Ardente.

Glu-B3x[00114] locus: 2+4+15+16[00114] syn: Glu-B3g[00114]

tv: Claro de Balazote.

Glu-B3y[00114] locus: 1+3+14+18[00114] syn: Glu-B3h[00114]

tv: Alaga.

Glu-B3z[10116] locus: 6.1[10116] syn: 6.1

tv: Buck Cristal[10116].

Glu-B3aa[10215] locus: 1+3+13*+16[10215] syn: Glu-B3l[10215]

tv: Blancal de Nules[10215].

Glu-B3ab[10804]

v: Hope[10804]; Nanbukomugi[10804].

Glu-B3ac[10804]

v: ACA 801[10804]; Klein Proteo[10804]; Thesee[10804].

Glu-B3ad[10804]

v: AC Vista[10804]; Heilo[10804]; Opata 85[10804]; Ruso[10804].

Glu-B3ae[11490] locus: 1+3+16[11490]

tv: *T. turgidum* ssp. *durum* accession 56 (CWI57386)[11490].

Glu-B3af[11490] locus: 1+3+17[11490]

tv: *T. turgidum* ssp. *durum* accession 74 (CWI71827)[11490].

Glu-B3ag[11490] locus: 2+4+16[11490]

tv: *T. turgidum* ssp. *durum* accession 46 (CWI56913)[11490].

Glu-B3ah[11490] locus: 8+9+16[11490]

tv: *T. turgidum* ssp. *durum* accession 65 (CWI57719)[11490].

Glu-B3ai[11490] locus: 2+4+14+18[11490]

tv: *T. turgidum* ssp. *durum* accession 62 (CWI57615)[11490].

Glu-B3aj[11490] locus: 19[11490]

tv: *T. turgidum* ssp. *durum* accession 77 (CWI73342)[11490].

Glu-B3ak[11490] locus: 2+4+6*+15+19[11490]

tv: *T. turgidum* ssp. *durum* accession 69 (CWI71627)[11490].

Glu-B3al[11490] locus: 2+4+7*+15+16[11490]

tv: *T. turgidum* ssp. *durum* accession 61 (CWI57614)[11490].

Glu-B3am[11490] locus: 1+3+6*+13'+17[11490]

tv: *T. turgidum* ssp. *durum* accession 72 (CWI71759)[11490].

Glu-B3an[11490] locus: 8+9+13'+17[11490]

tv: *T. turgidum* ssp. *durum* accession 58 (CWI57522)[11490].

Glu-B3ao[11490] locus: 1+3+8'+17[11490]

tv: *T. turgidum* ssp. *durum* accession 50 (CWI57256)[11490].

Glu-B3ap[11490] locus: 2+4+6*+9'+14+19[11490]

tv: *T. turgidum* ssp. *durum* accession 78 (CWI73350)[11490].

Glu-B3aq[11493] locus: 2+4+8+15+19[11492]

tv: *T. turgidum* ssp. *durum* landraces BGE045634[11492]; MGB-2963[11493].

Glu-B3ar[11493] locus: 1+3+7+15+18[11493]

tv: *T. turgidum* ssp. *durum* landrace MGB-16563[11493].

Glu-B3as[11493] locus: 1+3+8+13+16+19[11493]

tv: *T. turgidum* ssp. *durum* landrace MGB-3152[11493].

Glu-B3at[11493] locus: 2+4+17[11493]

tv: *T. turgidum* ssp. *durum* landrace MGB-3125[11493].

Glu-B3au[11493] locus: 2+4+7+15+19[11493]

tv: *T. turgidum* ssp. *durum* landrace MGB-5963[11493].

Glu-B3av[11493] locus: 9+13+16[11493]

tv: *T. turgidum* ssp. *durum* landrace MGB-3101[11493].

Glu-B3aw[11492] locus: 1+3+8+13+15+18[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047502[11492].

Glu-B3ax[11492] locus: 1+3+13*+19[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047504, BGE047506[11492].

Glu-B3ay[11492] locus: 1+3+14+15[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047521[11492].

Glu-B3az[11492] locus: 1+16[11492]

tv: *T. turgidum* ssp. *dicoccon* BGE045645, BGE047503[11492].

Glu-B3ba[11492] locus: 2+4+7+13*+15+19[11492]

tv: *T. turgidum* ssp. *durum* BGE045651[11492].

Glu-B3bb[11492] locus: 2+4+15[11492]

tv: *T. turgidum* ssp. *durum* BGE047516[11492].

Glu-B3bc[11492] locus: 2+4+15+17+21[11492]

tv: *T. turgidum* ssp. *turgidum* BGE048494[11492].

Glu-B3bd[11492] locus: 4+(7**)+13+15+19[11492]

tv: *T. turgidum* ssp. *dicoccon* BGE045628[11492].

The designation of subunit 7** as encoded by **Glu-A3** was deduced from its electrophoretic mobility and awaits confirmation through mapping studies[11492]; the subunit was therefore referenced by ◗[11492].

Glu-B3be[11492] locus: 4+(7**)+13+15+21[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047511[11492].

The designation of subunit 7** as encoded by GLU-A3 was deduced from its electrophoretic mobility and awaits confirmation through mapping studies[11492]; the subunit was therefore referenced by ◗[11492].

Glu-B3bf[11492] locus: 4+(7**)+15+19[11492]

tv: *T. turgidum* ssp. *dicoccon* BGE045629, BGE045676, BGE047499, BGE048499[11492].

The designation of subunit 7** as encoded by GLU-A3 was deduced from its electrophoretic mobility and awaits confirmation by mapping studies[11492]; the subunit was therefore referenced by ▸[11492].

Glu-B3bg[11492] locus: 4+7***+13+16[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047531[11492].

Glu-B3bh[11492] locus: 4+7***+15+19[11492]

tv: *T. turgidum* ssp. *durum* BGE045657[11492].

Glu-B3bi[11492] locus: 7+9+14+16[11492]

tv: *T. turgidum* ssp. *durum* BGE047533[11492].

Glu-B3bj[11492] locus: 7+13*+15+18[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047512[11492].

Glu-B3bk[11492] locus: 7***+8a*+14+17[11492]

tv: *T. turgidum* ssp. *durum* BGE047507[11492].

Glu-B3bl[11492] locus: 7***+8a*+14*+15+19[11492]

tv: *T. turgidum* ssp. *turgidum* durum wheat landrace BGE048495[11492].

Glu-B3bm[11492] locus: 7***+8a*+14*+16+21[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047535[11492].

Glu-B3bn[11492] locus: 8+9+14+18[11492]

tv: *T. turgidum* ssp. *durum* BGE045667[11492].

Glu-B3bo[11492] locus: 8+13+18[11492]

tv: *T. turgidum* ssp. *dicoccon* BGE048901[11492].

Glu-B3bp[11492] locus: 8+13*+16[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047510[11492].

Glu-B3bq[11492] locus: 8a*+13*+15+19[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047519[11492].

Glu-B3br[11492] locus: 8a*+13*+16[11492]

tv: *T. turgidum* ssp. *dicoccon* BGE047498[11492].

Glu-B3bs[1149] locus: (13**)+14+18[11492]

tv: *T. turgidum* ssp. *turgidum* BGE045632, BGE047532, BGE048498[11492].

The designation of subunit 13** as encoded by GLU-B3 was deduced from its electrophoretic mobility and awaits confirmation by mapping studies[11492]; the subunit was therefore referenced by ▸[11492].

Glu-B3bt[11492] locus: (13**)+14+19[11492]

tv: *T. turgidum* ssp. *turgidum* BGE047513, BGE048496[11492].

The designation of subunit 13** as encoded by GLU-B3 was deduced from its electrophoretic mobility and awaits confirmation through mapping studies[11492]; the subunit was therefore referenced by ▸[11492].

Glu-B3bu[11539] locus: 7***+8a*+14*+16+19[11539]

tv: *T. turgidum* ssp. *turgidum* BGE013100[11539].

Glu-B3bv[11539] locus: 13+15+19[11539]

tv: *T. turgidum* ssp. *turgidum* BGE020942[11539].

Glu-B3bw[11539] locus: 13+17+19[11539]

tv: *T. turgidum* ssp. *durum* BGE013622[11539].

Glu-B3bx[11539] locus: 1+3+7*+15+19[11539]

tv: *T. turgidum* ssp. *durum* BGE013590[11539].

According to [11492], this subunit (subunit 7*) is equivalent to 6.1 in [10116].

Glu-B3by[11539] locus: 1**+2+4+15+17+19[11539]

tv: *T. turgidum* ssp. *durum* BGE08366[11539].

Glu-B3bz[11539] locus: 1*+2+4+15+16[11539]

tv: *T. turgidum* ssp. *turgidum* BGE12537[11539].

Glu-B3ca[11540] locus: 1+3+13+19[11540]

tv: *T. turgidum* ssp. *durum* BGE018639[11540].

Glu-B3cb[11540] locus: 13*+18[11540]

tv: *T. turgidum* ssp. *durum* BGE018657[11540].

Glu-B3cc[11540] locus: 13+14+18[11540]

tv: *T. turgidum* ssp. *durum* BGE013724[11540].

Glu-B3cd[11540] locus: 2+4+13+15+17[11540]

tv: *T. turgidum* ssp. *durum* BGE030927[11540].

Glu-B3ce[476, 02110] locus: 4+6*+15+19[02110]

tv: Duramba-B, Duramba-D, Langdon; Mourisco Fino.

GLU-D3

Glu-D3[707, 1358] locus: 1DS[707, 1358]

v: CS.

Glu-D3a[481]

v: CS.

Glu-D3b[481]

v: Gabo.

Glu-D3c[481]

v: Insignia, Cappelle Desprez.

Glu-D3d[481]

v: Jufy-1[10813]; Norin-61A.

Glu-D3e[481]

v: Orca, Thatcher.

Glu-D3f[10548]

v: Cheyenne[10548].

Glu-D3g[10558]

v: Hira-1[10558].

Glu-D3h[10558]

v: India 115[10558].

Glu-D3i[10558]

v: Bolac[10558].

Glu-D3j[10558]

v: Hira-2[10558].

Glu-D3k [10558]

v: Lincoln[10558].

Glu-D3l [10804]

v: Heilo[10804]; Jing411[10804]; Pepital[10804]; Thesee[10804].

Glu-D3m [10804]

v: Darius[10804].

Glu-D3n [10804]

v: Fengmai 27[10804].

ungrouped

Glu-E3[480] locus: 1ES[480]

su: CS/*E. elongata*.

Glu-S^{l}3[480, 1228] locus: 1S^{l}[480]. 1S^{1}S[1228]

su: CS/*Ae. longissima*[480, 1228]. **ma**: In *Ae. longissima 2*/*Ae. longissima 10* glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one another in [1228] as follows: *GLU-S^{l}*1 – 15.9 cM – *GPI-S^{l}*1 – 38 cM – *GLI-S^{l}*4 – 7.1 cM – *GLU-S^{l}*3 – 0.9 cM – *GLI-S^{l}*1 – 5.6 cM – *GLI-S^{l}*5. *GLU-S^{l}*1 is located in 1S^{l}L and the other loci are in 1S^{1}S.

Glu-U3[480] locus: 1U[480]

su: CS/*Ae. umbellulata*.

A series of papers[00106, 00107, 00108, 00109] describe considerable variation in primitive wheats not present in bread wheat (A genome species *T. boeoticum*, *T. urartu*, *T. thaoudar*, *T. aegilopoides*, *T. monococcum*, and D-genome species *T. tauschii*) for the low molecular weight subunits, sufficient to use them as a source for potentially changing flour properties in bread wheat.

In[00110], variants for LMW glutenin subunits were reported from study of 24 accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). Nine of these showed two electrophoretic bands for LMW subunits, arbitrarily designated 'a' and 'b', that appeared to be associated with good bread-making quality. The isolation of a new low-molecular-weight glutenin subunit gene, located on chromosome 1D, was reported in [0350].

GLU-4

The following loci, **GLU-D4** and **GLU-D5**, encoding low molecular weight subunits of glutenin (30-32 kDa) were described in [02111]; the proteins encoded by them were first observed earlier[02114, 02115], and the former was later tentatively assigned the symbol GLU-4[02116], before its chromosomal location was established and the locus definitively named as **GLU-D4** in [02111]. While this locus is located on chromosome 1D (in accordance with the position on the group 1 chromosomes of the remaining glutenin encoding loci found to date), the locus **GLU-D5** is located on chromosome 7D. In SDS-PAGE, the proteins from both loci are detected only in the presence of 4-vinylpyridine added to the sample extract. Their amino acid compositions do not match those of the major prolamin groups; nonetheless, they classify as glutenins based upon solubility, immunological behaviour and N-terminal amino acid sequence (the latter suggesting an evolutionary link with the major (B and C) low molecular weight glutenin subunits).

Glu-D4[02111] locus: 1D[02111]

su: CS/Langdon 1D(1A); CS/Langdon 1D(1B)[02111].

Glu-D4a[02111]

v: J 24.

Glu-D4b[02111]

v: PBW 154.

Glu-D4c[02111] locus: Null allele

v: NI 4.

GLU-5

Glu-D5[02111] locus: 7D[02111]

su: CS/Langdon 7D(7A); CS/Langdon 7D(7B)[02111].

Glu-D5a[02111]

v: PBW 154.

Glu-D5b[02111] locus: Null allele

v: K 68.

A collection of 173 *Ae. tauschii* accessions were analysed for low molecular weight glutenin subunits by SDS-PAGE[02112]; 33 different patterns for B-subunits and 43 for C-subunits were identified, some of which were of identical electrophoretic mobility to those observed in common wheat. Also observed were subunits with the same mobilities as the D-subunits and as the subunits encoded by the **GLU-D4** and **GLU-D5** loci. This variation represents a source of novel germplasm of potential value for breeding programmes aimed at improving the D-genome of common wheat in the context of bread-making quality.

2.3.2 Gliadins

These are heterogeneous mixtures of alcohol-soluble polypeptides without quaternary structure. The GLI-1 loci are compound and are now considered to comprise the omega-gliadin and gamma gliadin[982, 1415] multigene families[494], which in some circumstances may be divided into *GLI-1-1* and *GLI-1-2*, respectively. The LMW glutenin multigene families, which are closely linked to the GLI-1 loci[588], are listed separately as the GLU-3 set[1358]; information on map distance and gene order in relation to GLU-3 and the centromere is given in the preamble for the GLU-3 loci. There is evidence that a few of the omega-gliadin genes are separated from the main omega-gliadin gene cluster[993].

A catalogue of common wheat gliadin genes and alleles is provided in ▶[11437].

Variation at the GLI-1 loci was described earlier[634, 996, 1126] and applied in mapping experiments[196, 422, 1120, 1125, 1243]. A rational system of naming the alleles was produced by Dr. E.V. Metakovsky[988]. This nomenclature is reproduced below. A considerable number of alleles were added to the original list given in ▶[988] and referenced here accordingly. A few alleles have been deleted, because, following much detailed comparison, there is now doubt that they can be reliably distinguished from existing alleles[9981]. The allelic letter in these cases has not been reused. To facilitate practical use of the list, the aim was to give at least three standard cultivars from a range of countries for each allele[9981]. This was achieved for majority of entries and is a change from the original list compiled from ▶[988], where up to two standards were given. While the three or more standards described almost always include the original standards, some were replaced for various reasons, such as international awareness of the cultivar, availability of seed, or the ease with which an allele can be identified in a particular genetic background[9981]. In the original list, where two cultivars were given as prototypes for an allele, the first named was from the USSR and the second from elsewhere; this is no longer the case, although care was taken to include a Russian cultivar where possible, to maintain a wide base of germplasm in which the alleles are available, as well as to acknowledge the research groups in the country where much of the pioneering work was carried out.

For discussion of null alleles at the GLI-1 and GLI-2 loci, see ▶[9984].

Recombination was observed within the gliadin multigene family at *XGli-A1*[277]. These closely linked genes may correspond to GLI-A1 and **GLI-A5**, but they were temporarily designated *XGLI-A1.1* and *XGLI-A1.2* until orthology with GLI-A1 and/or **GLI-A5** is established.

Note: The catalogue entries reproduced here only refer to alleles in *T. aestivum*; there is, however, enormous variation in gliadins in the close relatives of wheat; see, for example,[989] for studies in *T. monococcum* (more than 80 gliadin electrophoretic patterns observed in 109 accessions),[990] for studies in *T. boeoticum* (more than 50 electrophoretic patterns in 60 accessions), and ▶[1076] studies in *T. durum* (19 electrophoretic patterns, referring only to variation in the omego-gliadins, in 243 accessions). In ▶[00110], variants for omega-gliadins were reported from study of 24 accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). In ▶[00111], in a study of common wheat and durum from Portugal, the authors used the nomenclature system described in ▶[00112] for the omega-gliadins. In ▶[00116], a comparison between spelt and common wheat was carried out for the gliadins using a nomenclature system described in ▶[00118].

The GLI-1 loci may be recognised by probes pcP387[372] and pTag1436[65], and by specific microsatellite primers[252]. Furthermore, it was shown that probe pTag1436 differentiates gliadin alleles rather well; using this probe, families of gliadin alleles and some of their relationships were described[9988].

Twenty eight gamma-gliadin gene sequences from GenBank were grouped into nine subgroups in [10063]. Primers were developed against some of the subgroups and the chromosomal locations of the gamma-gliadin genes were determined[10063].

Based upon morphological observation and RFLP analysis, it was proposed that the cultivar 'Chinese Spring' is a strain of the landrace 'Chengdu-guangtou' from the Chengdu Plain, Sichuan Province; this proposal is supported by the observation that CS and the landrace share the same alleles at all nine GLI-1, GLI-2 and GLU-1 loci {see 01102}.

PCR primers GAG5 and GAG6 were applied to 35 cultivars of closely related spelt and hexaploid wheat, and to eight cultivars of durum, to yield products originating from two gamma-gliadin genes mapped to chromosomes 1B (termed GAG56B) and 1D (termed GAG56D)[01103]. Two alleles for GAG56D (differing in a 9 bp deletion/duplication and single nucleotide polymorphism) were found, one a new allele and the other previously published[01104]. Meanwhile two alleles found for GAG56B among the durum wheats correlated with the presence of gluten quality markers, gamma-gliadins 42 or 45.

1B and 1D sulphur-poor omega-gliadins in cultivar Butte 86 were characterised by RP-HPLC, SDS-PAGE, two-dimensional PAGE, amino acid composition determination and sequencing, matrix assisted laser desorption ionisation-time of flight mass spectrometry and circular dichroism spectroscopy to reveal the detailed nature of the peptides belonging to the two groups, and showing that the complexity of mixtures of the peptides of the 1B group was greater than that of the 1D group[01105]. Although circular dichroism spectra were similar for the two groups of peptides, and suggested a mainly flexible random structure, there was evidence for a significant amount of left-handed polyproline II helical conformation in the case of the 1D components. The authors placed some of the results in the context of the possible ancestor of the B-genome and relationships with the barley C-hordeins and rye omega-secalins.

Eleven new gliadin alleles were found in a collection of 52 Spanish landraces of common wheat[03141]. A new family of low-molecular-weight gliadin genes located on groups 4 and 7 were reported in [10117]. They appear to influence rheological properties and seem to be closely related to the 17kDa epsilon hordein, important in beer foam stability.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated **Ch1** to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci GLI-1 and GLU-3. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated[10307].

Transcriptome analysis showed the presence of proteins called avenin-like a and b. The former contained a duplicated sequence of about 120 residues and corresponded to the LMW-gliadins. The latter was not previously characterized but may form part of the glutenin fraction and hence influence quality. These avenin-like proteins showed higher expression levels in three *Aegilops* species (*Ae. caudata*, *Ae. cylindrica* and *Ae. tauschii*) than in common wheat[10321].

Four new classes of low molecular weight proteins related to gliadins, though not sufficiently similar to be classified as such, were reported in [02113]. One of the classes has no close association to previously described wheat endosperm proteins.

GLI-1

GLI-A1

Gli-A1[1125, 1334] locus: 1AS[150, 634, 1334, 1607] syn: Gld 1A[1415]

s: CS*/Cheyenne[634]. **v**: CS[150, 1334, 1607].

Gli-A1a[988]

v: Castan[991]; CS[988]; Mara[9986]; Mentana[9986]; Millewa[00119].

Gli-A1b [988]

v: Bezostaya 1, Mercia[988]; Tracy[991].

Gli-A1c [988]

v: Ukrainka[998]; Gazul[9985]; Sava[994]; Hopps[00119].

Gli-A1d [988]

v: Dankowska[988]; Cabezorro[9985].

Gli-A1e [988]

v: Falchetto[988]; Open[991]; Touzelle[991].

Gli-A1f [988]

v: Mironovskaya 808, Maris Freeman[988]; Arminda[991].

Note: An allele ***Gli-A1f**** is mentioned in [03130].

Gli-A1g [988]

v: Gabo[988]; Adalid[9985].

Gli-A1h [988]

v: Sadovo I[988]; Predela[9981]; Krajinka[9981].

Gli-A1i [988]

v: Saratovskaya 36[988].

Gli-A1j [988]

v: Lutescens 62[988].

Gli-A1k [988]

v: Courtot[991]; Skala (heterogeneous)[988]; Soissons[991]; Spada[9986].

Gli-A1l [988]

v: Lesostepka 75[988]; David[9986]; Salmone[9986]; Mura[9981].

Gli-A1m [988]

v: Marquis[988]; Dneprovskaya 521[988]; Carat[991]; Liocorno[9986].

Gli-A1n [988]

v: Intensivnaya[988].

Gli-A1o [988]

v: Odesskaya 16 (heterogeneous)[988]; Oderzo[9986]; Cappelle-Desprez[991]; Capitole[991].

Gli-A1p [988]

v: Pyrotrix 28[988]; Zagore[9981].

Gli-A1q [988]

v: Akmolinka 1[988].

Gli-A1r [988]

v: Ranniaya 73[988]; Barbilla[9985].

Gli-A1s

Although reported[9986], this allele is omitted because it requires further confirmation[9981].

Gli-A1t [9985]

v: Jeja del Pais[9985]; Milturum 553[9981]; Strela[9981].

Gli-A1u [9985]

v: Candeal Alcala[9985].

Gli-A1v [9981]

v: Japhet[9981]; Rouge de Bordeaux[9981].

Gli-A1w [9984, 9987] locus: Null allele

v: Saratovskaya 29 (mutant)[9987]; E. Mottin[9981].

Gli-A1x [10805] syn: Gli-A1^{m}a[10805]

dv: PI 191146, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1y [10805] syn: Gli-A1^{m}b[10805]

dv: PI 190947 *T. monococcum* ssp. *monococcum* [10805].

Gli-A1z [10805] syn: Gli-A1^{m}c[10805]

dv: PI 190946, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1aa [10805] syn: Gli-A1^{m}d[10805]

dv: PI 191097, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1ab [10805] syn: Gli-A1^{m}e[10805]

dv: BGE-020466, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1ac [10805] syn: Gli-A1^{m}f[10805]

dv: BGE-013626, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1ad [10805] syn: Gli-A1^{m}g[10805]

dv: BGE-013628, *T. monococcum* ssp. *monococcum* [10805].

Gli-A1ae [10811] syn: Gli-A^{u}1-I[10811]

dv: PI-428333, *T. urartu* [10811].

Gli-A1af [10811] syn: Gli-A^{u}1-II[10811]

dv: PI-428319, *T. urartu* [10811].

Gli-A1ag [10811] syn: Gli-A^{u}1-III[10811]

dv: PI-428335, *T. urartu* [10811].

Gli-A1ah [10811] syn: Gli-A^{u}1-IV[10811]

dv: PI-428323, *T. urartu* [10811].

Gli-A1ai [10811] syn: Gli-A^{u}1-V[10811]

dv: PI-428231, *T. urartu* [10811].

Gli-A1aj [10811] syn: Gli-A^{u}1-VI[10811]

dv: PI-428194, *T. urartu* [10811].

Gli-A1ak [10811] syn: Gli-A^{u}1-VII[10811]

dv: PI-428256, *T. urartu* [10811].

Gli-A1al [10811] syn: Gli-A^{u}1-VIII[10811]

dv: PI-428234, *T. urartu* [10811].

Gli-A1am [10811] syn: Gli-A^{u}1-IX[10811]

dv: PI-428320, *T. urartu* [10811].

Gli-A1an [10811] syn: Gli-A^{u}1-X[10811]

dv: PI-428255, *T. urartu* [10811].

Gli-A1ao[10811] syn: Gli-A^{u}1-XI[10811]

dv: PI-428241, *T. urartu*[10811].

Gli-A1ap[10811] syn: Gli-A^{u}1-XII[10811]

dv: PI-428235, *T. urartu*[10811].

Gli-A1aq[10811] syn: Gli-A^{u}1-XIII[10811]

dv: PI-428183, *T. urartu*[10811].

Gli-A1ar[10811] syn: Gli-A^{u}1-XIV[10811]

dv: PI-428317, *T. urartu*[10811].

Gli-A1as[10811] syn: Gli-A^{u}1-XV[10811]

dv: PI-427328, *T. urartu*[10811].

Gli-A1at[10811] syn: Gli-A^{u}1-XVI[10811]

dv: PI-428327, *T. urartu*[10811].

Gli-A1au[10811] syn: Gli-A^{u}1-XVII[10811]

dv: PI-428253, *T. urartu*[10811].

Gli-A1av[10811] syn: Gli-A^{u}1-XVIII[10811]

dv: PI-428224, *T. urartu*[10811].

Gli-A1aw[10811] syn: Gli-A^{u}1-XIX[10811]

dv: PI-538727, *T. urartu*[10811].

Gli-A1ax[10811] syn: Gli-A^{u}1-XX[10811]

dv: PI-428211, *T. urartu*[10811].

Gli-A1ay[10811] syn: Gli-A^{u}1-XXI[10811]

dv: PI-538724, *T. urartu*[10811].

Gli-A1az[10811] syn: Gli-A^{u}1-XXII[10811]

dv: PI-428191, *T. urartu*[10811].

Gli-A1ba[10811] syn: Gli-A^{u}1-XXIII[10811]

dv: TRI-6735, *T. urartu*[10811].

Gli-A1bb[10811] syn: Gli-A^{u}1-XXIV[10811]

dv: TRI-11494, *T. urartu*[10811].

Gli-A1bc[10811] syn: Gli-A^{u}1-XXV[10811]

dv: TRI-6734, *T. urartu*[10811].

Gli-A1bd[10811] syn: Gli-A^{u}1-XXVI[10811]

dv: TRI-11496, *T. urartu*[10811].

GLI-B1

Gli-B1[1125, 1607] locus: 1BS[150, 634].1B[1607] syn: Gld 1B[1243, 1415], Gld-B4[420], Gld-B2[420], Gld-B6[420], Gld-B5[420], Gld-B3[420], Gld-B1[420]

s: CS*/Cheyenne[634]. **v**: CS[150, 1607].

Gli-B1a[988]

v: CS[988].

Gli-B1b[988]

v: Bezostaya 1[988]; Carat[991]; Marquis[988]; Liocorno[9986]; Soissons[991].

Gli-B1c[988]

v: Siete Cerros 66[988]; Prinqual[991]; Loreto[9986].

Gli-B1d[988]

v: Dneprovskaya 521[988]; Chopin[991]; Petrel[991]; Tiberio[9986]; Yecora[9985]; Neepawa[995]; Suneca[00119].

Gli-B1e[988]

v: Apexal[991]; Fournil[991]; Lutescens 62[988]; Oderzo[9986].

Gli-B1f[988]

v: Capitole[991]; Cappelle-Desprez[991]; Dankowska[988]; Maris Freeman[988]; Mercia[998].

Gli-B1g[988]

v: Champtal[991]; Galahad[988]; Mara[9986]; Sadovo 1[988]; Tracy[991].

Gli-B1h[988]

v: Cabezorro[9985]; Krasnodonka[988]; Pepital[991]; Rudi[991]; Tincurrin[00119].

Gli-B1i[988]

v: Ghurka[988]; Insignia[988].

Gli-B1j[988]

v: Cluj 650[988].

Gli-B1k[988]

v: Crverkapa[994]; De Carolis[9986]; Kremena[988]; Mentana[9986].

Gli-B1l[988]

v: Avrova[9981]; Clement[991]; Damier[991]; Fiocco[9986]; Kavkaz[9981].

Gli-B1l encodes secalins ssociated with the 1BL.1RS translocation.

Gli-B1m[988]

v: Costantino[9986]; Et.d'Choisy[991]; Pyrotrix 28[988].

Gli-B1n[988]

v: Intensivnaya[988].

Gli-B1o[988]

v: Aragon 03[9985]; Levent[988]; Pippo[9986]; San Rafael[9985].

Gli-B1p[988]

v: Inia 66[9985]; New Pusa 834[988].

Gli-B1q[9986]

v: Gallo[9986]; Goelent[991]; Goya[991].

Gli-B1r[995]

v: Chinook[995]; Gazul[9985]; Sevillano[9985].

Gli-B1s[9986]

v: Salmone[9986]; Resistente[9986]; E. Mottin[9981].

Gli-B1t[9985]

v: Jeja del Pais[9985].

Gli-B1u[9985]

v: Negrillo[9985].

Gli-B1v[9985]

v: Montjuich[9985].

Gli-B1w[9981]

v: Ardica[9981]; Barbilla (MCB-1017)[9981].

Gli-B1x[991, 9984, 9987] locus: Null allele

v: Touzelle[991]; Florence Aurora[9985].

Twelve microsatellite alleles plus a null allele were found at the GLI-B1 locus tightly linked to GLU-B3 in 112 bread wheat cultivars from Argentina[03123].

GLI-D1

Gli-D1[121, 1125] locus: 1DS[121, 150], {634, }.[1334, 1607] syn: Gld-D1[420], Gld-D3[420], Gld 1D[1415], Gld-D2[420]

s: CS*/Cheyenne[634]. **v**: CS[121, 150, 1334, 1607].

Gli-D1a[988]

v: CS[988]; Marquis[988]; Mentana[9986]; Prinqual[991]; Saratovskaya 36[988].

Gli-D1b[988]

v: Bezostaya 1[988]; Cappelle-Desprez[991]; Etoile d'Choisy[991]; Galahad[988].

Gli-D1c[988]

v: Skorospelka Uluchshennaya (biotype)[988, 9982].

Gli-D1d[988]

v: De Carolis[9986]; Solo[988].

Gli-D1e[988]

v: Gerek 79[988].

Gli-D1f[988]

v: Carlos[991]; Gabo[988]; Maris Freeman[988]; Orso[9986].

Gli-D1g[988]

v: Fournil[991]; Ghurka[988]; Mironovskaya 808[988]; Open[991].

Gli-D1h[988]

v: Sadovo I[988]; Zlatostrui[9981].

Gli-D1i[988]

v: Insignia[988]; Napayo (biotype)[995]; San Rafael[9985]; Tselinogradka[988].

Gli-D1j[988]

v: Aubain; Chinook[995]; Inia 66[9985]; Petrel[991]; Promin[988].

Gli-D1k[988]

v: Cargimarec[991]; Kremena[988]; Mara[9986]; Pippo[9986].

Gli-D1l[988]

v: Artaban[991]; Corin[991]; Longbow[988].

Gli-D1m[991]

v: Heurtebise[991].

Gli-D1n[981]

v: Blanquillo de Toledo (MCB-0950)[9981].

Gli-D1o[991, 9984, 9987] locus: Null allele

v: Darius[991]; Touzelle[991]; Saratovskaya 29 (mutant)[9987].

ungrouped

Gli-Ag^{i}1 locus: 1Ag^{i} [168]

ad: Vilmorin 27/*Th. intermedium*.

Gli-DT1[02109] locus: 1DS[02109]

v: L/18913 (synthetic). **dv**: *Ae. tauschii* AUS18913.

A locus designated **GLI-DT1** controlling an omega-gliadin of *Ae. tauschii* was mapped on the short arm of chromosome 1D between loci GLI-D1 (strictly *GLI-D^{t}1*) and GLU-D1 (strictly *GLU-D^{t}1*), 13.18 cM proximal to the former and 40.20 cM from the latter[02109]. The only omega-gliadin to date identified as being encoded by this locus, namely T1, is of unusually low electrophoretic mobility in SDS-PAGE gels and was formally thought to be a high molecular weight glutenin encoded by the *GLU-D^{t}1* locus of *Ae. tauschii* (see note following the GLU-D1 list in section 'Glutenins'). The authors speculate that, due to their similar relative map positions, the loci *GLI-A4, GLI-D4,* **GLI-R3**, *GLI-S^{l}4* and this locus, **GLI-DT1**, form a series of 'Gli-4' orthologous loci. However, this should be interpreted in the light of the above discussion on **GLI-A3** and *GLI-A4*.

Gli-DT1a[02109] locus: T1

v: L/18913 (synthetic). **dv**: *Ae. tauschii* AUS18913.

A 1,200 bp Dra I RFLP was identified as a gene-specific probe for the T1 omega-gliadin[10645].

Gli-E1[781] locus: 1ES[781]

ad: CS/*E. elongata*. ***GLI-H^{t}1***[1037]. 1H^{t}p[1037]; CS/*E. trachycaulum*.

Gli-H^{t}1[1037] locus: 1H^{t}p

ad: CS/*E. trachycaulum*

Gli-R1[1334] locus: 1RS[781, 1340], {1336, }.[1334] syn: SecR1[1356], Sec1[1336]

ad: CS/Imperial[781, 1334, 1336, 1340]; Holdfast/King II[1334, 1340]. **tr**: CS 1DS. Imperial 1RL[1356]. *Sec-12* and *Sec13* are given as allelic alternatives in 1BL.1RS translocation lines by ▶[03132].

Gli-R^{m}1[1340] locus: 1R^{m}S[1340]

ad: CS/*S. montanum*.

Gli-S^{l}1[573] locus: 1S^{l}[573]

ad: CS/*Ae. longissima*.

Gli-U1[1335] locus: 1U[150, 1335]

ad: CS/*Ae. umbellulata*.

Gli-V1[111, 1026] locus: 1V[111, 1026]

ad: CS/*D. Villosum*[1026]; Creso/*D. villosum*[111].

In barley, the B and C hordeins are controlled by the *HOR2* and *HOR1* loci, respectively, which are linked[1341] on chromosome 1HS[1063, 1153]. The map distances and homology of the proteins indicate that *HOR1*, the locus closest to the centromere, is equivalent to the omega-gliadins (*GLI-1-1*) in GLI-1[1338].

Three alleles at each of the *GLI-1-1* (omega gliadin) loci were noted[1358]. The complexity of the GLI-1 compound loci is further emphasized by a report of individual genes being separable by recombination, where *G1d-1A* (a block of gamma and omega genes) is separable by 0.3% from *Gld4-1A* (omega gliadins) which is in turn, separable by 1.5% from *Gld3-1A* (omega gliadins)[1103].

Variation was described elsewhere[634, 996, 1126] and applied in mapping experiments[107, 196, 422, 1120, 1125, 1243]. Sixteen combinations of GLI-B1 and 4 combinations of GLI-D1 subunits are listed in ▶[420]. Multiple alleles described in ▶[996], number 15 at GLI-A1, 18 at GLI-B1, and 8 at GLI-D1.

The Gli-1 alleles present in 57 Yugoslav wheat varieties were reported in ▶[994].

GLI-2

Prior to publication[988] allelic variation was demonstrated at all the wheat GLI-2 loci, including 13 alleles at GLI-A2, 11 at GLI-B2, and 10 at GLI-D2, in a study of 39 cultivars[996].

GLI-A2

Gli-A2[1125, 1334] locus: 6A[1334]. 6AS[1122] syn: Gld 6A[1415]

v: CS.

Gli-A2b[988]

v: Aradi[9985]; Bezostaya 1[988]; Rivoli[991]; Tiberio[9986].

Gli-A2c[988]

v: Eagle[00119]; Escualo[9985]; Loreto[9986]; Prinqual[991]; Siete Cerros 66[988].

Gli-A2d[988]

v: Dneprovskaya 521[988]; Kenyon (biobype)[995]; Mocho Sobarriba[9985].

Gli-A2e[988]

v: Cobra[991]; Mentana[9986]; Resistente[9986]; Sadovo 1[988]; Sevillano[9985].

Gli-A2f[988]

v: Adalid[9985]; Gala[991]; Maris Freeman[988]; Sistar[9986].

Gli-A2g[988]

v: Cappelle-Desprez[991]; Ducat[988]; Mahissa 1[9985]; Mara[9986].

Gli-A2h[988]

v: Apollo[991]; Basalt[9981]; Hereward[988]; Montjuich[9985]; N. Strampelli[9986].

Gli-A2i[988]

v: Krasnodonka[988]; Lesostepka 75[988].

Gli-A2j[988]

v: Avalon[9981]; Camp Remy[991]; E. Mottin[9981]; Recital[991].

Gli-A2k[988]

v: Akmolinka 1[988]; Estica[991]; Pyrotrix 28[988]; Renan[991]; Zena[9986].

Gli-A2l[988]

v: Chamorro[9985]; Champlein[991]; Longbow[988].

Gli-A2m[988]

v: Marquis[988]; Rex[991]; Suneca[00119].

Gli-A2n[988]

v: Mironovskaya 808[988].

Gli-A2o[988]

v: Calatrava[9985]; Castan[991]; Glenwari[9981]; Lontra[9986]; Touzelle[991].

Gli-A2p[988]

v: Cajeme 71[9985]; Capitole[991]; Clement[991]; Pliska[988]; S. Lorenzo[9986]; Yecora 70[9985].

Gli-A2q[988]

v: Candeal Alcala[9985]; Montcada[9985]; Saratovskaya 39[988].

Gli-A2r[988]

v: Genia I[991]; Open[991]; Riband[988].

Gli-A2s[988]

v: Saratovskaya 36[998].

Gli-A2t[988]

v: Courtot[991]; Prostor[9981]; Rinconada[9985]; Soissons[991].

Gli-A2u[988]

v: Aragon 03[9985]; Kirgizskaya Yubileinaya[988]; Saunders[995]; Titien[991].

Gli-A2v[988]

v: Kzyl-Bas[988].

Gli-A2w[988]

v: Bezenchukskaya 98 (biotype)[988].

Gli-A2x[988]

v: Solo[988].

Gli-A2y[9981]

v: Gentil Rosso 202[9981]; PI 191245[9981].

Gli-A2z[9986]

v: Gallo[9986]; Giuliana[9986].

Gli-A2aa[9985]

v: Navarro 122[9985].

Gli-A2ab[9985]

v: Navarro 150[9985].

Gli-A2ac[9981]

v: Blanquillo de Barcarrota (MCB-0893)[9981].

Gli-A2ad[9981]

v: Hembrilla Soria (MCB-1298)[9981].

Gli-A2ae[9981]

v: Candeal de S.Lorenzo Parrilla (MCB-0932)[9981].

Gli-A2af[9981]

v: Barbilla de Leon (MCB-1292)[9981].

Gli-A2ag[9981]

v: Gluclub[9981]; Tincurrin[9981].

Gli-A2ah[9981]

v: Candeal de Nava del Rey (MCB-0892)[9981].

Gli-A2ai[9981]

v: Blanquillo (MCB-0908)[9981].

Gli-A2aj[9984, 9987] locus: Null allele

v: Saratovskaya 29 (mutant)[9987].

Gli-A2ak[10805] syn: Gli-A2^{m}a[10805]

dv: BGE-013630, *T. monococcum* ssp. *monococcum*[10805].

Gli-A2al[10805] syn: Gli-A2^{m}b[10805]

dv: PI 094740, *T. monococcum* ssp. *monococcum*[10805].

Gli-A2am [10805] syn: Gli-A2^{m}c [10805]

dv: PI 190942, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2an [10805] syn: Gli-A2^{m}d [10805]

dv: PI 190947, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2ao [10805] syn: Gli-A2^{m}e [10805]

dv: PI 190946, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2ap [10805] syn: Gli-A2^{m}f [10805]

dv: BGE-013626, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2aq [10805] syn: Gli-A2^{m}g [10805]

dv: PI 191095, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2ar [10805] syn: Gli-A2^{m}h [10805]

dv: BGE-001937, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2as [10805] syn: Gli-A2^{m}i [10805]

dv: PI 191096, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2at [10805] syn: Gli-A2^{m}j [10805]

dv: BGE-020466, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2au [10805] syn: Gli-A2^{m}k [10805]

dv: BGE-001937, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2av [10805] syn: Gli-A2^{m}l [10805]

dv: BGE-029108, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2aw [10805] syn: Gli-A2^{m}m [10805]

dv: BGE-013627, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2ax [10805] syn: Gli-A2^{m}n [10805]

dv: BGE-001937, *T. monococcum* ssp. *monococcum* [10805].

Gli-A2ay [10811] syn: Gli-A^{u}2-I [10811]

dv: PI-428333, *T. urartu* [10811].

Gli-A2az [10811] syn: Gli-A^{u}2-II [10811]

dv: PI-428320, *T. urartu* [10811].

Gli-A2ba [10811] syn: Gli-A^{u}2-II [10811]

dv: PI-428230, *T. urartu* [10811].

Gli-A2bb [10811] syn: Gli-A^{u}2-IV [10811]

dv: PI-428319, *T. urartu* [10811].

Gli-A2bc [10811] syn: Gli-A^{u}2-V [10811]

dv: PI-428239, *T. urartu* [10811].

Gli-A2bd [10811] syn: Gli-A^{u}2-VI [10811]

dv: PI-428336, *T. urartu* [10811].

Gli-A2be [10811] syn: Gli-A^{u}2-VII [10811]

dv: PI-428235, *T. urartu* [10811].

Gli-A2bf [10811] syn: Gli-A^{u}2-VIII [10811]

dv: PI-428234, *T. urartu* [10811].

Gli-A2bg[10811] syn: Gli-A^{u}2-IX[10811]

dv: PI-428183, *T. urartu*[10811].

Gli-A2bh[10811] syn: Gli-A^{u}2-X[10811]

dv: PI-428256, *T. urartu*[10811].

Gli-A2bi[10811] syn: Gli-A^{u}2-XI[10811]

dv: PI-428255, *T. urartu*[10811].

Gli-A2bj[10811] syn: Gli-A^{u}2-XII[10811]

dv: PI-428224, *T. urartu*[10811].

Gli-A2bk[10811] syn: Gli-A^{u}2-XIII[10811]

dv: PI-428208, *T. urartu*[10811].

Gli-A2bl[10811] syn: Gli-A^{u}2-XIV[10811]

dv: PI-428202, *T. urartu*[10811].

Gli-A2bm[10811] syn: Gli-A^{u}2-XV[10811]

dv: PI-428217, *T. urartu*[10811].

Gli-A2bn[10811] syn: Gli-A^{u}2-XVI[10811]

dv: PI-427328, *T. urartu*[10811].

Gli-A2bo[10811] syn: Gli-A^{u}2-XVII[10811]

dv: PI-428317, *T. urartu*[10811].

Gli-A2bp[10811] syn: Gli-A^{u}2-XVIII[10811]

dv: PI-428253, *T. urartu*[10811].

Gli-A2bq[10811] syn: Gli-A^{u}2-XIX[10811]

dv: PI-538742, *T. urartu*[10811].

Gli-A2br[10811] syn: Gli-A^{u}2-XX[10811]

dv: PI-428232, *T. urartu*[10811].

Gli-A2bs[10811] syn: Gli-A^{u}2-XXI[10811]

dv: PI-428188, *T. urartu*[10811].

Gli-A2bt[10811] syn: Gli-A^{u}2-XXII[10811]

dv: PI-428244, *T. urartu*[10811].

Gli-A2bu[10811] syn: Gli-A^{u}2-XXIII[10811]

dv: PI-538733, *T. urartu*[10811].

Gli-A2bv[10811] syn: Gli-A^{u}2-XXIV[10811]

dv: PI-428212, *T. urartu*[10811].

Gli-A2bw[10811] syn: Gli-A^{u}2-XXV[10811]

dv: TRI-6734, *T. urartu*[10811].

Gli-A2bx[10811] syn: Gli-A^{u}2-XXVI[10811]

dv: PI-428254, *T. urartu*[10811].

Gli-A2a[988]

v: Cabezorro[9985]; CS[988]; Insignia[988]; Rieti DIV[9986].

GLI-B2

Gli-B2[1125, 1607] locus: 6BS[1122]. 6B[1607] syn: Gld 6B[1415]

v: CS.

Gli-B2a[988]

v: CS[988].

Gli-B2b[988]

v: Bezostaya 1[988]; Cobra[991]; Gladio[9986]; Sideral[991].

Gli-B2c[988]

v: Courtot[991]; Escuala[9985]; Gabo[988]; Loreto[9986]; Manital[9986]; Prinqual[991]; Siete Cerros 66[988]; Sinton[995]; Yecora 70[9985].

Gli-B2d[988]

v: Akmolinka 1[988]; Cesar[9981]; Friedland[991]; Tselinnaya 20[988].

Gli-B2e[988]

v: Arsenal[991]; Veronese[9986]; Zlatna Dolina[994].

Gli-B2f[988]

v: Basalt[9981]; Maris Freeman[988]; Master[991].

Gli-B2g[988]

v: Capitole[991]; Capelle-Desprez[991]; Galahad[988]; Forlani[9986].

Gli-B2h[988]

v: Castan[991]; Mentana[9986]; Pane 247[9985]; Partizanka[994]; Sadovo 1[988]; Sistar[9986].

Gli-B2i[988]

v: Insignia[988]; Robin[9981].

Gli-B2j[988]

v: Farnese[9986]; Funo R250[9986]; Novosadska Rana 1[994].

Gli-B2k[988]

v: Skala[988].

Gli-B2l[988]

v: Clement[991]; Longbow[988]; Tracy[991].

Gli-B2m[988]

v: Mironovskaya 808[988]; Open[991]; Renan[991].

Gli-B2n[988]

v: Japhet[9981]; Rouge de Bordeau[9981]; Solo[988].

Gli-B2o[988]

v: Hardi[9981]; Mara[9986]; Odesskaya 16[988]; Pippo[9986]; Rivoli[991]; Slavjanka[9981].

Gli-B2p[988]

v: Pliska[983]; Champtal[991]; Oderzo[9986]; Recital[991]; Gazul[9985].

Gli-B2q[988]

v: Saratovskaya 39[988].

Gli-B2r[991]

v: Arminda[991]; Estica[991]; Genial[991].

Gli-B2s [988]

v: Aquila[9981]; Saratovskaya 36[988].

Gli-B2t [988]

v: Tselinogradka[988].

Gli-B2u [988]

v: Kirgizskaya Yubileinaya[988].

Gli-B2v [988]

v: Declic[991]; Garant[991]; Libellula[9986]; Mahissa 1[9985]; Poljarka[988].

Gli-B2w [995, 9986]

v: Palata[9986]; Pembina[995]; Rieti DIV[9986].

Gli-B2x [994]

v: Super Zlatna (biotype)[994]; Prostor[9981]; 251/83[9981].

Gli-B2y [9986]

v: Centauro[9986]; E. Morandi[9986].

Gli-B2z [9985]

v: Maestro[9985].

Gli-B2aa [9986]

v: Salmone[9986]; E. Mottin[9981].

Gli-B2ab [991]

v: Bordier[9981]; Orepi[991].

Gli-B2ac [991]

v: Scipion[991]; Artaban[991]; Riol[991]; Lontra[9981].

Gli-B2ad [991]

v: Champion[991]; Chopin[991].

Gli-B2ae [991]

v: Priam[991]; Etoile d'Choisy[991]; Campeador[9985]; Krajinka (biotype)[994].

Gli-B2af [9985]

v: Montjuich[9985]; Mocho Sobarriba[9985].

Gli-B2ag [9981]

v: Jeja del Pais[9985]; Barbilla de Leon (MCB-1292)[9981].

Gli-B2ah [9981]

v: Rojo de Humanes (MCB-1262)[9981]; Grano de Miracolo[9981].

Gli-B2ai [9981]

v: Blanquillo (MCB-0908)[9981].

Gli-B2aj [9981]

v: Negrete de Malaga (MCB-1754)[9981].

Gli-B2ak [9981]

v: HY320[9981]; Leader[9981].

Gli-B2al [9981]

v: Dankowska[991].

Gli-B2am [9981]

v: TM-275[9981]; Uralochka[9981].

Gli-B2an [9981]

v: Eagle[9981]; Glenwari[9981].

Gli-B2ao [9981]

v: Olympic[9981]; Mokoan[9981].

Gli-B2ap [9981]

v: Veda[9981]; Magnif 27[9981].

Gli-B2aq [9981]

v: Winglen[9981]; Isis[9981].

Gli-B2ar [9981]

v: Arbon[9981]; Roazon[9981].

Gli-B2as [9981]

v: Strela[9981]; Sredneuralskaya[9981].

Gli-B2at [9981]

v: Ranee[9981]; Javelin 48[9981].

Gli-B2au [9984, 9987] locus: Null allele

v: Saratovskaya 29[9987].

GLI-D2

Gli-D2 [1125, 1334] locus: 6DS[1122]. 6D[1334] syn: Gld 6D[1415]

v: CS.

Gli-D2a [988]

v: CS[988]; Maris Freeman[988]; Sistar[9986]; Tracy[991].

Gli-D2b [988]

v: Bezostaya 1[988]; Cobra[991]; Farnese[9986]; Partizanka[994].

Gli-D2c [988]

v: Escualo[9985]; Eridano[9986]; Rieti DIV[9986]; Siete Cerros 66[988].

Gli-D2d [988]

v: Dneprovskaya 521[988].

Gli-D2e [988]

v: Dollar[9985]; Lada[9981]; Mironovskaya 808[988]; Open[991].

Gli-D2f [988]

v: Creneau[991]; Kirgizskaya Yubileinaya[988]; Rempart[991].

Gli-D2g [988]

v: Capelle-Desprez[991]; Futur[991]; Galahad[988]; Ghurka[988]; Mec[9986].

Gli-D2h [988]

v: Capitole[991]; Chinook[995]; Eagle[00119]; Garant[991]; Sadovo 1[988]; Thatcher[995].

Gli-D2i [988]

v: Insignia 49[00119]; Lario[9986].

Gli-D2j[988]

v: Arcane[991]; Gallo[9986]; Gazul[9985]; Inia 66[9985]; Mentana[9986].

Gli-D2k[988]

v: Crvencapa[944]; Kzyl-Bas[988]; Skala[988].

Gli-D2l

Omitted. No reliable differences compared to existing alleles[9981].

Gli-D2m[988]

v: Marquis[988]; Rex[991]; Rinconada[9985]; Suneca[119]; Veronese[9986]; Yecora 70[9985].

Gli-D2n[988]

v: Castan[991]; Champlein[991]; Mahissa 1[9985]; Mercia[988]; Pippo[9986].

Gli-D2o[988]

v: Omskaya 12[988].

Cultivars Salmone and Resistente, which carry ***Gli-D2aa***[9981], were erroneously given as standards for allele ***Gli-D2o*** in [9986].

Gli-D2p[988]

v: New Pusa[988].

Gli-D2q[988]

v: Cook[9981]; E. Mottin[9981]; Fournil[991]; Volshebnitsa (biotype)[988]; Winglen[9981]; Soissons[991].

Gli-D2r[988]

v: Kremena[988]; Mara[9986]; Montcada[9985].

Gli-D2s[988]

v: Akmolinka 1[988]; Bezenchukskaya 98[988]; Selkirk (biotype)[995].

Gli-D2t[9986]

v: Golia[9986]; Gabo[9981]; Manital[9986]; Bokal[9981].

Gli-D2u[9986]

v: Loreto[9986]; Martial[991]; Cibalka[9981].

Gli-D2v[991]

v: Epiroux[991]; Arbon[991].

Gli-D2w[9985]

v: Navarro 150[9985]; Javelin[9981]; Hopps[9981]; Canaleja[9985].

Gli-D2x[9985]

v: Montjuich[9985]; Blanquillo[9985].

Gli-D2y[9985]

v: Candeal Alcala[9985].

Gli-D2z[9985]

v: Aragon 03[9985].

Gli-D2aa[9981]

v: Salmone[9981]; Resistente[9981].

Gli-D2ab[9981]

v: Rojo de Boadilla de Campos (MCB-1031)[9981].

Gli-D2ac [9981]

v: Albatros[9981].

Gli-D2ad [9981]

v: Hembrilla Soria (MCB-1298)[9981].

Gli-D2ae [9984, 9987] locus: Null allele

v: Saratovskaya 29 (mutant) {9987.

GLI-2 alleles were determined in *57* Yugoslav wheat varieties[994].

GLI-R2

Gli-R2[781] locus: 2R, 2RS syn: Sec 2

ad: CS/Imperial[781, 1336, 1340], **ad**: Holdfast/King II[1340]

Gli-R2a[03116] locus: d1 syn: d1[03116]

v: Carnac hexaploid triticale[03116].

Gli-R2b[03116] locus: d2 syn: d2[03116]

v: Mostral hexaploid triticale[03116].

Gli-R2c[03116] locus: t1 syn: t1[03116]

v: Alamo hexaploid triticale[03116].

Gli-R2d[03116] locus: Null[03116]

v: Triticor hexaploid triticale[03116].

Gli-R2e[03115] locus: t2 syn: t2[03115]

v: Tornado hexaploid triticale[03115].

Gli-R^{m}2[1339] locus: 6R^{m} [1339, 1340]

ad: CS/*S. montanum*.

The location of **Gli-R2** in *S. cereale* is thought to have evolved from *S. montanum*[1339] via a translocation between 2R and 6R[1530].

ungrouped

Gli-Ag^{i}2[374] locus: 6Ag^{i} [374]

ad: Vilmorin 27/*Th. intermedium*.

Gli-S^{l}2[573] locus: 6S^{l} [573]

ad, su: CS/*Ae. longissima*.

Gli-U2[1335] locus: 6U[1335]

ad: CS/*Ae. umbellulata*.

Gli-V2[111] locus: 6VS[111]

ad: Creso/*D. villosum*.

GLI-3

A GLI-3 set of loci coding for omega-type gliadins are located 22 to 31 cM proximal to GLI-1 on the short arms of group 1 chromosomes[422, 589, 1403].

Gli-A3[1119, 1403] locus: 1AS[1403] syn: Gld-2-1A[1416]

v: Bezostaya 1.

Each of the following **GLI-A3** alleles, apart from ***Gli-A3d***, which is a null, controls one minor omega-gliadin with molecular mass about 41k that occurs in the middle of the omega-region of APAGE fractionation. Gliadins controlled by these alleles differ in electrophoretic mobility in APAGE in that the fastest of three known **GLI-A3**-gliadins is controlled by ***Gli-A3a*** and the slowest by ***Gli-A3c***[9983].

Gli-A3a[9983]

v: CS, Prinqual, Courtot, Tselinogradka, Bezenchukskaya 98.

Gli-A3b[9983]

v: Bezostaya 1.

Gli-A3c[9983]

v: Anda.

Gli-A3d[9983] locus: Null[9983]

v: Saratovskaya 210, Kharkovskaya 6, Richelle.

Gli-B3[422, 1119] locus: 1BS[422, 589] syn: Glu-B2[589], Gld-B6[422]

s: CS*/Thatcher1B[422]. **v**: Sicco[589].

Gli-B3a[422, 589, 1119]

v: CS.

Gli-B3b[589]

v: Sicco.

Gli-B3c[422, 1119]

s: CS*/Thatcher1B.

Gli-R3[164] locus: 1RS[164]

al: Four inbred lines (R2, J14, 8t, E2666).

Gli-S^{l}3[1228] locus: 1S^{1}S[1228]

ad, su: CS/*Ae. longissima*. **ma**: In *Ae. longissima 2*/*Ae. longissima 10*, three gliadin loci, one glucose phosphate isomerase, and two glutenin loci were mapped relative to one another[1228] as follows: *GLU-S^{l}1* – 15.9 cM – *GPI-S^{l}1* – 38 cM – *GLI-S^{l}4* – 7.1 cM – *GLU-S^{l}3* – 0.9 cM – *GLI-S^{l}1* – 5.6 cM – *GLI-S^{l}5*. *GLU-S^{l}1* is located in 1S^{l}L and the other loci are in 1S^{l}S.

Gli-V3[111] locus: 4VL[111]

ad: Creso/*D. villosum*.

GLI-4

It is not clear how *GLI-S^{l}4* and *GLI-S^{l}5* relate to the GLI-4 and GLI-5 sets described below. A locus designated *GLI-A4* controlling omega-gliadins in cv. Perzivan biotype 2 was mapped at 10 cM proximal to GLI-A1 on the short arm of chromosome 1A[1205].

However, Metakovsky *et al.*[9983] have since shown that this locus and **GLI-A3** are, in fact, the same locus. Furthermore, Dubcovsky et al.[277] did not find evidence for the simultaneous presence of both **GLI-A3** and *GLI-A4* in five 1A or 1A^{m} mapping populations and concluded that *GLI-A4* should be considered **GLI-A3** until conclusive evidence for the former is obtained. For these reasons, variation at the locus *GLI-A4* is not considered.

GLI-5

GLI-5 loci controlling omega-gliadins were mapped to the short arms of chromosomes 1A and 1B, distal to GLI-1[1147]. The map distance between **GLI-B5** and GLI-B1 was estimated as 1.4 cM (recombination value of 1.4 +/- 0.4%), although there was significant variation in recombination ranging from 0% to 5.9% over the six crosses analysed. This variation was attributed to genotypic influence on the frequency of recombination.

Gli-A5[1147] locus: 1AS[1147]

v: Salmone.

Gli-A5a[9983] locus: Null[9983]

v: CS.

Gli-A5b[9983]

v: Marquis.

Allele ***Gli-A5b*** controls two slow-moving, easily-recognizable omega-gliadins. It is present in all common wheat cultivars having alleles ***Gli-A1m*** and ***Gli-A1r*** (and, probably, in those having ***Gli-A1e***, ***Gli-A1l*** and ***Gli-A1q***), because earlier (for example, in ▶[988]) two minor omega-gliadins encoded by ***Gli-A5b*** were considered controlled by these GLI-A1 alleles[9983]

Gli-B5[1147] locus: 1BS[1147]

v: Salmone.

Gli-B5a[1147]

v: CS.

Gli-B5b[1147]

v: Salmone.

In ▶[988], omega-gliadins controlled by **GLI-B5** (allele ***Gli-B5b***) were attributed to alleles at the GLI-B1 locus (alleles ***Gli-B1c***, *i, k, m, n* and *o*).

GLI-6

Gli-A6[993, 9983] locus: 1AS[9983]

GLI-A6 was first explicitly described in ▶[9983] but was first observed without designation in ▶[993]. There is strong evidence that it is distinct from **GLI-A3** and **GLI-A5**, mapping distally to GLI-A1, with which it recombines at a frequency of 2-5%. Currently three alleles are known, of which ***Gli-A6c*** is particularly well-described in ▶[9983]: the molecular mass of the omega-gliadin controlled by this allele is slightly lower than those of the omega-gliadins controlled by **GLI-A3** alleles. In ▶[988], the omega-gliadin controlled by ***Gli-A6c*** was attributed to ***Gli-A1f***. ***Gli-A6c*** is rather frequent in common wheat and may relate to dough quality (preliminary data[9983]).

Gli-A6a[9983] locus: Null[9983]

v: CS; Bezostaya 1.

Gli-A6b[9983]

v: Bezenchukskaya 98.

Gli-A6c[9983]

v: Courtot, Anda, Mironovskaya 808.

GLI-7

Gli-A7[10547] locus: 1DS[10547]

dv: AUS18913[10547].

The gamma-gliadin encoded by this locus co-segregated with the T1 omega-gliadin encoded by the *GLI-D^{t}T1* locus (currently included in the Catalogue as locus (**GLI-DT1**). **GLI-A7** was located 0.69 cM from *GLI-D^{t}1*[10547].

2.3.3 Other endosperm storage proteins

Triticin proteins The triticin proteins[1360] or [Triplet proteins[1357]] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species[1360]. Triticin gene segments including the hypervariable region were PCR-amplified, with preferential amplification of **TRI-D1** for the only pair of primers giving consistent results[10322].

Triticin proteins

The triticin proteins[1360] or [Triplet proteins[1357]] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species[1360]. Triticin gene segments including its hypervariable region were PCR-amplified, with preferential amplification of **Tri-D1** for the only pair of primers giving consistent results[10322].

Tri-A1[1357, 1358] locus: 1AS[1357]

v: CS.

Tri-A1a syn: cs[1358]

v: CS.

Tri-A1b syn: h[1358]

v: Hope.

Tri-D1[707, 1357, 1358] locus: 1DS[1357]

v: CS.

Tri-D1a syn: cs[1358]

v: CS.

Tri-D1b syn: i[1358]

v: India 115.

2.3.4 Salt soluble globulins

GLO-1 are endosperm proteins (23-26 kDa) soluble in salt but not in water[455].

GLO-1

Glo-A1[455] locus: 1AS[455]

v: CS. **ma**: Distally located: **GLO-A1**(distal) – 5.2 cM – GLI-A1[1077].

Glo-B1[455] locus: 1BS[455]

v: CS.

Glo-D1[455] locus: 1DS[455]

v: CS. **ma**: Distally located: **GLO-D1**(distal) – 2.9 cM – GLI-D1[1077].

Glo-E1[455] locus: 1ES[455]

ad: CS/*E. elongata*.

Glo-R1[455] locus: 1RS[455]

ad: CS/Imperial. **su**: 1B/(1R), eg., Salzmunde 14/44.

2.4 Non-storage proteins

2.4.1 Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator

SPA-1

Spa-A1[10908] locus: 1AL[10909]

v: Recital[10909].

Spa-B1[10908] locus: 1BL[10909]

v: Recital[10908]. **ma**: **Glu-B1** - 1.3 cM - **Spa-B1**[10909].

Spa-B1a[10908]

v: Chinese Spring[10909]; Recital[10908]; Australian genotypes listed in ▶[10908].

Spa-B1b[10908]

v: Renan[10909]; Australian genotypes listed in ▶[10908].

Spa-D1[10908] locus: 1DL[10909]

v: Recital[10909].

After testing an ealier hypothesis that SPA genes affected wheat quality, analyses conducted by both[10908, 10909] obtained no evidence supporting a significant effect and attributed any variation to the closely linked GLU-B1 locus.

2.4.2 Grain softness protein

GSP-1

Gsp-1[1185]

Gsp-A1[614] locus: 5A[383, 614] syn: GSP[614]

v: CS[614, 0383]; Rosella (GenBank AF177218)[383].

Gsp-B1[614] locus: 5B[614] syn: GSP[614]

v: CS[614]; Glenlea[0385].

In[1185] sequence of clone TSF33 from cv. Soft Falcon (GenBank X80379) was identical to this allele, as are ESTs for cv. CS (dbEST BJ235798) and cv. CNN (dbEST BE423845).

Gsp-D1[614] locus: 5DS[614] syn: GSP[614]

In ▶[1185] sequence of clone TSF69 from cv Soft Falcon (GenBank S72696) is identical, as are ESTs for cv CS (dbEST BJ237450) and cv CNN (dbEST BE422565).
This locus has a large deletion encompassing genes *Pina-D1, Pinb-D1* and *Gsp-D1*[10077].

Gsp-D1a[614, 1185, 10077, 0383, 0385]

v: CS[614]; Glenlea[0385]. **dv**: *Ae. tauschii* CPI1110799 (GenBank AF177219)[0383]. **ma**: Co-segregation of **Gsp-D1** and **Ha**[614].

Gsp-D1b[03105]

dv: *Ae. tauschii* TA1583 (GenBank AY252079) ***Pina-D1a***, ***Pinb-D1a***[03105]; TA2475 (GenBank AY252087) ***Pina-D1a***, ***Pina-D1i***[03105].

Gsp-D1c[03105]

dv: *Ae. tauschii* TA2369 (GenBank AY252081) ***Pina-D1c***, ***Pinb-D1h***[03105]; CPI110799 (GenBank AF177219)[0383].

Gsp-D1d

dv: *Ae. tauschii* TA2536 (GenBank 252093) ***Pina-D1c***, *Pinb-D2i*[03105]; TA2374 (GenBank AY252046) ***Pina-D1d***, ***Pinb-D1i***[03105]; TA2458 (GenBank AY252084) ***Pina-D1e***, ***Pinb-D1i***[03105]; TA2436 (GenBank AY252048) ***Pina-D1f***, ***Pinb-D1i***[03105].

Gsp-D1e

dv: *Ae. tauschii* TA2527 (GenBank AY252066) ***Pina-D1c***, ***Pinb-D1h***[03105]; TA2512 (GenBank AY252092) ***Pina-D1d***, ***Pinb-D1i***[03105]; TA2495 (GenBank AY252091) ***Pina-D1e***, ***Pinb-D1i***[03105].

Gsp-D1f

dv: *Ae. tauschii* TA1649 (GenBank AY252063) ***Pina-D1d***, ***Pinb-D1h***[03105]; TA2455 (GenBank AY252073) ***Pina-D1d***, ***Pinb-D1i***[03105].

Gsp-D1g

dv: *Ae. tauschii* TA1599 (GenBank AY252062) ***Pina-D1a***, ***Pinb-D1j***[03105].

Gsp-D1h

dv: *Ae. tauschii* TA1691 (GenBank AY252064) ***Pina-D1a***, ***Pinb-D1j***[03105].

Gsp-D1i[03105]

v: Yecora Rojo (GenBank AY255771) ***Pina-D1b***, ***Pinb-D1a***[03105].

Gsp-D1j[10077]

s: CS*/Red Egyptian 5D, **Pina-D1**, **Pinb-D1** and **Gsp-D1**[10077].

In [1185] the sequence of clone TSF69 from cv. Soft Falcon (GenBank S72696) is identical, as are ESTs for cv CS (dbEST BJ237450) and cv CNN (dbEST BE422565). This locus has a large deletion encompassing genes **PINA-D1**, **PINA-D1** and **GSP-D1**[10077].

In[1185] partial-sequence clone TSF61 from cv. Soft Falcon (GenBank X80380) was identical to this allele.

2.4.3 Histone H1 proteins

HSTH1-1

HstH1-A1[0215] locus: 5AL[0215]

v: CS[0215].

HstH1-B1[0215] locus: 5BL[0215]

v: CS[0215].

HstH1-D1[0215] locus: 5DL[0215]

v: CS[0215].

HstH1-D1a[0215]

v: CS[0215]; 18 others[0215].

HstH1-D1b[0215]

v: Grekum 114[0215]; Kirgizsky Karlik[0215].

HSTH1-2

HstH1-A2[0215] locus: 5AL[0215]

v: CS[0215].

HstH1-A2a[0215]

v: CS[0215].

HstH1-A2b[0215] locus: Null allele[0215]

v: Mara[0215]; 10 others[0215].

HstH1-B2[0215] locus: 5BL[0215]

v: CS[0215].

HstH1-B2a[0215]

v: CS[0215]; 19 others[0215].

HstH1-B2b[0215]

v: Excelsior[0215].

HstH1-D2[0215] locus: 5DL[0215]

v: CS[0215].

The relationship of this gene series with a *Hst-A1, Hst-B1, Hst-D1* series in group 5 chromosomes[0216] based on DNA hybridization studies was not established.

2.4.4 Iodine binding factor

A monomeric water-soluble protein from mature grain which preferentially binds iodine[818].

IBF-1

Ibf-A1[818] locus: 5AL[818]

v: CS.

Ibf-A1a[818]

v: CS.

Ibf-A1b[818]

v: Cappelle-Desprez.

Ibf-A1c[818]

v: Hope.

Ibf-A1d[818]

v: Chris.

Ibf-A1e[818]

v: Sears' Synthetic.

Ibf-Ag^{i}1[818] locus: [818]. 5Ag^{i} [818]

ad: Vilmorin/*Th. intermedium*.

Ibf-B1[818] locus: 5BL[818]

v: CS.

Ibf-B1a[818]

v: CS.

Ibf-B1b[818]

v: Cappelle-Desprez.

Ibf-B1c[818]

v: Ciano 67.

Ibf-B1d[818]

v: Sears' Synthetic.

Ibf-D1[818] locus: 5DL[818]

v: CS.

Ibf-D1a[818]

v: CS.

Ibf-D1b[818]

v: Cappelle-Desprez.

Ibf-D1c[818]

v: Purple Pericarp.

Ibf-D1d[818]

v: Sears' Synthetic.

Ibf-E1[818] locus: 5EL[818]

ad: CS/*E. elongata*.

Ibf-H1[818] locus: 4H[818]

ad: CS/Betzes.

Ibf-R1[818] locus: 5RL[818]

ad: CS/Imperial, CS/KingII.

Ibf-S^{l}1[818] locus: 5S^{l} [818]

ad: CS/*Ae. sharonensis*.

Ibf-U1[818] locus: 5U[818]

ad: CS/*Ae. umbellulata*.

2.4.5 Lectins

LEC-1

Lec-A1 locus: 1AL[1427]

v: CS.

Lec-B1 locus: 1B[1427]

s: CS*/Hope 1B.

Lec-D1 locus: 1DL[1427]

v: CS.

Lec-U1 locus: 1U[1427]

ad: CS/*Ae. umbellulata*.

2.4.6 Lipopurothionins

PUR-1

Pur-A1[351] locus: 1AL[351]

v: CS[351].

A PCR marker specific for **PUR-A1** was developed in [9976].

Pur-B1[351] locus: 1BL[351]

v: CS[351].

A PCR marker specific for **PUR-B1** was developed in [9976].

Pur-D1[351] locus: 1DL[351]

v: CS[351].

PCR marker specific for **PUR-D1** was developed in [9976].

A locus in chromosome 5DS affects the level of lipopurothionin[351].

Pur-R1 locus: 1RL[1261]

= 1RS.1BL.

ad: CS/Imperial. **su**: Several 1R(1B) lines. **tr**: Aurora, Kavkaz. A PCR marker specific for **PUR-R1** was developed in [9976].

2.4.7 Puroindolines and grain softness protein

Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). The name 'puroindoline' and the complete amino acid sequence of puroindoline from cv. Camp Remy was given in [0382]. Hard grain texture in hexaploid wheat results from unique changes in the puroindoline amino acid sequence or, currently, four null forms[0295] of the completely linked genes (max. map distance 4.3 cM)[452]. Tetraploid (AABB, AAGG) wheats lack puroindolines and are consequently very hard[03103]. A searchable database of wheat varieties and their puroindoline genotype is available at http://www.wsu.edu/~wwql/php/puroindoline.php. Grain softness protein-1 is a closely related gene which is closely located to the puroindoline genes[1185, 03111]. 'GenBank' and 'dbEST' refer to sequence databases available at NCBI (also available throught EMBL and DDB).

Reviews[10522, 10523] provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave[10524] reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al.[10525, 10526] developed a CS line (PI 651012) carrying a 5A^{m}S.5AS translocation from *T. monococcum*; the translocated chromatin carries A-genome *Pina, Pinb* and **Gsp-1** alleles that confer softer kernel texture.

PINA-1

Pina-A1 03103, 03104, 03108

dv: *T. urartu* unspecified accession 03103; TA763 (GenBank AJ302094) 03104, 03108; TA808 (GenBank AJ302095) 03104, 03108.

Pina-A^{m}1 0083 locus: 5A^{m}S 0083

dv: *T. monococcum* DV92 (cultivated), G3116 (spp. *aegilopoides*) (GenBank AJ242715) 0083; unspecified acession (GenBank AJ249933) 03103; PI 277138 (GenBank AJ302093) 03104; PI 418582 (GenBank AJ302092) 03104; *T. monococcum* spp. *monococcum* TA2025, TA2026 (GenBank AY622786), TA2037 (GenBank AJ242715) 03108; *T. monococcum* spp. *aegilopoides* TA183, TA291, TA546, TA581 (GenBank AY622786) 03108.

In *T. monococcum PINa-A^{m}1* is completely linked to *GSP-A^{m}1* 0083.

Pina-D1 452 locus: 5DS 452

v: CS (GenBank DQ363911) 03108; Capitole (GenBank X69914) 03110.

This locus has a large deletion encompassing genes *PINa-D1, PINb-D1* and **GSP-D1**. This allelic combination confers a harder kernel texture than ***Pina-D1a***/***Pinb-D1b*** 10077.

Pina-D1a 452

v: Bellevue 0249; Capitole (GenBank X69914) 03110; Courtot 0249; Fortuna 0249; Galaxie 0249; Heron 1035; Renan (GenBank CR626934) 10440; Soissons 0249. **v2**: Aurelio ***Pinb-D1a*** 0249; Bezostaja ***Pinb-D1b*** 0249; Bilancia ***Pinb-D1a*** 0249; Bolero ***Pinb-D1a*** 0249; Brasilia ***Pinb-D1b*** 0249; Centauro ***Pinb-D1a*** 0249; Cerere ***Pinb-D1b*** 0249; CS ***Pinb-D1a*** 452, 0249; Colfiorito ***Pinb-D1b*** 0249; Cologna 21 ***Pinb-D1b*** 0249; David ***Pinb-D1b*** 0249; Democrat ***Pinb-D1b*** 0249; Etruria ***Pinb-D1b*** 0249; Francia ***Pinb-D1b*** 0249; Gemini ***Pinb-D1b*** 0249; Genio ***Pinb-D1b*** 0249; Gladio ***Pinb-D1b*** 0249; Lampo ***Pinb-D1a*** 0249; Leone ***Pinb-D1a*** 0249; Leopardo ***Pinb-D1a*** 0249; Libero ***Pinb-D1a*** 0249; Livio ***Pinb-D1a*** 0249; Marberg ***Pinb-D1b*** 0249; Mentana ***Pinb-D1a*** 0249; Mieti ***Pinb-D1b*** 0249; Mose *Pinb- D1a* 0249; Neviana ***Pinb-D1a*** 0249; Newana ***Pinb-D1b*** 0249; Oscar ***Pinb-D1a*** 0249; Pandas ***Pinb-D1b*** 0249; Pascal ***Pinb-D1b*** 0249; Penawawa ***Pinb-D1a*** 03104; Sagittario ***Pinb-D1b*** 0249; Salgemma ***Pinb-D1b*** 0249; Saliente ***Pinb-D1b*** 0249; Salmone ***Pinb-D1b*** 0249; Serena ***Pinb-D1a*** 0249; Serio ***Pinb-D1b*** 0249; Veda ***Pinb-D1b*** 0249; Zena ***Pinb-D1b*** 0249. **dv**: *Ae. tauschii* upspecified accession (GenBank AJ249935) 03103; TA2475 (GenBank AY252037) ***Pinb-D1i***, ***Gsp-D1b*** 03105; TA1599 (GenBank AY252011) ***Pinb-D1j***, ***Gsp-D1g*** 03105; TA1691 (GanBank AY252013) ***Pinb-D1j***, ***Gsp-D1h*** 03105; *Ae. tauschii* unidentified accession (GenBank AJ249935) 03103; *Ae. tauschii* CPI 110799 (GenBank CR626926) 10440.

Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats that carry a hardness mutation in puroindoline b 452, 1035, 0204, 0295, 0082.

Pina-D1b 1035 locus: Null allele

i: Falcon/7*Heron, Heron/7*Falcon 03109; Gamenya Seln. 0203, 0298; Heron/7*Falcon sel. 0203, 0298; PI 644080 (Alpowa/ID377s//7*Alpowa) 10429; Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar and Explorer 10527. **v**: Butte 86 1035; Eridano 0249; Falcon 1035; Glenlea (GenBank AB262660). This BAC clone also contains ***Pinb-D1a*** 10431; Kalyansona 0249; Super X 0249; Yecora Rojo 0204. **v2**: Amidon ***Pinb-D1a*** 0249; Ciano ***Pinb-D1a*** 0249; Dorico ***Pinb-D1a*** 0249; Golia ***Pinb-D1a*** 0249; Guadalupe ***Pinb-D1a*** 0249; Barra ***Pinb-D1a*** 0249; Inia 66 ***Pinb-D1a*** 0249; Indice ***Pinb-D1a*** 0249; Jecora ***Pinb-D1a*** 0249; Manital ***Pinb-D1a*** 0249; Mendos ***Pinb-D1a*** 0249; Padus ***Pinb-D1a*** 0249; Prinqual ***Pinb-D1a*** 0249; Sibilia ***Pinb-D1a*** 0249.

Present only in some hard hexaploid wheats. ***Pina-D1b*** is associated with harder texture than ***Pinb-D1b*** 0177, 0206.

This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls 10391, 10428.

Pina-D1c 03105

dv: *Ae. tauschii* TA2369 (GenBank AY252031) ***Pinb-D1h***, ***Gsp-D1c***; TA2527 (GenBank AY252015) ***Pinb-D1h***, ***Gsp-D1e*** 03108; *Ae. tauschii* TA10 (GenBank AY649746) 03108.

Pina-D1d[03105]

dv: *Ae. tauschii* PI 452131 (GenBank AJ302098) ***Pinb-D1i***[03104]; PI 554318 (GenBank AJ302099) ***Pinb-D1k***[03104]; TA1649 (GenBank AY252012) ***Pinb-D1h***, ***Gsp-D1f***[03105]; TA2374 (GenBank AY251996) ***Pinb-D1i***, ***Gsp-D1d***[03105]; TA2512 (GenBank AY252042) ***Pinb-D1i***, ***Gsp-D1e***[03105]; TA2455 (GenBank AY252022) ***Pinb-D1i***, ***Gsp-D1f***[03105]; TA2536 (GenBank AY252043)[03105]; *Ae. tauschii* TA 1704 (GenBank AY649744)[03108].

Pina-D1e[03105]

dv: *Ae. tauschii* TA2458 (GenBank AY252034) ***Pinb-D1i***, ***Gsp-D1d***[03105]; TA2495 (GenBank AY252041) ***Pinb-D1i***, ***Gsp-D1e***[03105].

Pina-D1f[03105]

dv: *Ae. tauschii* TA2436 (GenBank AY251998) ***Pinb-D1i***, ***Gsp-D1d***[03105].

Pina-D1g[03105]

dv: *Ae. tauschii* TA1583 (GenBank AY252029) ***Pinb-D1a***, ***Gsp-D1b***[03105].

Pina-D1h[10118]

v: *X. aegilotriticum* CIGM86.946-1B-0B-0PR-0B (GenBank AY573898) ***Pinb-D1o***[10118].

Pina-D1i[10118]

v: *X. aegilotriticum* CIGM87.2784-1B-0PR-0B (GenBank AY573899) ***Pinb-D1k***[10118].

Pina-D1j[10118]

v: *X. aegilotriticum* CIGM88.1363-0B (GenBank AY573900) ***Pinb-D1o***[10118].

Pina-D1k[10077] syn: homonym: Pina-D1b/Pinb-D1h(t)

s: CS*/Red Egyptian 5D substitution line, ***Pinb-D1q***, ***Gsp-D1i***[10077]. **v**: Bindokku[10305]; Cheyenne-A[10305]; Chosen 68[10305]; Gaiyuerui[10316]; KT020-584[10432]; Saiiku 18[10305]; Saiiku 44[10305]; Safangmai[10316]; Tachun2[10316]; ZM2851[10316]; ZM2855[10316].

This allele is currently used to denote a large deletion of undetermined size that involves *PINa-D1, PINb-D1* and **GSP-D1**[10077]. The deletion of both puroindolines is associated with harder kernel texture than other known puroindoline hardness alleles[10077, 10305, 10432].

Pina-D1l[10168] syn: Pina-D1c[10168]

v: Baikezaomai Chinese landraces[10208]; Chengduguangtou[10208]; Guangtouxiaomai[10208]; Sanyuehuang[10208]; Xiaoyuhua[10208]. **v2**: Fortuna (USA) ***Pinb-D1a***[10168]; Glenman ***Pinb-D1a***[10168].

Pina-D1l has a C deletion leading to an open reading frame shift and premature stop codon; PINA null, hard kernel texture[10208].

Pina-D1m[10208]

v: Hongheshang (GenBank EF620907)[10208]. C-to-T substitution: Proline-35 to serine; hard kernel texture[10208].

Pina-D1n[10208]

v: Baimangchun[10208]; Hongheshang (GenBank EF620907)[10208]; Xianmai (GenBank EF620908)[10208]; Yazuixiaomai Chinese landraces[10208]; Yazuizi[10208]; Zhuantoubaike[10208].

G-to-A substitution: Tryptophan-43 to stop codon; PINA null hard kernel texture[10208].

Pina-D1o[10311]

dv: *Ae. tauschii* RM0182 (GenBank AY608595)[10311].

Pina-D1p[10316]

v: *T. aestivum* Jing 771 (GenBank AY599893)[10316].

Pina-D1q[10316]

v: U29 (GenBank AB181238)[10316]; Muu-27 (homonym ‘a2’, ***Pina-D1p***)[10316].

Pina-S1[03108]

dv: *Ae. speltoides* PI 393494 (GenBank AJ302096)[03104]; PI 369616 (GenBank AJ302097)[03104]; *Ae. speltoides* spp. *speltoides* TA2368 (GenBank AY622787), TA1789 (GenBank AY622788)[03108]; *Ae. speltoides* spp. *ligustica* TA1777 (GenBank AY622789)[03108].

Pina-S^{b}1[03108]

dv: *Ae. bicornis* spp. *typica* TA1954, TA1942[03108].

Pina-S^{l}1[03108]

dv: *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622790)[03108]; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622791)[03108].

Pina-S^{s}1[03108]

dv: *Ae. searsii* TA1837, TA1355 (GenBank AY622792)[03108].

Pina-S^{sh}1[03108]

dv: *Ae. sharonensis* TA1999 (GenBank AY622796)[03108].

PINB-1

Pinb-A1[03104, 03108]

dv: *T. urartu* TA763 (GenBank AJ302103)[03104]; TA808 (GenBank AJ302104)[03104, 03108].

Pinb-D1 locus: 5DS

v: CS[452], **v**: Capitole (GenBank X69912)[03110]

Pinb-D1a[452]

v: Hill 81[452]. **v2**: Adder ***Pina-D1a***[0317]; Amidon ***Pina-D1b***[0249]; Aurelio ***Pina-D1a***[0249]; Barra ***Pina-D1b***[0249]; Bilancia ***Pina-D1a***[0249]; Bolero ***Pina-D1a***[0249]; Centauro ***Pina-D1a***[0249]; CS ***Pina-D1a***[452, 0249]; Ciano ***Pina-D1b***[0249]; Dorico ***Pina-D1b***[0249]; Fortuna (USA) ***Pina-D1b***[0249]; Glenman ***Pina-D1b***[0249]; Golia ***Pina-D1b***[0249]; Guadalupe ***Pina-D1b***[0249]; Inia 66 ***Pina-D1b***[0249]; Jecora ***Pina-D1b***[0249]; Idice ***Pina-D1b***[0249]; Karl ***Pina-D1a***[0317]; Lampo ***Pina-D1a***[0249]; Leone ***Pina-D1a***[0249]; Leopardo ***Pina-D1a***[0249]; Libero ***Pina-D1a***[0249]; Livio ***Pina-D1a***[0249]; Manital ***Pina-D1b***[0249]; Mendos ***Pina-D1b***[0249]; Mentana ***Pina-D1a***[0249]; Mose ***Pina-D1a***[0249]; Neviano ***Pina-D1a***[0249]; Oscar ***Pina-D1a***[0249]; Padus ***Pina-D1b***[0249]; Penawawa ***Pina-D1a***[03104]; Prinqual ***Pina-D1b***[0249]; Serena ***Pina-D1a***[0249]; Sibilia ***Pina-D1b***[0249]; Sigyn II ***Pina-D1a***[0317]. **dv**: *Ae. tauschii* unspecified accession (GenBank AJ249936)[03103]; TA1583 (GenBank AY251981) ***Pina-D1a***, ***Gsp-D1b***[03105].

Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the ***Pinb-D1b***, *-D1c, -D1d, -D1e*, or *-D1f* mutations[452, 1035, 0204, 0295, 0082].

Pinb-D1b[452] locus: 5DS[452]

i: Paha*2/Early Blackhull/5*Paha[0203, 0298]; Early Blackhull der./5*Nugaines seln.[0203, 0298]; hard sib sel. from Weston[03107]; PI 644081 (Alpowa/ND2603//7*Alpowa)[10429]. **s**: CS*7/Cheyenne 5D[452]. **v**: Thatcher[0204]; Wanser[452]; hard component of Turkey[0204]; Cheyenne (GenBank DQ363914)[10315]; Renan (GenBank CR626934)[10440]. **v2**: Bastion ***Pina-D1a***[0317]; Bezostaya ***Pina-D1a***[0249]; Brasilia ***Pina-D1a***[0249]; Cerere ***Pina-D1a***[0249]; Colfiorito ***Pina-D1a***[0249]; Cologna 21 ***Pina-D1a***[0249]; David ***Pina-D1a***[0249]; Democrat ***Pina-D1a***[0249]; Etruria ***Pina-D1a***[0249]; Francia ***Pina-D1a***[0249]; Gemini ***Pina-D1a***[0249]; Genio ***Pina-D1a***[0249]; Gladio ***Pina-D1a***[0249]; Marberg ***Pina-D1a***[0249]; Mieti ***Pina-D1a***[0249]; Newana ***Pina-D1a***[0249]; Pandas ***Pina-D1a***[0249]; Pascal ***Pina-D1a***[0249]; Sagittario ***Pina-D1a***[0249]; Salgemma ***Pina-D1a***[0249]; Saliente ***Pina-D1a***[0249]; Salmone ***Pina-D1a***[0249]; Serio ***Pina-D1a***[0249]; Veda ***Pina-D1a***[0249]; Zena ***Pina-D1a***[0249].

Pinb-D1b is a “loss-of-function” mutation resulting from the replacement of a glycine by a serine at position 46[452].

Pinb-D1c[0082]

i: PI 644082 (Alpowa/Red Bobs//7*Alpowa)[10429]. **v**: Avle[0082]; Bjorke[0082]; Portal[0082]; Reno[0082]; Tjalve[0082].

Pinb-D1c is a “loss-of-function” mutation resulting from the replacement of a leucine by a proline at position 60[0082].

Pinb-D1d[0082]

i: PI 644083 (Alpowa/Mjolner//7*Alpowa)[10429]. **v**: Bercy[0082]; Mjolner[0082]; Soissons (homonym ‘b1’)[10433].

Pinb-D1d is a “loss-of-function” mutation resulting from the replacement of a tryptophan by an arginine at position 44[0082].

Pinb-D1e[0204]

i: PI 644084 (Alpowa/Canadian Red//7*Alpowa)[10429]. **v**: Gehun[0204]; Canadian Red[0204]; Chiefkan[0204]; Yunxianxiaomai[10427].

Pinb-D1e is a “loss-of-function” mutation resulting from the replacement of a tryptophan by a stop codon at position 39[0204].

Pinb-D1f[0204]

i: PI 644085 (Alpowa/Sevier//7*Alpowa)[10429]. **v**: Abyssinia AV12.4[10430]; The hard component of Utac[0204].

Pinb-D1f is a “loss-of-function” mutation resulting from the replacement of a tryptophan by a stop codon at position 44[0204].

Pinb-D1g[0204]

i: PI 644086 (Alpowa/Andrews//7*Alpowa)[10429]. **v**: Andrews[0204].

Pinb-D1g is a “loss-of-function” mutation resulting from the replacement of a cysteine by a stop codon at position 56[0204].

Pinb-D1h[03105]

dv: *Ae. tauschii* TA2369 (GenBank AY251983) ***Pina-D1c***, ***Gsp-D1c***[03105]; TA2527 (GenBank AY251965) ***Pina-D1c***, ***Gsp-D1e***[03105]; TA1649 (GenBank AY251963) ***Pina-D1d***, ***Gsp-D1f***[03105]; TA10 (GenBank AY649748)[03108]; CPI110799 (GenBank AY159804)[10037].

Pinb-D1i[03105]

dv: *Ae. tauschii* TA2475 (GenBank AY251989) ***Pina-D1a***, ***Gsp-D1b***[03105]; TA2536 (GenBank AY251993) ***Pina-D1c***, ***Gsp-D1d***[03105]; TA2374 (GenBank AY251948) ***Pina-D1d***, ***Gsp-D1d***[03105]; TA2512 (GenBank AY251992) ***Pina-D1d***, ***Gsp-D1e***[03105]; TA2455 (GenBank AY251972) ***Pina-D1d***, ***Gsp-D1f***[03105]; TA2458 (GenBank AY251986) ***Pina-D1e***, ***Gsp-D1d***[03105]; TA2495 (GenBank AY251991) ***Pina-D1e***, ***Gsp-D1e***; TA2436 (GenBank AY251947) ***Pina-D1f***, ***Gsp-D1d***[03105]; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747)[10315, 03108]; *Ae. tauschii* isolate Q03-002 (GenBank DQ257553) (referred to as allele 2)[10314]; *Ae. tauschii* CPI 110799 (GenBank CR626926)[10440].

Q03-002, TA1704, and TA2381 were incorrectly assigned ***Pinb-D1w*** in the 2006 supplement.

Pinb-D1j[03105]

dv: *Ae. tauschii* TA1599 (GenBank AY251962) ***Pina-D1a***, ***Gsp-D1g***[03105]; TA1691 (GenBank AY251964) ***Pina-D1a***, ***Gsp-D1h***[03105]; *Ae. tauschii* TA1691 (GenBank AY251946)[03108].

Pinb-D1k

dv: *Ae. tauschii* PI 554318 (GenBank AJ302108) ***Pina-D1d***[03104].

Pinb-D1l[10119]

v: GaoCheng8901[10119, 10208] reported ***Pinb-D1b*** in Gaocheng 8901.

Pinb-D1m[10118]

v: *X. aegilotriticum* CIGM87.2783-1B-0PR-0B (GenBank AY573901) ***Pina-D1c***[10118].

Pinb-D1n[10118]

v: *X. aegilotriticum* CIGM92.1708 (GenBank AY573902) ***Pina-D1d***[10118].

Pinb-D1o[10118]

v: *X. aegilotriticum* CIGM93.247 (GenBank AY573903) ***Pina-D1e***[10118].

Pinb-D1p [10121] syn: Pinb-D1z[10316]

v: Dahuangpi (GenBank AY581889)[10316]; Nongda 3213[10121]; Nongda 3395[10121]; Qindao landrace[10305]; Qitoubai[10305]; Shijiazhuang 34[10305]; Zigan[10305].

The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213. Homonym: ***Pinb-D1i(t)*** [10305]. This homonym sequence (allele) was incorrectly assigned ***Pinb-D1z***, *'b3'*, ***Pinb-D1u***.

Pinb-D1q [10077]

s: CS*/Red Egyptian 5D substitution line, ***Pina-D1k***, ***Gsp-D1i***[10077]. **v**: Jingdong 11 (GenBank EF620909)[10313].

This allele was used originally (2004 supplement) in combination with ***Pina-D1k*** and ***Gsp-D1i*** to denote the large deletion that encompasses *PINa-D1, PINb-D1,* and **GSP-D1**[10077] (cf. *Pins-D1k*). The haplotype nomenclature of this deletion is under review. ***Pinb-D1q*** is currently used to denote the C-to-G SNP at position 218[10313].

Pinb-D1r [10209] syn: Pinb-D1h[10209]

v: Hyb65 (NCBI AJ619022)[10209].

G insertion: open reading frame shift and premature stop codon; hard kernel texture[10209].

Pinb-D1s [10209]

v: NI5439 (NCBI AJ619021)[10209].

G insertion as in ***Pinb-D1r*** and an A-to-G substitution; hard kernel texture[10209].

Pinb-D1t [10208]

v: Guangtouxianmai (GenBank EF620910)[10208]; Hongma[10208]. G-to-C substitution: Glycine-47 to arginine; hard kernel texture[10208].

Pinb-D1u [10427]

v: Tiekemai (GenBank EF620911)[10427]; 31 hard Yunnan endemic wheats (*T. aestivum* ssp. *yunnanense* King)[10427].

Possesses a G deletion at position 127 leading to a shift in ORF[10427].

Pinb-D1v [10305, 10316] syn: Pinb-D1i(t)[10305], Pinb-D1r[10316]

v: Qingdao Landrace 1[10305]; Qitoubai[10305]; Shijiazhuang 34[10305]; Tachun 3 (GenBank AY598029)[10316]; Zigan[10305]; homonym 'b5'[10316].

The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in {10305] are ***Pinb-D1p*** as listed above for that allele. The following variety/sequence was assigned ***Pinb-D1y*** in the 2006 supplement; but the original assignment of ▶[10316] is now unchanged.

Pinb-D1w [10314] syn: Pinb-D1q[10316]

v: Jing 771 (GenBank AY640304, AB180737)[10316]; homonym 'b4'[10316]. **dv**: *Ae. tauschii* 002 (GenBank DQ257553)[10314]; *Ae. tauschii* ssp. *tauschii* TA1704 (GenBank AY649747)[10315]; *Ae. tauschii* ssp. *anathera* TA2381 (GenBank AY649747[10315].

This variety/sequence was incorrectly assigned ***Pinb-D1x*** in the 2006 supplement; the original assignment of ▶[10316] is now unchanged.

Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2)[10314]; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747)[10315]; *Ae. tauschii* CPI 110799 (GenBank CR626926)[10440] were incorrectly assigned this allele in the 2006 supplement; they are ***Pinb-D1i*** as listed above.

Pinb-D1x [10528]

v: Kashibaipi (GenBank AM909618)[10528].

Pinb-D1y

The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in ▶[10305] is ***Pinb-D1v*** as listed above. The original assignment of ▶[10316] is now unchanged. Currently there is no assignment for this allele.

Pinb-D1aa [10391]

v: Changmangtoulongbai (GenBank EF620912)[10391]; Hongtutou 1[10391]; Hongtutou 2[10391].

Pinb-D1ab [10432]

v: KU3062[10432]; KU3069[10432]; Tuokexunyihao[10528].

Pinb-D1ac [10570]

v: Kashibaipi[10570]; Red Star[10570].

G to A substitution at position 257 and C to T substitution at position 382[10570].

2.4.8 Serine protease inhibitors alias serpins

Serine proteinase inhibitors or serpins are salt soluble proteins (~43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.

SRP-1

Srp-A1 [10754] locus: 5AL[10754]

Srp-B1 [10754] locus: 5BL[10754] syn: Srp5B[10754]

Srp-B1a [10754] syn: Srp5Ba[10754]

v: Etawah[10755]; Federation[10755]; Frame[10755]; Pugsley[10754]; Stylet[10755].

Srp-B1b [10754] locus: Null allele

v: Correll[10755]; EGA Eagle Rock[10755]; Gladius[10755]; Yitpi[10755].

This allele reduced milling yield by 0.4%[10755].

Srp-D1 [10754] locus: 5DL[10754]

2.4.9 Starch granule proteins

The proteins, designated SGP-1, are starch synthases, encoded by **SsII-A1**, **SsII-B1** and **SsII-D1**[0042].

SGP-1

P-D1 [1615] locus: 7DS[1615]

v: CS. See also.

Sgp-A1 [1615] locus: 7AS[1615]

v: CS.

Sgp-A1a [1615]

v: CS.

Sgp-A1b [1615] locus: Null allele

v: Chosen 30, Chosen 57.

Sgp-A1c [1615]

v: Hua Non 9.

Sgp-B1 [1615] locus: 7BS[1615]

v: CS.

Sgp-B1a [1615]

v: CS.

Sgp-B1b[1615] locus: Null allele

v: K79.

Sgp-B1c[1615]

v: Gnatruche.

Sgp-B1d[1615]

v: Waratah.

Sgp-D1[1615] locus: 7DS

v: CS

Sgp-D1a[1615]

v: CS.

Sgp-D1b[1615] locus: Null allele

v: T116.

SGP-2

Sgp-A2[1615]

v: CS.

Sgp-B2[1615]

v: CS.

Sgp-D2[1615]

v: CS.

SGP-3

Sgp-A3[1615] locus: 7AS[1615]

v: CS.

Sgp-A3a[1615]

v: CS.

Sgp-A3b[1615] locus: Null allele

v: Norin 61.

Sgp-B3[1615] locus: 7BS[1615]

v: CS.

Sgp-B3a[1615]

v: CS.

Sgp-B3b[1615] locus: Null allele

v: Crest.

Sgp-B3c[1615]

v: Spica.

Sgp-D3[1615] locus: 7DS[1615]

v: CS.

A triple null stock (SGP-1 null wheat) is reported in [0137]. Deletion mapping indicated that the gene order on the 7S arms is: centromere - SGP-1 – SGP-3 – *Wx*[1615].

2.4.10 Water soluble proteins

WSP-1 are monomeric grain endosperm proteins identified by their high pI's[817].

WSP-1

Wsp-A1[817] locus: 7AL[817]

v: CS.

Wsp-A1a[817]

v: CS.

Wsp-A1b[817]

v: Huntsman.

Wsp-A1c[817]

v: Hope.

Wsp-A1d[817]

v: Sicco.

Wsp-A1e[817]

v: Condor.

Wsp-B1[817] locus: 7BL[817]

v: CS.

Wsp-B1a[817]

v: CS.

Wsp-B1b[817]

v: Hope.

Wsp-B1c[817]

v: Condor.

Wsp-D1[817] locus: 7DL[817]

v: CS.

Wsp-D1a[817]

v: CS.

Wsp-D1b[817]

v: Sears' Synthetic IPSR 1190903.

Wsp-D1c[893]

v: T4 = Agatha[890, 893]; Indis[890, 892].

Wsp-E1[817] locus: 7E[817]

ad: CS/*E. elongata*.

Wsp-H1[817] locus: 7H[817]

ad: CS/Betzes.

Wsp-H^{ch}1[817] locus: 7H^{ch} [817]

ad: CS/*H. chilense*.

Wsp-S^{l}1[817] locus: 7S^{l} [817]

ad: CS/*Ae. sharonensis*.

Wsp-V1[817] locus: 7V[817]

ad: CS/*D. villosum*.

2.4.11 Waxy proteins

Waxy protein (granule-bound starch synthase = ADP glucose starch glycosyl transferase, EC 2.4 1.21 = GBSSI) is tightly bound within endosperm starch granules and is involved in the synthesis of amylose[1616]. Waxy variants, characterised by starch granules containing increased amylopectin and reduced amylose, are preferred for Japaness white salted or “udon” noodles[1650]. Similar waxy phenotypes are controlled by orthologous genes in barley, maize and rice but are not known to occur in rye[725]. All combinations of the null alleles were produced in Chinese Spring[0018]. Partial genomic clones of various diploid, tetraploid, and hexaploid wheats were sequenced[0278, 0279].

A multiplex PCR assay for identifying waxy genotypes is described in ▶[10032].

WX-1

Wx-A1[180, 1053] locus: 7AS[180, 1053] syn: Wx-B1[1053, 1054], Xwx-7A[179, 180]

v: CS. **ma**: Variation in the microsatellite gene *Xsun1-7A* provides a co-dominant marker for this locus[116].

Wx-A1a[1054] syn: Wx-B1a[1054]

v: Bao Hua[10989]; CS; Hoshuu. **tv**: Langdon[10989].

Wx-A1b[1054] locus: Null allele syn: Wx-B1b[1054]

v: California[10032]; Kanto 79; Kanto 107; Shino[10032]; Shirodaruma[1617]; Sturdy[1617, 10032]. **v2**: Mochi-Otome ***Wx-B1b Wx-D1b***[10032]; Nebarigoshi *Wx-b1b*[10032]. **tv**: Asrodur[0111]; MG826[03101].

A variant allele was present in one Iranian and one Italian accession[03101]. The complete genomic sequences for the ***Wx-A1a*** allele from CS[0073] and the cDNA sequence for the ***Wx-A1b*** allele from Kanto 107[0075] were determined.

Wx-A1c[1617]

v: Pakistan Zairaishi selection[10629]; QT105[1617]; WB6[1617].

Wx-A1d[1616]

tv: *T. dicoccoides* KU 8937B[1616].

Wx-A1e[1616]

tv: KU 3659[10629]; *T. durum* KU 3655 and KU 3659[1616].

Wx-A1f[10187] locus: Null allele

v: Turkey-124[10187]; Turkey-140[10187]; Turkey-171[10187]; Turkey-280[10187]; Turkey-299[10187].

Lines with this allele produce a PCR product with a 173 bp insertion in an exon[10187].

Wx-A1g syn: Wx-A1’[10587]

v: PI 348476[10587]; Spelt accessions PI 348576[10587]; 2778 Epeautre Noir Velu[10587].

Wx-A1h[10763] locus: Null allele

tv: Buck Topacio[10763].

This is probably a unique allele possessing a 1 bp deletion in exon 6 leading to frameshift and a stop codon: partial sequence GQ120523[10763].

Wx-A1i[10989]

v: KU9259[10989].

Wx-A1j[10989, 10990]

v: M1[10989].

Functional markers for ***Wx-A1c***, ***Wx-A1d***, ***Wx-A1e*** and *Wx-Ali* were developed from DNA sequences[10990].

Wx-B1[180, 1053] locus: 4AL[180, 1054] syn: Wx-A1[1053, 1054], XWx-4B[179, 180], XWx-4A[961]

v: CS. **tv**: A variant allele was present in three accessions[03101].

A dominant PCR marker for identifying heterozygotes at the **Wx-B1** locus is reported in ▸[10732].

Wx-B1a[1054] syn: Wx-A1a[1054]

v: CS; Joshuu.

The complete genomic sequence for ***Wx-B1a*** from CS was determined[0073].

Wx-B1b[1054] locus: Null allele syn: Wx-A1b[1054]

v: Kanto 79[1617]; Kanto 82[1617]; Kanto 107[1617]; Norin 98[1617]; Gabo[1617]; Reward[10032]; Satanta[1617]; Yukon[10032]. **v2**: Mochi-Otome ***Wx-A1b Wx-D1b***[10032]; Nebarigoshi ***Wx-A1b***[10032]. **v**: For list of Australian wheats, see ▸[1650]. **tv**: Blaquetta (BG-13701)[0111].

An ELISA-based method was developed for distinguishing wheat lines carrying this null allele[10325].

Wx-B1c[1617]

v: AF24[10629]; Chousen 40[0094]; Cikotaba[1617, 10629]; Junguk 12[1617, 10629].

Wx-B1d[1616]

tv: *T. durum* KU 4213D[1616]; KU 4213D[10629]; KU 4224C[1616].

Wx-B1e[0027]

v: Blue Boy II[0027]; Canthatch[0027]; Eureka[0027]; Gotz[0027]; Norin 44[0027]; Turkey Red[0027].

Wx-B1f[0111]

tv: BG-12413[0111]; BG-12415[0111].

Wx-B^{S}1g[10587]

al: *Ae. speltoides* 33[10587].

Wx-B^{SL}1h[10587]

al: *Ae. longissima* 12[10587].

Wx-D1[180, 1053] locus: 7DS[180, 1053] syn: XWx-7D[179, 180]

v: CS.

Isolation of a wheat cDNA encoding **WX-A1** and **WX-D1** was reported in ▸[0123, 0167], respectively.

Wx-D1a[1054]

v: CS.

Wx-D1b[1617] locus: Null allele

v: Bai Huo (Baihuomai)[1617]; DHWx12[0117]. **v2**: Mochi-Otome ***Wx-A1b Wx-B1b***[10032]. **ma**: STS marker *Xsun1-7D* produces a distinct band of about 260 bp (compared with the standard 840 bp), indicative of a smaller PCR product, but the gene is non-functional[0117, 0077]; *Xsun4(Wx)-7D* is a perfect marker[0118].

The complete genomic sequence for ***Wx-D1a*** from CS[0073] and the cDNA sequence for the ***Wx-D1b*** allele from Bai Huo[0075] were determined.

Wx-D1c[1617]

v: Scoutland[1617].

Wx-D1d[0118]

v: K107Wx1[0118]; K107Wx2[0118]; One Iranian and one Italian accession[03101].

Wx-D1e[0117] locus: Null allele[0117]

v: NP150[0117].

STS marker *Xsun1-7D* failed to produce a PCR product {0117].

Wx-D1f syn: Wx-d1e[0234]

v: Tanikei A6599-4[0234].Relative to Kanto 107, Tanikei A6599-4 carries an alanine to threonine substitution at position 258 in the mature protein[0234].

Wx-D^{DN}1g[10587]

al: *Ae. ventricosa* 12[10587].

Various hard and soft wheats with alleles ***Wx-A1b***, ***Wx-B1b*** and ***Wx-D1b*** are listed in [0304]. 15% of Chinese wheats possessed **Wx-B1** null alleles[10357].

Isolation of genomic sequences for the genes encoding granule-bound starch synthase (*GBSSI* or *WX*) in *T. monococcum*, *Ae. speltoides* and *Ae. tauschii* was reported in [0168]. Cloning of a second set of *GBSSI* or *waxy* genes, *GBSSII*, which were shown to be located on chromosomes 2AL, 2B and 2D, was reported in [0167].

2.5 Enzyme Inhibitors

Inhibitors of alpha-amylase and subtilisin

2.5.1 Inhibitors of alpha-amylase and subtilisin

ISA-1

Isa-A1[908] locus: 2AL[908]

v: CS.

Isa-A1a[908]

v: CS.

Isa-A1b[908] locus: Null allele

v: Cajeme 71.

Isa-B1[908] locus: 2BL[908]

v: CS.

Isa-B1a[908]

v: CS.

Isa-B1b[908]

v: Bihar.

Isa-D1[908] locus: 2DL[908]

v: CS.

Chromosome 3BS has duplicated loci controlling two dimeric inhibitors of exogenous a-amylases, one known as 0.53 or Inh I[1260], and the other as WDA I-3[1260]. Chromosome 3DS has a homoeologous locus controlling a dimeric inhibitor of exogenous a-amylases, known as 0.19 or Inh III[1260, 0124], that is closely related to 0.53/Inh I. Intervarietal polymorphism for the WDA-3 protein was identified by isoelectric focussing of water-soluble endosperm proteins[0124]. This was interchromosomely mapped on 3BS using both a DH population of Cranbrook/Halberd, and a set of RILs of Opata 85/W-7984 (ITMI population)[0125].

Three genome allele specific primer sets were designed for the 3BS and 3DS alpha-amylase inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu*, *Triticum monococcum*, *Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24 kDa dimeric alpha-amylase inhibitors in cultivated wheat are encoded by a multigene family[10323], previously proposed in [10324], as the result of phylogenetic analysis of sequences characterized by cSNPs.

2.5.2 Inhibitors (dimeric) of heterologous alpha-amylases

Chromosome 3BS has duplicated loci controlling two dimeric inhibitors of exogenous a-amylases, one known as 0.53 or Inh I[1260], and the other as WDA I-3[1260]. Chromosome 3DS has a homoeologous locus controlling a

dimeric inhibitor of exogenous a-amylases, known as 0.19 or Inh III[1260, 0124], that is closely related to 0.53/Inh I. Intervarietal polymorphism for the WDA-3 protein was identified by isoelectric focussing of water-soluble endosperm proteins[0124]. This was interchromosomely mapped on 3BS using both a DH population of Cranbrook/Halberd, and a set of RILs of Opata 85/W-7984 (ITMI population)[0125].
Three genome allele specific primer sets were designed for the 3BS and 3DS alpha-amylase inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu*, *Triticum monococcum*, *Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24kDa dimeric alpha-amylase inhibitors in cultivated wheat are encoded by a multigene family[10323], previously proposed in [10324], as the result of phylogenetic analysis of sequences characterized by cSNPs.

IHA-1

IHA-B1.2

Iha-B1.2[0124] locus: 3BS

v: CS[0124].

Iha-B1.2a[0124] locus: 3BS[0124]

v: CS[0124, 0125].

Iha-B1.2b[0125] locus: Null allele

v: Cadoux[0125]; Cranbrook[0125]; Tasman[0125].

Iha-D1[1260] locus: 3DS[1260]

v: CS[1260].

ungrouped

Iha-B1.1[1260] locus: 3BS[1260]

v: CS[1260].

2.5.3 Subtilisin inhibition

SI-1

Si-H1[528] locus: 2H[528] syn: Isa 1[528]

ad: CS/Betzes.

Si-R1[529] locus: 2RS[701].2R[529]

ad: CS/Imperial, Holdfast/King II.

SI-2

Si-B2[701] locus: 1BS[701]

su: Bersee (Koga II).

Si-D2[701] locus: 1DS[701]

v: Koga II.

Si-H2[528, 701] locus: 1H[528] syn: Ica 2[528], Ica 1[528]

ad: CS/Betzes.

Si-R2[529, 701] locus: 1RS[701]. 1R[529]

ad: CS/Imperial[529]. **tr**: Gabo 1BL.1RS[701].

Si-S^{l}2[701] locus: 1S^{l}[701]

ad: CS/*Ae. longissima*.

Si-U2[701] locus: 1U[701]

ad: CS/*Ae. umbellulata*.

Considerable genetic variation for *Si-2* was noted in [701]. A chromosome location for **Si-H2** on 1HL was inferred in [528] but questioned in [701].
Three subunits of the wheat tetrameric inhibitor of insect a-amylase, CM1, CM3 and CM16, with homology to the dimeric and monomeric a-amylase inhibitors and the trypsin inhibitors, were located by Southern analysis of cDNAs pCT1, pCT2, and pCT3 to 4A, 4B, 4D; 7A, 7B, 7D; and 4A, 4B, 4D, respectively[427].

Genes encoding proteins which inhibit the action of mammalian and insect, but not cereal, a-amylases, were located in chromosomes 3BS, 3DS and 6DS of Chinese Spring[1260]. Also, genes encoding inhibitors of insect a-amylases were located in *H. chilense* chromosomes $4H^{ch}$ and $7H^{ch}$ [1262].

2.5.4 Trypsin inhibition

TI-1

Ti-H1 locus: 3H[528] syn: Itc 1[528]

ad: CS/Betzes.

Ti-R1 locus: 3R[529]

ad: CS/Imperial.

TI-2

Ti-A2[699] locus: 5AL[699]

v: CS.

Ti-Ag^{i}2[699] locus: 5Ag^{i} [699]

ad: Vilmorin 27/*Th. intermedium*.

Ti-B2[699] locus: 5BL[699]

v: CS.

Ti-D2[699] locus: 5DL[699]

v: CS.

Ti-D2a[699]

v: CS.

Ti-D2b[699]

v: Champlein.

Ti-D2c[699]

v: Synthetic.

Ti-M^{t}2[699] locus: 5M^{t} [699]

ad: CS/*Ae. mutica*.

Ti-R2[699] locus: 5RL[699]

ad: CS/Imperial. **su**: CS/King II.

Ti-S^{l}2[699] locus: 5S^{l}L[699]

ad: CS/*Ae. sharonensis*.

Ti-U2[699] locus: 1U[699]

ad: CS/*Ae. umbellulata*.

3.1 Abiotic Stress Responses: Dehydrin-response Element Binding Factors

DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers as probes for an orthologous *Dreb1* gene series was placed on chromosomes 3A, 3B and 3D[10729]. SNPs in **DREB-B1** permitted mapping in chromosome 3BL in the ITMI (Opata 85/W7984) mapping population. See also section 2.2.42.

DREB-1

Dreb-A1[10729] locus: 3A[10729]

Dreb-B1[10729] locus: 3BL[10729]

ma: *Xmwg818-3B* – 27.3 cM – **Dreb-B1** – 11.2 cM – *Xfbb117-3B*[10729].

Dreb-B1a[10729]

v: Opata 85[10729].

Dreb-B1b[10729]

v: Synthetic W7984[10729].

Dreb-D1[10729] locus: 3D[10729]

3.2 Reaction to Barley Yellow Dwarf Virus

Disease: Barley yellow dwarf; Cereal yellow dwarf

BDV1

Bdv1[1363, 1379] locus: 7D[1379]. 7DS[1363]

i: Jupeteco 73R (compared to Jupeteco 73S)[1363]. **v**: Anza[1379]; Condor BW3991[1379]; Tyrant BW3872[1379]; Hahn BW4097[1379]; Parrot BW10817[1379]; Siren BW18643[1379]; Many CIMMYT genotypes. **Bdv1** is completely linked with **Ltn**, **Sr57**, **Lr34** and **Yr18**. See **Ltn**, **Lr34**, **Yr18**. Note: BW = CIMMYT wheat accession number.

BDV2

Bdv2[58] locus: 7DL = T7DS.7DL-7Ai#1L, 7D = T7DS-7Ai#1S.7Ai#1L group

Derived from *Th. intermedium*.

7D = T7DS-7Ai#1S.7Ai#1L group. 7DL = T7DS.7DL-7Ai#1L[552, 0182]. **tr**: TC14[59, 0201]; H960642[0182]. **v**: Glover (with TC6)[10491]; Mackellar = LH64C (from tissue culture)[10177]; TC14*2/Hartog[0225]; TC14*2/Spear[0201]; TC14*2/Tatiara[0225]; Yw243, Yw443, Yw642 and Yw1029 (derived by *ph1* induced recombination) see ▸[10177]. **ma**: Distal 10% of 7DL, translocation point between RFLP markers *Xpsr680* and *Xpsr965*[0182]; Complete association with *Xpsr129-7D*, *Xpsr548-7D*, *XksuD2-7D*, *XcslH81-7D*, and *Xgwm37-7D* selected as a diagnostic marker[0225]; Two RGAP and 1 RAPD markers developed for the Yw series also effective for at least TC14[10177].
7D = T7DS-7Ai#1S.7Ai#1L[552] **tr**: TC5, TC6, TC8, TC9, TC10[59].
1B = T1BS-7Ai#1S.7Ai#1L[552] TC7[447].
7Ai#1S[552] **su**: TAF2[59]; Lines 5395 & 5395-243AA[552].

Small recombinant segments are described in a *pontin* series of lines: recombinants were obtained with **Lr19** but not with **Sr25**[11097].

BDV3

Bdv3[10159] locus: 7DS.7DL-7EL[10157]

BDV3 in wheat shows distored inheritance that varies with genetic background

Derived from *Th. intermedium* cv. Ohahe[10158]

v: P961341 PI 634825[10157]; P98134[10159]. **ad**: P107[10159]. **su**: P29 (7D(7E)[10156]. **ma**: A SSR-.

BDV marker is described in ▸[10159].

Further translocation lines with **Bdv3** are described in ▸[10882].

3.3 Reaction to *Bipolaris sorokiniana*

Diseases: Spot blotch and common root rot. Spot blotch

The pathogen harbours Tox A in common with *Parastagonospora nodorum*, *Parastagonospora avenaria tritici* and *Pyrenophora tritici-repentis* [11255, 11768].

SB1

Sb1 [10855] locus: 7DS

Partial resistance 7DS [10855, 10856].

i: HUW234Ltn+ [10855]. **v**: Saar [10856]; Lines with **Lr34**/**Yr18**/**Pm38**/**Sr57** – see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*, Reaction to *Blumeria graminis*, Reaction to *Puccinia graminis*, Leaf tip necrosis. **ma**: Pleiotropic or closely linked with **Lr34**/**Yr18**/**Pm38**/**Sr57** located between *Xgwm1220-7DS* and *Xswm10-7DS* (1.0 cM interval) [10856]; see also Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia graminis* and Reaction to *Blumeria graminis*. **c**: Putative ABC transporter [10648].

SB2

Sb2 [11255] locus: 5BL [11255] syn: QSb.bhu-5B [11255]

bin: 5BL1-0.55-0.75. **v**: Ning 8201 [11255]; Yangmai 6 [11255]; YS116 [11255]. **ma**: *Xgwm639-5B* – 1.4 cM – **Sb2** – 0.06 cM – *Xgwm1043-5B* [11255].

sb2 syn: Tsn1 [11255]

v: Duster [11376]; Sonalika [11255]. Presumably all genotypes with **Tsn1**.

SB3

Sb3 [11256] locus: 3BS [11256]

bin: 3BS8-0.78 -1.00. **v**: Line 621-7-1 [11256]. **ma**: **Sb3**/*XWGGC3959* were mapped to a 2.2 cM interval between *Xbarc133*/*Xbarc147*/*Xcfp30-3B*/*XWGGC5911* and *XWGGC4320* [11255]; *XWGGC12798* – 0.08 cM – *SB3XW GGC9893/XWGGC10235* – 0.07 cM – *XWGGC6119* [11255].

SB4

Sb4 [11592] locus: 4BL [11592]

v: Line 7H9094 [11592]. **ma**: *YK12831* – 1.18 cM – SB4/*YK12828* – 0.01 cM – *YK13104* [11592].

Line 7H9094 was selected from a segregating F_4 line from a cross of resistant cultivars GY17 and Zhongyu 1211 [11592].

QTL

Yangmai 6 (R) / Sonalika (S): RIL population: AUDPC was controlled by four QTLs derived from Yangmai 6, viz. *QSb.bhu-2AL* (*Xbarc353-2A* – *Xgwm445-2A*, R^2=0.148), *QSb.bhu-2BS* (*Xgwm148-2B* – *Xgwm375-2B*, R^2=0.205), *QSb.bhu-5BL* (*Xgwm67-5BL* – *Xgwm371-5BL*, R^2=0.386) and *QSb.bhu-6DL* (*Xbarc173-6D* – *Xgwm732-6DL*, R^2=0.225) [10719].

3.4 Reaction to *Blumeria graminis* DC

Disease: Powdery Mildew.
Resistance genes and their molecular associations are reviewed in [10141].

3.4.1 Designated genes for resistance

Note: Chancellor, used as a susceptible genetic background, for some near-isogenic lines probably carries **Pm10** and **Pm15** [1479]. 33 NILs, including 22 resistance genes and 3 genetic backgrounds are listed in [10389].

PM1

Pm1

Pm1a[562] locus: 7AL[1305].7A[1293] syn: Mla[348], Pm1[130], Mlt[1175]

i: Axminster/8*Chancellor[132]; CI 14114 = As II/8*Chancellor[132]; CI 13836/8*Chancellor[132]; Kenya C6041/5*Federation[1168]; Norka/8*Chancellor[132]. **s**: CS*5/Axminster 7A[1293]. **v**: Anfield[98]; As II[130]; Axminster[130, 1175]; Birdproof[165]; Bonus[1554]; CI 13836[130]; Converse[1175]; Fedka[939]; Festival[1554]; Fram I[130]; Huron CI 3315[1175, 1554]; Kenora[1554]; Kenya W744 = C6041[130, 1175]; Norka[130, 1175]; Pika[130]; Sweden W1230[1554]; Thew[1175]; TU 4[130]; Zhengzhou 871124[570]. **v2**: Anfield **Pm9**[1287]; BGRC 44514 ***Pm3a***[1628]; Mephisto **Pm2 Pm9**[540]; Normandie **Pm2 Pm9**[165]; Pompe **Pm9**[1287]; Ring **Pm9**[1287]; Sappo **Pm2** ***Pm4b*** (Carries **Lr20**)[310]; Solo **Pm2** ***Pm4b***[52]. **ma**: Co-seg. with *Xcdo347-7A* using NILs[864]; Co-segregation or close linkage with three RAPDs; one RAPD converted to a STS[570]; Note: In Solo, **Pm1** is translocated to chromosome 7D[52]; Complete cosegregation of several markers including *Xcdo347-7A*, *Xpsr121-7A*, *Xpsr680-7A*, *Xpsr687-7A*, *Xbzh232(Tha)-7A*, *Xrgc607-7A* and *Xsts638-7A* with **Pm1** and **Lr20** was reported in ▶[323]. **c**: Encodes a nucleotide-binding, leucine rich repeat protein with close similarity to **Pm21**[11509].

Reference[11402] provides further evidence for a non-recombinogenic region in distal chromosome arm 7AL. The region appeared to have re-arrangements involving all three homoeologous group 7 chromosomes. This casts doubt regarding an allelic series at the PM1 locus[11509].

Pm1b[562]

v: MocZlatka[562].

Pm1c[562] syn: Pm18[562, 853]

v: Blaukorn[0011]; M1N[562, 1628]; M1N was described as an undesignated subline of Weihenstephan M1[540]. **ma**: AFLP marker 18M2 was diagnostic for ***Pm1c***[0011].

Pm1d[562]

v: *T. spelta* var. *duhamelianum* TRI2258[562]. **ma**: AFLP marker 18M1 – various **Pm1** alleles 0.9 cM[0011].

Pm1e[0322] syn: Pm22[1134]

v: Elia[1134]; Est Mottin[1134]; Ovest[1134]; Tudest[1134]; Virest[1134].

PM2

TraesCS5D01G044600[11503].

Pm2[130] locus: 5D[1007]. 5DS syn: Mlu,Mlx

TraesCS5D01G044600[11503].

Pm2a[130, 1088, 1175, 11049] locus: 5DS[945] syn: Mlu[1175], Mlx[1088], Pm2[130], Pm48[10935]

i: CI 14118 = Ulka/8*Chancellor[132]; CI 14119 = CI 12632/8*Chancellor[132]; Federation*4/Ulka[1168]. **v**: Avalon[96]; Bounty[96]; Claire[11678]; Fenman[96]; Galahad[1531]; H8810/47[130]; Longbow[1531]; Maris Beacon[1592]; Maris Nimrod[1592]; Maris Sportsman[96]; Maris Templar[1592]; Mattis[11678]; Norman[96]; Orestis[1079]; PI 92378[1168]; PI 181374[1168]; Sea Island[130]; Sentry[96]; S2303[945]; Synthetic(Iumillo/*Ae. tauschii*)[1168]; Tobasco[11678].TP 114/2*Starke deriv[626]; Ulka[130, 1175]; XX186 = *T. durum* Santa Maria/*Ae. squarrosa* BGRC 1458 **Pm19**[853]. **v2**: Apollo ***Pm4b*** **Pm8**[541]; Brigand **Pm6**[96]; Brimstone **Pm6**[1531]; CI 12632 **Pm6**[130]; CI 12633 **Pm6**[133]; Compal ***Pm4b***[854]; Crossbow **Pm5 Pm6**[98]; Gawain **Pm6**[1531]; Halle Stamm 13471 **Mld**[97]; Heiduck **Pm6**[541]; Hustler **Pm6**[96]; Hornet **Pm8**[1531]; Kinsman **Pm6**[96]; Mardler **Pm6**[96]; Maris Dove **Mld**[1592]; Maris Fundin **Pm6**[96]; Maris Huntsman **Pm6**[1592]; Mephisto **Pm1 Pm9**[540]; Normandie **Pm1 Pm9**[165]; Parade **Pm5 Pm6**[1531]; Rendezvous ***Pm4b*** **Pm6**[1531]; Solo **Pm1** ***Pm4b***[52]; Timmo ***Pm4b***[96]; TP 114 **Pm6**[626]; Virtue **Pm6**[96]; Walter ***Pm4b*** **Pm6**[1428]. **dv**: *Ae. squarrosa* BGRC 1458[853]; Forty accessions of *Ae. tauschii*[852]. **ma**: **Pm2** – 3.5 cM – *Xbcd1871-5D* using F2s[864]; *Xcfd81-5D* – 2.0 cM – **Pm2**[10366]. **c**: NBS-LRR structure[11270]. GenBank LN999386, protein CZT14023.1. The *TraesCS5D01G044600* allele in susceptible CS and Taichung 29 differed from the ***Pm2a*** allele by a 7 bp deletion in the first intron[11503]. Several alleged alleles at the **Pm2** locus were are likely ***Pm2a***[11503]. Allelism of ***Pm2a*** and ***Pm2b*** was based on more than 7,600 F_2 plants. Tobasco was independently reported to have ***Pm3a***[10843].

Pm2b [11049, 11075] syn: PmKM2939[11049], PmPB3558[11049]

Putatively derived from *Agropyron cristatum* [*PmPB3558*[11049], *PmKM2939*[11049]].

bin: C-5DS1-0-0.63. **v**: KM2939[11049]; PB3558[11075]. **ma**: *Xscar112* – 0.5 cM – ***Pm2b*** – 1.3 cM – *Xscar203*/*Xmag6176*/*Xcfd81-5D*[11049]; *Xcfd81-5D* – 5.5 cM – *PmPB3558* – 3.9 cM – *Xbwm25* – 0.9 cM – *Xbwm21* – 0.9 cM – *Xbwm20*[11075].

Deleted: Identified as ***Pm2a***[11503].

Pm2c[11061] locus: 5DS[11061] syn: PmNM[11061]

bin: 5DS-1-0-0.63. **v**: Niaomai[11061]. **ma**: *Xcfd81-5D* – 0.4/0.1 cM – ***Pm2c*** – 7.5/4.9 cM – *Xcfd78-5D*[11061].

Deleted: Identified as ***Pm2a***[11503].

Several alleles of **Pm2** with wheat and alien origins have been reported in Chinese genotypes – see temporary designations. The complex nature of temporarily named powdery mildew resistance genes in the **Pm2** region is discussed in ▶[11380]. Several alleged alleles at the **Pm2** locus are likely ***Pm2a***[11503].

PM3

PM3 has 92.9% identity with PM8 at the protein level[11398].

Pm3 locus: 1A

PM3 has 92.9% identity with PM8 at the protein level[11398].

Pm3a[130, 132] locus: 1A[1007].1AS[943, 947] syn: Mla[1168]

i: Asosan/8*Chancellor[132] = CI 14120; Asosan/3*Federation[1168]. **v**: Asosan[130, 1168]; BGRC 44514 ***Pm1a***[1628]; Coker 797[786]; Florida 301[786]; Florida 302[786]; Hadden[97]; Halle Stamm[97]; Madrid[10843]; Merker[10843]; Norin 3[1134]; Norin 29[1134]; PI 46890[1439]; Robigus[10843]; Saluda[786]; Tabasco[10843]; Tyler[1419]. **ma**: *Xbcd1434-1A* – 1.3 cM – **Pm3** using NILs[864]; *Xwhs179-1A* – 3.3 cM – **Pm3**[522]. *Xgdm33-1A* – 2.3 cM – **Pm3**/*Xpsp2999-1A*[313]. Sequence AY939880[10292].

Tobasco was independently reported to have ***Pm2a***[11678], **Pm48**[10935].

Pm3b[130, 132] locus: 1A[1007] syn: Mlc[165], Pm3j[10405]

i: Chul*8/Chancellor = CI 14121[132]; *T. sphaerococcum**8/Chancellor = CI 15887[539]. **v**: Chul[165]; Enorm[10843]. **ma**: *Xbcd1434-1A* – 1.3 cM – ***Pm3b*** using NILs[864]. **c**: The isolation of ***Pm3b*** is reported in ▶[10064]. The ***Pm3b*** gene (GenBank AY325736) is a coiled-coil NBS-LRR type of disease resistance gene[10064].

Pm3c[130, 132] locus: 1A[134, 1007] syn: Pmi[10405], Mls[1175], Pm3i

i: Sonora/8*Chancellor[132] = CI 14122; Sonora/4* Federation[1168]; Triticale/8*Chancellor[539]. **s**: CS*7/Indian 1°[134]. **v**: Borenos[854]; Cawnpore[1628]; CI 3008[130]; CI 4546[130]; Hindukush[1628]; Indian[1175]; Sonora[130, 1168]; Sturgeon[1175]. **c**: Sequence DQ251587, DQ517917[10405].

Pm3d[1628] locus: 1A syn: Mlk[434], Ml-k[540, 10405]. 1°[1628], Pm3h

v: Axona[0313]; Cornette[0313]; Herold[540]; Indian 4[0313]; Kadett[0313]; Kanzler[0011]; Kleiber[0313]; Kolibri[540, 542, 1628]; Ralle[540]; Socrates (heterogeneous)[540]; Star (heterogeneous)[540]; Syros[540]; Vergas[10843]. **v2**: Kadett ***Pm4b***[540]; Turbo ***Pm4b***[540]. **c**: Sequence AY9398881[10292]. DQ251488, DQ517518[10405].

Pm3e[1628]

v: Sydney University Accession W150 = AUS 6449[939, 1628]. **v2**: Cortez **Pm5** allele[10843]. **ma**: ***Pm3e*** – 7.1 cM – *Xwmc818-1A*[10843].

Pm3f[1628]

i: Michigan Amber/8*Chancellor[1628]; This allele was distinguished from ***Pm3c*** with only one of 13 pathogen cultures. **v**: Viza[10843]. **c**: Sequence DQ071554[10292].

Pm3g[0070] locus: 1AS[0313] 1A[0070] syn: Mlar[854]

v: Avo[1629]; Aristide[1629]; Champetre[0313]; Courtot[1629]; Lutin[0313]; Oradian[0313]; Rubens[0313]; Soissons[0313]; Valois[0313]. **ma**: ***Pm3g*** – 5.2 cM – **Gli-A5** – 1.9 cM – **Gli-A1**[0070]; ***Pm3g*** was completely linked to microsatellite *Xpsp2999*[313]. **c**: Sequence DQ251489, DQ517919[10405].

The ***Pm3a***, ***Pm3b***, ***Pm3d*** and ***Pm3f*** alleles form a true allelic series based on sequence analysis[10292]. Following the cloning and sequencing of ***Pm3b***[10064], 6 other alleles were sequenced[10405]. The Chinese Spring (susceptible) allele, *Pm3CS*, considered to be ancestral and present in many hexaploid and tetraploid wheats, was also transcribed[10405, 10406]. Other wheats possessed a truncated sequence (e.g. Kavkaz), or were null[10405, 10406]. Unique markers were developed for all 8 transcribed alleles, and for individual alleles[10405].

Alleles ***Pm3b***, ***Pm3d***, and ***Pm3f*** were detected in Scandinavian varieties using allele-specific markers[10681].

PM4

TraesSYM2A03G00828360[11774].

Pm4[131]

[131] *TraesSYM2A03G00828360*[11774].

Pm4a[1464] locus: 2AL[1464] syn: Pm4[131]

i: CI 14123 = Khapli/8*Chancellor[131]; CI 14124 = Yuma/8*Chancellor[131]. **v**: Aikang 58[11753]; Steinwedel*2/Khapli[939]; Yangmai 10[10176]; Yangmai 11[10176]. **tv**: Khapli[131]; Valgerado[97]; Yuma[131]. **ma**: Co-seg with *Xbcd1231-2A.2* & *Xcdo678-2A* using F2s[864]; *Xbcd1231-2A.1* – 1.5 cM – **Pm4** – 1.56 cM – *Xbcd292-2A*[864]; ***Pm4a*** – 3.5 cM – AFLP markers *4aM1* and *4aM2*[11]; *Xbcd1231-2A* was converted to a STS marker and to a ***Pm4a***-specific dominant PCR marker[10176]; *Xgwm356-2A* – 4.8 cM – ***Pm4a***[10176]. **c**: Similar structure to ***Pm4b***[11525].

Pm4b[1464] locus: 2°[52]. 2AL[1464] syn: Mle[1591]

i: Federation*7/*T. carthlicum* W804[1464]; VPM1/7*Bainong 3217[11287]. **v**: Achill[540]; Ajax[540]; Arkas[540]; Armada[96]; Atlantis[11]; Boheme[11]; Botri (heterogeneous)[854]; ELS[1591]; Facta[854]; Factor (heterogeneous)[854]; Fakon[854]; Fazit[854]; Hermes[540]; Horizont[540]; Maris Halberd; Max[540]; Olymp[540]; Orbis[540]; RE714[1220]; Renan[16]; Ronos[1079]; S-25[52]; S-28[52]; TP 229[626, 1591]; Weihenstephan M1[1591]; VPM1[97]. **v2**: Apollo **Pm2 Pm8**[541, 802]; Boxer **Pm5**[541]; Compal **Pm2**[854]; Kadett ***Pm3d***[540]; Kronjuwel **Pm8**[541]; Mission **Pm5**[541, 1531]; Rang **Pm1**[52]; Rendezvous **Pm2 Pm6**[1531]; Solo **Pm1 Pm2**[52, 540]; Sorbas **Pm6**[541]; Timmo **Pm2 Pm6**[96]; Turbo ***Pm3d***[540]; **v**: Xiaomaomai[11774]; Walter **Pm2 Pm6**[1428]. **ma**: ***Pm4b*** – 4.8 cM – *Xgbx3119b-2A*[272]; *Xgwm382-2A* – +/-10 cM – ***Pm4b*** – +/-2 cM – *XgbxG303-2*[354]; STS241 – 4.9 cM – ***Pm4b*** – 7.1 cM – SRAP *Me8/Em7*$_{220}$ – 4.7 cM – *Xgwm382-2A*[10553]; *Xics13* – 1.3 cM – ***Pm4b*** – 1.7 cM – *Xics43* covering a 6.7 Mb physical region[11287]. **c**: Encodes a putative chimeric protein of a serine/threonine kinase and multiple C2 domains and transmembrane regions; ***Pm4b*** undergoes alternative splicing to generate two isoforms, both of which are essential for resistance function[11525]. Genbank: Pm4b_V1 CDS: MT783929; Pm4b_V2 CDS, MT783930. Closest homologue of the C2 domain of ***Pm4b*** in CS is *TraesCS2A01G557900*.

Pm4c[10583] locus: 2AL[10583] syn: Pm23[1618]

– earlier reported on 5AL[1618].

v2: 81-7241 **Pm8** suppressed[1618, 10583]. **ma**: *Xbarc122-2* – 1.4 cM – ***Pm4c*** – 3.5 cM – *Xgwm356-2*[10583].

Pm4b and ***Pm4c*** are identical at the nucleotide level[11774].

Pm4d[10744] locus: 2AL[10744]

bin: 2AL1-0.85-1.00. **v**: GR18-1[11701]; SYMattis[11525, 11775]; Tianmin 668[11702]; Tm27d2 = WW St2022/Tm27//Amor = TRI 29584[10744]. **dv**: *T. monococcum* Tm27[10744]. **v**: **ma**: A 218 bp fragment was amplified with STS marker *ResPm4* as were other **Pm4** alleles[10744], Located within the intervals 75.889 – 78.702 Mb[11701] and 76.148 – 76.803[11702]..

Pm4e[11317] locus: 2AL[11317]

v: D29[11317]. **ma**: *Xgdm93-2A* – 4.9 cM – ***Pm4e***/*Xsts_bcd1231* – 1.8 cM – *Xhbg327-2A*[113017]; *Xwgrc763-2A* – 0.13 cM – ***Pm4e***/*Xwgrc872-2A*/*Xwgrc869-2A* – 0.58 cM – *Xwgrc982-2A*, a region of about 6.1 Mb[11335].

Pm4d and ***Pm4e*** are identical at the nucleotide level[11774].

A recessive resistance gene (*pmXXM*[11661]) in Xiaomaomai had a similar protein structure to ***Pm4d***, ***Pm4e*** and *Pm4h*[11661].

Pm4f

v: WATDE0571[11775].

Pm4g

v: WW-740[11775]. ***Pm4h***; WW-474[11774]. ***Pm4i***; WATDE0048[11775]. ***Pm4j***; WATDE0592[11775].

Add note at end of **Pm4** section: Some variants of PM4 confer resistance to wheat blast[11632, 11735, 11775] – see Reaction to *Magnaporthe grisea*.

PM5

TraesCS7B02G441700 (susceptible allele) (chr7B: 706.811-706.816 Mb)[11533].

Pm5

c: CS (susceptible allele): *TraesCS7B02G441700* (chr7B: 706.811-706.816 Mb); GenBank MK955157.

Pm5a[0257] locus: 7B[964].7BL[771] syn: Pm5[787], mlH[771]

Pm5a was transferred to hexaploid wheat from *T. dicoccum* via Hope and H-44. Recessive.

i: Hope/8* Chancellor = CI 14125[570]. **s**: CS*6/Hope 7B[771, 964]. **v**: Alidos[854]; Aotea[964]; Caldwell[786]; Ga 1123[786]; Galaxie[0257]; Glenwari[964]; Hardired[786]; Hope[964]; H-44[964]; Kontrast[854]; Kormoran[1079]; Kutulukskaya[257]; Lambros[0257]; Lawrence[964]; Navid[0257]; Pagode[0257]; Redcoat[97]; Redman[964]; Regina[0257]; Renown[964]; Selpek[540]; Sicco[96, 0257]; Spica[964]; Tarasque[0257]; Warigo[964]; Zolotistaya[0257]. **v2**: Arthur **Pm6**[786]; Coker 983 **Pm6**[786]; Double Crop **Pm6**[786]; Granada **Pm8**[541]; Saar **Pm38 Pm39**[10481]; Sensor **Pm8**[541]. **c**: GenBank MK955160.

Pm5b[0257] syn: Mli[540, 558]

v: Aquila[96, 541]; Carimulti[541]; Cariplus[541]; Cucurova[0257]; Dolomit[541]; Falke[541]; Flanders[96]; Fruhprobst[0257]; Ilona[0257]; Ibis[96]; Kirkpinar-79[0257]; Kontrast[0257]; Kormoran[541]; Krata[541]; Markant[541]; Mercia[1531]; Milan[541]; Nadadores[0257]; Reiher[541]; Rektor[541]; Rothwell Perdix[96]; Siete Cerros[0257]; Severin[541]; Sicco[96]; Sperber[541]; Tukan[541]; Una[0257]; Urban[541]; Wattines[541]; Wettiness[0257]. **v2**: Bert **Pm6**[541]; Boxer ***Pm4b***[541]; Crossbow **Pm2 Pm6**[98]; Kristall **Pm8**[541]; Mission ***Pm4b***[541, 1531]; Parade **Pm2 Pm6**[1531]. **c**: GenBank MK955159.

Pm5c[257, 0257] locus: 7B[0257]

v: *T. sphaerococcum* cv. Kolandi[0257].

Pm5d[0257] locus: 7B[0257]

bin: 7BL 0.86-1.00[10542]. **i**: IGV 1-455 = CI 10904/7*Prins[0257]; CI 10904/7*Starke[0257]. **v**: Dream[10542]. **ma**: *Xgwm611-7B* – 2.1 cM – ***Pm5d*** – 2.0 cM – *Xgwm577-7B* – 1.0 cM – *Xwmc581-7B*[10542]. c Same sequence as ***Pm5e***[11533].

Pm5e[0258] locus: ; *PmAL11* [11708] syn: mlfz[0259]

Recessive and hemizygous effective[0258]; usually dominant[11708].

i: H962R {11707). **v**: AL11[11708]. Baiyouyantiao (previously published as *PmBYYT*[11533]); Fuzhuang 30[0258]; Hongquanmong (previously published as *PmH*[11533]; Mazhamai (previously published as *Mlmz*[11533]); Tangmai 4 (previously published as **PmTm4**[10961, 11533, 11533]); Xiaobaidongmai (previously published as *Pmxbd*[11533, 0258]). **ma**: *Xgwm1267-7B* – 6.6 cM – ***Pm5e*** – 12.6 cM – $Xubc405_{628}$*-2B*[0258]. KASP marker *AL11-K2488*[11708]. **c**: Identified as a CC-NBS-LRR[11533]. GenBank MK955156.

Although Duanganmang (*PmDGM*) had an identical sequence and UTR to ***Pm5e***, a second completely linked gene was postulated to account for a different response pattern to the ***Pm5e*** control[11705].

Genotype lists:[10405, 10406, 0313]

PM6

Pm6[627] locus: 2B[1088] syn: Mlf[626]

i: CI 13250/7*Prins[0069]; CI 12559/8*Prins[0069]; Eight Prins derivatives[10576]; PI 170914/7*Prins 6 NILs based on Prins[0139, 0069]. **v**: 1969 IVGS Line C[626]; Abe[97, 1256]; Coker747[786, 1079]; Mengavi[97]; Oasis[786]; Timgalen[98]; TP 114/2*Starke deriv. B[626]. **v2**: Arthur ***Pm5a***[97, 786]; Brigand **Pm2**[96]; Brimstone **Pm2**[1531]; CI 12632 **Pm2**[626,

[1088]; CI 12633 **Pm2**[626, 1088]; Crossbow **Pm2 Pm5**[98]; Double Crop ***Pm5a***[786]; Garwain **Pm2**[1531]; Greif ***Pm5a***[0011]; Heiduck **Pm2**[541]; Hustler **Pm2**[96]; Kinsman **Pm2**[96]; Mardler **Pm2**[96]; Maris Fundin **Pm2**[96]; Maris Huntsman **Pm2**[1592]; Parade **Pm2 Pm5**[1531]; Rendezvous **Pm2** ***Pm4b***[1531]; Sorbas ***Pm4b***[541]; Timmo **Pm2** ***Pm4b***[96]; TP 114 **Pm2**[626]; Virtue **Pm2**[96]; Walter **Pm2** ***Pm4b***[1428]. **ma**: Close linkage with *Xbcd135-2B* (1.5+-1.4 cM), *Xbcd307-2B* (4.7 +- 2.5 cM) and *Xbcd266-2B* (4.5 +- 2.4 cM)[69]; Mapped to the interval *Xbcd35-2B-Xpsr934-2B*[139]; However, the fact that Timgalen and a 'CI12632/Cc' line lacked the critical *T. timopheevii* markers[0139] is cause for concern; RFLP marker *Xbcd135-2B* was converted to STS markers *NAU/STS*$_{BCD135-1}$ and *NAU/STS*$_{BCD135-2}$ which showed linkage of 0.8 cM with **Pm6**[10576]. **Pm6** was localized to a 0.9 Mb physical region in chromosome 2BL[11451].

PM7

Pm7 locus: 4BL[270, 271, 389]

Derived from *S. cereale* cv. Rosen. = T4BS.4BL-5RL[543], but more recently revised to T4BS.4BL-2R#IL[380, 389].

i: Transec/8*Chancellor. **v**: Transfed[269]; Transec[273].

PM8

Pm8 locus: 1BL.1RS. 1R(1B)

Derived from Petkus rye – see **Yr9**, **Lr26**, **Sr31**.

i: MA1 and MA2, four-breakpoint double translocation lines 1RS-1BS-1RS-1BS. 1BL in Pavon[0084]. **v**: Corinthian[1531]; Dauntless[1531]; Ambassador[1531]; Disponent[541]; GR876[753]; Halle Stamm[97]; Hammer[98]; Others[1208]; ST1-25[201]; Slejpner[1531]; Stetson[1531]; Stuart[96]. **v2**: Apollo **Pm2** ***Pm4b***[541]; Granada **Pm5**[541]; Hornet **Pm2**[1531]; Kristall **Pm5**[541]; Kronjuwel ***Pm4b***[541]; Sensor **Pm5**[541]. **tv**: Cando*2/Veery = KS91WGRC14[381].

1BS/1RS recombinants 2.9 cM proximal to **Gli-B1**/*GluB3*[0084]. Crosses between three lines with **Pm8** and Helami-105, a 1BL.1RS line with **Pm17**, indicated that **Pm8** and **Pm17** were allelic[524]. Earlier, these genes were reported to be genetically independent[1463]. ma: **Pm8** is located between *Gli/Glu3* and rust resistance genes **Sr31**, **Lr26** and **Yr9**[11354]. An STS marker distinguished **Pm8** from **Pm17**[0186]. **Pm8** is located between *Gli/Glu3* and rust resistance genes **Sr31**, **Lr26** and **Yr9**[11354]. c: GenBank KF572030. **Pm8** is an orthologue of **Pm3** and an allele of **Pm17** in the rye genome[11276, 11398]. **Pm8** has 92.9% identity with **Pm3** at the protein level[11398].

PM9

Pm9[347] locus: 7AL.7A[347]

v: N14[562]. **v2**: Anfield ***Pm1a***[1287]; Mephisto ***Pm1a*** **Pm2**[540]; Normandie ***Pm1a*** **Pm2**[347]; Pompe ***Pm1a***[1287]; Ring ***Pm1a***[1287].

PM10

Pm10[1482] locus: 1D[1482]

v: Norin 4[1482]; Norin 26[1482]; Norin 29[1482]; Penjamo 62[1482]; Shinchunaga[1482]. **v2**: *T. spelta duhamelianum* **Pm11**[1481].

Pm10 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*.

PM11

Pm11[1481] locus: 6BS[1481]

v: Chinese Spring[1481]; Salmon[1481]; *T. compactum* No. 44[1481]. **v2**: *T. spelta duhamelianum* **Pm10**[1481].

Pm11 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*

PM12

Pm12[1017] locus: 6B = 6BS-6SS.6SL[572, 598]. 6S^{1}S[598]

Derived from *Ae. speltoides*. The earlier location of 6A[1017] was not correct.

v: Wembley*6/*Ae. speltoides* #31[598, 1017]. **al**: *Ae. speltoides* CL214008 = K[1017]. **ma**: **Pm12** was mapped to a translocated segment proximal to *Xpsr551-6B*[598]; Secondary recombination analysis indicated that **Pm12** was located in the long arm of 6S between *Xwmc105* and *Xcau127*[10517].

PM13

Pm13

Derived from *Ae. longissima* accession TL01.

T3BL.3BS-3S^{l}#1S. **v**: Recombinant N12-3 containing 2.82 Mb of 3S^{l}[11756]. **al**: *Ae longissima* TL01, TL20, TA1910[11756]. **ma**: STS marker *Xutv13*[0036]; several other markers located in introgressed segments[0036].
3B[173] = T3BL.3BS-3S^{l}#1S[389] **v**: R1A[174]; R1B[0055]; R4A[0055]; R6A[0055]. **ma**: **Pm13** was mapped to a translocated 3S^{l}S segment distal to *Xcdo-460-3B*[0036]; Two markers, *AelMLKL-1* and *AelMLKL-8*, developed[11756].
3D[173] = T3DL.3DS-3S^{l}#1S[389]. **v**: R2A[0055]; R2B[0055]. **tv**: R1D[174]. 3S^{l}#1S. **al**: *Ae. longissima*.
c: Encodes a mixed lineage kinase domain kinase-like (MLKL) or kinase fusion protein (FLP)[11756].

PM14

Pm14[1478] locus: 6B[1478]

v2: Akabozu *Pm10Pm15*[1478]; Kokeshikomugi **Pm15**[1478]; Norin 10 **Pm15**[1478].

Pm14 and **Pm15** were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

PM15

Pm15[1478] locus: 7DS[1478]

v2: Akabozu **Pm14**[1478]; Chinese Spring **Pm11**[1478]; Kokeshikomugi **Pm14**[1478]; Norin 4 **Pm10**[1478]; Norin 10 **Pm14**[1478]; Norin 26 **Pm10**[1478]; Shinchunaga **Pm10**[1478]; *T. macha subletschumicum* **Pm10**[1478]; *T. compactum* No. 44 **Pm11**[1478].

Pm14 and **Pm15** were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

PM16

Pm16[1201] locus: 4A[1201]. 5B[10217]

v: Line 70281 = Norman/*3 Beijing 837[10217]; Norman lines with resistance from *T. dicoccoides* CL1060025[1201]. **tv**: *T. dicoccoides* CL1060025[1201]. **ma**: **Pm16** – 5.3 cM – *Xgwm159-5B*[10217].

To account for the different chromosome locations a 4A-4B translocation was suggested[10217]. Based on the 5B location and similar disease responses **Pm16** and **Pm30** may be the same[10217].

PM17

Pm17[97, 544, 838] locus: 1AS = T1AL.1R#2S[185, 389, 1624]

v: Amigo[561]; Century[216]; Embrapa 16[11355]; Hugenoot[11355]; McCormack[10758]; Nekota[21]; Neobrara[21]; TAM107[216]; TAM200[216]; TAM201[216]; TAM202[21]; TAM303[10758]; Tribute[10758]; TXGH13622[11355]. **al**: Insave rye Nr 10458[11398]. **c**: **Pm17** shares 96% nucleotide identity with **Pm8** (83% at the protein level) and low but significant identity with *Pm3CS*[11355]. GenBank MH077963.

1BS = T1BL.1R#2S[561] v2: Helami 105 **Pm5**[561]. ma: A STS marker distinguished **Pm17** from

Pm8[0286]; **Pm7** – 7.8 cM – *Xmwg68-1R* – 10.9 cM – *Sec-1* in 1RS[10167].

Pm8 and **Pm17** were reported to be allelic[524], see note under **Pm8**.

Pm17 is allelic with **Pm8** in rye and orthologue of **Pm3**[11398].

PM18

PM19

Pm19[853] locus: 7D[853]

v: *T. durum* 'Moroccos 183'/*Ae. tauschii* AE 457/78[853]. **v2**: Synthetic XX186 **Pm2**[853]. **dv**: *Ae. tauschii*[853].

PM20

Pm20[386] locus: 6BL = T6BS.6R#2L[386, 389, 543] syn: M1P6L[543]

v: KS93WGRC28 = PI 583795[382, 386]; 6RL. **su**: 6R{6D}[543]. **ad**: 6R addition[543]. **al**: Prolific rye[543].

PM21

Pm21[1177] locus: 6AS = T6AL.6VS#2[1177, 11714]

bin: 6VS 0.45-0.58[10859]. **v**: Yangmai 18[11352]; 9 independent translocations[1177]; A derivative named HP33 was described as a 'cryptic' translocation[11275]. **ma**: RAPD *OPH17*$_{1900}$ (synonym 'OPH17-1900') was associated with **Pm21** and RAPD *OPH17*$_{1000}$ (synonym OPH17-1000') with its absence[1176]; RAPD OPH17$_{1400}$ and SCAR markers SCAR$_{1400}$ and SCAR$_{1265}$ associated with **Pm21** are described in [14]; Marker NAU/*Xibao15*, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying **Pm21**[10519]; Potentially useful markers are provided in [10918]. Genetic mapping in a resistant × susceptible *D. villosum* cross identified two RGA candidate loci (markers 6VS-09.4 and 6VS.09.4b) co-segregating with **Pm21** and overlapped by an EMS-induced susceptible mutation[11352]. **c**: **Pm21** is likely the serine/threonine kinase gene *Stpk-V*[10859]. *NLR-V1*, one of two *NLR-V* genes in HP33, was identified as the candidate for **Pm21**[11275]. GenBank MF716955.

Silencing of *NLR-V1* compromised **Pm21** resistance in the T6AL.6VS lines described below and decreased the level of resistance in the T6DL.6VS lines described below[11275]. Marker *6VS-09.4* but not marker *6VS-09.4b* was deleted in a susceptible mutant indicating that the former was **Pm21** – the protein product had a CC-NBS -LRR structure – GenBank MF370199[11353]. This gene was different from *Stpk-V*[11275] but was quite similar to *NLR-V1*[11353].

6AL.6AS-6VS#2S[11578].

Pm21, **PmV** and **Pm12** were shown to be orthologous and diagnostic markers for each gene were developed in [11704].

See also **PmV**. See also PM31.

Three lines, Pm97033, Pm97034 and Pm07035, with a 6DL.6VS translocation were developed from a different source of *H. villosa*[10194]. These may carry **Pm21**.

See also **PmV**.

PM22

PM23

PM24

TraesCS1D02G058900; *AET1Gv20142700*. This locus is also named RMG1 (*RWT4*) – see Reaction to *Magnaporthe grisea*.

Pm24[571, 11414] locus: 6D[571]. 1DS[0150] syn: Pm24a[571], Pm24b[10994], WTK3[11414]

bin: 1DS5-0.54-1.00. **v**: Baihulu[10994, 11414]; Chiyacao[571]; Hongmangmai[11414]; Hulutou[11413, 11414]. **ma**: *Xgwm789-1D*/*Xgwm603-1D* – 2.4 cM – **Pm24**/*Xgwm1291-1D* – 3.6 cM – *Xbarc229-1D*[10109, 10957]; *Xgwm789*/*Xgwm603-1D* – 2.4 cM – **Pm24** – 6 cM – *Xbarc229-1D*[10109, 10957, 10994]. Located in a 9.3 cM region flanked by *Xgwm337-1D* and *Xcfd83*/*Xcfd72-1D*[11413]. **c**: **Pm24** encodes a tandem kinase protein with putative pseudokinase domains. The gene was designated *Wheat Tandem Kinase 3* (**WTK3**) – this gain of function mutation was conferred by a 6 bp deletion of lysine/glycine codons (K400G401) in the KIN1 domain[11414]. GenBank MK950855. The same candidate gene was predicted for *PmDTM* in Datoumai (11556), but according to those results Chiyacao, Hulutou and Datoumai showed differential responses to an array of *Bgt* isolates[11414].

PM25

Pm25[1343] locus: 1A[1343] syn: PmTmb[1343, 1344]

v: PI 599035 = NC94-3778[1344]. **v2**: NC96BGTA5 = Saluda*3/PI 427662 ***Pm3a***[1343]. **dv**: *T. monococcum* PI 427662[1343]. **ma**: Linked with 3 RAPDs, the nearest, OPAG04950, at 12.8 +/- 4.0 cM[1343]; Associated with 3 RAPDs[1344].

PM26

Pm26[0001] locus: 2BS[0001]

Recessive[0001].

s: Bethlehem*8/*T. turgidum* var. *dicoccoides* 2BS[0001]. **tv**: *T. turgidum* var. *dicoccoides* TTD140[0001]. **ma**: Co-segregation with *Xwg516-2B*[0001].

PM27

Pm27[0002] locus: 6B (6B-6G)[0002]

v: Line 146-155-T[0002]. **tv**: *T. timopheevii* var. *timopheevii* K-38555[0022]. **ma**: 6BS … *Xpsr8*/*Xpsr964-6B* – **Pm27** – *Xpsr154*/*Xpsr546-6B* … 6BL[0002]; Co- segregation with *Xpsr3131-6B*[0002].

PM28

Pm28[0022] locus: 1B[0022]

v: Meri[0022].

PM29

Pm29[0129] locus: 7DL

Derived from *Ae. ovata*.

v: Pova[0129]. **ma**: Location confirmed by co-segregation with molecular markers[0129].

PM30

Pm30[0163] locus: 5BS[0163] syn: MIC20

v: 87-1/C20//2*8866 Seletion[0163]. **ma**: **Pm30** – 5.6 cM – *Xgwm159-5B*[0163].

Pm30 could be the same as **Pm16**[10217].

PM31

Deleted. This gene designation[0301] is not valid; subsequent studies[10918] showed the gene is **Pm21**.

Pm31[0301] locus: 6AL[0301] syn: mlG[0301]

v: G-305-M/781//3*Jing411[0301]. **tv**: *T. dicoccoides* G-305-M[0301]. **ma**: cent **Pm31** – 0.6 cM – *Xpsp3029.1-6A* – 2.5 cM – *Xpsp3071-6A*[0301].

PM32

Pm32[10025] locus: 1B=1BL.1SS[10025]

Derived from *Ae. speltoides*[10025].

v: L501 = Rodina*6/*Ae. speltoides*[10025].

PM33

Pm33[10205] locus: 2BL[10205] syn: PmPS5B[10205]

v: Am9 = *T. carthlicum* PS5/*Ae. umbellulata* Y39[10205]. **tv2**: *T. carthlicum* PS5 *PmPS5A*[10205]. **ma**: *Xgwm536-2B* – 18.1 cM – **Pm33** – 1.1 cM – *Xwmc317-2B* – 1.1 cM – *Xgwm111-2B* – 1.8 cM – *Xgwm383-2B*[10205].

PM34

Pm34[10241] locus: 5DL[10241]

v: PI 604033 = NC97BGTD7 = Saluda*3/*Ae. tauschii* TA2492[10241]. **dv**: *Ae. tauschii* TA2492[10241]. **ma**: *Xbarc177-5D* – 5.4 cM – 2.6 cM – *Xbarc144-5D*[10241].

PM35

Pm35[10342] locus: 5DL[10342]

v: NC96BGTD3 = PI 603250 = Saluda*3/TA2377[10342]. **dv**: *Ae. tauschii* ssp. *strangulata* TA2377[10342]. **ma**: *Xcfd26-5D* – 11.9 cM – **Pm35**[10342].

PM36

Pm36[10356] locus: 5BL[10356]

bin: 5BL6-0.55-0.76[10356]. **tv**: MG-FN14999, a durum backcross line 5BIL-29[10356]; *T. turgidum* ssp. *dicoccoides* MG29896[10356]. **ma**: *Xcfd7-5B* – 10.7 cM – **Pm36** – 0.8 cM – *EST BJ261636* – 8.9 cM – *Xwmc75-5D*[10356]; 5BIL-42 identified as the derivative with shortest *T dicoccoides* segment; *IWB7454* (537.36 Mb, Svevo RefSeq) – PM36 – *IWB22904* (538.44 Mb)[11709].

PM37

Pm37[10372] locus: 7AL[10274, 10372]

v: PI 615588 = NC99BgTAG11 = Saluda*3/PI 427315[10372]. **tv**: PI 427315 = *T. timopheevii* ssp. *Ameriacum*[10372]. **ma**: **Pm37** (PmAG11) was about 15 cM proximal to a cluster of markers that earlier co-segregated with **Pm1**[10372]; A cross indicated linkage between **Pm37** and **Pm1**[10372]; *Xgwm332-7A* – 0.5 cM – **Pm37** – 0.5 cM – *Xwmc790-7A* – 15.5 cM – **Pm1**[10372].

A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3/PI 427772[10479]. A single resistance gene was identified on chromosome 7AL in hexaploid germplasm NC96BGT4 (a *T. monococcum* derivative). This gene was proximal to **Pm1** and considered to be different from **Pm37**, although possibly allelic[10274].

PM38

TraesCS7D03G0183600

Pm38[10373] locus: 7DS

TraesCS7D03G0183600

Adult plant resistance 7DS[10374].

i: RL6058 = Tc*6/PI 58548[10374]. **v**: Lines with **Sr57**/**Lr34**/**Yr18**. **v2**: Saar ***Pm5a*** **Pm39**[10481]. **ma**: *Xgwm1220-7D* – 0.9 cM – **Lr34**/**Yr18**/**Pm38** – 2.7 cM[10374]. **c**: ABC transporter; See **Lr34**.

This gene is identical to **Yr18**, **Sr57**, **Lr34** and **Ltn** and confers stem rust resistance in some genetic backgrounds; see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*.

PM39

Pm39[10481] locus: 1BL

Adult plant resistance 1BL[10480, 10481].

i: Avocet-R+**Lr46**/**Yr29** = Avocet-R*3//Lalb mono 1B*4/Pavon 76[10480]. **v**: Genotypes with **Lr46**/**Yr29**; see Reaction to *Puccinia triticina*, Reaction to *P. striiformis*. **v2**: Saar (CID: 160299, SID: 188) ***Pm5a*** **Pm38**[10481]. **ma**: *Xwmc719-1BL* – 4.3 cM – **Lr46**/**Yr29**/**Pm39** – 2.5 cM – *Xhbe248-1BL*[10481].

PM40

Pm40[10539] locus: 7BS[10539]

Derived from *Th. intermedium*[10539]. **Pm40** was not derived from *Th. intermedium*[11710].

bin: C-7BS-1-0.27. **v**: GRY19[10539]; Partial amphiploid TAI7047[10539]; Yu[10539]; PI 672538[11710]; Yu24[10539]. **ma**: *Xwmc426-7B* – 5.9 cM – *Xwmc334-7B* – 0.2 cM – **Pm40** – 0.7 cM – *Xgwm297-7B* – 1.2 cM – *Xwmc364-7B*[10539]; *Xwmc-7B* – 0.58 cM – **Pm40** – 0.26 cM – *BF291338*[11710]. Flanked by EST markers *BF478514* and *BF291338*[11711]. **c**: *TraesCS7B01G164000*, an NLR with an additional NBS region was identified as a candidate[11711].

PM41

Pm41[10551] locus: 3BL[10551]

Derived from *T. dicoccoides*.

bin: 0.63-1.00. **v**: XXX = 87-1*4/Langdon/IW2[10551]. **tv**: Langdon/IW2 Seln. XXX[10551]; *T. dicoccoides* IW2[10551]. **ma**: *BE489472* – 0.8 cM – **Pm41** – 1.9 cM – *Xwmc687-3B*[10551]. **c**: Encodes a unique CC-NBS-LRR gene[11454]. GenBank MN395289. Orthologs: in **tv**: Zavitan (*TRIDC3BG077810*) and Svevo (*TRITD3Bv1G261150.1*), and common wheat cv. Claire, but not in Chinese Spring[11454].

Pm41 and associated marker alleles showed strongly distored inheritance with reduced frequencies relative to Langdon alleles[10551].

PM42

Pm42[10559] locus: 2BS[10559]

Derived from *T. dicoccoides*. Recessive.

bin: 2BS-0.75-0.84. **v**: P63 = Yanda 1817/G303-1M/3*Jing 411[10559]. **tv**: *T. dicoccoides* G303-1M[10559]. **ma**: *BF146221* – 0.9 cM – **Pm42** – *Xgwm148-2B*[10559].

PM43

Pm43[10560] locus: 2DL[10560]

Derived from *Th. intermedium*.

v: Line CH5025 = 76216-96/TAI7045//2*Jing 411[10560]; Partial amphiploid TAI7045[10560]. **al**: *Th. intermedium* Z1141[10560]. **ma**: *Xwmc41-2D* – 2.3 cM – **Pm43** – 4.2 cM – *Xbarc11-2D*[10560].

PM44

Pm44[10790] locus: 3AS[10790]

v: Hombar[10790]. **ma**: Flanked by SSR markers distally located in chromosome arm 3AS[10790]. CURATOR'S NOTE: This gene nane was based on a pre-publication request; the publication cannot be located.

PM45

Pm45[10791] locus: 6DS[10791] syn: Pm57-6D[10790]

v: Line NWG0099[10791]. **v2**: D57[10791]. **ma**: Close linkages are reported in the draft manuscript.

PM46

Pm46[10847] locus: 4DL[10678, 10847]

Partial resistance.

bin: Distal to break point 0.56 FL[10678]. **i**: RL6077 = Thatcher*6/PI 250413[10678, 10847]. **v**: Chapingo 48[11070]. **ma**: Pleiotropic or closely linked with **Lr67**/**Yr46**/**Sr55**/**Ltn3** and aassociated with *Xgwm165-4D* and *Xgwm192-4DL*[10678, 10847]. **c**: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmenbrane helices[11070].

PM47

Pm47[10912] locus: 7BS[10912] syn: PmHYLZ[10912]

Reccessive.

bin: 7BS1-0.27-1.00. **v**: Hongyanglazi[10912]. **ma**: *Xgpw2119-7B* – 7.5 cM – *BE606897* – 1.7 cM – **Pm47** – 3.6 cM ascob – *Xgwm46-7A*[10912].

PM48

Pm48[10935] locus: 5DS[10935] syn: Pm46[10935]

Identified as ***Pm2a***[11678].

bin: 5DS1. **v**: Tabasco[10935]. **ma**: *Xgwm205-5D* – 17.6 cM – **Pm48** – 1.3 cM – *Xmp510(BE498794)* – 1.8 cM – *Xcfd81-5D*[10935].

PM49

Pm49[10937, 10938] locus: 2BS[10937] syn: MI5323[10937]

bin: 2BS-0.84-1.00. **tv**: *T. dicoccum* MG5323[10937]. **ma**: *Xcau516-2B* – 7.2 cM – **Pm49** – 4.1 cM – *XCA695634*[10937].

PM50

Pm50[10942] locus: 2AL[10942]

bin: C-2AL1-0.85. **v**: K2 TRI29907[10942]. **tv**: *T. dicoccum* M129[10942]. **ma**: *Xgwm294-2A* – 2.9 cM – **Pm50**[10942].

K2 is a backcross derivative of German winter wheat cv. Alcedeo with *T. dicoccum* accession M129 as donor of mildew resistance[10942].

PM51

Pm51[11026] locus: 2BL[11026] syn: PmCH86[11026]

Putative *Th. ponticum* derivative.

bin: 2BL6-0.89-1.00. **v**: CH7086[11026]. **ma**: *Xwmc332-2B* – 3.2 cM – **Pm51** – 1.5 cM – *BQ246670*[11026].

PM52

Pm52[11028, 11029] locus: 2BL[11028] syn: MILX90[11028, 11029]

bin: 2BL-0.35-0.50. **v**: DH51302[11715]; Jimai 22[11714]; Liangxing 99[11028, 11029, 11716]; Shimai 26[11715]. **ma**: *Xcfd73-2B* – 5.3 cM – *Xwmc441-2B* – 0.2 cM – *XBE604758* – **Pm52** – 2.9 cM – *Xgwm120-2B*[11028]; *XBE604758* – 5.5 cM – *Xics34* – **Pm52** – 0.8 cM – *Xics30* – 6 additional *ics* markers – *Xgwm120*[11029]. Located in a 533.6 – 612.9 Mb interval[11716].

PM53

Curator's note: A publication of this gene could not be located.

Pm53[11045] locus: 5BL[11045] syn: PmNC-S16[11045]

Derived from *Ae. speltoides*.

v: NC09BGTS16, PI 669386 = Saluda*3/TAU829[11045]. **al**: *Ae. speltoides* TAU829[11045]. **ma**: *Xwmc759*/*Xgwm499-5B*/*IWA6024* – 0.7 cM – **Pm53** – *IWA2454* – 5.9 cM – *Xgwm408-5B*[11045].

PM54

Pm54[11050] locus: 6BL[11050] syn: PmA2K[11050]

bin: 6BL-0.450-1.00. **v**: AGS2000 PI 612956[11050]. **ma**: *Xgpw2344-6B* – 1.00 cM – *wPt-9256* – **Pm54** – 1.2 cM – *Xbarc134-6B*[11050].

PM55

c: CC-NBS-LRRR[11742].

Pm55[11108, 11109] locus: 5AS (5VS.5AL)[11108]. 5DS (5VS.5DL)[11109] syn: Pm5VS[11108, 11109]

Derived from *Dasypyrum villosum*.

v: NAU421[11108]; NAU415[11108, 11109]. **ma**: A 730 bp *5EST-237* band is associated with chromosome 5VS[11109]; 5VS also carries puroindoline genes; therefore all lines with this gene will be soft (5VS.5DL) or supersoft (5VS.5AL).

The backgrounds of NAU415 and NAU 421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.

Pm55a[11742] locus: *Pm55* [11108]. 5AS (5AL 5VS#4S)[11108] syn: Pm5VS#4S[11108, 11109]

Growth stage and tissue-specific.

v: NAU185[11742].

This allele has a closely linked dominant inhibitor[11742].

The backgrounds of NAU415 and NAU 421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.

Pm55b[11742] locus: 5DS (5DL.5VS)[11109]

v: NAU421[11108]; NAU415[11108, 11109]; NAU[11742]; TF5V-1[11742]. **ma**: A 730 bp *5EST-237* band is associated with chromosome 5VS[11109].

5VS also carries puroindoline genes; therefore all lines with this gene will be soft (5VS.5DL) or supersoft (5VS.5AL).

Pm55a and ***Pm55b*** interact differently with the ***Pm55a*** inhibitor *SuPm55*[11742].

PM56

Pm56[11155] locus: 6AS (T6AL.6RS)[11155]

Derived from *S. cereale*.

v: LM47-6[11155]. **al**: *S. cereale* cv. Qinling[11155].

Study of misdivision products from a double monosomic 6A, 6R located **Pm56** to the subterminal region of 6RS[11155].

PM57

Pm57[11159] locus: 2BL (T2BS.2BL-2S^{S}#1)[11159]

Derived from *Ae. searsii*.

v: Line 89-346, TA5108[11159]; Line 89(5)69, TA5109[11159]; Line898(6)88[11728]; TA5109[11728]. **ad**: BCS+2S^{S}#1 TA3581[11159]. **c**: Encodes a tandom kinase with putative kinase-pseudokinse domains followed by a von Willebrand domain and orthologue of **Lr9** (88.3% amino acid similarity)[11728].

Line 89-346 has a 28% distal *Ae. searsii* segment and line 89(5)69 has a 33% distal *Ae. searsii* segment[11159].

PM58

Pm58[11171] locus: 2DS[11171] syn: PmTA1662[11171]

Derived from *Ae. tauschii*.

v: U6714-A-011, PI 682090[11320]; U6714-B-056, PI 682089[11320]. **dv**: *Ae. tauschii* TA1662[11171]. **ma**: Co-segregation with KASP^{TM}markers *K-TP331370, KTP338253, K-Tp15990* and *K-Tp313873*[11171]. Co-segregating marker *Xkasp68500* developed from *AET2Gv20068500* distinguished TA1662 from random common wheat accessions[11749].

PM59

Pm59[11214] locus: 7AL[11214] syn: Pm181356[11214]

bin: 7AL15-0.00-1.00. **v**: PI 181356[11214]. **ma**: *Xwmc525-7A* – 1.8 cM – *Xmag1759* – 0.5 cM – *Pm18156* – 5.7 cM – *Xmag1714* – 20.0 cM – *Xcfa2257-7A*[11214].

PM60

Pm60 locus: 7AL[11250] syn: PmR2[11250]

ex *T. urartu*[11250].

ex *T. dicoccoides*[11551]. *TRIDC7AG077150*.

bin: 7AL16-0.86-1.00. **dv**: PI 428196[11250]; PI 428210[11250]; PI 428215[11250]; PI 428306[11250]; PI 428309[11250]; PI 428310[11250]; PI 538737[11250]; PI 538751[11250]. **c**: NBS-LRR; the sequence in PI 428309 (GenBank. **v**: 3D249 (derivative of WE18)[11608], Ruta[11551]. **itv**: WEW G18-6/LDN RIL 154[11551]; G18-16[10886, 11551]. **t*v:*** *MIWE18*[11608]; *MIIW72*[10545, 11609], **MIIW172**[11095], **PmG16**[10886, 11551] v Ruta[11551]. **ma**: *Xuhw386-7A* – 0.3 cM – **Pm60** – 1.4 cM – *Xuhw-7A*[11551].

MF996807) is 4,365 bp. The sequence in PI 428215 (designated *Pm60a*; GenBank MF996808) has a 240 bp insertion relative to PI 428309 whereas PI 428210 (designated *Pm60b*, GenBank MF996806) lacks the same sequence, which corresponds to two LRRs[11250]. Transformants with *Pm60a* conferred resistance to a lower number of *Bgt* isolates than transformants with **Pm60** or *Pm60b*[11663].

PI 428210 carries an adjacent gene (possibly a paralog) that conferred resistance to a *Bgt* isolate virulent to **Pm60** and *Pm60b*[11663].

Two of three resistant haplotypes of **Pm60** were transferred to common wheat (11651}.

Further resistant haplotypes were identified for *MlIWE6* (MW375704) and *MlIW113* and *PmIW226* (MW375704)[11761]. Evidence of allelic variation was also presented[11761].

The cloned PM60 sequences from the diploid and tetraploid sources differed by 8 SNP that changed 6 amino acids[11551].

pm60

dv: G1812[11250].

Gene **PmU**, flanked by *Xwmc273-7A* and *Xpsp3003-7A*, was transferred to common wheat from *T. urartu* accession UR206 (JIC 10100015)[11402]. *Xwmc273-7A* was 7.8 cM proximal to PM60[11250].

PM61

Pm61[11290] locus: 4AL[11290]

bin: 4AL4-0.8-1.00. **v**: Xuxusanyuehuang[11290]. **ma**: *Xgwm160-4A* – 0.23 cM – **Pm61** – 0.23 cM – *Xicsx79*[11290].

Pm61 was considered to be at a different locus to **MlIW30**, a dominant gene in *T. dicoccoides* accession IW30 and its hexaploid derivative Line 2L6[11289].

PM62

Pm62[11321] locus: 2BS.2VL#5[11321] syn: Pm2VL[11321].

Adult-plant resistance.

v: NAU1823[11321]. **ma**: *X2L4g9P4/Hae111*[11159].

PM63

Pm63[11331] locus: 2BL[11331] syn: Pm628024[11331]

bin: 2BL6-0.89-1.00. PI 628024[11331]. **v**: PI 628024[11331]. **ma**: *Xwmc175-2B* – 1.7 cM – *Xstars419-2B* – 0.6 cM – **Pm63** – 1.1 cM – *Xbcd135.2* – *2B*; 710.3 – 723.4 in the CS RefSeq 1.0[11331].

PM64

Pm64[11346] locus: 2BL[11346] syn: PmWE35[11346]

bin: 2BL4-0.5-0.89. **v**: WE35[11346]. **tv**: *T. dicoccoides* G-573-1[11346]. **ma**: *Xwmc175-2B* – 1.12 cM – **Pm64**/*Xgwm47-2B* – 2.18 cM – *Xwmc332-2B*[11346]. Complete repulsion linkage with **Yr5** in 644 F_3 lines[11346].

PM65

Pm65[11356] locus: 2AL[11356] syn: PmXM208[11356]

v: Xinmai 208[11356]. **ma**: *Xhbg327-2A* – 4.4 cM – *XresPm4/XTaAetPR5* – 0.6 cM – **PmXM208** – 1.6 cM – *Xbarc122-2A*[11356]. An allelism test of **Pm65** and ***Pm4a*** showed a recombination value of 10.3 cM based on the frequency of susceptible F_2 plants[11356].

Pm351817[11752]

Putative **Pm65** allele[11752].

v: PI 351817[11752]. **ma**: *Stars-KASP662* (771.21 Mb, CS RefSeq 2.1) – 0.9 cM – ***Pm351817*** – 0.6 cM – *Stars-KASP656* (771.81 Mb). 2.5 cM proximal to a marker for **Pm4**[11752].

PM66

Pm66[11364] locus: 4BS (4BL·4S^{l}#7S)[11364]

v: TA3465[11364]. **al**: *Ae. longissima* (unknown accession). **ma**: 4S^{l}S markers developed in [11364].

PM67

Pm67[11426] locus: 1D (1DL.1VS#5)[11426] syn: *Pm1V#5*[11426]

v: NAU18105[11426]. **su**: NAU18103 (1V(1D))[11426]. **al**: *Dasypyrum villosum* 011140[11426].

Lines with **Pm67** showed complete immunity as seedlings but adult plants produced some conidial development on leaves whereas the culms, leaf sheaths and spikes were mildew-free[11426].

PM68

Pm68[11466] locus: 2BS[11466]

bin: 2BS-0.84-1.00. **tv**: *T. durum* TRI 1796[11466]. **ma**: *Xdw04* (*TRITD2Bv1G010030*, chr2B:21587671-21591163) – 0.22 cM – PM68 – 0.22 cM – *Xdw12* (*TRITD2Bv1G010880*, chr2B:23374401-23375310) – 3.0 Mb – PM26/*Xcau516-2B* (*TRITD2Bv1G012960*, chr2B:26398438-26414596) – 36.8 cM – PM42[11466].

PM69

Pm69[11541] locus: 6BL[11302] syn: PmG3M[11302]

bin: 6BL-0.7-1.00. **v**: Ruta + **Pm69**[11627]. **itv**: Svevo + **Pm69**[11627]. **tv**: *T. dicoccoides* G-305-3M[11302, 11627] TD116180 (University of Haifa Wild Cereal Gene Bank), CGN19852 (Netherlands Centre for Genetic Resources)[11541]. **ma**: *Xgpw7262-6B* – 6.9 cM – PM69 (**PmG3M**) – 4.5 cM – *Xedm149-6B*[11302]. **c**: **Pm69** comprises Rx_N with RanGAP interaction sites, NB-ARC, and LRR domains[11627]. GenBank KY825226.1.

Collinearity analyses indicated homoeology with SR13[11627].

PM70

Pm70[11724] locus: 3BS (by association with *Sr2* and *Lr27* [11723]

s: CS (Hope 3B)[11723]. **v**: Hope[11723]. **tv**: Yaroslav emmer[11723]. **ma**: Association of **Pm70** with **Sr2**, **Sr27** and *Pbc1*[11723].

MLO

Mlo mutants in barley confer durable resistance to powdery mildew; most *mlo* mutants have deleterious effects on plant growth and morphology, but a few selected for negligible deleterious effects have been widely used in barley breeding. Most species have *MLO* homologs. *MLO* is considered a gene for susceptibility since overexpression leads to increased haustorial index[11743]. ***TaMLO-A1***, ***TaMLO-B1*** and ***TaMlo-D1*** located in chromosome arms 5AL, 4BL and 4DL[11743] are 98% and 99% identical at the nucleotide and protein levels, respectively[11744].

Plants with combined *Tamlo-A1*, *Tamlo-B1* and *Tamlo-D1* mutations were resistant to powdery mildew[11744] but exhibit abnormal growth[11745]. A mutant with a 304 bp targeted deletion in *TaMLO-4B* had normal phenotype when combined with the mutant orthologs[11745]. This mutation led to ectopic activation ofa closely linked gene *TaTMT3B* (*Tonoplast monosaccharide transportase 3*, *TraesCS4B02G322000*) leading to a normal plant phenotype[11745].

A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3/PI 427772[10479]. A single resistance gene was identified on chromosome 7AL in hexaploid germplasm NC96BGT4 (a *T. monococcum* derivative). This gene was proximal to **Pm1** and considered to be different from **Pm37**, although possibly allelic[10274].

Genotype lists

Chinese wheats[572, 1608]; Finnish wheats[0028]; French wheats[1629]; Hungarian wheats[02104]; Western Siberian wheats[1101]. Others[10405, 10406, 0313]

Complex genotypes
Drabent (heterogeneous) **Pm2** ***Pm4b*** **Pm9**/**Pm1 Pm2** ***Pm4b*** **Pm9**[1287];
Nemares **Pm1 Pm2** ***Pm4b*** **Pm6 Pm9**[1287];
Planet, Sappo & Walter **Pm1 Pm2** ***Pm4b*** **Pm9**[96, 97, 540, 1287, 1428] Scandinavian wheats[10681].

3.4.2 Suppressors of *Pm* resistance genes

Some wheats which on the basis of cytological and rust tests carry 1RS from Petkus rye, do not express resistance due to presence of a suppressor[385]. Zeller & Hsam[1625] located a suppressor of **Pm8** and **Pm17** in chromosome 7D of Caribo. Mildew resistance was suppressed in Florida, Heinrich, Ikarus, Olymp and Sabina, which are derivatives of Caribo with 1BL.1RS. According to Ren *et al.*[1209], **SuPm8** does not suppress **Pm17**. Hanusova *et al.*[492] listed 16 wheats that carry a suppressor of **Pm8**; 111 wheats did not carry the suppressor. In contrast, a high frequency of suppression occurred in CIMMYT wheats[108, 1208]. Further genotypes are identified in [491, 11025]. Although Line 81-7241 carries **Pm8** as well as ***Pm23***, evidence was presented to indicate that **Pm8** was suppressed in Line 81-7241[1618] and, by inference, indicated that Chinese Spring possessed **SuPm8**.

SuPm8[1209] locus: 1AS[1209]

v: Wheats with ***Gli-A1a***[1209] including CS; Lists in [108, 491, 1208].

Pm8 was suppressed when locus **Pm3** is transcribed (including Chinese Spring and Thatcher which have no currently detectable **Pm3** resistance alleles)[10828].

3.4.3 Temporarily designated genes for resistance to *Blumeria graminis*

MI-Ad[854]

v: Adlungs Alemannen[854].

MI-Br[854]

v: Bretonischer Bartweizen[854].

MI-Ga[854]

v: Garnet[854]; Many old German cultivars[854].

MI3D32[10892] locus: 5BL[10892]

bin: 5BL 0.59-0.76. **tv**: *T. dicoccoides* I222[10892]. **v**: 3D232[10892]. **ma**: *Xwmc415-5B* – 1.3 cM – *MI3D232* – 3.3 cM – *CJ832481*[10892]; Co-segregation with 8 EST markers including an NBS-LRR analogue[10892].

MI92145E8-9[11436] locus: 2AL[11436]

bin: 2AL1-0-0.85. **v**: Line 92145E8-9[11436]. **ma**: *Xwmc181-2A* – 9.3 cM – *Xsdauk682-2A* – 2.8 cM – **MI92145E8-9** – 0.8 cM – *Xsdauk-2A* – 18.7 cM – *Xgwm356-2*[11436].

MIAB10[10873] locus: 2BL[10873]

bin: 2BL6 0.89-1.00. **v**: NC97BGTAB10, PI 604036[10873]. **tv**: *T. dicoccoides* PI 471746[10873]. **ma**: *Xwmc445-2B* – 7 cM – **MIAB10**[10873].

MId[96] locus: 4B[97]

v2: Halle 13471 **Pm2**[96]; H8810/47 **Pm2**[96]; Maris Dove **Pm2**[96]. **tv**: *T. durum* line[96].

MIHLT[18057] locus: 1DS[11257] syn: Pm24[11414]

v: Hulutou[11257]. **ma**: *Xgwm-1D* – 1.7 cM – *Xwggc3026* – 1.5 cM – **MIHLT** – 2.1 cM – *Xwggc3148* – 4.0 cM – *Xcfd83-1D*[11257].

MIIW30[11289] locus: 4AL[11289] syn: MLIW30[11289]

bin: Line 2L6[11289]. **v**: Line 2L6[11289]. **tv**: *T. dicoccoides* IW30[11289]. **ma**: *Xbarc78-4A* – 1.00 cM – *XB1g2020.2* – 0.1 cM – *MIIw30* – 0.1 cM – *XB1g2000.2* – 2.6 cM – *Xgwm350-4A*[11289].

MIIw72[10545] locus: 7AL[10545]

See **Pm60**.

bin: FL 0.86[10545]. **tv**: *T. dicoccoides* IW72[10545]. **ma**: *Xmag1759-7A* – 8.2 cM – *MIIW72* – 3.3 cM – *Xmag2185-7A* – 1.6 cM – *Xgwm344-7A*[10545].

MIIw170[10921] locus: 2BS

bin: 2BS3-0.84-1.00[10921]. **tv**: *T. dicoccoides* IW170[10921]. **ma**: *XcauG2* – 0.6 cM – **MIIw170**/*Xcfd238-2B* – 2.15 cM – *XcauG8*/*BF201235*/*Xwmc243-2B*[10921]; **Iw1** – 18.77 cM – **MIIw170**[10921].

This gene is located in the same region as **Pm26**[10921].

MIIW172[11095] locus: 7AL[11095]

bin: 7AL-16-0.86-0.90. **tv**: *T. dicoccoides* IW172[11095]. **ma**: *WGGC4664/WGGC4665/WGGC4668* – 0.44 cM – **MIIW172** – 0.7 cM – *WGGC4659*[11095].

mljy[0339] locus: 7B[339]

Recessive, hemizygous-effective[0339]

v2: Jieyan 94-1-1 **Pm8**[0339].

MIm80[10393] locus: 7AL[10393]

dv: *T. monococcum* ssp. *aegilopoides* M80[10393]. **ma**: *Xmag1757*/*Xmag1759* – 3.6 cM – **MIm80** – 0.7 cM – *Xmag2166*/*Xgwm344-7A*[10393]; *Xwggc4655* – 0.29 cM – **MIm80** – 0.57 cM – *Xwgrc253*/*Xwgrc271*[11190].

MIm2033 and **MIm80** appeared to be allelic and their relative locations suggest they are allelic with **Pm1**[10393].

MIm2033[10393] locus: 7AL[10393]

dv: *T. monococcum* TA2033[10393]. **ma**: *Xmag1757*/*Xmag2185* – 2.7 cM – **MIm2033**/*Xmag2185* – 1.3 cM – *Xgwm344-7A*[10393]; *Xmag1757* – 5.9 cM – **MIm2033**/*Xmag2185*/*Xgwm344*/*Xgwm146-7A* – 4.7 cM – *Xmag1986*[10393]; *Xmag1757*/*Xmag1714*/*Xmag1759* – **MIm2033** – 0.9 cM – *Xmag2185*/*Xgwm344-7A*[10393]; *Xwgrc353*/*Xwggc4659* – 0.84 cM – **MIm2033**/*Xmag8626*/*Xmag9060*/*Xmag2185*/*Xmag5240* – 0.06 cM – *Xmag8415*/*Xmag8220*[11190].

MLNCD1[11004] locus: 7DS[11004]

bin: 7DS4-0.61-1.00[11004]. **v**: NC96BGD1 PI 597348[11004]; Saluda*3/TA2570[11004]. **ma**: *Xgwm635-7D* – 5.5 & 8.3 cM – *MlNCD1* – 16.2 cM & 13.6 cM – *Xgpw328-7D*[11004].

MINFS10[11666] locus: 4AL[11666]

tv: *T. turgidum* ssp. *dicoccoides* NFS10[11666]. **ma**: Located to a 0.3 cM interval of 2.1 Mb (729275816-731365462) in CS refseq 1.0[11666].

Considered to be located at a different locus to **Pm61** and **MIIW30**[11666].

mlRd30[10175] locus: 7AL

Reccesive 7AL[10175].

v: RD30[10175]; TA2682c[10175]. **ma**: *Xgwm344-7A* – 1.8 cM – **mlRD30** – 2.3 cM – *Xksuh9-7A*[10175].

TA2682c carries a second dominant gene located in chromosome 1A[10175].

MIre[1220] locus: 6AL[0142]

v2: RE714 ***Pm4b***[1220, 0142]. **tv**: *T. dicoccum* 119[1220].

MIre showed a residual effect on the quantitative expression of APR in the presence of *B. graminis* pathotypes considered virulent for **MIre** in standard seedling tests[0016]. In addition to **MIre**, a QTL for resistance effective at the seedling stage was associated with microsatellite marker *Xgwm174-5D*[0142].

mlsy[339, 0339] locus: 7B[0339]

Recessive, hemizygous-effective[0339]

v: Siyan 94-2-1[0339].

MITd1055[10029]

tv: *T. dicoccoides* 1055[10029].

MIUM15[11216] locus: 7AL[11216]

Derived from *Aegilops neglecta*.

bin: 7AL15-0.99-1.00. **v**: NC09BGTUM15[11216]. **al**: *Ae. neglecta* TTCC 223[11216]. **ma**: *Xwmc525-7A*/*IWA8057* – 0.7 cM – *Xcfa2257-7A* – 0.4 cM – **MIUM15** – 0.8 cM – *Xcfa2240-7A* – 2.8 cM – *Xmag2185* – 3.4 cM – *IWA2929*5 – 4.0 cM – *IWA4434*[11216].

MIWE74[11589] locus: 2BS[11589]

v: WE74[11589]. **tv**: *T. dicoccoides* G-748-M[11589]. **ma**: Mapped to a 799.9 kb region corresponding to physical region 25.48-26.28 in CHr2_Zavitan v2.0 (26.59-27.01 in IWGSC RefSeq v1.0)[11589]. The relationship to **Pm26** and *MlIW170* was not established[11589].
v: WE74 = YD1817/G-748-M//7*ND01[11665]. **tv**: *T. dicoccoides* G-748-M[11665]. **ma**: Co-segregated with *WGGBD425*[11665].Located in the same region as **Pm26**, *MlIW170*, and **MIWE74**[11665].

MIxbd[0259] locus: 7B[0259]

Recessive and hemizygous-effective[0258]

v: Xiaobaidong[0258].

MIzec1[10127, 10227] locus: 2BL[10127] syn: MLZec[10127]

v: Zecoi 1 = Ralle*3/*T. dicoccoides* Mo49[10127]. **tv**: *T. dicoccoides* Mo49[10127]. **ma**: Distally located in chromosome 2BL[10127]; *Xwmc356-2B* – 2.0 cM – *PmZec1*[10127].

Pm2Mb[11662] locus: 2DL[11662]

v: 2DL-2M^{b}L translocation lines. **ad**: CS + 2M^{b} TA7733[11662]. **ma**: Mapped to a FL 0.49 – 0.667 region containing 19 2Mb-specific markers[11662].

Pm6SI[11597] locus: 6A and 6B[11597]

Derived from *Ae. longissimum*.

ad: CS + 6S^{l}#3 TA7548[11597]. **v**: T27 (Ti6AS.6AL-6S^{l}#3-6AL)[11597]; R43 (T6BS.6BL-6S^{l}#3^{l}#3[11597]. **al**: *Ae. longissimum* TA1910 (11597). **ma**: Mapped to a distal 6S^{l}#3 interval of 42.8 Mb flanked by markers *Ael58410* and *Ael5799* {11597).

Pm6S^{l} conferred resistance to 28 of 30 Chinese *Bgt* isolates[11597].

Pm10V-2[11380] locus: 5DS[11380]

bin: 5DS-0-0.63. **v**: 10V-2[11380]. **ma**: *Xbwm25-5D*/*Xswgi066-5D* – 1.2 cM – **Pm10V-2**/several markers – 1.2 cM – *Xcfd-5D*[11380].

Pm2026[10604] locus: 5A^{m}L[10604] syn: pm2026[10604]

Recessive[10604].

bin: 5AL17-0.78-1.00[10604]. **dv**: *T. monococcum* TA2026[10604]. **ma**: *Xcfd39-5A* – 1.8 cM – *Xcfd1493-5A*/*Xmg2170-5A* – 0.9 cM – **Pm2026** – 2.5 cM – *Xgwm126-5A*[10604].

PmAF7DS[11291] locus: 7DS {M10891}

v: Arina[11291]. **ma**: *Xpsr160-7D* – 1.3 cM – *Xgwm350a-7D* – 4.7 cM – **PmAF7DS** – 9.9 cM – *Xbarc184*/*Xgwm111-7D*[11291].

Three of 61 Israeli *Bgt* isolates were avirulent: all three isolates were from tetraploid wheat accessions. It is possible that the gene may be present in many common wheat accessions.

PmAS846[10926, 10927] locus: 5BL[10926]

bin: 5BL14-0.75-0.76. **v**: N9134[10926]; N9738[10927]. **tv**: *T. dicoccoides* AS846[10926]. **ma**: *XMAG2498-5B* – 1.3 cM – **Pm36**/*XBJ261635* – 1.1 cM – **PmAS846** – 1.3 cM – *XFCP1-5B*[10927].

PmCn17[10686] locus: 1BS=1BL.1RS[10686]

v: Chuannong 17[10686]. **al**: *S. cereale* R14[10686].

pmDHT[11447] locus: 7BL[11447]

Recessive.

v: Dahongtou S761[11447]. **ma**: *XBE443877*/*Xwmc526-7B* – 0.8 cM – **pmDHT** – 0.8 cM – *Xgwm611*/*Xwmc581-7B* – 0.9 cM – *XBF473539*/*Xgwm577-7B* – 0.9 cM – *Xgwm577-7B*[11447].

PmG16[10886] locus: 7AL[10886]

bin: 7AL16 0.86-0.90. **tv**: *T. dicoccoides* G18-16[10886]. **ma**: *Xgwm1061*/*Xgwm344-7A* – 1.2 cM – **PmG16**/*wPt-1424*/*wPt6019* – 2.4 cM – *wPt-0494*/*wPt9217*/*Xwmc809-7A*[10886].

PmHHXM syn: PmXNM[11748]

v: Xiaonanmai[11748]. **ma**: *PmXnm* was flanked by markers *caps213923* (744.11 Mb) and *kasp511718* (744.41 Mb)[11748].
v: Honghuaxiaomai[11565]. **ma**: Located in a 1.77 Mb (0.18 cM) region flanked by *Xkasp475200* and *Xhnu522*[11565].

PmHNK[10706] locus: 3BL[10706]

v: Zhoumai 22[10706]. **ma**: *Xgwm108-3BL* – 10.3 cM – **PmHNK** – 3.8 cM – *Xwmc291-3BL*[10706].

PmHNK54[10897] locus: 2AL[10897]

bin: 2AL1 C-0.85. **v**: Zheng9754[10897]. **ma**: *Xgwm372-2A* – 5.0 cM – **PmHNK54** – 6.0 cM – *Xgwm312-2A*[10897].

PmHo[11176] locus: 2AL[11176]

v: Mv Hombar[11176]. **ma**: *XwPt-665330* – 0.3 cM – **PmHo** – 0.1 cM – *XwPt-3114*[11176].

PmHYM[11732] locus: *pmHYM* [11732]. 7BL[11732]

Recessive.

v: Hongyoumai[11732]. **ma**: Allelic with ***Pm5e*** and *mlXBD* and differed in specificity from lines carrying ***Pm5a***, ***Pm5b***, ***Pm5e*** and *MlXBD*[11732].

PmJM23[11445] locus: 5DS[11445]

v: Jimai 23[11445]. **ma**: *Xytu3004* – 0.7 cM – **PmJM23**/*Xytu201*/*Xbwm21*/*Xcfd81-5D* – 1.8 cM – *Xswgi068*/*Xbwm20*[11445].

PmKN0816[11598] locus: 2BL[11598]

v: KN0816[11598]. **ma**: Mapped to a region of chromosome carrying **Pm6**, **Pm33**, **Pm51**, **Pm64** and **PmQ** but distinguished from each other by specificity[11598].

PmLK906[10476] locus: 2AL[10476, 10477]

Resistance is recessive[10476, 10477].

v: Lankao 90(6)21-12[10476]; Zhengzhou 9754[10476]. **ma**: *TacsAetPR5-2A*/**Pm4** – 3.9 cM – *Xgwm265-2A* – 3.72 cM – **Pm39** – 6.15 cM – *Xgdm93-2A*[10476, 10477]; *TacsAetPR5-2A* was converted to an STS marker[10477].

PmLS5082[11629] locus: 2BL[11629]

v: LS5082[11629]. **ma**: Located in the interval 710.3 – 711.0 Mb[11629].

PmLX66[11162] locus: 5DS[11162]

PmLX66 was allelic with **Pm2**[11162].

v: Liangxing 66[11162]. Identified as ***Pm2a***[11503].

PmNJ3946[11677] locus: 3AS[11677]

dv: *T. monococcum* Line NJ3946[11677]; PI 191097 = TA2032[11677]. **ma**: *Xbarc294-3A* – 1.1 cM – **PmNJ3946** – 0.8 cM – *Xwgrc5153-3A*[11677].

PmPBDH[11647] locus: 4AL[11647]

v: PBDH[11647]. **ma**: Mapped to a 3.2 cM interval, 719.1-726.2 Mb (CS RefSeq 1.0)[11647].

Cytology failed to detect a putative *Agropyrum cristatum* segment in PBDH[11647].

PmPs5A[10205] locus: 2AL[10205]

v: AM4[10205]. **tv2**: *T. turgidum* subsp. *carthlicum* pS5 **Pm33**[10205]. **ma**: *Xgwm356-2A* – 10.2 cM – *PmPS5A*; *PmPS5A* is located at or near the **Pm4** locus[10205].

PmQ[11461]

Recessive.

v: Hongxinmai[11461]. **ma**: *Xstars419-2B* – 0.6 cM – *Xicsq405 2B* – 0.8 cM – **PmQ** – 0.2 cM – *XWGGBH913-2B*[11461].

PmQ is very close to **Pm51**, **Pm63** and **Pm64**.

PmSGD[11453] locus: 7BL[11453]

Recessive.

v: Shangeda[11453]. **ma**: *SNP2-58* – 0.4 cM – **PmSGD** – 0.8 cM – *SNP2-46*[11453].

PmTb7A.1[11130] locus: 7AL[11130]

bin: 7AL 18-0.90-1.00. **dv**: *T. boeoticum* PAU5088 **PmTb7A.2**[11130]. **ma**: Mapped to a 4.3 region flanked by *wPt4553* and *Xcfa2019-7A*[11130]; Estimated to be 46 cM proximal to **Pm1**[11130].

PmTb7A.2[11130] locus: 7AL[11130]

dv: *T. boeoticum* PAU5088 **PmTb7A.1**[11130]. **ma**: Mapped to a 0.8 cM region flanked by *MAG1759* and *MAG2185b* in the region of **Pm1**[11130].

PmTm4[10961] locus: 7BL[10961]

bin: 7BL10-0.78-1.00. **v**: Tanmai4[10961]. **ma**: *Xgwm611-7B* – 7.0 cM – **PmTm4** – 14.6 cM – *Xest92* – 2.9 cM – *Xbarc1073*/*Xbarc82-7B*[10961]; *XWGGC6892* – 0.6 cM – **PmTm4**/*XWGGC5746* – 0.03 cM – *XWGGC891*[11452].

PmTR1 & PmTR3[11686] locus: 6RS[11686]

SECCE6Rv1G0382290.

v: TR1 and TR3 were described as stable wheat lines derived from different triticale sources; TR1 had post-seedling ('age-dependent') resistance and TR3 had all stage resistance. **c**: These genes were shown to be allelic and the different responses were attributed to differences in expression[11686]. Both proteins had similarity to **Pm12** and **Pm21**, but differed from Pm8, **Pm17** and **Pm50**[11686].

PmTx45[11374] locus: 4BL[11374]

Recessive.

bin: 4BL5-0.85-1.00. **v**: Tian Xuan 45[11374]. **ma**: *Ax-110673642* – 3.0 cM – **PmTx45** – 2.6 cM – *ILP4B01G266900*[11374].

PmU[11251] locus: 7AL[11251]

dv: UR206[11251]. **ma**: *Xwmc273-7A* – 2.2 cM – **PmU** – 3.8 cM – *Xpsp3003-7A*[11251].

PmU was transferred to, and was effective in, common wheat.

PmV[11703]

T6DL.6VS#4S[11703].

v: Yangmai 22[11703].

PmW14[11162] locus: 5DS[11162]

PmW14 is allelic with **Pm2**[11162].

v: Wennong 14[11162]. Identified as ***Pm2a***[11503].

PmWE99[11162, 11166] locus: 2BS[11166]

Derived from *Thinopyrum intermedium*.

bin: 2BS-0.84-1.00. **v**: WE99. **ma**: *Pmwe99* – 10.4 cM – *Xgwm148-2B* – 3.1 cM – *Xbarc55-2B*[11162].

GISH failed to detect alien chromatin.

Pmx[11009] locus: 2AL[11009]

Reccessive.

bin: 2AL1-0.58-1.00. **v**: Xiaohongpi[11009]. **ma**: *Xhbg327-2A* – 0.6 cM – **Pmx**/*Xsts-bcd1231* – 8.9 cM – *XresPm4*/*Xgpw4456-2A*[11009].

This gene and close markers showed distorted segregation ratios and some discrepancy of markers relative to **Pm4** alleles[11009].

PmXQ-0508[11734] locus: 2AS[11734]

v: Line XQ00508[11734]. **ma**: Located to 226.7 kb interrval[11734].

All F_2 plants in crosses with lines having **Pm26** (1,226 plants), **Pm42** (1,198 plants) and **Pm26** (1,583 plants) were resistant to the test isolate but the response arraye of the lines appeared to be diferente[11734].

PmY39[10367] locus: 2U(2B)[10367]

su: Laizhou 953*4/Am9 (Am9 = *Ae. umbellulata* Y39/*T. turgidum* ssp. *carthlicum* PS5)[10367]. **dv**: *Ae. umbellulata* Y39[10367]. **ma**: Associated with 2U markers *Xgwm257*, *Xgwm296* and *Xgwm319*[10367].

PmYm66[10619] locus: 2AL[10619]

v: Yumai 66[10619]. **ma**: *XKsum193-2A* – 2.4 cM & 3.6 cM – **PmYm66**[10619].

Unnnamed resistance gene[11612]. *WTK4*[11612]. 7D[11612]. dv: *Ae. tauschii* Ent-079[11612]; Ent-080[11612]; Ent-085[11612]; Ent-102[11612]. v: Synthetic derivatives of the above diploid accessions[11612]. ma: Located within a 60 kb insertion relative to the AL8/78 reference genome in region 4.76 – 5.06 Mb[11612]. c: Wheat tandom kinase; MW295405[11612].

A normally inherited resistance to powdery mildew in wheat-*Th. intermedium* translocation line 08-723 (?B-?S^t.6AL) was reported in [11035].

3.4.4 QTLs for resistance to *Blumeria graminis*

QTL: Several QTLs were detected in two RE714/Hardi populations when tested at two growth stages and with different cultures over three years. The most persistent and effective QTL was located in the vicinity of *Xgwm174-5D*[0272]. Three QTLs, *QPm.vt-1B*, *QPm.vt-2A* and *QPm.vt-2B*, with additive gene action, accounted for 50% of the variation in a population developed from Becker/Massey[0284]. These QTLs were confirmed by the addition of extra markers to the Becker/Massey map and in a separate analysis of USG 3209 (A Massey derivative)/Jaypee (susceptible)[10505]. USG 3209 possessed **Pm8** (1BL.1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL[10505]. QTLs on chromosomes 1A, 2A, 2B, 3A, 5D, 6A and 7B were detected in a RE714/Festin population in multiple locations and over multiple years. The QTL on chromosome 5D was detected in all environments and all years and was associated with markers *Xgwm639-5D* and *Xgwm174-5D*. Resistance was contributed by RE714. A QTL coinciding with *MlRE* on 6A was also detected in all environments. The QTL on chromosome 5D and 6A accounted for 45% to 61% of the phenotypic variation[0354].

PmSE5785[11084] locus: 2DL[11084]

Recessive 2DL[11084].

v: SE5785, Snipe/Yav79//Dack/Teal/3/*Ae. squarrosa 877*[11084]; NO7728-1[11084]; NO7728-2[11084]. **ma**: *Xbarc59-2D* – 3.6 cM – *PmSe5785* – 4.6 cM – *Xwmc817-2*[11084]. Bainong 64(R)/Jingshuan 16(S). DH lines: Four QTL from Bainong 64: *Qpm.caas.1A*. *Xbarc148-1A* – *Xgwmc550-1A* interval. R^2=0.074-0.099; *QPm.caas-4DL* proximal to *Xwmc331-4D*. R^2=0.15-0.23; *QPm.caas-6BS*, proximal to *Xbarc79-6BS*, R^2=0.09-0.13; and *QPm.caas-7AL*, proximal to *Xbarc174-7AL*, R^2=0.067-0.071[10680].

QPm-tut-4A[11154] locus: 4AL[11154]

v: DT4AL-TM Line 8.1[11154]. **tv**: *T. militinae* (AAGG)[11154].

The 7G segment carrying this resistance likely replaces most of the 7BS segment known to be part of chromosome 4A[11154].

QPm.ipk-2B[0255] locus: 2BS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Resistance was contributed by Opata[0255]. **ma**: Associated with *Xcdo405-2B* and *Xmwg950-2B*[0255].

QPm.ipk-4B[0255] locus: 4B[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Resistance was contributed by W-7984[0255]. **ma**: Associated with *Xcdo795-4B* and *Xbcd1262-4B*[0255].

QPm.ipk-7D[0255] locus: 7DS[0255]

v: Opata/W-7984 (ITMI) RI mapping population[0255]; Resistance was contributed by Opata[0255]. **ma**: Associated with *Xwg834-7D* and *Xbcd1872-7D*[0255].

QPm.sfr-1A[0051] locus: 1A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr1201-1A* and *Xpsr941-1A*[0051].

QPm.sfr-1B[0051] locus: 1B[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xsfr3(LRR)-1B* and *Xpsr593-1B*[0051].

QPm.sfr-1D[0051] locus: 1D[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr168-1D* and *Xglk558-1D*[0051].

QPm.sfr-2A[0051] locus: 2A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr380-2A* and *Xglk293-2A*[0051].

QPm.sfr-2D[0051] locus: 2D[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr932-2D* and *Xpsr331-2D*[0051].

QPm.sfr-3A[0051] locus: 3A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xpsr598-3A* and *Xpsr570-3A*[0051].

QPm.sfr-3D[0051] locus: 3D[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr1196-3D* and *Xsfr2(Lrk10)-3D*[0051].

QPm.sfr-4A.1[0051] locus: 4A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xgwm111-4A* and *Xpsr934-4A*[0051].

QPm.sfr-4A.2[0051] locus: 4A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xmwg710-4A* and *Xglk128-4A*[0051].

QPm.sfr-4B[0051] locus: 4B[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xpsr593-4B* and *Xpsr1112-4B*[0051].

QPm.sfr-4D[0051] locus: 4D[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xglk302-4D* and *Xpsr1101-4D*[0051].

QPm.sfr-5A.1[0051] locus: 5A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr644-5A* and *Xpsr945-5A*[0051].

QPm.sfr-5A.2[0051] locus: 5A[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr1194-5A* and *Xpsr918-5A*[0051].

QPm.sfr-5B[0051] locus: 5B[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0051]. **ma**: Associated with *Xpsr580-5B* and *Xpsr143-5B*[0051].

QPm.sfr-6B[0051] locus: 6B[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xpsr167-6B* and *Xpsr964-6B*[0051].

QPm.sfr-7B.1[0051] locus: 7B[0051]

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xpsr593-7B* and *Xpsr129-7B*[0051].

QPm.sfr-7B.2[0051] locus: 7B[0051]

This QTL corresponds to **Pm5**[0051].

v: Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno[0051]. **ma**: Associated with *Xglk750-7B* and *Xmwg710-7B*[0051].

Additional temporarily named genes and QTL are listed in [11655].

QTL

Ae. tauschii ***ClAe8*** **(R)** / *Ae. tauschii* **PI 574467 (S)**: Resistance conferred by recessive genes *pmAeCl8_2DS* (14.48 – 16.32 Mb) and *pmAeCl8_7DS* {4.72 – 4.98 MB); the former overlapped the location of dominant **Pm58** and the latter was likely *WTK4* located in a ~60 kb insertion and encoding a wheat tandom kinase[11695].

Avocet R(S) / Saar (R): F6 RILs: QTL located on chromosomes 1BL (close to *Xwmc44-1B*) (**Pm39**), 7DS (*Xgwm1220-7D*) (**Pm38**) and 4BL (*XwPt-6209*) (resistance allele from Avocet R[10481].

AGS 2000 (*Pm3a* + Pm8) / Pioneer 26R61 (Pm8): *QSuSuPm.uga-1AS*(**SuPm8**) with an inhibitory effect on powdery mildew response was located at or near ***Pm3a***. *QPm.uga-7AL* from Pioneer 26R61 flanked by *Xcfa2257-7A* and *Xwmc525-7A* was in the region of the **Pm1** locus, even though the test culture was virulent for known **Pm1** alleles[11025].

CI 13227(S) / Suwon 92(R): SSD population: APR (field resistance) was closely associated with **Hg**. *Xpsp2999-1A* and *Xpm3B.1* and *Xpm3B.2* were designed from the ***Pm3b*** sequence {REF}.

Fukuho-Komugi / Oligoculm: DH population: QTL for adult plant resistance located on 1AS (R^2=22%, **Pm3** region, *Xgdm33* – *Xpsp2999*), 2BL (R^2=8%, *Xwmc877.1-Xwmc435.1*) and 7DS (R^2=10%) derived from Fukuho-komugi, and 4BL (R^2=6% at one of two sites, *Xgwm373-Xgwm251*) from Oligoculm[10335]. The QTL on 7DS, flanked by *Xgwm295.1-7D* and **Ltn**, is likely to be **Lr34**/**Yr18**.

Jingdong 8 / Aikang 58 (R): RIL population: ***Pm4a*** and several QTL from both parents[11753].

Liangxing 99 / Zhongzuo 9504: RIL population: A QTL *Qaprpm.caas.2B* in the same region as **Pm52** and APR QTL *Qaprpm.caas.7A* in a 1.3 cM region flanked by *Xicscl726*-7AL and *XicsK128-7A*[11716].

Lumai 21(R) / Jingshuang 16(S): F_3 lines: Three QTLs from Lumai 21: *QPm.caas-2BS*, *Xbarc98-2BS* – *Xbarc1147-2BS* interval, R^2=0.106-0.206; *QPm.caas-2BL*, *Xbarc1139-2BL* – *Xgwm47-2BL* interval, R^2=0.052-0.101; and *QPm.caas-2DL*, *Xwmc18-2DL* – *Xcfd233-2DL* interval, R^2=0.057-0.116[10707].

RE9001(R) / Courtot(S): RIL population: *QPm.inra-2B* (R^2 = 10.3-36.6%), in the vicinity of **Pm6**, was consistent over environments[10360]. Eleven QTL, detected in at least one environment were identified by CIM[10360].

SHA3 / CBRD(S) / Naxos(R): RIL population: A major QTL on chromosome 1AS accounted for 35% of the phenotypic variation; other QTL from Naxos were on 2DL, 2BL and 7AL. Although SHA3/CBRD possessed a **Pm3** allele suppressed **Pm8** which appeared to be effective in Norway[10934].

Tianmin 668 / Jingshuang 16: RIL population: Three QTL in chromosome arms 2AS (3,573 – 4.347 Mb), 2BL (56.844 – 70.698 Mb), and 5AL (4.412 – 4.719 Mb) were detected in Tianmin 666; ***Pm4d*** (2AL) identified in the same line was not effective in the field[11702].

3.5 Reaction to *Cephalosporium gramineum*

Disease: Cephalosporium stripe QTL: Coda (more resistant)/Brundage (less resistant): RIL population: 7 QTLs identified based on whiteheads; three from Coda – *QCs.org-2D.1* (nearest marker C, R^2=0.11), *QCs.orp-2B* (nearest marker *Xwmc453-2B*, R^2=0.08), and *QCs.orp-5B* (nearest marker *Xgwm639-5A*, R^2=0.12) and four from Brundage (*QCs.orp-2D.2* (nearest marker *Xbarc206-2D*, R^2=0.04), *QCs.orp-48* (nearest marker *wpt-3908*, R^2=0.05), *QCs.orp-5A.1* (nearest marker *wpt-3563*, R^2=0.08), *QCs.orp-5A.2* (nearest marker **B1**, R^2=0.05)[10836].

3.6 Reaction to *Cephus* spp.

Pest: Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*. Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).

Tetraploid wheat

Qsf.spa-3B[10351]

See Stem solidness.

3.7 Reaction to *Cochliobolus sativus* Ito & Kurib.

Disease: Cochliobolus root rot.

CRR

Crr[764] locus: 5BL[764, 765]

Recessive.

v: Apex[764]; Cadet[765].

3.8 Reaction to *Colletotrichum cereale*

RCC1

Rcc1[10939] locus: 5AL[10939]

v: Chinese Spring[10939]; Norin 4[10939]; Shinchunaga[10939]. **ma**: *Xbarc165-5A* – 1.2 cM – **Rcc1** – 12.8 cM; *Xgwm671-5A* – 0.7 cM – *Xwmc415-5A*[10939].

rcc1[10939]

v: Hope[10939].

Susceptibility to this non-pathogen of common wheat is rare, with only one susceptible genotype being documented. A few susceptible tetraploid genotypes were identified[10939].

3.9 Reaction to *Diuraphis noxia* (Mordvilko)

Insect pest: Russian aphid, Russian wheat aphid.

DN1

Dn1[286] locus: 7DS[0211].7D[1288]

bin: 7DS-0.36-0.73[11225]. **i**: Betta-Dn1:PI 634768[10277, 0211, 0004]; Caledon[0004]; Gariep[0004]; Karee-Dn1[0211]; Limpopo-Dn1[0004]; Tugela-Dn1:PI 591932[10277, 0211, 0004]. **v**: PI 137739[286]. **ma**: *Xgwm111-7D*$_{210}$ – 3.20 +/- 0.20 cM – **Dn1**[0211].

VIGS silencing of *5AL-B4* on chromosome 5A compromised resistance conferred by **Dn1** suggesting a decoy role[11333].

Tests of allelism indicated that **Dn1**, **Dn2**, **Dn5**, **Dn6**, and **Dnx** and four uncharacterized lines were identical or closely linked[11225].

DN2

Dn2[286] locus: 7DL[863].7DS[286]

i: Betta-Dn2:PI 634769[286, 10277]; Karee-Dn2:PI 663774[286, 10277]; Tugela-Dn2: PI 634772[286, 10277]. **v**: PI 262660[286, 863]. **ma**: *XksuA1-7D* – 9.8 cM – **Dn2**[863]; Myburg et al.[9968] identified two SCAR markers that mapped 3.3 cM proximal to **Dn2**[9968]; *Xgwm111-7D*$_{200}$ – 3.05 +/- 0.18 cM – **Dn2**[286]; *XksuA1-7D* – 9.9 cM – **Dn2** – 2.8 cM – *Xgwm437-7D*[0353].

According to Saidi & Quick[1250], **Dn1** and **Dn2** are probably allelic. Reference stocks with each gene showed allelism with a gene in PI 262605.

DN3

Dn3[1086]

Recessive.

v: *Ae. tauschii* SQ24/*T. turgidum* TD65[1086]. **dv**: *Ae. tauschii* SQ24[1086].

DN4

Dn4[1250] locus: 1DL[863], 1DS[11225]

i: Yumar[10397]. **v**: Ankor[10397]; CORWAI[260]; CI 2401[260]; Halt[0209]; PI 151918[260]; PI 372129[1250]; Prairie Red[10397]. **ma**: *Xabc156-1D* – 11.6 cM – **Dn4**[863]; *Xgwm106-1D* – 7.4 cM – **Dn4** – 12.9 cM – *Xgwm337-1D*[0352]; *Xgwm106-1D* – 5.9 cM – **Dn4** – 9.2 cM – *Xgwm337-1D*[10128].

Dn4 and an uncharacterized gene in PI 151918 were allelic or tightly linked[11225].

DN5

Dn5[1249] locus: 7D[259]. 7DS[286]. 7DL[287, 10310, 10396]

i: Betta-DN5[286]; Palmiet derivative 92RL28[287]; Palmiet DN5[0004]. **v**: STARS – 9302W-sib[259]; PI 294994[259]. **ma**: A SCAR marker developed from the RAPD fragment OPF14$_{1083}$ mapped 5.5 cM proximal to **Dn5**[0172]; *Xgwm111-7D*$_{220}$ – less than 3.20 cM – **Dn5**[286].

Issues relating to the confused arm location and mapping of **Dn5** is discussed in [10310]. Genetic mapping indicated that **Dn5** is located in chromosome 7DS, but cytological analysis showed it was located in 7DL[10396]. It was also suggested[10396] that the Palmiet Dn5 line[0004] may not have **Dn5**[10396].

DN6

Dn6[1250] locus: 7D

bin: 2AL1-0.85-1.00. **v**: CI 6501[260]; PI 243781[1249, 1250]. **ma**: **Dn6** – 3.0 cM – *Xgwm111*[352]. *Xgwm44-7D* – 11.6 cM – *Xgwm111-7D* – 3.0 cM – **Dn6**[11225].

DN7

Dn7[9918] locus: 1R[9918]. 1B = 1BL.1RS[9918] syn: Dn2414[10478]

Derived from *S. cereale* cv. Turkey 77[9918]

v: 93M45-14[9918]; 94M370[10188]; STARS 02RWA2414-11[10474]. **ma**: *Xbcd1434-1R* – 1.4 cM – **Dn7** – 7.4 cM – *Xksud14-1R*[10188]; *Xhor2-1R* – 1.7 cM – **Dn7** – 1.0 cM – *Xscb241-1R*[10474]; Marker *Xrems1303*$_{320}$ was amplified only in genotypes resistant to biotype 3 and presumably possessing **Dn7**[10474].

DN8

Dn8[286, 0211] locus: 7DS[286]

i: Karee-Dn8:PI 634775[10277]. **v2**: PI 294994 *Dn5Dn9*[286]. **ma**: *Xgwm635-7D*$_{100}$ – less than 3.20 cM – **Dn8**[286].

DN9

Dn9[286, 0211] locus: 1DL[286]

i: Betta-DN9:PI 634770[10277]. **v2**: PI 294994 *Dn5Dn8*[286]. **ma**: *Xgwm642-7D*$_{180}$ – less than 3.20 cM – **Dn9**[286].

DN10

Dn10[11211]

bin: 7DL-0.1-077. **v**: PI 682675[11211]. **ma**: *Xcfd14*-7D – 2.3 cM – *Xgwm437-7D* – 9 cM – **Dn10** – 29.1 cM – *Xwmc488-7D*[11211]; *Xcfd14*-7D – 3.6 cM – *Xgwm437-7D* – 11.3 cM – **Dn10** – 35 cM – *Xwmc488-7D*[11211]; **Dn626580** – 2.0 cM – **Dn2401** – 8.4 cM – *Dn624151*[11211].

Temporary designations

Dn1881[10145] locus: 7BS[10145]

tv: Line 1881[10145]. **ma**: *Xgwm46-7BS* – 10.1 cM – **Dn1881** – 12.8 cM – *Xgwm333-7BL*[10145].

Dn2401[11078] locus: 7DS[11078]

v: CI2401, PI 97812[11078]. **bin**: 7DS-0.37-0.61[11211]. **ma**: *Xbarc214-7D* – 1.1 cM – **Dn2401** – 1.8 cM – *Xgwm473 -7D*[11078].

Dn100695[11226] locus: 7DS M19026}

v: IG 100695[11226]. **ma**: *Xgwm44-7D* – 13 cM – *Xcfd14-7D* – 15.7 cM – **Dn100695**.

Dn626580[10981] locus: 7DS[10981]

v: PI 626580[10981]. **ma**: **Dn626580** – 1.8 cM – *Xbarc214-7D* – 3.2 cM – *Xgwm473-7D* – 3.2 cM – *Xgwm473-7D*[10981].

Dnx[286, 0211] locus: 7DS[286]

v: PI 220127[286]. **ma**: *Xgwm111-7D*$_{210}$ – 1.52 +/- 0.15 cM – **Dnx**[286].

Dnx was considered to be located at a locus different from **Dn1**, **Dn2** or **Dn5**[286], which were likely to be identical or allelic.

QTL: QTLs for antixenosis were associated with *Xpsr687-7D* (7DS) and *Xgwm437-7D* (7DL) in CS/CS (Synthetic 7D)[10136]. Separate antibiotic effects were demonstrated for the same chromosome[10136].

A QTL, *QDn.unlp.6A*, for antixenosis was associated with *Xgwm1393-6AL* and *Xgwm1150-6AL* in a CS/CS(Synthetic 6A) DH population[10216].

3.10 Reaction to *Eurygaster Integriceps*

Sunn pest

EI1

Ei1[11201] locus: 4BS[11201]

bin: 4BS4-C-0.27. **ma**: *IWB73001* – **Ei1**/*BS00022785* – *IWB9610*[11201].

3.11 Reaction to *Fusarium* spp.

3.11.1 Disease: Fusarium head scab, scab

Type II resistance. Whereas much of the recent genetic work involved FHB caused by *F. graminearum*, according to ▶[10514], *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction and DON/NIV contamination. Mesterhazy et al.[0006] reported a strong genetic correlation in resistance to different species of *Fusarium*.

FHB1

Fhb1[10214, 10403] locus: 3BS[9925] syn: QFhs.ndsu-3BS[175, 9925]

i: HC374/3*98B69-147[10214]; Sumai 3*5/Thatcher[10214]. **v**: HC-147-126[10444]; Rollag[11071]. **v2**: Alsen **Fhb5**[11071, 11237]; BW278 **Fhb2**[10225]; Carberry **Fhb5**[11237]; ND744 **Fhb5**[11237]; ND3085 **Fhb5**[11237]; Sumai 5 **Fhb2 Fhb5**[10314, 11237]. **ma**: *XSTS3B-80* – 0.2 cM – **Fhb1** – 1.1 cM – *XSTS3B-142*[10214]; Placed in a 1.2 cM interval flanked by *XSTS3B-189* and *XSTS3B-206*[10403]; *Xgwm389-3B* – 3.0 cM – **Sr2**/*csr2* – 0.4 cM – *Xgwm389-3B* – 2.0 cM – **Fhb1**/*UMN10*/UMN$_{v2}$ (coupling)[11210]. *Xgwm493-3B* and *Xgwm533-3B* were

confirmed as useful markers[11237]. **c**: A pore-forming toxin-like gene product encodes a chimeric lectin with two agglutinin domains and an ETX/MTXZ toxin domain[11205].

The relationship of **Fhb1** to **Fhs1** or *Fhsb2*[1096] is unknown. Lines combining **Fhb1**and **Sr2** are reported in [11170]; **Fhb1** is located about 2 cM proximal to **Sr2**. SYN1/Ocoroni DH population: three

QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%)[11165].

A marker study found that 14 of 66 wheats with putative FHB resistance shared markers indicative of the 3BS QTL in Ning 7840, Sumai 3, Wangshuibai and possibly Wuhan 3, plus Japanese landraces Shinchunaga and Shirasu No 1[10115]. The original source may be the landrace 'Taiwan Wheat' rather than Funo[10115].

FHS1

Fhs1[1096]

v: Line A[1096]. **v2**: Ning 7840 **Fhs2**[1096].

FHB2

Fhb2[10225] locus: 6BS[10225]

v: pbE85[10444]. **v2**: BW278 **Fhb1**[10225]; Sumai 3 **Fhb1**[10225]. **ma**: *Xgwm133-6B* – 4 cM – **Fhb2** – 2 cM – *Xgwm644-6B*[10225].

The relationship of **Fhb2** to **Fhs1** or **Fhs2**[1096] is unknown.

FHS2

Fhs2[1096]

v: Line B[1096]. **v2**: Ning 7840 **Fhs1**[1096].

A major QTL was associated with several linked AFLP markers tentatively located in chromosome 7BL of Ning 7840[0005].

FHB3

Fhb3[10529] locus: 7DS = T7AL.7Lr#1S[10529]

v: TA 5608[10529]. **al**: *Leymus racemosus*[10529]. **ma**: Three PCR markers, *Be586744-STS, BE404728-STS* and *BE586111-STS*, were developed[10529]. The level of type 2 resistance conferred by **Fhb3** was similar to that of Sumai 3[10529].

FHB4

Fhb4[10884] locus: 4BL[10282, 10883] syn: Qfhi.nau-4B[10282]

bin: 4BL5-0.86-1.00. **i**: Mianyang 99-323*4/Nanda 2419/Wangshibai[10885]. **v2**: Wangshuibai **Fhb5**[10884]. **ma**: Located in a 1.7 cM segment flanked by *Xhbg226-4B* and *Xgwm149*/*Xmag4580-4B*[10883].

Although plants with *Fhb-4* were taller than the recurrent parent, the height difference was not associated with the **Rht-B1** locus[10885].

Type I resistance (% infected plants) in this cross was attributed to 10 chromosome regions among which **Qfhi.nau-4B** (*Xwmc349-4B* – *Xgwm149-4B* – r^2 = 0.75), *XFhi.nau-5A* (*Xwmc96-5A* – *Xgwm304-5A* – R^2 = 0.27) and *Qfhi.nau-5B* (*Xgwm408-5B* – *Xbarc140-5B*) from Wangshuibai were detected in at least 3 of 4 years[10282]. A significant additive effect of QTL on 6D and 2A was also observed[10282].

FHB5

Fhb5[10896] locus: 5AS[10896] syn: Qfhi.nau-5A[10282], Qfhs.ifa-5A[10076]

bin: C-5AS3-0.75. **i**: Mianyan 99-323 and PH691 backcross derivatives selected for **Qfhi.nau-5A**[10896]. **v2**: Alsen **Fhb1**[11237]; Carberry **Fhb1**[11237]; ND744 **Fhb1**[11237]; ND3085 **Fhb1**[11237]; Sumai 5 **Fhb1 Fhb2**[10314, 11237]; Wangshuibai *Fh4b*[10896]. **ma**: Mapped to a 0.3 cM interval between *Xbarc117*/*Xbarc358*/*Xgwm293*/*Xgwm304-5A* and *Xgwm415-5A*[10896].

Closely linked in coupling with *Qflw.nau-5A* for narrow leaf width, but recombination is reported in [11041].

According to [11487] **Fhb5** might be the same as *Qfhs.ifa-5Ac* but the issue remained ambivalent.

FHB6

Fhb6[11048] locus: 1AS[11048]

Derived from *Elymus tsukushiensis* syn. *Roegneria kamoji* 1AS[11048].

T1AL.1AS-1E^{ts}#1S[11048] **v**: TA5660, KS14WRRC61[11048].
T1AL.1AS-1E^{ts}#1S[11048] **v**: TA5093[11048]. **ma**: Three CAPS and one KASPar SNP (*wg1S-snp1*) markers were developed[11048].
TW.1E^{ts}#1S[11048] **v**: TA5655[11048].

TA5660 is in Chinese Spring background; TA5093 is in Everest background.

FHB7

Fhb7[657, 11060, 11118] syn: FhbLoP[11118]

Derived from *Thinopyrum ponticum* [*FhbLoP*[11118]].

T7DS.7DL-7el$_2$L[11060] **v**: SDAU1881[11060].
T7DS.7DL-7el$_2$L[11060] **v**: SDAU1886[11060]. **ma**: Flanked by 7el$_2$ markers *Xcfa2240* and *XsdauK66* in a 1.7 cM interval[11060]. Located to a 245 kb region flanked by *Xsdau86* and *Xsdau88*[11483].
T7DS.7el$_2$[657] **v**: KS24-2[657].
c: Gene Tel7E01T1020600.1 encodes a glutathione S-transferase that detoxifies trichothecene toxin[11483]. Sequence data can be found at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA540081

FHB8

Fhb8[11676] locus: 7D[11676]

i: Wangshuibai/4*PH691 7D-NIL1[11676]; Wangshuibai/4*PH691 7D-NIL2[11676]. **v2**: Wangshuibai **Fhb1 Fhb2 Fhb4 Fhb5**[11676]. **ma**: *Xwgrb1500* (93.9 Mb, RefSeq 1.0) – *Fbhb8*/*Xwgrb1587* – *Xwgrb1559* (96.5 Mb)[11676].

FHB9

Fhb9[11727] locus: 2DL[11727] syn: QFhb-2DL[11719]

v: Shi4185/Shijiazhuang8 RIL92 (11727}; Ji5625/Wheaton NILs[11719]. **v2**: Shi4185 + additional QTL in chr. 4A, 3D and 5D[11727]; Ji5625[11719]. **ma**: Located in an 8.0 Mb (2.21 cM) region (KASP-525 – KAS-12056, 525.9 – 533.8, Mb, CS RefSeq 2.1)[11727]; 524.9 – 531.0 Mb[11719].

ungrouped

Qfhs.crc-2BL [10445]

tv: Strongfield[10445]. **ma**: Spanning 16 cM, this QTL peaking on *Xgwm55-2B* explained 23% of the phenotypic variation[10445].

Qfhs.crc-6BS [10445]

tv: *T. turgidum* var. *carthlicum* cv. Blackbird[10445]. **ma**: Spanning 23 cM and peaking on *Xwmc397* this QTL accounted for 23% of the phenotypic variation[10445].

Qfhs.fcu-7AL [10401]

sutv: LDN-DIC 7A[10401]. **tv**: *T. turgidum* var. *dicoccoides* PI 78742[10401]. **ma**: Located in an interval 39.6 cM thie QTL accounted for 19% of the phenotypic variation in a RIL population of Langdon/LDN-DIC 7A; nearest marker *Xbarc121-7AL* [10401].

Qfhs.ifa-5A [10076] locus: 5A[240, 10076]

Associated mainly with resistance to fungal penetration[10073].

v: Remus/CM-82036[10076]. **ma**: Associated with markers *Xgwm293-5A*, *Xgwm304-5A*, *Xgwm1057-5A*, *Xbarc117-5A*, *Xbarc186-5A*, *Xbarc100-5A* and *Xbarc40-5A* [10073]. Fine mapping divided this QTL into two components, *Qfhs.ifa-5Ac* located in the centromere region at 245.9 Mbp and a less effective *Qfhs.ifa*

5AS located at 290 Mbp. Both QTL were significantly associated with higher anther extrusion and plant height[11487].

QFhs.inra-2A[10069]

ma: Associated with *Xgwm382c-2A* (LOD=6.3, R^2=14.4%).

QFhs.inra-2B[10069]

ma: Associated with *Xgwm374-2B* (LOD=7.6, R^2=12%).

QFhs.inra-3A[10069]

ma: Associated with *Xbcd372-3A* (LOD=3.7, R^2=6.2%).

QFhs.inra-3B[10069]

ma: Associated with *Xgwm383b-3B* (LOD=5.4, R^2=10.5%).

QFhs.inra-5A.1[10069]

ma: Associated with *Xpsr170a-5A* (LOD=3.8, R^2=5%).

QFhs.inra-5A.2[10069]

ma: Associated with *Xgwm639b-5A* 8LOD=6.6, R^2=14%).

QFhs.inra-5A.3[10069]

ma: Associated with **B1** (LOD=6.3, R^2=8.5%).

QFhs.inra-5D[10069]

ma: Associated with *Xcfd29-5D* (LOD=4.4, R^2=7%).

QFhs.inra-6D[10069]

ma: Associated with *Xcfd42-6D* (LOD=2.7, R^2=6.6%).

QFhs.ndsu-2A[175, 9925, 0175] locus: 2AL[9925]

v: Sumai 3/Stoa RI mapping population; the QTL was contributed by Stoa[9925]. **ma**: Association with RFLP *XksuH16-2A* (LOD >3)[175, 9925].

QFhs.ndsu-3AS[10402, 10482] locus: 3AS[372]

sutv: LDN-DIC3A[10402]. **tv**: *T. turgidum* var. *dicoccoides*. Recombinant substitution lines LDN and LDN(Dic-3A). The resistant allele was contributed by *T. dicoccoides*[372]. **ma**: Associated with *Xgwm2-3A* (explained 37% of the phenotypic variation)[372]; located in a 29.3 cM interval with peak marker *Xgwm2-3A*[10402]; *QFhs.ndsu-3AS* was placed within a 11.5 cM region flanked by TRAP marker loci *Xfcp401-3A* and *Xfcp397.2-3A*[10482]; This gene was transferred to durum cultivars using the closely linked marker *Xgwm2-3A*[11367]. This gene is unlikely to be a homoeologue of Qfhs.ndsu-3BS = **Fhb1**[10482].

QFhs.ndsu-3B[9925, 0175] locus: 3BS[9925]

v: Sumai 3/Stoa RI mapping population; the QTL was contributed by Sumai 3[9925, 0175]. **ma**: Association with *Xbcd907-3B.2* (LOD >3)[9925] and microsatellite markers *Xgwm1533-3B* and *Xgwm493-3B*[0175]; *QFhs.ndsu-3B* from Sumai 3 was associated with microsatellite loci *Xgwm533-3B* and *Xgwm274-3B* in certain Sumai 3 derivatives[10062]. In Ning 894037 the QTL has the same location and similar SSR bands to Sumai 3[10085]. STS marker SRST.3B1 was mapped between *Xgwm533-3B* and *Xgwm389-3B* and associated with *QFhs.ndsu-3B*[10072]. *QFhs.ndsu.3B* was associated with markers *Xgwm533-3B*, *Xbard133-3B*, *Xbarc147-3B* and *Xgwm493-3B*[10073].

This QTL explained 42% of the variation in Sumai 3/Stoa[0175].

QFhs.pur-2D[10085]

v: Alondra[10085]. **ma**: Located on 2DS between SSR markers *Xgwm296-2D* and *Xgwm261-2D*[10085].

QFhs.pur-7El[10489] locus: 7DS.7DL-7el$_2$[10489]. 7el$_2$[10489]

su: K2630[10489]. **v**: K11695 = 7DS.7DL-7el$_2$[10489]; KS10-2 = 7el$_2$S.7el$_2$L-7DL[10489]; KS24-1 and KS24-2 = 7DS.7el$_2$[10489]. **ma**: *Qfhs.pur-7el$_2$* was flanked by *BE445653* and *Xcfa2270-7D*[10489]; These markers were also present in KS10-2[10489]. See FHB7.

QTLs for resistance to *Fusarium graminearum* detected in the cross Renan/Recital[10069]. All resistance alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percent of variation explained by the QT (R^2) are average of three years of field tests.

Two additional QTL for resistance to *Fusarium graminearum* were identified in the croSumai3/Stoa[0175]. The QTL on 4BS was associated with *Xwg909-4B* and the QTL on 6BS was associated with *Xbarc101-6B* and *Xbcd1383-6B*[0175]. The QTL associated with markers *Xgwm493-3B*/*Xgwm533-3B* (explaining 24.8 % of the variation), and *Xbarc101-6B*/*Xbcd1383-6B* were also identified in a RIL population from the cross ND2603/Butte 86[0175]. In addition, one QTL on chromosome 3AL associated with *Xbcd941-3A* and one on chromosome 6AS associated with *XksuH4-6A* were identified in RILs from the cross ND2603/Butte 86[0175].

Two major genes with additive effects were reported in crosses between Sumai 3 (resistant) and two susceptible cultivars[0174]. One of the genes was assigned to 5AL based on linkage to the dominant awn suppressor **B1** (RF 15.1-21.4%).

Dream*4/Lynx lines were developed by selection of QTL on chromosomes 6AL, 7BS and 2BL. Lines carrying *QFhs.lfl-6AL* and *QFhs.lfl-7BS* were more resistant than lines lacking them; the 2BL QTL effect was not verified[10470].

Wuhan-1 / Nyubai[10623]: Two QTLs were located on chromosomes 2DL and 3BS (distal)[10020]. A QTL for seedling resistance in the Wuhan/Nyubai population was associated with the *Qwmc75-5B* locus, R^2 = 0.138. The relationship of this resistance to crown rot resistance was unknown[10624] (see Reaction to *F. pseudograminearum*).

Of 54 lines with reported FHB resistance, 6, including CM-82036, Ning 7840 and Wuhan 3, had the same 5-marker haplotype as Sumai 3, and 4 lines possessed 4 of the markers. Twenty-nine lines, including Frontana, had no marker allele in common with Sumai 3, whereas 13 lines had 1 to 3 alleles in common with it[10113]. *Qfhs.ndsu-3B* and the 5 marker loci were placed in 3BS deletion bin 0.78-0.87[10144].

Haplotype diversity among a large number of FHB resistant and susceptible (mainly Canadian) germplasms indicated similarities in Asian, Brazilian and other materials[10173]. Brazilian cv. Maringa was more similar to Asian types than to other Brazilian lines[10173].

For review see [0283]. A review of 52 mapping studies is provided in {10593

Bobwhite plants transformed with AtNPR1, an *Arabidopsis thaliana* gene that regulates SAR activities, displayed a heritable type II response equal to that of Sumai 3[10237].

Associations between response to FHB caused by *F. culmorum* and the semi-dwarfing locus **Rht-D1** in crosses Apache/Biscay, Romanus/Pirat and History/Rubens (Biscay, Pirat and Rubens carry ***Rht-D1b***) were reported in [10574]. Genotypes with the semi-dwarf alleles tended to be more susceptible. }.

QTL

Remus / CM-82036 (a Sumai 3 derivative): DH population: Resistance QTL on chromosome 3BS associated with *Xgwm493-3B* and *Xgwm533-3B*[0240]. Additional QTL in this cross were detected on chromosome 5A, associated with *Xgwm293-5A* and *Xgwm304-5A*, and possibly on 1B, associated with **Glu-B1**[0240].

Alve (S) / Line 685 R: DH population: QTL on chromosomes 4D (**Rht-D1**), 3BS, 5A and 2BL[10972]. Two resistance QTL were needed to counteract the negative effect of the ***Rht-D1b*** semi-dwarfing allele[10972].

Arina (R) / Forno (S): Three QTLs, *QFhs.fal-6DL* (R^2=22%), *QFhs.fal-5BL.1* (in Forno, R^2=14%) and *QFhs.fal.4AL* (R^2=10%) and 5 minor QTLs in 2AL, 3AL, 3BL, 3DS and 5DL were detected[10172].

Arina / Riband DH lines: QTL affecting ADUPC were identified in 1BL(2), 2B, 4DS, 6BL and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of ***Rht-D1a*** rather than height *per se*[10464].

Baishanyuehuang (R) / Jagger (S): RIL population: Four genes/QTLs derived from the resistant parent included *Fhd1* (R^2=0.16), *Qfhb.hwwg-3BS c*(R^2=0.09), *Qfhb.hwwg-3A* (R^2=0.05-0.08) and *Qfhd.hwwg-5A* (R^2=0.05 in one trial)[10950].

Cansas (moderately resistant) / Ritmo (susceptible): Map based analysis across environments revealed seven QTL, *QFhs.whs-1BS* (1RS), *QFhs.whs-3B* (not **Fhb1**), *QFhs.whs-3DL*, *QFhs.whs-5BL* '(renamed *Qfhs.lfl-1BL* in [10768])', *QFhs.whs-7AL* and *QFhs.whs-7BL* (cumultatively, R^2 = 0.56). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread[10503]. There were significant correlations of FHB response with height and heading date[10503]. *Qfhs.lfl-1BL* was

verified in $F_{4:7}$ lines and detected in Biscay, History and Pirat[10768]. The renamed *Qfhs.lfl-1BL* reduced FHB severity by 42% relative to lines lacking it[10698]. This gene was also present in Biscay, History and Pirat[10698].

CS / CS(Sumai 3 7A): *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for Type II and 24% of phenotypic variance for Type III resistance[10798].

Chris / Frontana: In a reciprocal backcross analysis of Chris monosomics/Frontana, Frontana chromosomes 3A, 6A and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B and 7A increased the same traits[10398]. Further study of the 3A, 6A and 4D reciprocal substitution lines indicated that chromosome 3A of Frontana had the largest effect on incidence, severity, spread and kernel damage, 4D less so and 6A possibly not at all[10900].

DH181(R)(Sumai 3 / HY 386 Seln.): QTL identified in 2DS, 3AS, 3BS, 3B Cent. region, 4DL, 5AS, 6BS[10213].

Dream(R) / Lynx(S): RIL population: Following inoculation with *F. culmorum* 4 QTL for AUDPC were identified on chromosomes 6AL (R^2=19%), 1B (12%), 2BL (11%) and 7BS (21%). The resistance allele in 1B came from Lynx and was associated with T1BL.1RS[10260].

Chokwang (R) / Clark (S): *Qfhb.ksu-5DL.1* associated with *Xbarc239-5D* (R^2=0.24)[10276], *Qfhb.ksu-4BL.1* associated with *Xbarc1096-4B* (R^2=0.13)[10276], and *Qfhs.ksu-3BS.1* marginally associated with the region of **Fhb1** (R^2=0.1)[10276].Ernie (Res)/MO94-317 (Sus): 243 F8 RIL population. Four QTLs from Ernie detected as follows: *Qfhs.umc-2B*, linked to *Xgwm278-2BS*, R^2 = 0.04[10456]; *Qfhs.umc-3B*, linked to *Xgwm285-3BS*, R^2 = 0.13[10456]; *Qfhs.umc-4B*, linked to *Xgwm495-4BL*, R^2 = 0.09[10456]. *Qfhs.umc-5A*, linked to *Xgwm165-5A*, R^2 = 0.17[10456]. Evidence was provided to suggest the QTL acted additively[10456].

Frontana (R) / Remus (S): Major QTLs in chromosomes 3AL (*Xgwm270-3AL* – *Xdupw227-3A* region) and 5A (*Xgwm129-5A* – *Xbarc-5A* region) accounted for 16% and 9% of the phenotypic variation (mainly type 1 resistance) over 3 years[10174].

Frontana (MR) / Seri82 (S): F3 and F3:5 populations: QTLs were located in chromosomes 1BL (R^2=7.9%), flanked by AFLP markers, 3AL (R^2=7.7%), flanked by *Xgwm720-3A* and *Xgwm121-3A*, and 7AS (R^2=7.6%), flanked by anAFLP and *Xgwm233-7A* [10349].

G16-92 (R) / Hussar (S): Two QTL for resistance to *F. culmorum* were identified on chromosome 1A (resistance from Hussar) (R^2 = 0.01) and 2B (resistance from G16-92) (R^2 = 0.14)[10588].

Glenn (R) / MN00261-4 (S): RIL population: three of 15 QTL for FHB response and heading date were stable and explained >10% of the phenotypic variation; these were located on chromosome arms 5BL, 6BS (possibly **Fhb2**) and 7AS[11568].

Grandin (S) / PI 277012 (I): DH population: Two QTLs, *Qfhb.rwg-5A.1* on 5AS ($R^2$0.06-0.2) and *Qfhb.rwg-5A.2* on 5AL (R^2=0.12-0.2) conferred type I and II resistance and reduced DON content[0147]. The new QTL on 5AL was closely but not completely linked with gene **q** which is present in PI 277012[10860].

Hobbit Sib / *T. macha* **4A**: DH population: Type I resistance and DON accumulation:: Both traits were assigned to a small region distal to *Xgwm601-4A* and cosegregating with *Xgwm165-4A* [10254].

Huapei 57-2 / Patterson: Four QTL on chromosomes 3BS (associated with *Xbarc133-3B*), 3BL (*Xgwm247-3B*) and 3AS (*Xgwm5-3A*) from Huapei 57-2, and 5BL (*Xbarc59-5B*) from Patterson[10026]. Huapei 57-2, Ning 7840 and Sumai 3 carried common alleles in the *Xgwm533-3B*, *Xgwm493-3B*, *Xbarc147-3B* and *Xbarc133-3B* region[10026].

Luke (S) / AQ24788-83 (R): RIL population: *QFhb.cau-7DL* near marker *Xgwm428-7DL* was equally effective as **Fhb1**[11358].

Nanda2419 (S) / Wangshuibai (R): 8 QTLs were identified; those with large effects were associated with *Xgwm533-3B.3* – *Xgwm533-3B.1* (W), *Xwmc539-6B* (W) and *Xs1021m-2B* – *Xgwm47-2B* [10190].

Nanda 2419 / Wangshuibai: Backcross-derived NILs with *Qfh.nau-2B*, *Qfhs.nau-3B*, **Qfhi.nau-4B** (syn. **Fhb4**), and **Qfhi.nau-5A** were developed with Mianyang 99-323 as the recurrent parent[10884]. Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTLs, four from Wangshuibai. Those with the largest effects included *QFdk.nau-2B* (from Nanda 2419), *QFdk.nau-3B* and *QFdk.nau-4B* [10577] with each accounting for more than 20% of the phenotypic variation.

Ning 7840 / Clark: QTLs were located in chr. 3BS, 2BL and 2AS. The most effective QTL was probably in the interval flanked by deletions 3BS-3 and -8 and was close to *Xgwm533-3B* and *Xbarc147-3B* [0328]. RIL population: Three resistance gene analogue (RGA) sequences putatively assigned to chromosome 1AL

explained 3.37-12.73% of the phenotypic variation in FHB response among F7 and F10 populations[10364]. STS marker FHBSTS1A-160 was developed from one of the RGA.

Patterson (mod sus) / Fundulea 201R RILS: QTLs accounting for 19% and 13% of phenotypic variation were found on chromosomes 1BL (*Xbarc8-1BS – Xgwm131-1BL* region) and 3AS (*Xgwm674-3A*/*Xbarc67-3A* region)[10114]. Two weak QTLs were possibly associated with chromosomes 3D (Patterson allele) and 5AS[10114].

Patterson (open florets) / Goldfield (closed florets): RILs: narrow flower opening was correlated with FHB resistance. The major QTL effect associated with narrow flower opening and low FHB incidence occurred in map interval *Xbarc200 – Xgwm210* (29% of variation in FHB incidence); these genes were probably located in chromosome 2BS[10243].

Pelikan (S) / G93010 (= Bussard / Ning 8026) (R): *Qfhs.lfl-7BS*/*5BL* and *Qfhs.lfl-6BS* (probably **Fhb2**) from Ning 8026 reduced disease severity by 30% and 24%, respectively, and by 46% when combined[10594]. Other resistance genes were located on chromosomes 1AS (*Qfhs.lfl-1AS* from Pelikan), and 2AL and 7AL (from Ning 8026)[10594].

PI 672538 (R) / L661 (S): F_2:F_3 population. QTL identified in chromosomes 2B and 3B. The latter was considered different from **Fhb1**[11648].

Renan / Recital: Of the QTLs for resistance detected in the cross all alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percentages of variation explained by the QTL (R^2) were averages of three years of field tests[10069].

Spark (MR) / Rialto (S): DH population: Of nine QTLs identified across all environments, seven alleles for resistance came from Spark and two from Rialto. The largest effect on Type 1 resistance (*Xfhs.jic-4D.2*) was associated with the ***Rht-D1b*** allele in Rialto which made lines more susceptible. Other QTLs occurred on chromosomes 1B (1B.1R), 4D (*Qfhs.jic-4D.2*), 2A,3A (each, 2 QTLs), 5A and 7A. *Xfhs.jic-4D.2* had little effect on Type 2 resistance[10603].

Soissons (relative resistant) / Orvantis (susceptible): Increased susceptibility associated with the ***Rht-D1b*** allele was further confirmed in crosses of semi-dwarf cultivars Apache, History and Romanus[10793].

Sumai3 (R) / Y1193-6 (S): RIL population: Three resistance QTL on chromosomes 3BS, 6BL and 2DS with R^2 values of 0.26, 0.11 and 0.19, respectively; the last was derived from Y1193-6[11001].

SYN1 / Ocoroni DH population: three QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%)[11165].

Treho (S) / Heyne (MR): RIL population: Three QTLs from Heyne, viz *Qfhb.hwwg-3AS* (R^2, up to 0.18), *Qfhb.hwwg-4DL* (R^2=0.14-0.23) and *Qfhb.hwwg-4AL* (R^2, up to 0.18)[11005].

W14(R) / Pioneer 2684(S) population: QTL in 3BS and 5AS accounted for 33%, 35% and 31% of the phenotypic variation for disease spread, kernel infection and DON accumulation in greenhouse experiments, and 34% and 26% of variation for FHB incidence and severity in the field[10239]. Flanking markers were *Xbarc133-3B* & *Xgwm493-3B* and *Xbarc117-5A* & *Xbarc56-5A* [10239].

Wuhan-1 / Maringa: Field resistance: QTLs were located on chromosomes 2DS, 3BS (proximal) and 4B[10020]. Resistance to DON accumulation: QTLs were located on chromosomes 2DL and 5DS[10020].

VA00W-38 (mod. R) / Pioneer26R46 (S): RIL population: Consistent QTL from VA00W-38 detected on chromosomes 1BL, 2A, 2DL, 5B, 6A and 7A explained 6.5-21.3% of the phenotypic variation; one QTL from 24R46 was identified on chromosome 7A[11022]. Major QTL on 2DL, 6A and 5B decreased FHB index, Fusarium damaged kernels, and DON, respectively[11022]. Veery (S)/CJ9306 (R): Four QTLs, *XQFhs.ndsu-3BS* (*Xgwm533b – Xgwm493*), *QFhs.nau-2DL* (*Xgwm157 – Xwmc-041*), *QFhs.nau-1AS* (– *Xbarc148*) and *QFhs.nau-7BS* (*Xgwm400 – Xgwm573*) accounted for 31, 16, 10 and 7%, respectively, of the average phenotypic variation over three years[10490]

Wangshuibai / Alondra 'S': A stable QTL was associated with *Xgwm533-3B* in each of 3 years, QTLs in 5B (*Xgwm335-5B*), 2D and 7A were detected in 2 years[10268].

Wangshuibai / Annong 8455: RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosome 3B (R^2=0.17) and 2A (R^2=0.12) and for DON levels in 5A (R^2=0.13), 2A (R^2=0.85) and 3B (R^2=0.06)[10447]. The regions involved were *Xgwm533-3B – Xbarc133-3B*, *Xgwm425-2A*, and *Xgwm186-5A – Xgwm156-5A* [10447].

Wangshuibai / Seri 82: F3:F5 populations: QTL on chromosome 3BS (*Xgwm533-3B – Xs18/m12-3B*) and 2DL (*Xgwm539-2D – Xs15/m24-2D*) accounted for 17% and 11%, respectively, of the phenotypic variance[10264].

Wangshuibai (R) / Wheaton (S): QTLs located in chromosome 3BS (*Xbarc147-3B*, R^2=37% & *Xbarc344-3B*, R^2=7%), 7AL (*Xwms1083-7A*, R^2=10%) and 1BL (*Xwms759-1B*, R^2=12%)[10200].

Wheaton (I) / Haiyanzhong: RIL population: Four QTLs, *Qfhb.uhgl-7D* [syn. *Qhb.hyz-7D*], nearest marker *Xwmc121-7D*, R^2=0.16-0.2), *Qfhb.uhgl-6B.1* [*Qhb.hyz-6B.1*], R^2=0.4), *Qfhb.uhgl.6B.2* [*Qhb.hyz-6B.2*], R^2=0.07), *Qfhb.uhgl-5A* [*Qhb.hyz-5A*], R^2=0.04-0.07) were from Haiyanzhong, and *Qfhb.uhgl-1A* [*Qhb.hyz-1A*], R^2=0.05) was from Wheaton[10837].

Ben*2 / Tunisian 108: BIL population: nine QTL for FHB resistance of which new QTL *Qfhb.ndsu-2B* and *Qfhb.ndsu-3BL* and *Qfhb.ndsu-5A* and *Qfhb.ndsu-7BL* were the most important[11382].

Langdon / Langdon (DIC-2A): RICL population: Increased susceptibility of the *T. dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22 cM interval spanned by *Xgwm558-2A* and *Xgwm445-2A*[10613].

Strongfield / *T. carthlicum* **(Blackbird)**: Field resistance identified in chromosome 2BL (*Xgwm55-2B*), and 6BL (*Xwmc397-6B*) (coincident with **Fhb2**[10225].

T. dicoccum line Td161 crossed to three durum parents: small effect QTL were detected on chromosomes 3B, 4B, 6A, 6B and 7B; all except the 6A QTL were located at previously known positions[10993].

T. dicoccoides **Mt. Gerizim#36** / ***2** *T. durum* **Helidur**: F_6 lines: two QTL for type2 resistance located on chromosome 3A (*Xbarc45-3A – Xbarc67-3A* and 6B (*Xs13m22-2 – Xgwm626-6B*[11088].

3.11.2 Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species.

QTL

2-49 / W21MMT70: DH lines: Three QTLs fo seedling resistance, viz. *QCr.usq-1D.1*, and a weaker QTL on chromosome 7A from 2-49 and *QCr.usq-3B.1* (R^2=0.41) from W22MMT70[10883].

2-49 (partially resistant) / Janz (susceptible): DH population: Analysis of partial seedling resistance indicated major QTL in chromosomes 1D (R^2=0.21) and 1A (R^2=0.09) and minor QTL in 2A, 2B (from Janz), 4B and 7B[10132].

W21NMT70 / Mendos: DH population: three consistent QTLs for seedling resistance were identified with CIM; these were located in chromosome 5D and 2D (resistance alleles from W21NMT70) and 2B (resistance allele from Mendos)[10358].

Kukri (R) / Janz (S): DH population: Simple interval mapping in the region Pst1 ACG.Mse1 CAC – *Xgwm251-4B* accounted for 48% of the variation in crown rot response[10034].

Lang (S) / *T. spelta* **CSCR6 (R)**: RIL population: tested under controlled conditions with *F. pseudograminearum* and *F. graminearum*: *Qcrs.cpi-3BL* from CSCR6, R^2=0.49 and *Qcrs.cpi-4B* from Lang R^2=0.23[10703]. Six of 9 NIL pairs made by MAS for *Xgwm01081-3B* earlier located near the 3BL QTL[10703] in CSCR6 showed significant differences (P <0.01) in crown rot response[10891].*Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495*; R^2 up to 0.49, validated in other crosses[10723]. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23[10723]. Shishoumai (R)/Sanyuehuang (S): $F_{2:3}$ population. *Qfcr.sicau.1B-4* – 641.36 – 645.13 Mb – reduced the crown rot response by up to 39.7% of the phenotypic variation[11674].

Sunco / 2-49: DH population: Three QTLs for seedling resistance, viz. *QCr.usq-1D.1* and *QCr.usq-4B.1* (R^2=0.19) from 2-49 and *QCr.usq-2B.1* from Sunco[10883].

Sunco / Macon: RIL population: QTLs were located in chromosomes 2B, 3B, 4B and 4D. *Qcrs.wsu-3BL* from Macon and flanked by *Xgwm299-3B* was the most effective[10932].

Sunco / Otis: RIL population: QTLs were located in chromosomes 2B, 3B, 4B and 7A. *Qcrs.wsu-3BL* from Otis was the most effective[10932].

UC1110 / PI 610750: RIL population: Three QTL had an additive effect: *QFCR.heau-6A* (R^2 = 0.078 – 0.102) from UC1110; and *QFCR.heau-2A* (R^2 = 0.052 – 0.070) and *QFCR.heau-2D* (R^2 = 0.072 – 0.093) from PI 610750[11548].

Wuhan / Nyubai: A QTL for seedling resistance to *F. graminearum* was associated with the *Qwmc75-5B* locus, R^2 = 0.138. The relationship of this resistance to crown rot resistance is unknown[10624]Three crosses involving EGA Wylie: *Qcrs.cpi-5Ds* (R^2 = 0.31) and *Qcrs.cpi-2DL* (R^2 = 0.221). Two additional QTL on chromosome 4BS were associated with plant height[11243].Nine NIL sets derived from three crosses of Australian wheat cultivars and *T. spelta* CSCR6: *Qcrs.cpi* was flanked by *Xcfp1822-3B* and *Xgwm181-3B*[11244].

3.12 Reaction to *Heterodera avenae* Woll.., *H. filipjeva* (Madzhidov) Stelter

Cereal root eelworm; cereal cyst nematode.

CRE1

Cre1 locus: 2BL[1579, 1580]. 2B[1388] syn: Cre[1388]

i: AP = Prins*8/AUS10894[1579]. **v**: AUS 10894[1056]; Beulah[10013]; Chara[10163]; Goldmark[10013]; Goroke[10013]; Kellalac[10013]; Loros CI 3779[10013]; Mira[10163]; Mitre[10163]; Ouyen[10013]; RE8670[10013]; Silverstar[10013]; VI252[10013]; VI727[10013]. **ma**: *Xglk605-2B* – 7.3 cM – **Cre1** – 8.4 cM – *Xcdo588-2B*/*Xabc451-2B*[1579]; A PCR-based assay was developed from *Xglk605-2B*[1580]; Co-segregation with *Xcsl107-2B*. Four of 6 land varieties possessed *Xcsl107-2B*. A variant haplotype of *Xcsl107-2B* was present in AUS4930[10013]; *Xcdo36-2B* – 7.5 cM – *Xbcd1231-2B*/*XAtPPr5*/*Xcsl107-2B*/**Cre1**[10013].

CRE2

Cre2[238] locus: $6M^v$ [9991]

Derived from *Ae. ventricosa* 10[238, 9991].

v2: H-93-8 **Cre6**[238]. Although H-93-8 is a double M^v(5A), $7M^v$(7D) substitution line, **Cre2** was presumed to be located in a separate undetected translocated $6M^v$ segment[9991].

CRE3

Cre3 locus: 2DL[328] syn: CcnD1[329],Ccn-D1[328]

v: Synthetic hexaploids[329]. **dv**: *Ae. tauschii* accessions AUS 18912[328]; AUS 18913[328]; CPI 110809[329]; CPI 110810[328]. **ma**: Co-linearity with 2BL for *Xcdo-36-2D* and *XAtPPr5*/*Xbcd1231-2D*/*G4*/*G12*/**Cre3** (see **Cre1**)[10013].

CRE5

Cre5[0107] locus: 2AS[0107] syn: CreX[9, 0183], QCre-ma2A[11394]

Derived from *Ae. ventricosa*[0107, 0009]. = 2A-2N^v-6N^v.

v: VPM1[0107]; Many VPM1 derivatives[0107]. **v2**: Madsen **Cre9**[11102].

Notable exceptions of lines with **Lr37**, **Sr38** and **Yr17**, but lacking **Cre5** include Trident and Line L22[0107]; however a contribution of the **Cre5** region was detected in Trident/Molineux[10343]. su: Moisson 6N^v(6D)[0183]. dv: *Ae. ventricosa* 10[0183]. ma: Associated with the *Xgwm359-2A* (R^2=8%) – *Xwmc177-2A* (R^2=7%) region in Trident/Molineux[10343].

Two resistance gene analogues similar to the candidate gene **Cre3** were isolated from the *Ae. ventricosa* segment carrying **Cre5**.

Cre5 conferred resistance to *H. avenae* but not to *H. filipjevi*[11394].

CRE6

Cre6[0138] locus: 5N^v [0138]

Derived from *Ae. ventricosa*[0138].

ad: Moisson + 5N^v [0138]. **v**: H-93-35[0138]. **v2**: H-93-8 **Cre2**[0138].

CRE7

Cre7[104, 0104] syn: CreAet[0105]

Derived from *Ae. triuncialis*[0105].

v: TR353 derivatives[0105].

CRE8

Cre8[220, 0220] locus: 6BL[0220], on basis of linkage with *Xbcd1-6B* and *Xcdo347-6B* [220] syn: CreF[12, 138]

v: Barunga[220]; Festiguay[12, 220]; Frame[138, 220]; Molineaux[220]. **ma**: Linked to RFLP loci *Xbcd1-6B* and *Xcdo347-6B*. The 6B location of the *Xcdo347* probe used in this study was confirmed by nulli-tetrasomic analysis[220]; Associated with the *Xgwm147-6B* (R^2 = 24%) – *Xcdo247-6B* (R^2 = 12%) region in Trident/Molineux[10343]; The map in ▶[10343] was reversed: **Cre9** was located closer to the end of chromosome 6BL[11081]; Six markers that can be screened by KASP™ and *wri15* developed from a SNP were reported[11081].

CRE9

Cre9[11394] syn: QCre-ma7D[11394]

v: VPM-1/Moisson 951[11394]. v2 Madsen **Cre5**[11394]; VPM-1 **Cre5**[11394]. **ma**: Flanked by *Xics7D-27-7D* and *BS00129645*[11394]. KASP markers *BS00021745*, *BS00150072*, and *BS00154302* were developed[11394].

Cre9 conferred resistance to Chinese isolates of *H. filipjevi* but not to *H. avenae*.

CRE

Cre4 locus: 2D[328] syn: Ccn-D2[328],CcnD2[329]

dv: *Ae. tauschii* accessions AUS 18914[329]; CPI 110813[328].

Temporary designations

CreR[133, 318, 0133, 0318] locus: 6RL[133]

ad: Wheat + 6R[318]; Wheat + 6RL[318]; Various deletion stocks[318]. **su**: CS + 6R(6D)[133]. **al**: Rye accession T701-4-6[133]; Triticale T-701[318]. **ma**: Cent … *XksuF37* 3.7 cM – **CreR**[133]; Deletion mapping indicated **CreR** was located near **Got-R2**[318].

CreY[10486] locus: 3BL

Derived from *Ae. variabilis* 3BL[590].

v: Line X[10487]. **ma**: Co-segregation with RAPD $OpY16_{1065}$[0103] which was converted to SCAR16[10486].

May be the same gene as **Rkn-mn1** (see reaction to *Meloidogyne naasi*).

ungrouped

QCre.pau-1A[10749] locus: 1AS[10749]

dv: *T. monococcum* Tm 14087 *QCre.pau-2A*[10749]. **ma**: *QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. boeoticum* Tb 5088/Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890*[10749]; R^2=0.26[10749].

QCre.pau-1A was transferred to tetraploid and hexaploid lines[10749].

QCre.pau-2A[10749] locus: 2AS[10749]

dv: *T. monococcum* Tm 14087 *QCre.pau-1A*[10749]. **ma**: *QCre.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A*[10749]; R^2=0.13[10749].

Qcre.src-1B

was located to the *Xwmc719-1B* (R^2=12%) – *Xgwm140-1B* (R^2=12%) region in Trident/Molineux[10343].

For review[11309].

3.13 Reaction to *Magnaporthe* spp.

3.13.1 Reaction to *Magnaporthe grisea* (Herbert) Barr: Syn. *Pyricularia oryzae*

M. grisea is a pathogen of blast on many graminaceous species, the best known of which is rice. In Brazil a related form has become a pathogen of wheat. The wheat pathotype(s) (MoT) is different from those attacking other species such as rice, oat, millets and weeping lovegrass.

RMG1

TraesJAG1D03G00423690; *TraesCS1D02G058900*; this locus is also named PM24[11414, 11632]

Rmg1{10461; 10462},[0333] locus: 1D[10462] syn: Rwt4[0302]

s: CS (Cheyenne 1D)[10462]. v1: Cheyenne[10462]; Norin 26[10462]; Shin-chunaga[10462]. **v2**: Norin 4 **Rmg6**[11470, 0302]. c Candidate gene encodes a 916 amino acid protein with a wheat tandom kinase (WTK) domain[11632].

Rmg1 was present in 87% of surveyed genotypes[11470].

RMG2

Rmg2[10461] locus: 7A[10461]

i: CS (Thatcher 7A)[10461]. **v2**: Thatcher **Rmg3**[10461].

RMG3

Rmg3[10461] locus: 6B[10461]

i: CS (Thatcher 6B)[10461]. **v2**: Thatcher **Rmg2**[10461].

RMG4

Rmg4[10639] locus: 4A[10639]

v: Norin 4[10639]; Norin 26[10639]; Norin 29[10639]; P168[10639]; Shin-chunaga[10639]; *T. compactum* No. 24[10639]. Confers resistance to *Digitaria* isolate Dig41 at 26C[10639].

RMG6

Rmg6{10948 11504} locus: 1DS[10948]. v1: Chinese Spring[10948]; Shin-Chunaga[10948], Transfed[11470] syn: Rwt3[11470, 11504]

TraesCS1D02G029900.

v2: Chinese Spring **Rmg9**[11504], Norin 4 **Rmg1**[10948, 11470]. **ma**: *Xwmc432-1D* – 9.6 cM – RMG6 – 6.6 cM – *Xwmc222-1D*[10948]; 11.60 – 11.80 Mb[11632]. **c**: Candidate gene encodes an NRL with 1,069 amino acids (11632}. **Rmg6** was present in 77% of surveyed genotypes 11470}. *Xwmc432-1D* – RMG9 – 5.0 cM – RMG6 – *Xwmc222-1D*[11504].

A second gene in chromosome 1D designated **Rwt4**[0302] (*TraesCS1D02G058900*[11632]) (was present in CS and Norin 4. c: **Rwt4** was identified as wheat tandom kinase[11632].

Genes **Rwt3** and **Rwt4** were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

Rmg6 and a second gene with a weaker effect conferred resistance to a selected *Triticum x Lolium* isolate[10948].

RMG5

Rmg5[10639] locus: 6D[10639]

s: CS (Red Egyptian 6D)[10639]. **v**: Red Egyptian[10639]. Confers resistance to *Digitaria* isolate Dig41 at 26C[10639].

RMG7

Rmg7[11046, 11083] locus: 2AL[11083]

tv: *T. dicoccum* KU112[11046]; KU120[11046]; KU1222[11046]. **ma**: *Xcfd50-2A* – 5.6 cM – **Rmg7** – 15.1 cM – *Xhbg327-2A*[11083]. **c**: The sequence of **Rmg7** was identical to ***Pm4a***[11735]. **Rmg7** has the same specificity as **Rmg8**[11735].

Rmg7 and **Rmg8** recognise the same *Avr-Rmg8* effector[11775].

RMG8

Rmg8[11083] locus: 2BL[11083]

bin: 2BL6-0.89-1.00. **v**: S615[11083]. **ma**: *Xwmc317-2B* – 12.1 cM – **Rmg8** – 22.4 cM – *Xbarc159-2B*[11083]. **c**: The nucleotide sequence of **Rmg8** was identical to ***Pm4f***[11735]. **Rmg8** has the same specificity as **Rmg7**[11735].

According to [11083] markers linked to *RMG8* were independent of those linked to RMG7. The ***Pm4a*** allele in some accessions is located in chromosome 2B[11735].

Among PM4 alleles ***Pm4a***, ***Pm4b*** and ***Pm4d*** conferred resistance to both MoT and *Bgt*; *Pm5f* conferred resistance to MoT but not *Bgt*, and ***Pm4f*** was ineffective against both pathogens[11735].

RMG9

Rmg9[11504] locus: 1D[11504]. v2 Chinese Spring *Rmg6* [11504] syn: Rwt6[11504]

ma: *Xwmc432-1D* – RMG9 – 5.0 cM – RMG6 – *Xwmc222-1D*[11504].

RMG10

Rmg10[11736] locus: 2DS[11736]

v: Line 6051 (amphiploid Langdon/KU-2097) Permanent genbank accession number needed[11736]. **dv**: *Ae. tauschii* KU-2097[11736]. **ma**: *Xbarc-2D* – 7.8 cM – *Ms-4* – 7.8 cM – RMG10 – 8.3 cM – *MS12* – 4.7 cM – *Xwmc503-2D*[11736].

RMG11

Rmg11[11755] locus: 7AS[11755]

tv: *T. dicoccum* St19, KU-114[11755]. ma *IMT_5* – 1.0 cM – RMG11 – *IMT_6/IMT_7* – 1.1 cM – *Xgwm635-7A*[11755].

The **Rmg11** resistance remained effective at 30ºC[11755].

Temporary designations

RmgGR119[11652]

v: GR119 **Rmg8**[11652].

RmgTd(t)[10949] locus: 7BL[10949]

tv: *T. dicoccoides* KU109[10949]. **ma**: *Xhbg338-7B* – 10.5 cM – **Rmg7**[10949].

RmgTd(t) was detected with a white culture of an *Avena* pathogen isolate backcrossed to a wheat isolate. A virulence to **RmgTd(t)** was completely associated with white color of the pathgen isolate[10949]. The white color appeared as a mutant variant during backcrossing.

The wheat blast pathogen became established on wheat cultivar Anahuac (*rmg1 rmg6*) in Brazil in the mid-1980s. It was initially avirulent on cultivars such as IAC-5 with **Rmg6** but later acquired virulence allowing it to attack most wheat genotypes[11470].

3.13.2 Reaction to *Magnaporthe oryzae*

RMG8

Rmg8

Rmg8 also confers resistance to the wheat form of the pathogen. Its response is not sufficiently effective when present alone, but is enhanced in the presence of **RmgGR119**[11263].

AVR-Rmg8 was isolated and shown to be a small protein with a putative signal peptide. This protein was recognized by both **Rmg8** and **Rmg7**[11272].

RmgGR119[11263]

v: GR119[11263].

RmgGR119 confers resistance to the wheat form of the pathogen and its response is enhanced in combination with **Rmg8**[11263].

Near-isogenic lines with the T2A-2NS translocation from *Ae. ventricosa* displayed reduced levels of spike blast, but there was little effect on seedling leaf blast response[11265]: v: Milan; VPM1.

Wheat cultivars carrying the 2NS translocation from *Aegilops ventricosa* had 50.4 to 72.3% less head blast than those without 2NS when inoculated with an older isolate (MoT) of *Magnaporthe oryzae* (*Triticum* pathotype) under growth chamber conditions. When inoculated with recently collected isolates from wheat, cultivars with 2NS had 64.0 to 80.5% less head blast[11127].

A review of wheat blast[11776].

3.14 Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

Insect pest: Hessian fly.

H1

H1[1087]

i: Dawson/3*Poso, 6179[1087]. v2: Big Club 43 **H2**[1441]; Dawson **H2**[166, 1087]; Poso 42 **H2**[1441].

H2

H2[1087]

i: Dawson/3*Poso, 6232[1087]. v2: Big Club 43 **H1**[1441]; Dawson **H1**[166, 1087]; Poso 42 **H1**[1441].

H3

H3[156] locus: 5A[425, 1105]

Recessive. Based on the location of **H9** on chromosome 1AS, **H3** may also be located on chromosome 1AS[10231, 10252].

i: Carol = Newton-207*5/Larned[1107]. v: Ace[426]; Arthur[426]; Becker[749]; Cardinal[750]; Dual[1273]; Frankenmuth[341]; Georgia 1123[426]; GR855[751]; GR876[753]; Ike[10252]; Ionia[426]; Larned[824]; Logan[426]; Monon[157]; Norkan[904]; Ottawa[547]; Purdue B 36162 A13-12[156]; PI 468960[1439]; Redcoat[1273]; Reed[1273]; Riley[1273]; Roland[148]; Russell[426]; Shawnee[547]; Titan[747]; Todd[426]; W38[156]. v2: Clara Fay **H6**[375]. ma: Cosegregation of **H3** and a RAPD[296].

Allan et al.[19] considered that **H3** and **H4** might be allelic. Also suggested by Shands and Cartwright[1317]. Linkage of 10.5 +/- 2% involving **H3** and ***Pm3a*** in PI 468960 was attributed to a chromosome 1A/5A translocation[1437].

H4

H4 locus: 1AS[11634] syn: h4[1441]

Recessive. **H4** confered resistance to race A, but not to race B.

v: Dixon[1441]; Java[1441]. ma: Mapped to interval 6.64 – 728 Mb[11634]. KASP markers developed[11634].

H5

H5[1317] locus: 1AS[1222]

Temperature sensitive[1413].

v: Abe[162]; Arthur 71[162]; Beau[875]; Downy[1223]; Magnum[10252]; Oasis[1109]; Ribeiro[1317]; Sullivan[1110]. tv: Giorgio 331-4[1090]; PI 94567-6[1317]; PI 94571-14[1317]. ma: Cosegregation of **H5** and two RAPDs[296].

H6

H6[19] locus: 5A[425]

Based on the location of **H9** on chromosome 1AS, **H6** may also be located on chromosome 1AS[10231, 10252].

i: Erin = Newton-207*7/Arthur 71[1107]; Flynn = Newton-207*7/Knox 62[1107]. v: Adder[1319]; Benhur[426]; Caldwell[1421]; Compton[1318]; CI 12855[19]; Excel[752]; Fillmore[1106]; Knox 62[426]; Lathrop[426]. v2: Clara Fay **H3**[375]. tv: Purdue 4835 A4-6[1105]. tv2: PI 94587 **H11** **H16**[19]. ma: Cosegregation with three RAPDs[296].

H7 and H8

H7 locus: 6AS[11511]; 5D[26]

ma: Mapped as a major QTL (PVE 0.61 – 0.78) in a 6 Mb interval flanked by GBS6A205 and GBS6A215[11511].

With relocation of **H7** to chromosome arm 6AS there are issues of overlap with **H31**.

H7 & H8[425]

Duplicate factors. **H7** is located in chromosome 5D[26].

v: Adena[748]; Seneca[26, 425].

H8 locus: 2B[11511]

ma: Mapped as a minor QTL (PVE, 0.03 – 0.05)[11511].

The **H7** and **H8** genes were variously described as duplicate[26], complementary and additive[11511].

H9

H9[1420] locus: 1AS[10231, 10252]. 5A[162]

i: Iris = Newton-207*7/Ella[1107]. **v**: Ella[875]; Line 822-34[162]. **v2**: Elva CI 17714 **H10**[162]; Line 812-24 **H10**[1421]; Line 817-2 **H10**[1421]; Stella **H10**[875]. **ma**: Cosegregation with two RAPDs[296]; *STS-Pm* – 1.7 cM – *SOP005*$_{909}$ – 0.6 cM – *Xksu11*/*Xcnl76*/*Xgdm3* – 0.5 cM – *Xgwm176*/*Xpsp2999*/*Xcfa2153-1A* – 0.5 cM – *Xbarc263-1A* – 1.2 cM – **H9** – *Xwmc24-1A*[10231]; *Xcfa2153-1A* – 0.5 cM – **H9** – 0.3 cM – *Xbarc263-1A*[10252].

H10

H10[1104] locus: 1AS[10252]. 5A[162]

May be identical to H9[10252].

i: Joy = Newton-207*3/IN76529A5-3-3[1107]. **v**: IN76529[875]. **v2**: Elva CI 17714 **H9**[162]; Line 817-2**H9**[162]; Stella **H9**[875]. **ma**: Cosegregation with one RAPD and close linkage to another RAPD[296]; *Xcfa2153-1A* – 0.5 cM – **H10** – 1.3 cM – *Xbarc263-1A*[10252]; *Xrapd9-2-1000*/*Xpsp2999-1A*/*Xgps7072-1A* – 2.2 cM – **H10**[10252].

H11

H11[1422] locus: 1A[1222]. 1AS[10252]

i: Karen = Newton-207*4/IN916-1-3-1-47-1[1107]. **v**: Kay[375, 875]; Line 916[1422]; Line 920[1422]; Line 941[1422]. **tv2**: *T. turgidum* PI 94587 **H6 H16**[1422]. **ma**: Close linkage with two RAPDs[296]; *Xcfa2153-1A* – 0.3 cM – **H11** 1.7 cM – *Xbarc363-1A*[10252].

H12

H12[1092] locus: 5A[1098]

i: Lola = Newton-207*4/Luso[1107]. **v**: Luso[1092]. **ma**: Cosegregation with one RAPD and close linkage of **H12** to another RAPD[296].

H13

H13[1104] locus: 6DS[10251, 10388]. 6DL[441]

i: Molly = Newton-207*7/3/KU221-19/Eagle/KS806[1107]. **v**: AGS 2010[11008]; AGS 2026 PI 658065[11008]; KS81H1640HF[441]; Oglethrope PI 657986[11008]; PI 562619[10388]; SW34=Langdon/*Ae. tauschii* RL 5544[10388]; *T. turgidum* var. *durum* cv. Gulab KU 134/*Ae. tauschii* KU 2076, KU 221-14[525]; *T. turgidum* var. *persicum straminium* KU 138/*Ae. tauschii* KU 2076, KU221-19[525]. **dv**: *Ae. tauschii* KU 2076[525]. **ma**: Cosegregation with a RAPD[296]; *Xgdm36-6D* – 2.7 cM – **H13**/*Xcfd132-6D* – 1.1 cM – *Xcfd213-6D*[10251]; *Xcfd132-6D* – 3.7 cM – **H13**[10388].

H14

H14[875] locus: 5A[875]

tv: IN 81601A2-3-3[875]. **tv2**: ELS 6404-160 **H15**[875]. **ma**: Cosegregation with a RAPD[296].

H15

H15[875] locus: 5A[875].Based on the location of *H9* on chromosome 1AS, *H15* may also be located on chromosome 1AS[10231]

tv: IN81602C5-3-3[875]. **tv2**: ELS 6404-160 **H14**[875].

H16

H16[1106] locus: 5A[1098]. 1AS[11058]

bin: 1AS-3-0.86-1.00. **v**: P921682[11058]. **tv**: IN 80164H5-2-9[1106]; N80164[1097]. **tv2**: PI 94587 **H6 H11**[1106]. **ma**: Cosegregation of **H16** and a RAPD[296]; *Xpsp2999-1A* – 3.7 cM – **H16** – 5.5 cM – *Xbarc263*/*Xwem6B-1A*[11058].

H17

H17[1090] locus: 5A[1090]. 1AS[11058]

bin: 1AS-3-0.86-1.00. **v**: P921680[11058]. **tv**: PI 428435[1090]. **ma**: Cosegregation of **H17** and a RAPD[296]; *Xpsp2999-1A* – 6.27 cM – **H17** – 5.1 cM – *Xbard263*/*Xwem6B-1A*[11058].

H18

H18[1090]

v: Marquillo[426, 874]; Redlant[10715]; Shield[198].

H19

H19[1089]

tv: PI 422297[1089]; This germplasm possesses a second gene which is allelic or closely linked with **H16**[1089]; IN84702[1097]. **tv2**: PI 422297 **H29**[1097].

H20

H20[25] locus: 2B[25]

tv: Jori[25].

H21

H21 locus: 2B[383]. = 2BS.2R#2L[389]

v: Hamlet = KS89WGRC8[1312]; KSWR 69-2-4-3[383]; KS85HF 011-5[383]. **ad**: KSWR 297h-1-1-9[383]. **al**: Chaupon rye[383]. **ma**: A RAPD amplified by primer OPE-13 was shown to co-segregate with **H21**[9938]; STS primer set SJ07 was developed to identify 2RL, and hence **H21**[233].

H22

H22[1199] locus: 1D[1199]. 1DS[10381]

v: KS86WGRC1[1199]; KS85WGRC01=*Ae. tauschii* TA1644/Newton//Wichita[1199]; PI 572542[10388]. **ma**: *Xgdm33-1D* – 1.0 cM – **H22** – 0.3 cM – *Xhor2KV-1D* – 0.5 cM – *Xgpw7082-1D*[10381].

H23

H23[1199] locus: 6DS[10251]. 6DL[1199]. 6D[442]

v: KS89WGRC03 = TA1642/2*Wichita[442, 10251]; PI 535766[10388]. **al**: *Ae. tauschii* TA1642[10251]. **ma**: **H23** – 6.9 cM – *XksuH4-6D*[861]; Maps to same region as **H13**[10262].

H24

H24[1199] locus: 6DL[861]. 3D[442, 1199]

v: KS89WGRC6[442]; PI 535769[10388]. **ma**: **H24** – 5.9 cM – *Xbcd451-6D*/*Xcdo482-6D*[861].

H25

H25 locus: 6B[384]

= T6BS.6BL-6R#1L[389]

v: 88HF16 = WGRC17[384]. 4B[384] = T4BS.4BL-6R#1L[389] 88HF79, 88HF80 = WGRC18, 88HF81, 88HF117 = WGRC19[384]. 4A[384] = Ti4AS.4AL-6R#1L-4AL[389] 89HF17, 89HF18, 89HF25, 88HF32, 88HF51, 88HF89 = WGRC20[384]. 6R. **al**: Balbo rye[384].

H26

H26 locus: 4D[217]. 3DL[10388]

bin: 3DL3-0.81-1.00. **v**: KS92WGRC26[217]; SW8 = Langdon/*Ae. tauschii* Clae 25[10388]. **dv**: *Ae. tauschii* TA2473[217]. **ma**: *Xcfd211-3D* – 7.5 cM – **H26** – 2.9 cM – *Xwgc7330-3D* – 4.0 cM – *Xgwm3-3D*[10388]. *Xrwgs-3D* – 3.2 cM – **H26**/*Xrwgs11-3D* – 1.0 cM – *Xrwgs12-3D*[10846].

H26 is very close to **H32**[10846].

H27

H27[235] locus: $4M^{v}$[235]

su: H-93-33[235]. **al**: *Ae. ventricosa* No. 10[235]; *Ae. ventricosa* No. 11[235].

H28

H28[171] locus: 5^{A}[171]

tv: PI 59190[171].

H29

H29[1095] locus: 5A[1097] syn: H27[171]

tv: PI 422297 **H19**[1097].

H30

H30[256, 0256]

Derived from *Ae. triuncialis*[0256].

v: TR-3531[256]. **al**: *Ae. Triuncialis*[256].

H31

H31[332, 0332] locus: 5BS[332]

v: P961696[332]. **tv**: CI 3984[332]. **ma**: STS marker *Xupw4148-5B* – 3 cM – **H31**[332].

H32

H32[10137] locus: 3DL[10137]

bin: 3DL3-0.81-1.00. **v**: Synthetic W7984[10137]. **ma**: *Xgwm3-3D* – 1.7 cM – **H32** – 1.7 cM – *Xcfd-3D*[10137]; *Xrwgs10-3D* – 0.5 cM – **H32**/*Xrwgs11-3D* – 0.5 cM – *Xrwgs12-3D*[10846]. KASP markers developed[11633]. H32 is very close to **H26**[10846].

H33

H33[10954] locus: 3AS[10954]

v: Line 97211[10954]. **tv**: PI 134942[10954]. **ma**: *Xgwm218-3A* – 10 & 7 cM – **H33** – 28 & 25 cM – *Xhbg-3A*[10954].

H34

H34[11018] locus: 6BS[11018] syn: *Qhf.hwwg-6B*[11018]

v: Clark[11018]. **ma**: Flanked by *Xsnp921-6B* and *Xsnp2745-6B* within a 4.5 cM region, R^2 = 0.38-0.42[11018].

Halotype analysis was used to postulate *Ae. tauschii*-derived genes **H13**, **H22**, **H23**, **H26** and **H32** in a set of synthetic wheat lines[10983].

H35

H35

in chromosome arm 3BS and ***H36*** in chromosome arm 7AS were named for one major and one minor QTL in common wheat line SD06165[11512].

Temporary designations

Hdic[10262] locus: 1AS[10262]

v: KS99WGRC42[10262]. tv *T. dicoccum* PI 94641[10262]. **ma**: *Xcfa2153-1A* – 1.4 cM – **Hdic** – 0.6 cM – *Xgwm33-1A*[10262].

HNC09MDD14 locus: 6DS[10843] syn: Hf-NC09MDD14[10844]

v: NC09MDD14 PI 656395[10843]. **dv**: *Ae. tauschii* TA2492 and/or TA2377[10843]. **ma**: *Xgdm36-6D* – 1.5 cM – **HNC09MDD14**/*Xcfd123-6D*[10843]; *HNC09MDD12* could be allelic to, but is different from, **H13**[10843].

HR61[11008] locus: 6AL[11008]

bin: 6AL8-0.90-1.00[11008]. **v**: 26R61 PI 612153[11008]. **ma**: Mapped as a QTL (R^2=0.63) flanked by *Xgwm427-6A* and *wPt-731936*[11008].

H_{WGRC4}[10251] locus: 6DS[10251]

v: KS89WGRC04 = TA 1695/3*Wichita[10251]. **ma**: Allelic with **H13**[10251].

A recombination value of 12.0% between leaf-rust reaction (possibly **Lr10**) and Hessian-fly reaction in Selection 5240 was reported[18].

ungrouped

Mds-1A[11327] locus:[11327]. 3AS[11327] syn: Mds-1

v: No allelic variation demonstrated. **c**: EST CD453475, GenBank JN162442; **Mds-1A** encodes a 151 amino-acid protein with 96% identity with HSP16.9[11327]. Homoeologues are present in chromosomes 3B and 3D. Silencing of **Mds-1** expression caused immunity in otherwise FHB-susceptible genotypes[11327].

QH.icd-2A[11510] locus: 2AL

Putatively derived from *T. dicoccum*[11510].

ma: Linked with *Ax-94980581*[11510].

QH.icd-5B[11510] locus: 5BS

tv: DWHF01[11510].

Possible overlap with **H31**[11510].

Qhara.icd-6B[11510] locus: 6BS

tv: *T. timopheevii* subsp. *ameniacum* derivatives: DWHF02[11510]; Chaoui[11510]; Icamoram7d {11510; Marouane[11510]; Nassira[11510]. **ma**: Linked with *Ax-95181449*[11510].

Qhf.hwwg-1A[11018] locus: 1AS[11018]

v: Clark **H34**[11018]. **ma**: Closely linked to *Xwgm33-1A*[11018]; Located within a 6 cM region flanked by *Xwgm33-1A* and *Xsnp5150-6B*, R^2=0.1[11018].

QHf.hwwg-6BS[11635] locus: 6BS[11635]

v: Chokwang[11635]. **ma**: Located to interval 6BS 6.029 – 10.779 Mb (CS RefSeq v2.0)[11635]. KASP markers developed[11635].

QHft.nc-7D

in chromosome arm 7DS conferring tolerance to Hessian fly in line LA03136E71 is reported in [11513].

QTL

Duster (R) / Billings: DH population: *QHf.osu.1A.2* (Syn. *QHf.osu-1A^d*), R^2 = 0.88, delimited to a 2.7 cM region flanked by *GBS07851* and *GBS10205*[11324]. This was a distinct locus 11.2 cM proximal to *QHf.osu.1A*.

Jagger (S) / 2174 9 (R): RIL population: *QHf.osu-1A* (Syn. *Qhf.osu*[74] (R^2 = 0.70) and *QHf.osu-2A* (R^2 = 0.18)[11325]. The QTL in chromosome 1A appeared to be co-linear with several previously named *H* genes in tetraploid wheat; the gene in 2A was in repulsion with the 2N segment present in Jagger[11325].

3.15 Reaction to *Meloidogyne* spp.

Root rot nematode, root knot eelworm

RKN1

Rkn1[632] locus: 6D[10799] syn: Rkn[632]

dv: *Ae. tauschii* G3489. **v**: Prosquare, a synthetic hexaploid of Produra/*Ae. tauschii* G3489[632].

RKN2

Rkn2[1621] locus: 3B[590] syn: Rkn-mn1[1621]

Derived from *Ae. peregriina (variabilis)* [1621].

v: X8 = CS/*Ae. peregrina* No. 1//Rescler/3/Lutin[1620]; X35[1620, 1621]. **ma**: Co-segregation with RAPD *OpY16*$_{1065}$ and close linkage with several markers including **Est-B5**[103]; converted to SCAR Y16[10486]; May be the same as **CreY** (see reaction to *Heterodera avenae*) on chromosome 3S^{V} from *Ae. variabilis* translocated to 3BL[10800].

RKN3

Rkn3[10801, 11264] locus: 2NS translocation into 2AS

Derived from *Ae. ventricosa* 2NS translocation into 2AS[10801].

v: VPM1, Lassik (PI 653535)[10801]. **ma**: Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation[10801].

3.16 Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*

Disease: Septoria tritici blotch

STB1

Stb1 locus: 5BL[10123] syn: Slb1[1586]

bin: FL 5BL-11 – 5BL-14[10123]. **v**: Bulgaria 88[1586]; Oasis[1586]; P881072-75-1[10123]; SO852[10123]; Sullivan[1586]. **ma**: Close linkage with 2 RAPD markers at >0.68 and 1.4 cM in P881072-75-1[10123]; Cent *barc74-5B* – 2.8 cM – **Stb1**[10123].

STB2

Stb2 locus: 1BS[10976]. 3BS[10105] syn: Slb2[1586]

v: Nova Prata[1586]; Veranopolis[1586]. **ma**: *Xgwm389-3B*/*Xgwm533-3B* – 1.0 cM – **Stb2** – 3.7 cM – *Xgwm493-3B*[10105]; **Stb2** is neither on 3BS nor linked with *Xgwm389-3B*[10976]; *Xwmc406-1B* – 6.0 cM – **Stb2** – 5.0 cM – *Xbarc008-1B*[10976].

STB3

Stb3 locus: 7AS[10556, 11191]. 6D,[10105] (according to ▶[10556] this location is not correct syn: Slb3[1586]

v: Israel 493[1586]. **ma**: *Xcfa2028-7A* – 12.4 cM – **Stb3**/*Xwmc83-7A* – 2.1 cM – *Xbarc222-7A*[11191].

STB4

Stb4[1410] locus: 7DS[10140]. 7D[326]

v: Cleo[1410]; Gene[10010]; Tadinia[1410, 10140]; Tadorna[1410]. **ma**: *XAGG/CAT10* – 4.0 cM – **Stb4** – 0.7 cM – *Xgwm111-7D* – 1.4 cM – *XATCG/CAAA5* Cent[10140]; **Stb4** – 0.7 cM – *Xgwm111-7D*[10140].

Stb4 segregated independently of **Stb1** but its relationship with **Stb2** and **Stb3** is unknown. Genetic analysis of Tadinia indicated single gene segregation (assumed to be **Stb4**) with a Californian culture but a different single gene segregated with South American isolates[10140].

STB5

Stb5[0186] locus: 7DS[0186]

Identified using *M. graminicola* IPO94269[0186]. Derived from *Ae. tauschii* accession 37-1[0186].

v: Baldus[11446]; Bezostaya[0187]; Chaucer[11446]; Hereward[0187]; Israel 493[11446]; Longbow[11446]; Olaf[11446]; Sears' Synthetic[0186]; Senat[11446]; Shafir[0]; Veranopolis[11446]; Vivant[0187]. **su**: CS*8/(Syn7D)[0186]. **dv**: *Ae. tauschii* 37-1[0186]. **ma**: ***Rc3*** – 6.6 cM – **Stb5** – 7.2 cM – *Xgwm44-7D* – Centromere[186]; **Stb6** – 2 cM – *Xgwm369-3A*[0187].

STB6

Stb6[0187] locus: 3AS[0187] syn: TaWAKL4[11434]

Confers resistance to *M. graminicola* isolate IPO323 but not to isolate IPO94269[0187].

v: Amigo[10448]; Arina[10448]; Amada[10448]; Atlas 66[10448]; Ble Seigle[10448]; Bon Fermier[10448]; Cadenza[11434]; Chinese Spring[10448]; Bezostaya 1[10495]; Flame[187, 11434]; Gene[10448]; Heines Kolben[10448]; Hereward[10448]; Poros[10448]; Senat[10448]; Shafir[10448]; Tadinia[10448]. **v2**: Bulgaria 88 **Stb1**[10448]; Israel 493 **Stb3**[10448]; Kavkaz-K4500 **Stb7 Stb10 Stb12**[10011]; TE9111 **Stb7 Stb11**[10012]; Veranopolis **Stb2**[10448]. tv **Stb6** is common in *T. dicoccum*[11434]. **ma**: A resistance gene from Senat located at or near the **Stb6** locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS[10067]; *Xgwm369-3A* – 4.3 cM – **Stb6** – 3.8 cM – *Xgwm132-3A*[11434]. **c**: Encodes a wall-associated receptor kinase (WAK)-like protein[11434].

STB7

Stb7[0311] locus: 4AL[0311]

v: ST6 = Estanzuela Federal. **v2**: Kavkaz-K4500 **Stb6 Stb10 Stb12**[10011]; TE9111 **Stb6 Stb11**[10012]. **ma**: *Xwmc219-4A* – 0.8 cM – *Xwmc-4A* – 0.3 cM – **Stb7**[0311]; **Stb7** was closer to *Xwmc313-4A* than to *Xwmc219-4A*[10011].

STB8

Stb8[0326] locus: 7BL[0326]

v: Synthetic hexaploid W7984 (parent of ITMI population)[0326]. **ma**: *Xgwm146-7B* – 3.5 cM – **Stb8** – 5.3 cM – *Xgwm577-7B*[0326].

STB9

Stb9[10027] locus: 2BL

Culture IPO89011 2BL[10027].

v: Courtot[10027]; Tonic[10027]. **ma**: *Xfbb226-2B* – 3 cM – **Stb9** – 9 cM – *XksuF1b-2B*[10027].

STB10

Stb10[10011] locus: 1D[10011]

Confers resistance to cultures IPO94269 and ISR8036, but not to IPO87019[10011].

v2: Gene **Stb5**[11446]; Frontana **Stb5**[11446]; Kavkaz-K4500 L.6.A.4 **Stb6 Stb7 Stb12** = JIC.W9995[10011]; Mentana **Stb5**[11446]. **ma**: Associated with *Xgwm848-1D*[10011].

STB11

Stb11[10012] locus: 1BS[10012]

Confers resistance to isolate IPO90012[10012].

v: JIC W 9996; TE9111. **v2**: TE9111 **Stb6 Stb7**[10012]. **ma**: Distal to *Xbarc008-1B*[10012].

STB12

Stb12[10011] locus: 4AL[10011]

Confers resistance to cultures ISR398, ISR8036 and IPO87019[10011].

v2: Kavkaz-K4500 **Stb6 Stb7 Stb10**[10011]. **ma**: **Stb12** was closer to *Xwmc219-4A* than to *Xwmc313-4A*[10011].

STB13

Stb13[10347] locus: 7BL[10347]

Confers resistance to Canadian cultures MG96-13 and MG2[10347]

v: DH line 90S05B*01[10347]; DH line 98S08C*03[10347]. **v2**: Salamouni **Stb14**[10347]. **ma**: *Xwmc396-7B* – 9 cM – **Stb13**[10347]; *Xwmc396-7B* – 7 cM – **Stb13**[10347].

STB14

Stb14[10348] locus: 3BS[10348]

Confers resistance to Canadian isolate MG2 but not to MG96-13[10347]

v: DH line 98S08A*09[10348]. **v2**: Salamouni **Stb13**[10347]. **ma**: *Xwmc500-3B* – 2 cM – **Stb14** – 5 cM – *Xwmc623-3B*[10348].

STB15

Stb15[10341] locus: 6AS[10341]

Confers resistance to Ethiopian culture IPO88004[10341]

v: Riband[10341]. **v2**: Arina **Stb6**[10341]. **ma**: **Stb15** – 14 cM – *Xpsr904-6A*[10341].

STB16

Stb16[10879] locus: 3DL[10879] syn: Stb16q

Seedling and adult plant resistance [**Stb16q**[10879]].

v2: Synthetic W-7976 **Stb17**[10879]. **ma**: Associated with *Xgwm494-3D* and mapped as a QTL, R^2=0.4-0.7 in seedling tests and 0.28-0.31 in mature plants[10879].

STB17

Stb17[10879] locus: 5AL

Adult plant resistance 5AL[10879].

v2: Synthetic W-7976 **Stb16**[10879]. **ma**: Associated with *Xhbg247-5A* and mapped as a QTL, R^2=0.12-0.32[10879].

STB18

Stb18[10827] locus: 6DS[10827]

Confers resistance to IPO0323, IPO98022, IPO98046[10827]

v2: Balance **Stb6 Stb11**[10827]. **ma**: Mapped as a QTL located in a 8.8 cM region spanned by *Xgpw3087-6D* and *Xgpw5176-6D*[10827].

STB19

Stb19[11360] locus: 1DS[11360]

Derived from synthetic wheat.

v: Lorikeet[11360]. **ma**: KASP markers snp_4909967 and snp_1218021[11360].

See [11332, 11361] for reviews.

Temporary designation

TmStb1[11446]

Resistance to IPO323.

dv: *T. monococcum* MDR043[11446].

ungrouped

QStb.riso-2B

was mapped on chromosome arm 2BL linked to SSR marker *Xwmc175-2B* (LOD>5, R^2>17%)[10067].

QStb.riso-3A.2

was mapped on chromosome arm 3AS linked to SSR markers *Xwmc489-3A*, *Xwmc388-3A* and *Xwmc505-3A* (LOD >4, R^2 >18%). Also detected at the seedling stage[10067]. *Xgwm369-3A* is present on chromosome arm 3AS[0187]. A resistance gene from Senat located at or near the STB6 was mapped 5 cM from *Xgwm369-3A* on chromosome arm 3AS[10067].

QStb.riso-6B

was mapped on the centromeric region between SSR markers *Xwmc494-6B* and *Xwmc341-6B* (LOD >16, R^2 >68%). Also detected at the seedling stage[10067].

QStb.riso-7B

was mapped on chromosome 7B close to SSR marker *Xwmc517-7B* (LOD>4, R^2 >11%)[10067].

Four QTLs for resistance to *Mycosphaerella graminicola* were identified in replicated field experiments in a double haploid population from **Savannah (susceptible) / Senat (resistant)**. Senat contributed all the alleles providing resistance[10067].

ITMI Population: Three QTL, *QStb.ipk-1DS*, *QStb.ipk-2DS* and *QStb.ipk-6DS* conferred seedling-stage resistance to 2 isolates, whereas 2 QTL *QStb.ipk-3DL* and *QStb.ipk-7BL* conferred separate adult-stage resistances to each isolate[10151].

A weak QTL, *QStb.psr-7D.1*, giving partial resistance to Portuguese isolate IPO92006, was detected in the *Xcdo475b-7B* – *Xswm5-7B* region in chromosome 7DS[10341].

For a review of qualitative and quantitative resistance[11439].

QTL

Apache / Balance: Analyses with a panel of *M. graminicola* cultures identified QTLs on chromosomes 1BS (Apache, considered to be **Stb11**), 3AS (Balance, considered to be **Stb6**), 6DS (Balance, named as **Stb18**), 7DS (Apache, considered to be **Stb4**) and 7DL (Apache)[10827].

Florett / Biscay (S): RIL population: two QTLs for APR were located on chromosomes 3B and 6D[10901].

Solitar (R) / Mazurka (S): DH population: Resistance under field conditions was associated with QTL on chromosomes 5A, 6D and 7D which accounted for 20% of the genotypic variation; all three were derived from Solitar, but there was no evidence that **Stb6** and **Stb11**, also present in Solitar, were involved[10984].

Spelt HRTI1410 (R) / three wheat parents: 135 DH lines: mapped using SNP polymorphisms common to all three S parents: four QTL identified on chromosome 5AL (74.2 – 82.4 cM; r^2 = 0.18); 4B (52.9 – 56.9 cm, r^2 = 0.09) contributed by the susceptible parents; and 7B.1 (41.2 – 57.0 cM, r^2 = 0.09), and 7B.2 (58.2 – 67.4 cM, r^2 = 0.15) contributed by the susceptible parents[11430].

Steele-ND (R) / ND735 (S): RIL population: A consistent QTL (R^2=0.1) for seedling resistance flanked by DArT markers *XwPt-7101* and *X377410* was mapped to chromosome 5BL in the region of **Stb1**[10992]. Two other QTLs on chromosomes 1D and 7A were detected in single experiments[10992].

Tuareg / Biscay (S): RIL population: two QTLs for APR were located on chromosomes 4B and 6B[10901].

3.17 Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude

Disease: Septoria nodorum blotch, Stagonospora nodorum blotch.

3.17.1 Genes for resistance

SNB1

Snb1[856] locus: 3AL[856]

v: Red Chief[856]. **v2**: EE8 **Snb2**[856].

SNB2

Snb2[856] locus: 2AL[856]

v2: EE8 **Snb1**[856].

SNB3

Snb3[1594] locus: 5DL[1594]

s: CS*/Synthetic 5D[1594]. **v**: Synthetic[1594]. **dv**: *Ae. Tauschii*[1594].

Temporary names

SnbTM[856, 857] locus: 3A[857]. 3AL[856]

v: Cooker[10210]; Hadden[10210]; Missouri[10210]; Red Chief[10210]; 811WWMN 2095[10210]; 86ISMN 2137[10210]. **tv**: *T. timopheevii*/2*Wakooma[856]; *T. timopheevii* PI 290518. *T. timopheevii* derivatives: S3-6[857]; S9-10[857]; S12-1[857]. **ma**: *UBC521*$_{650}$ – 15 cM – **SnbTM** – 13.1 cM – *RC37*$_{510}$[212].

UBC521$_{650}$ was converted to a SCAR marker[0212].

Allelism of the hexaploid wheat gene and the *T. timopheevii* **SnbTM** was suspected but not confirmed.

A QTL analysis of SNB response in the **ITMI population** found significant effects associated with chromosome 1B (probably **Snn1**) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B[10009]. An additional QTL on 7BL was effective at a later stage of disease development[10009].

ITMI population: A major QTL, coinciding with **Snn1**, was located in chromosome 1BS (R^2 = 0.58, 5 days after inoculation), minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL[10009]. P91193D1 (partially resistant)/P92201D5 (partially resistant) RIL populations were tested in Indiana and Western Australia for glume resistance. Two QTL were identified: *Qng.pur-2DL.1* from P91193D1 (R^2 = 12.3 in Indiana and 38.1% in WA, respectively; *Xgwm526.1-2D* – *Xcfd50.2-2D*) and *QSng.pur-2DL.2* from P99201D5 (R^2 = 6.9% and 11.2%, respectively; *Xcfd50.3-2D* – *wPT9848*)[10471].

A summary of QTL analyses is provided in [10726].

QTL

Arina / Forno: RIL population[10065]. Two QTLs for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in. *QSng.sfr-3BL* was associated with marker *Xgwm389-3B* and explained 31.2% of the variation with resistance contributed by Arina[10065]. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1% of the variation. Resistance was contributed by Forno[10065]. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTLs for plant height and heading time[10065]. *QSng.sfr-3BS* peaked 0.6 cm proximal to *Xsun2-3B*[10465]. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes[10465].

Br34 / Grandin: Three QTLs with resistance effects from BR34; *Qsnb.fcu-5BL.1* (**Tsn1**), R^2 = 0.63, *Qsnb.fcu5BL.2*, R^2 = 0.06, and *Qsnb.fcu-1BS* (vicinity of **Snn1**), R^2 = 0.10[10458]. QTL analysis of the RIL population with Culture Sn6 revealed four QTLs, *Qsnb.fcu-2DS* (R^2 = 0.3 – 0.49) associated with **Snn2**, *Qsnb.fcu-5BL* (R^2 = 0.14 – 0.2) associated with **Tsn1**, *Qsnb.fcu-5AL* (R^2 = 0 – 0.13) associated with *Xfcp13-5A*, and *Qsnb.fcu-1BS* (R^2 = 0 – 0.11) associated with *Xgdm125-1BS*[10507].

Forno (S) / Oberkulmer spelt (R): Among 204 RILs leaf and glume response were genetically different but correlated (R^2=0.52). Ten QTLs for glume blotch (SNG) resistance were detected, 6 from Forno. A major QTL (R^2=35.8%) was associated with q. Eleven QTLs (4 from Forno) affected leaf blotch; 3 of these (chromosome 3D, 4B and 7B) with R^2>13% were considered potential candidates for MAS[10250].

HRWSN125 (R) / WAWHT2074 (S): Constant detection of *QSnl.daw-2DL* for flag leaf resistance, and *QSng.daw-4BL* for glume resistance over two years[10584].

Liwilla / Begra: DH population: Four QTLs, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B and 5D. A longer incubation period and lower disease intensity were contributed by Liwilla[10045]. A QTL, *QSnl.ihar-6AL*, identified in DH lines of Alba (R)/Begra (S) accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period[10143].

Salamouni / Katepwa: RIL population: Two QTLs. *QSnb.fcu-1A* (**Snn4**) (R^2=0.24) and *QSnb.fcu-7A* (R^2=0.16) were associated with SNB response to isolate Sn99CH 1A7a[10867].

Langdon / Langdon (*T. turgidum* ssp. *dicoccoides* **Israel-A 5B)**: *QSnb.ndsu-5B* located 8.3 cM proximal to **tsn1** for tan spot resistance; R^2 = 0.38[10597].

3.17.2 Sensitivity to SNB toxins (necrotrophic effectors)

A discussion on the origin and role of host-specific toxins is provided in [10726].

TSN1

Tsn1[346, 10207, 10458]

Sensitive to SnToxA, which is functionally identical to Ptr ToxA[10459].

v: Cheyenne[7]; Forno[10725]; Hope[7]; Jagger[7]; Kulm[346, 10030, 10458]; ND495[7]; Timstein[7]; Trenton[315]. **dv**: Two *Ae. speltoides* accessions[10756]. **tv**: Langdon[10458]; Some *T. dicoccoides* accessions[10756]. **c**: **Tsn1** has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA[10756]. See reaction to *Pyrenophora tritici repentis*[10458].

tsn1[346, 10207] locus: 5BL[346]

Insensitivity (disease resistance) is recessive[346].

v: AC Barrie[10153]; AC Cadillac[10153]; AC Elsa[10153]; BR34[7]; CEP17[7]; Chinese Spring[7]; Erik[7, 10030]; Hadden[10155]; Laura[10153]; Line 6B-365[10155]; Red Chief[10155]; 1A807[7]; 1A905[7]; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122. **v2**: Grandin **Snn2 Snn3**[10507]. **tv**: Altar 84[7]; D87450[7]; *T. dicoccoides* Israel A[10506]. **ma**: *Xbcd1030-5B* – 5.7 cM – **tsn1** – 16.5 cM – *Xwg583-5B*[346]; – 3.7 cM – *Xbcd1030-5B*[7]; *Xfgcg7-5B* – 0.4 cM – **Tsn1**/*Xfcg17-5B* – 0.2 cM – *Xfcg9-5B*[10207]; *Xfcg17-5B* – 0.2 cM – **Tsn1** – 0.6 cM – *Xfcg9-5B*[10207]; *Xfcp1-5B* and *Xfcp2-5B* delineated **Tsn1** to an interval of about 1 cM[10337]. **Tsn1** was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1*/*XBE425878*/*Xfcc1*/*XBE443610*[10413]; This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B*[10724].

Australian cultivars with **Tsn1** and **tsn1** are listed in [10540].

SNN1

Snn1[10008] locus: *TaWAK* [11341]. 1BS[10008]

Sensitivity to SnTox1 is dominant[10008]

bin: 1BS.sat.18. **s**: CS-DIC 1B[10008]. **v**: CS[10008]; Grandin[10008]; Kulm[10008]; M-6[10960]; ND495[10008]. **ma**: **Snn1** – 4.7 cM – *XksuD14-1B*[10008]; *XksuD14.2-1BS* – 0.4 cM – **Snn1**/*XBE498831*/*XBF474204* – 0.4 cM *Xpsp3000-1BS*/*XBE422980*/*XBE637568*/*ZBE605202*[10727]; *XksuD14.2* – 0.34 cM – **Snn1**/*XBE498831*/*XBF474204* – 0.12 cM – *XBF29322* – 0.04 cM – *Xpsp3000-1BS*/*XBE422980*/*XBE637568*/*XBF605202*[10727]; *Xfcp618-1B* – 1.9. cM – **Snn1** – 0.16 cM – *Xfcp624-1B*[11433] KASP marker *Bs00093078_51* was developed at Wang map position 8.361 in the UK MAGIC population[11133]. **c**: **Snn1** encodes a wall-associated kinase (WAK)[11341]. GenBank: KP091701.

Lebsock durum carried an intact **Snn1** but it was not expressed[11433].

Snn1 was present in some *T. dicoccum* accessions, 73% of durum accessions and 16% of common wheat accessions[11341].

snn1

i: CS*/*T. dicoccoides* 1B[10008]. **su**: CS/Hope 1B[11341]. **v**: Br34[10008]; Erik[10008]; Opata 85[10008].

SNN2

Snn2[10507] locus: 2DS[10507]

Sensitivity to SnTox2 is dominant[10507].

v: BG223[10507]. **v2**: Grandin **Tsn1 Snn3**[10507]. **ma**: *Xgwm614-2D* – 7.6 cM – **Snn2** – 5.9 cM – *Xbarc95-2D*[10507]; *XTC253803* – 3.6 cM – **Snn2** – 0.4 cM – *Xcfd-2D*[10724].

snn2

v: Atlas 66[10724]; Br34[10507]; Cheyenne[10724]; Chinese Spring[10724]; Jagger[10724]; Opata 85[10724]; Salamouni[10724]; TAM 105[10724].

SNN3

Snn3[10507, 10728] locus: 5BS

Sensitivity to SnTox3 is dominant[10728]

bin: 5BS-6[10507], **v**: BG220[10960], **v2**: Grandin **Tsn1 Snn2**[10507, 10728], **ma**: **Snn3** - 1.4 cM - *Xcfd20-5BS*[10507]

snn3

v: BR34[10507].

Snn3-B1 locus: *Snn3* [10507, 10728]. 5BS[10507, 10728, 11637]

Sensitivity to SnTox3 is dominant[10728]

bin: 5BS-6[10507]. **v**: BG220[10960]; Hope[11637]; Katepwa[11637]; Opata 85[11637]; Timstein[11637]; Sumai 3[11637]. 39% of a panel of wheat accessions[11637]. **dv**: 2.4% of a panel of *Ae. speltoides* accessions[11637]. **v2**: Grandin **Tsn1 Snn2**[10507, 10728]. **ma**: **Snn3** – 1.4 cM – *Xcfd20-5BS*[10507].

Snn3-D1 locus: (11637}. 5DS[11637]

dv: *Ae. tauschii* TA2377[11637]. 12% of a panel of *Ae. tauschii* accessions[11637]. **ma**: *Xbarc130-5D* – 1.3 cm – *SNN3-B3*/*Xcfd18*/*Xhbg-5D* – 1.3 cM – *XBE446811* – 1.6 cM – *Xgwm190-5D*[11637].

These likely homoeologous genes (*Snn3*-B1 and **Snn3-D1**) recognize the same pathogen effector (toxin)[11637].

SNN4

Snn4[10725] locus: 1AS[10725]

Sensitivity to SnTox4 is dominant[10725]

bin: 1AS3-0.86-1.00[10725]. **v**: Arina[10725]; Katepwa[10867]; Salamouni[10867]. **ma**: *XBG262267*/– 0.9 cM – **Snn4** – 1.6 cM – *Xcfd58.1-1AS*[10725].

snn4

v: Forno[10725].

SNN5

Snn5[10925] locus: 4BL[10925, 11205]

bin: 4BL5-0.85-1.00. **tv**: *T. carthlicum* PI 94749[10925]. **tv2**: Lebsock **Tsn1 Snn3-B1**[11203]. **ma**: *Xbarc163*/*Xcfd-4B* – 13.3 cM – **Snn5** – 2.8 cM – *Xwmc349-4B*[10925].

snn5[10925]

tv: LP749-29[10925]; PI 94749[10925].

SNN6

Snn6[11206] locus: 6AL[11206]

v: Opata 85[11206]; RIL ITMI137[11206]. **ma**: Flanked by *XBE424987* and *XBE403326*[11206].

snn6

v: Synthetic W-7984[11206].

SNN7

Snn7[11292] locus: 2DL[11292]

Sensitive to SnTox7.

bin: 2DL-9-0.75-1.00. **v**: Timstein[11292]. **ma**: *Xcdf267-2D* – 2.3 cM – *Xgdm6-2D* – 0.9 cM – **Snn7**/*Xcfd44-2D* – 1.8 cM – *Xgwm349-2D* – 11.3 cM – *Xgwm311-2D*[11292].

ungrouped

snn1tsn1

Atlas 66[10458]; BR34[10458]; Erik[10458]; Opata 85[10458]; ND688[10458].

QSnn.niab-5A.1[11133]

v: Identified in the UK MAGIC population[11133].

In a reevaluation study Faris and Friesen[10688] attributed all of the variation in SNB response to the presence or absence of *SnTox1*.

Genotype list in [10724].

ITMI population: A major QTL, coinciding with **Snn1**, was located in chromosome 1BS (R^2 = 0.58, 5 days after inoculation), minor QTLs were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL[10009].

Host sensitivity genes in US southern winter wheats are listed in [1241].

QTL
P91193D1 / P92201D5: RIL population: tested in USA and Australia: *QSng.pur-2DL.1* from P91103D1, R^2=0.123 (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, R^2=0.069 (Indiana) and 0.112 (South Perth)[10776].

3.18 Reaction to *Pratylenchus* spp.

Root lesion nematode; prats

3.18.1 Reaction to *Pratylenchus neglectus*

RLNN1

Rlnn1[0121, 0374] locus: 7AL[0121]

v: Excalibur[0121]; Krickauff[0121]. **ma**: Mapped between markers *Xpsr121-7A* and *Xgwm344-7A* and 9 cM proximal to **Lr20**[0374].

3.18.2 Reaction to *Pratylenchus thornei*

QTLs were located on chromosomes 2BS and 6DS[11501, 0122]. These QTL were fine mapped in a Sokoll (MR)/Krichauff DH population and further crosses: *QRlny.sk-2B* was mapped to a 1.4 cM/2.19 Mbp region; *QRLnt.sk-6D* was mapped to a 3.5 cM/1.77 Mbp region[11501, 11502].

3.19 Reaction to *Puccinia coronata* var. *hordei*.

CR1

Cr1[10956] locus: 5DL[10956]

v: Chris CItr 14108[10956]. **ma**: *Xwmc41.2-5D* – 11.3 cM – **Cr1** – 16.8 cM – *Xgdm63-5DL*[10956].

3.20 Reaction to *Puccinia graminis* Pers.

Disease: Black rust; black stem rust; stem rust.

Note: Some near-isogenic lines are based on Marquis. The genes present in the Marquis background are not listed for those NILs.

3.20.1 Genes for resistance

SR1

SR2

Sr2 locus: 3BS[499]

Recessive allele. Adult plant response

s: CS*6/Hope 3B[499]. **v2**: HD2009 **Sr30**[10632]; Warigo ***Sr7b*** **Sr17**[499]; Suneca ***Sr8a*** **Sr17**[485]; Hopps ***Sr9d***[499]; Lancer ***Sr9d*** **Sr17**[679]; Scout ***Sr9d*** **Sr17**[679]; See also ▸[499, 1040]. **ma**: *Xgwm389-3B* – 2.7 cM – **Sr2** – 1.1 cM – *Xglk683-3B*[358]; *Xglk683* (STS *Xsun2-3B*) – 0.5 cM – *Xgwm533-3B*[358]; These SSR loci were located within FL 0.87 - 0.75[0358]; All 27 lines with **Sr2** carried a 120 bp allele at *Xgwm533-3B*; A 120 bp allele in 4 cultivars lacking **Sr2** differed from the **Sr2** associated allele at 4 base positions[0358]; STMs for the *Xgwm533-3B* locus had increased specificity as markers for **Sr2**[10142]; Tightly linked CAPS marker *csSr2* based on a SNP proved superior to *Xgwm533-3B* as a marker for **Sr2**[10786]; *Xgwm389-3B* – 3.0 cM – **Sr2**/*csr2* – 0.4 cM – *Xgwm389-3B* – 2.0 cM – **Fhb1**/*UMN10*/*UMN* $_{v2}$ (coupling)[11210]; *Bs0006276* – 0.3 cM – **Yr57** – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B*[11480].

Sr2 is associated with pseudo-black chaff[742, 1102] and seedling chlorosis (see ▸[149]) and occurs very frequently in commercial wheats, especially in germplasm produced and distributed by CIMMYT. **Sr2** has probably remained effective since the 1920s.

Lines combining **Sr2** and **Fhb1** are reported in ▸[11170]; **Sr2** was located about 2 cM distal to **Fhb1**.

SR3 & SR4

Sr3 & Sr4[47]

v: Marquillo – based on early data. No stocks for the individual genes available.

SR5

Sr5[47] locus: 6D[939, 1308, 1626]. 6DS[939].

i: I **Sr5**-Ra[828]; I **Sr5**-Rb[828]; Sr5/7*LMPG[685]; Thatcher/10*Marquis[686]. **s**: CS*6/Thatcher 6D[1308]. **v**: Admonter Fruh[72]; Dacia[979]; Dong-Fang-Hong 2[564]; Dong-Fang-Hong 6[564]; Feng-Kong[563]; Hochzucht[46]; Hybrid 80-3[72]; Jubilejna[68]; Juna[76]; Kanred[1308]; Ke-Fang 1[564]; Stabil[72]; Viginta[71]; Vrakunski[72]. **v2**: Amika **Sr31**[76]; An-Hewi II ***Sr8a***[564]; Beijing 10 **SrTmp**[564]; Dong-Xie 3 **Sr31**[563]; Dong-Xie 4 **Sr31**[563]; Erythrospermum 974 ***Sr8a***[72]; Glenlea **Sr6** ***Sr9b***[327]; Istra **Sr31**[76]; Jing-Hong **Sr17**[564]; Jing-Hong 2 **Sr17**[564]; N.P.789 **Sr11**[1555]; Qing-Chung 5 **Sr6** **Sr11**[564]; Solaris **Sr31**[76]; Victor **Sr6** ***Sr8a***[979]. **ma**: Flanked by *Xbarc183-6D* and *wPt3879*[11232].

SR6

Sr6[687, 1167] locus: 2D[1293, 1308, 1577]. 2DS[942] syn: SrKa1[1167]

bin: 2DS5 – 0.47 – 1.00[10714]. **i**: I **Sr6**-Ra[828]; Kenya 58/10*Marquis[468, 675]; Sr6/9*LMPG[685]. **s**: CS*5/Red Egyptian 2D[1308]. **v**: Africa 43[669]; Eureka[468, 844]; Kenya stocks[669, 670, 673, 687, 689, 1167, 1557]; McMurachy[679]; Shield[198]. **v2**: Bowie ***Sr8a***[1553]; Eurga **Sr11**[1553]; Fortuna ***Sr7a***[679]; Gamut ***Sr9b*** **Sr11**[1555]; Glenlea (heterogeneous) **Sr5** ***Sr9b***[327]; Kentana 52 ***Sr7a***[678, 1577]; Kiric 66 ***Sr7b***[979]; Lerma Rojo 64 ***Sr7b*** ***Sr9a***[979]; No. 466 ***Sr9b*** **Sr10**[689]; Red Egyptian ***Sr8a*** ***Sr9a***[687, 1308]; Siete Cerros **Sr11**[33]; Victor I **Sr5** ***Sr8a***[979]. **ma**: **Sr6** – 1.1 cM – *Xwmc453-2D* – 0.4 cM – *Xcfd43-2D*[10714]; *Xgwm102-2D* – 0.9 cM – *Xgpw94049-2D* – 5.6 cM – **Sr6** z – 1.5 cM – *Xwmc453*/*Xcfd43-2D*[10870]. See also ▸[1553].

SR7

Sr7[830] locus: 4AL[939, 1308]. 4A[671, 830, 1293].

Sr7a[830] syn: Sr7[687]

i: Egypt Na101/6*Marquis[468]; Kenya 117A/6*Marquis[468]; ***Sr7a***/9*LMPG[685]. **s**: CS*7/Kenya Farmer 4B[830]; CS*8/Sapporo 4B[830]. **v**: Egypt Na101[669]; Jagger **Sr38**[11420]; Kenya stocks[669, 670, 673, 687, 689]; Sapporo Haru Komugi Ichigo[689]. **v2**: Egypt Na95 ***Sr9b*** **Sr10**[687]; Fortuna **Sr6**[679]; French Peace ***Sr9a*** **Sr13**[680]; Kentana 52

Sr6[689]; Khapstein **Sr13 Sr14**[674]; W3746 **Sr12**[1371]. **ma**: *Xwmc313-4A* – *SNP1067* – 0.8 cM – ***Sr7a*** – 2.7 cM – *Xbarc78-4A* – 2.7 cM – *SNP7126*[11420].

Sr7b[830]

i: I ***Sr7b*** -Ra[828]. **v2**: Warigo **Sr2 Sr17**[499]; Kiric 66 **Sr6**[979]; Roussalka ***Sr8a***[979]; Red Bobs **Sr10**[308]; Nell **Sr17**[1565]; PI 177906 **Sr28 SrTmp**[11419]; Spica **Sr17**[939]; Marquis **Sr18 Sr19 Sr20**[675, 830]. **ma** Located at 147-164 Mb in the Wang et al. (2014) consensus map[11419].

SR8

Sr8 locus: 6A[1293, 1308], 6AS[929, 1368]

Sr8155B was also reported to be located at locus[11758].

Sr8a[1368] syn: Sr8[687]

i: I Sr8a-Ra[828]; Red Egyptian/10*Marquis[686]; ***Sr8a***/9*LMPG[685]. **s**: CS*5/Red Egyptian 6A[1308]. **v**: Harvest[11418]; Marimp 3[979]; Mentana[844]; Strampelli[979]. **v2**: An-Hewi II **Sr5**[564]; E-Gan-Zao **Sr17**[564]; Erythrospermum 974 **Sr5**[72]; Frontana *b*[689]; Golden Valley **Sr17**[979]; Hartog **Sr2 Sr12**[127]; Magnif G ***Sr9b***[689]; Pitic 62 ***Sr9b***[33]; PI 177906 ***Sr7b*** **SrTmp**[11419]; Red Egyptian **Sr6** ***Sr9a***[687]; Rio Negro ***Sr9b***[689]; Roussalka ***Sr7b***[979]; SD4297 **Sr28**[11418]; Suneca **Sr2 Sr17**[485]; Victor 1 **Sr5 Sr6**[979]. **ma**: Terminally located; SNP markers within 2 cM[11416]. ***Sr8a*** – 2.2 cM – *Xgwm459-6* A[11418].

Sr8b[1368] syn: SrBB

v: Barleta Benvenuto[1368]; Klein Titan[1368]. **v2**: Bezostaya **Sr5**[979]; Klein Cometa **Sr30**[1368]. **tv**: According to Luig[841] one of the genes in Leeds is ***Sr8b***. **tv2**: Arrivato ***Sr9e*** **Sr13**[10607]. **ma**: ***Sr8b*** – 4.6 cM – *Xgwm334-6A*[10607].

This could be the gene located on chromosome 6A in ST464-A1[10473] and one of the genes present in ST464, a parent of Leeds.

Sr8155B was also reported to be located at locus[11758].

SR9

Sr9[676] locus: 2B[671, 677, 828, 1308], 2BL[944, 946, 951, 1307, 1582] syn: Sr9[676]

c: Encodes an NB-LRR immune receptor containing a long LRR domain[11747]. Ortholog of **Sr21** with about 85% identity[11747].

Sr9a[676] syn: Sr9[687]

i: I***Sr9a*** -Ra[828]; Red Egyptian/10*Marquis[686]; ***Sr9a***/9*LMPG[685]. **s**: CS*4/Red Egyptian 2B[1308]. **v2**: Red Egyptian **Sr6** ***Sr8a***[687]; French Peace ***Sr7a*** **Sr13**[680]; Excel ***Sr8a*** **Sr17**[752]. **ma**: *Xbarc101-2B*/*Xgwm12-2B* – 2.7 cM – *Xgwm47-2B* – 0.9 cM – ***Sr9a***/*Xwmc175-2B*[10472].

Sr9b[468] syn: SrKb1[468], Sr9[687]

i: Kenya 117A/10*Marquis[686]; ***Sr9b***/10*LMPG[685]. **s**: CS*7/Kenya Farmer 2B[939]. **v**: Gamenya[844]; Kenya stocks[67, 669, 673, 687, 689, 1557]. **v2**: Egypt Na95 ***Sr7a*** **Sr10**[636]; Festival **Sr15**[1553]; Frontana ***Sr8a***[689]; Gamut **Sr6** **Sr11**[1555]; Glenlea **Sr5 Sr6** heterogeneous[327]; Kenora **Sr15**[1553]; Magnif G ***Sr8a***[689]; No. 466 **Sr6 Sr10**[689]; Pitic 62 ***Sr8a***[33]; Rio Negro ***Sr8a***[689]; Robin **Sr11**[879]; Veadeira **Sr10**[687]. See also ▶[1553]. **c**: ***Sr9b*** differs from ***Sr9h*** and ***Sr9g*** by different single amino acids[11747].

See also ▶[1553].

Sr9c

Originally reserved for **Sr36**, but later **deleted**.

Sr9d[678, 831] syn: Sr1[47, 676, 677]

i: Hope/10*Marquis[677]; H-44/10*Marquis[677]; I Hope 2B-Ra[828]; ***Sr9d***/8*LMPG[685]. **v**: Hopps **Sr2**[1040]. **v2**: Lancer **Sr2 Sr17**[679]; Scout **Sr2 Sr17**[679]. **tv**: Arnautka[939]; Mindum[939]; Spelmar[939].

Sr9e[951] syn: Srv[1391], Srd1v[642], SrKn[11590]. TRITD2Bv1G223210

Srv[1391], ***Srd1v***[642], *SrKn*[11590]. *TRITD2Bv1G223210*.

v: Line Td31-5R PI 700734[11514, 11590]; SST 16[1324]; SST 33[785]; SST 66[785]; SST 3R[1324]; Vernstein[845]. **v2**: Combination III **Sr36**[841]; Sunstar ***Sr8a*** **Sr12**[939]. **tv**: ST464-A2[10473]; Svevo[11590]; Vernal emmer[1391]; CI 7778[845]; ***Sr9e*** occurs in many tetraploid wheats[939, 1378]. **tv2**: Arrivato ***Sr8b*** **Sr13**[10607]; Kronos **Sr13**[11590]; ST464 **Sr13**[10473]. **ma**: *Xgwm191-2B* – 5.5 cM – ***Sr9e*** – 0.7 cM – *Xgwm47-2B*[10607]. *SrKn* was mapped to a 0.29 cM region flanked by *pku4856F$_2$R$_2$* and *pku4917F$_3$R3*[11590].

Sr9f[826]

v: Chinese Spring[826]; Not present in the near-isogenic I***Sr9a***-Ra[826]. Deleted[11747]. The ***Sr9f*** homolog protein in CS is non-functional indicating that the gene named ***Sr9f*** in CS is not an **Sr9** allele[11747].

Sr9g[965]

s: CS*7/Marquis 2B **Sr16**[965]; CS*4/Thatcher 2B **Sr16**[965]. **v2**: Celebration **Sr12** **Sr16**[965]; Eagle **Sr26**[842]; Hochzucht **Sr5** **Sr12**[965]; Lee **Sr11** **Sr16**[965]. **tv**: Acme[965]; Iumillo[965]; Kubanka[965]. See also ▶[504]. **c**: ***Sr9g*** differs from ***Sr9h*** by a single amino acid[11747].

Sr9h[10057, 10858, 11010, 11147, 11149] locus: 2BL[10858, 11010] syn: SrWeb[10858], SrWLR[11485]

v: Matlabas[10058, 11486]; RL6203[11010]. **v2**: Gabo 56 CI 14035 **Sr11**[11010]; Gabo CI 12795 **Sr11**[11010]; Timstein CI 12347 **Sr11**[11010]; Webster RL6201 **Sr30**[10858]. **ma**: *Xgwm47-2B* – 1.4 cM – ***SrWeb*** – 12.5 cM – *Xwmc332-2B*[10858]; *wPt-3132* – 1.9 cM – ***Sr9h*** – 1.9 cM – *wPt-8460*[11010]; ***Sr9h*** – 20.7 cM – **Sr28**[11010]; *Xgwm47-2B* – 1.8 cM – ***Sr9h*** (***SrWLR***) – 7.0 cM – *Xwmc332-2B*[11485]; *AWA543-HRM* – ***Sr9h*** – *Xgwm47-2B*.

Although[11149] concluded that **Sr28** was present in VL404 and Janz it is more likely that the gene described is the linked gene ***Sr9h***. ***Sr9h*** was frequently present in landraces with field resistance to early isolates of the *Pgt* race Ug99 group[11147].

SR10

Sr10[687] locus: 2B[686, 939]

i: Egypt Na95/4*Marquis[468]. **v**: Federation[939]; Geneva[1412]; Hazen[49]; Kenya stocks[669, 670, 673, 687]. **v2**: Egypt Na95 ***Sr7a*** ***Sr9b***[687]; No. 466 **Sr6** ***Sr9b***[689]; Red Bobs ***Sr7b***[308].

SR11

Sr11[468] locus: 6BL[1297] 6B[671, 1143, 1293, 1309] syn: Sr11[687], Sr12[687]

i: I **Sr11**-Ra[828]; Lee/10*Marquis[686]. **s**: CS*7/Kenya Farmer 6B[830]; CS*9/Timstein 6B[1308]. **v**: Charter[844]; Flevina[72]; Gabo[687]; Kenya stocks[670, 673, 844, 1557]; Sonora 64[33]; Sylvia[71]; Timstein[687, 1308]; Tobari 66[33]; Yalta[844]. **v2**: Charter ***Sr9h***[11177]; Eurga **Sr6**[1553]; Gamut **Sr6** ***Sr9b***[1555]; Lee ***Sr9g*** **Sr16**[687]; N.P.790 **Sr5**[1555]; Qing-Chung 5 **Sr5** **Sr6**[564]; Robin ***Sr9b***[879]; Prospect **SrWld**[197]; Trident **Sr38**[11177]; See also ▶[1553]. **ma**: *KASP_6BL_IWB46893* – 0.3 cM – **Sr11**/*KASP_6BL_IWB10724* – 0.3 cM – *KASP_6BL_IWB72471*[11177].

A resistance gene allelic with **Sr11** was found in Chinese Spring[938], but the *P. graminis* culture for its detection was lost.

SR12

Sr12[1332] locus: 3BS or centromeric region[682, 968, 1332, 11103]. 3BL[11104]

Recessive.

s: CS*7/Marquis Selection 3B **Sr16**[1332]; CS*5/Thatcher 3B **Sr16**[1332]. **v**: Marquillo[682]; Tincurrin[939]; Windebri[939]. **v2**: Condor ***Sr8a***[11105]; Celebration *Sr9gSr16*[939]; Condor Thatcher *Sr5Sr9gSr16*[939]; RL6058 (a Thatcher derivative)[11104]; W3746 ***Sr7a***[1371]. **tv**: Postulated for several durums[1378]. **ma**: *IWA6086* – **Sr12** – *IWA4613*[11104].

Sr12 is more widespread and probably more effective in conferring resistance than is usually acknowledged[939]. Although the association of field resistance and **Sr12** was not definitive allelism or close linkage is clearly involved[11104].

SR13

Sr13[674] locus: 6AL

ma: *Xwmc59-6A* – 5.7 cM – **Sr13**[10607]; *CD926040* – **Sr13** – *BE471213*[10777]; CD926040 – SR13 – *BE471213*[10777]; Markers *Xgwm427-6A* and *AFSr13S* (proximal) and *Xdupw-6A* (distal) showed variable but close (<10 cM) linkage with SR13 in six durum crosses – these markers were variously applicable across durum backgrounds, but only *Xgwm427-6A* was variable in a range of hexaploid derivatives with **Sr13** likely originating from a single source[11146]. **c**: **Sr13** was identified as a CC-NBS-LRR gene with three resistance haplotypes in two specificities[11217]; later, four resistance haplotypes and four specificities[11584].

Sr13a[674, 11217, 11584] locus: 6AL[929]

bin: 6AL-8. **i**: Khapstein/9*LMPG[685, 11217]; Khapstein/10*Marquis ***Sr7b***[686]; **Sr13**/9*LMPG[685]. **v2**: Khapstein ***Sr7a*** **Sr14**[674]; Machete **Sr2**[10607]. **itv**: Rusty-KL-B[11584]; Rusty-KL-C[11584]. **tv**: Cando[11584]; Durox[11584]; Grenora[11584]; Kronos PI 576168[11217]; Lakoto[11584]; Maier[11217]; Mountrail[11584]; Renville[11217]; Strongfield[11584]; Transend[11584]; Wells[11584]. **tv2**: Khapli ***Sr7a*** **Sr14**[674]. **c**: KY825225 (Resistance haplotype R1)[11217].

Sr13b[11217, 11584]

itv: Im-C2[11584]; Im-7B[11584]; Rusty-14803[11584]. **tv**: Ben[11584]; Botno[11584]; Calvin[11584]; Carpio[11584]; D99656[11217]; D15143[11584]; Joppa[11584]; Kofa PI 584336{10777; 11217}; Lebsock[11584]; Leeds *Sr92* ***Sr8b***[11584]; Lloyd[11584]; Medora PI 496260[10777, 11217], CItr 7777[11584]; Munich[11584]; ND Grano[11584]; ND Riveland[11584]; Pierce[11584]; Rugby[11584]; Sceptre[10777, 11584]; Svevo[11584]; *T.* carthlicum PI 387696[11584]; *T. polonicum* CItr 14803[11584]; Tioga[11584]; Vic[11584]; Ward[11584]. **c**: GenBank KY225226 (Resistance haplotype R2)[11217].

Sr13c[11584]

itv: 8155-B2[11584]; 8155-C2[11584]; Rusty-SR464-C1[11584]; ST464-C1[10473, 11584]. **tv**: Alkabo[11584]; Altar 84[11584]; CItr 7771[11584]; D101073[11584]; Langdon[11217, 11584]; PI 352548[11584]; ST464 ***Sr9e***[10473, 11584]. **c**: GenBank KY924305 (Resistance haplotype R3)[11217].

Sr13d[11584]

itv: CAT-A1[11584]. **tv**: Camadi Abdu Tipo #103[11584]. **c**: MW033594 (Resistance haplotype R4)[11584].

Alleles of many of the **Sr13** genotypes listed under tv: were identified by sequence markers; those entries are likely to carry additional resistance genes.

Haplotypes of other germplasm previously listed are unknown: v2: French Peace ***Sr7a*** ***Sr9a***[680]. tv2: Arrivato ***Sr8b*** ***Sr9e***[10607].

Unspecified allele. tv:[11280].

A resistance gene in Khapstein/9*LMPG and believed to be **Sr13** was mapped in chromosome 6AL by Admassu et al.[10778]. However, the map location was more than 50 cM proximal to that reported in ▶[10777]. It was resolved in ▶[10779] that the resistance locus mapped in ▶[10778] could not be SR13.

SR14

Sr14[674] locus: 1BL[933]

i: Khapstein/10*Marquis[686]. **v**: Line A[933]. **v2**: Khapstein ***Sr7a*** **Sr13**[674]. **tv2**: Khapli **Sr13**[674].

SR15

Sr15[1554] locus: 7AL[1305]. 7A[1293, 1554]

v: Present in stocks possessing **Pm1** and **Lr20**[931, 1554]; See Reaction to *Blumeria graminis* and Reaction to *P. triticina*. **ma**: Associated with clustered markers[323].

SR16

Sr16[830] locus: 2B[830, 1308]. 2BL[1307] syn: Srrl2[1238]

i: I **Sr16**-Ra[828]; I Th3B-Ra[832]. **s**: CS*7/Marquis 2B ***Sr9g***[1581]; CS*4/Thatcher 2B ***Sr9g***[1308]; CS*5/Thatcher 3B **Sr12**[832]. **v2**: Thatcher **Sr5** ***Sr9g*** **Sr12**[939]; Lee ***Sr9g*** **Sr11**[939]. **Sr16** is allelic with a gene in Kota (*SrKt2*[932])[939].

SR17

Sr17 locus: 7B[771]. 7BL[964, 10565] syn: sr17[964]

Recessive.

s: CS*6/Hope 7B[964]. **v**: Forno[10511, 10565]. **v2**: E-Gan Zeo ***Sr8a***[564]; Golden Valley ***Sr8a***[979]; Jing-Hong 1 **Sr5**[564]; Jing-Hong 2 **Sr5**[564]; Lancer **Sr2** ***Sr9d***[679]; Nell ***Sr7b***[1565]; Scout **Sr2** ***Sr9d***[679]; Suneca **Sr2** ***Sr8a***[485]; Present in many stocks possessing **Pm5**[964]; See Reaction to *Blumeria graminis*. **ma**: *Xwmc273-7B* – 15.3 cM – **Sr17**[10565].

SR18

Sr18[54] locus: 1D[54, 1308, 1582] syn: SrMn1[1263], Srmq1[99], SrPs1[1263], SrG2[844], Srrl1[1238]

i: I Hope 1D-Ra[828]; **Sr18**/8*LMPG[685]. **s**: CS*6/Hope 1D[1308]. **v**: Present in the majority of wheat stocks[828].

Stocks **not** possessing **Sr18**: Brevit[54]; Chinese Spring[828]; Eureka[54]; Federation[54]; Gular[54]; Kenya C6042[54]; Koala[54]; Little Club[828]; Morocco[54]; Norka[54]; Prelude[828]; Yalta[54].

SR19

Sr19[29] locus: 2B[29]. 2BS[1582] syn: Srmq2[99]

v: Mq-B[29]. **v2**: Marquis ***Sr7b*** **Sr18** **Sr20**[29].

SR20

Sr20[29] locus: 2B[29] syn: Srmq3[1238], Srrl3[1238]

v: Mq-C[29]; Rl-C[29]. **v2**: Reliance **Sr5** **Sr16** **Sr18**[29]; Marquis ***Sr7b*** **Sr18** **Sr19**[29].

SR21

Sr21[1460] locus: 2AL[1460, 1464]

i: **Sr21**/8*LMPG[685]. **v**: CSSr21 {M10115}; Hexaploid derivatives of *T. monococcum*[939]. **tv**: Tetraploid derivatives of *T. monococcum*[939]. **dv**: Einkorn CI2433[1460, 11110]; Dv92 **Sr35**[10876]; G2919 **Sr35**[10876]; Various *monococcum* accessions. See also **Sr45** which has similar specificity to **Sr21**. **ma**: FD52726 – 0.25 cM – **Sr21** – 0.05 cM – EX594406[11110]. madv: *CJ961291* – 0.02 cM – **Sr21** – 0.04 cM – NLR pseudo-gene cluster[11315]; A diagnostic marker was developed from the cloned gene[11315]. **c**: **Sr21** is a CC-NBS-LRR gene of 4,872 bp; 44 diploid accessions with **Sr21** were classified as five haplotypes – viz. Haplotype R1, MG582649, 28 accessions including DV92 (and CSSr21); Hap R2, GenBank MG601519, six accessions; Hap R3, MG601520, one accession; Hap R4, MG601521); and six accessions, Hap R5, MG601522, three accessions[11315].

SR22

The stem rust resistance **Sr22** from *T. monococcum* was cloned and was shown to encode a CC-NBS-LRR gene[11404]. The gene model for the allele in susceptible CS is Ref Seq v1.1 *TraesCS7A02G499600*.

Sr22[1460] locus: 7A, 7AL

bin: 7AL-0.74-0.86, **bin**: 7AL-13 0.83-0.89[10869], **i**: Marquis*4//Stewart*3/*T. monococcum*[649, 1460], **i**: Sr22/9*LMPG[685], **i**: Others[1112], **v**: CS/3/Steinwedel*2//Spelmar/*T. boeoticum*[1460], **v**: Schomburgk[880], **v**: Steinwedel*2//Spelmar/*T. boeoticum*[1460], **v**: Others[1112], **v**: Recombinant line reported in[10772, 10773], **tv**: Spelmar/*T. boeoticum*[1460], **tv**: Stewart*6/*T. monococcum* RL 5244[649], **dv**: Various *T. monococcum* accessions[649, 1460], **ma**: Hexaploid derivatives with Sr22 carried 'alien' segments of varying lengths; the shortest segment was distal to Xpsr129-7A[1112], **ma**: See also[0158], **ma**: Xcfa2123-7A - 6 cM - Sr22 - 5.9 cM - Xcfa2019-7A[10263], **ma**: Multiplex marker cssu22 based on STS markers derived from cloned fragment csIH81 was developed in[10772], **ma**: This marker gave positive results for Sr22 in all recombinant lines including those reported in[10773], **ma**: Recombined lines with shortened introgressions from diploid wheat are reported in[10869], **ma**: the shortest was U5616020-154[10869]

Sr22a [11514] locus: 7A[649]. 7AL[1460] syn: Sr22[1460]

bin: 7AL-0.74-0.86; 7AL-13 0.83-0.89[10869]. **i**: Marquis*4//Stewart*3/*T. monococcum*[649, 1460]; **Sr22**/9*LMPG[685]; Others[1112]. **v**: CS/3/Steinwedel*2//Spelmar/*T. boeoticum*[1460]; Schomburgk[880]; Steinwedel*2//Spelmar/*T. boeoticum*[1460]; Others[1112]; Recombinant line reported in [10772, 10773]. **tv**: Spelmar/*T. boeoticum*[1460]; Stewart*6/*T. monococcum* RL 5244[649]. **dv**: Various *T. monococcum* accessions[649, 1460]. **ma**: Hexaploid derivatives with ***Sr22a*** carried 'alien' segments of varying lengths; the shortest segment was distal to *Xpsr129-7A*[1112]; See also[158]; *Xcfa2123-7A* – 6 cM – **Sr22** – 5.9 cM – *Xcfa2019-7A*[10263]; Multiplex marker *cssu22* based on STS markers derived from cloned fragment csIH81 was developed in [10772]; This marker gave positive results for **Sr22** in all recombinant lines including those reported in [10773]; Recombined lines with shortened introgressions from diploid wheat are reported in [10869]; the shortest was U5616020-154[10869]. **c**: **Sr22** encodes a CC-NBS-LRR protein with 941 aa[11213]. EBI LN883743, GenBank CUM44200.1.

Sr22b [11514] locus: 7A^{m}L {M11208} syn: SrTm5[11208]

dv: *T. monococcum* ssp. *monococcum* PI 277131-2 **Sr21** ***Sr22b*** **Sr60**[11208, 11385]; PI 306540 **Sr21** ***Sr22b*** **Sr60** **SrTm4**[11208, 11385]. **i**: PI 306540 (2x)/Kronos (4x)//Clear White (6x)///*3 Fielder[11514]; PI 700735[11514]. **ma**: ***SrTm5***/*IWB25012*/*IWB44281*/*IWB405527*/*Sr22GMF/GMR* – 0.8 cM – *IWB6942*[11208]; *pkw4995* (RefSeq v1.1 *TraesCS7A02G499500*) – 0.04 cM – ***SrTm5*** – 0.04 cM- *pkw4999* (RefSeq v1.1 *TraesCS7A02G499900*)[11514]. **c**: ***Sr22b*** has an insertion of a large (13.8-kb) retrotransposon in its second intron[11514].The predicted ***Sr22b*** NLR protein is 95.7 to 96.7% identical to proteins translated from six ***Sr22a*** resistant haplotypes[11514].

Allelism of ***Sr22a*** and ***Sr22b*** was based on more than 2,200 gametes[11514].

SR23

Sr23[950] locus: 2BS[939]. 4B[950]

The following chromosome locations are consistant with the finding that the first location was based on Rescue monosomics. Rescue differs from CS by a 2B-4B reciprocal translocation[939].

v: Exchange[950]; Warden[950]; **Sr23** is always associated with **Lr16**[950]. **v2**: Etoile de Choisy **Sr29**[950].

SR24

Sr24[956] locus: 3DL = T3DS.3DL-3Ae#1L[389, 956]

Derived from *Thin. elongatum*.

i: **Sr24**/9*LMPG[685]; Sears' 3D/*Ag* translocations[956, 1300]. **v**: Agent[956]; Blueboy II[956]; Collin[901]; Cloud[956]; Cody[1284]; Ernest[10845]; Fox[956]; Gamka[785]; Karee[785]; Keene[10845]; Kinko[785]; Palmiet[785]; Sage[825, 1024]; SST 23[1324]; SST 25[785]; SST 44 = T4R[785, 1324]; SST 102[785]; Torres[128]; Wilga[785]. **v2**: Siouxland **Sr31**[1283]; List of Australian genotypes[340]. 1BS[185] = T1BS = 1BS-3Ae#1L[389, 600]. **tr**: Amigo[389, 600, 1463]; Millenium[10845]; Teewon[389, 600]. Note: Amigo and some derivatives also carry a 1AL.1RS translocation with resistance from rye[1463]. 3Ae#1. **su**: Chinese Spring 3Ag {3D}[1304]; TAP48[389]. **ma**: *Xbarc71-3Ag* was considered a better marker for **Sr24** than STS **Sr24**#12[10845]. SR24 is completely linked in coupling with LR24[956] and often with red grain colour. See Reaction to *P. triticina*.

SR25

Sr25[956] locus: 7DL = T7DS.7DL-7Ae#1L[291, 388, 657, 956]

Derived from *Thin. elongatum*.

i: Sears' CS 7D/7Ag translocations[956, 1300]; **Sr25**/9*LMPG[685]. **v**: Agatha **Sr5** ***Sr9g*** **Sr12** **Sr16**[956] = T4[1323]; Mutant 28[388]; Misr 1 (Oasis/Skauz//4*BCN/3/2*Pastor)[11260].
7AL = T7A-7Ae#1L[330] Sears' 7A/7Ae#1L No. 12[330, 1304]; Sears' 7D/7Ag#11 carries neither **Sr25** nor **Lr19**[939].
7Ae#1L. **su**: Chinese Spring + 7Ae#1L(7D)[1304].

See **Lr19**, reaction to *Puccinia triticina*.

Sr25/**Lr19** often show complete linkage in wheat[956].

Knott[681] obtained two mutants (28 and 235) of Agatha with reduced levels of yellow pigment in the flour. One of these mutants lacked **Sr25**. Marais[890] reported that a gene very similar to **Sr25** was present in the putative Inia 66 x *Thin. distichum* derivative, Indis. Marais[890, 892] also obtained mutants with reduced yellow pigment in Indis derivatives and some of these lacked **Sr25**.

SR26

Sr26[956] locus: 6AL[364]

Derived from *Thin. elongatum*. = T6AS.6AL-6Ae#1L[388, 389].

i: **Sr26**/9*LMPG[685]. **v**: Avocet[364]; Flinders[1449]; Harrier[939]; Jabiru[956]; King[1451]; Kite[956]; Knott's 6A-6Ae#1L translocation to Thatcher[672]; Takari[253]. **v2**: Bass **Sr36**[1450]; Eagle ***Sr9g***[956]. **ma**: Detected with several RFLP probes[138]; A PCR marker, **Sr26**#43 was reported in ▶[10257]. Four KASP markers were developed for the original translocation (FL 0.85). WA-1 (AUS91435) a derivative with a shortened 6Ae#1 segment (FL 0.32), amplified only *sunKASP_224* and *sunKASP_225*[11336]. The latter was diagnostic for accession AGG91586WHEA *SrB*, a derivative of line WA-5 (AUS91436)[11338]. PCR markers based on NLR genes in homoeologous group 6 chromosomes were used to confirm that WA-2 Type 1 was the smallest secondary translocation carrying **Sr26**[11357].

Secondary recombinants with shortened 6AL#1L segments involving chromosomes 6A and 6D are reported in ▶[11141]; five 6A recombinants were accessioned in the Australian Winter Cereals Collection. c: Encodes an NLR protein; GenBank MN531843[11528].

SR27

Sr27 locus: 3A (T3A-3R) = T3AS.3R#1S[3, 389, 896, 10162]

Derived from *S. cereale*.

i: **Sr27**/9*LMPG[685, 10162]. **v**: WRT wheat-rye translocation, available in CS, Thatcher and Pembina backgrounds. Translocated from Imperial rye to Chinese Spring by Acosta[3, 10162]; Widespread in triticales[966, 1384, 10162]. 3A = T3AL.3RS[896]; W964 = 3RS.3AL.1/4* Inia 66[896]; W968 = 3RS.3AL.1/5* Condor[896]; W970 = 3RS.3AL.88/5*SST3[896]. 3B = T3BL.3R#1S[896]; W966 = 3RS.3BL.26/4*Inia 66[896]. **c**: **Sr27** encodes an NLR with closest similarity to **Sr13** among cloned wheat *Sr* alleles[11561].

SR28

Sr28[932] locus: 2BL[932]

i: Line AD[932]. **v**: SD 1691, CI 12499[11148]. **v2**: Kota ***Sr7b*** **Sr18**[932]; SD4297 ***Sr8a***[11419]. **ma**: *Xwmc332* – 1.4 cM – **Sr28** – 6.0 cM – *wPt-7007*[11148]; **Sr28** – 1.6 cM – *wPt-7004*[11148]; **Sr28** – 0.6 cM – *wPt-7004*[11148].

Although[11149] concluded that **Sr28** was present in VL404 and Janz it is more likely that the gene described is the linked gene ***Sr9h***.

The **Sr28** allele in SD4297 was originally reported as ***Sr9h***[11418].

SR29

Sr29[313] locus: 6DL[313]. 6DS[1626] syn: SrEC[955]

i: Prelude/8*Marquis//Etoile de Choisy[313]. **v**: Hana[71]; Hela[76]; Mara[68]; Slavia[76]; Vala[76]. **v2**: Etoile de Choisy **Sr23**[955].

SR30

Sr30[688] locus: 5DL[688] syn: SrW

i: **Sr30**/7*LMPG – Lines 1, 2, and 3[685]. **v**: Festiguay[688]; Mediterranean W1728[1369]; Webster[688]. **v2**: HD2009 **Sr2**[10632]; Klein Cometa ***Sr8b***[1368]; Relatively common in Australian and Mexican wheats. Various unnamed accessions[208, 1321]. **ma**: *Xcfd12-5D* – 9.0 cM – **Sr30** – 16.6 cM – *Xgwm292-5D*[10858].

According to ▶[10858] Webster RL6201 carries a second gene **SrW** that confers resistance to the race Ug99 group.

SR31

Sr31 locus: 1B = T1BL.1RS = T1BL.1R#1S[389] or 1R(1B)

Derived from *S. cereale* cv. Petkus. See also Reaction to *P. striiformis*, **Yr9**: Reaction to *P. triticina*, **Lr26** 1B = T1BL.1RS = T1BL.1R#1S[389] or 1R(1B).

i: MA1 and MA2 four-breakpoint double translocation lines 1RS-1BS-1RS.1BL in Pavon[84]. **v**: Amika (heterogeneous) **Sr5**[76]; Cougar[267]; Feng-Kang 2[563]; Feng-Kang 8[563]; Gamtoos[785]; GR876[753]; Jing-Dan 106[563]; Jan 7770-4[563]; Lu-Mai 1[563]; Rawhide (heterogenous)[267]; Yi 78-4078[563]. **v2**: Dong Xie 3 **Sr5**[563]; Dong Xie 4 **Sr5**[563]; Istra **Sr5**[76]; Solaris **Sr5**[76]; Siouxland **Sr24**[1283]. **tv**: Cando*2/Veery = KS91WGRC14[381]. **ma**: 1BS/1RS recombinants 4.4 cM proximal to **Gli-B1**/**Glu-B3**[84]; Several markers tightly linked with **Sr31** were indentified in [377]; A SCAR marker, SCSS30.2$_{576}$ was developed[10359]; *Xscm09-1R*$_{208}$[10845].

Sr31 seems to be different from the rye-derived gene in Amigo and related materials[10270].

SR32

Sr32 locus: 2A[939, 1304]. = T2AL.2S#1L-2S#1S[389]

Derived from *Ae. speltoides*.

v: C95.24[389]. 2B[1304] = T2BL-2S#1S[389]; C82.1 = P80-14.1-2[389]. 2D[1304] = T2DL-2S#1L.2S#1S[389]; C82.2 = P80-139.1-4[389, 1304]; C82.3 = P80-132.2-2[939, 1304]; C82.4 = P80-153.1-2[939, 1304]; Deben[10283].

C82.2 was shown to have two resistance genes – **Sr32** in the short arm isolated as 70type1 (AUS91442) and *SrAe1t* in the long arm isolated as 70typeII (AUS91441), 122typeII (AUS91444), and line 247 (AUS91446)[11779].

SR33

Sr33 locus: 1DS[620]. 1DL[650] syn: SrSQ[650]

v: RL 5405 = Tetra Canthatch/*Aegilops squarrosa* RL 5288[650]. **dv**: *Ae. tauschii* PI 603225[11012]; TOWWC0153 = TA2466[11685]. **ma**: linked with **Gli-D1**; *Xmwg60-1D* – 5.8 cM – **Sr33** – 2.2 cM – *Xwmg2083-1*[360]; *Xwmc432-1D* – 0.3 cM – *Xwmc336-1D* – 1.0 cM – **Sr33** – 4.2 cM – *Xwmc222*/*Xcfa2158-1D*[11012]; Flanked by *BE405778* and *BE499711* within a 1 cM region[10987]. **c**: **Sr33** encodes a CC-NBS-LRR protein and is orthologous to **Sr31**, **Sr50** and the barley powdery mildew locus *Mla*[10987]. GenBank KF031291, 4,639 bp; protein CUM44200.1. **Sr33** is a paralogue of **Sr66**[11685] with 83% homology[11405].

SR34

Sr34[967] locus: 2A[967]. = T2AS-2M#1L.2M#1S[389]

Derived from *Ae. comosa*.

v: CS 2A-2M 4/2[967]. 2D[967] = T2DS-2M#1L.2M#1S[389] **i**: **Sr34**/6*LMPG[685]. **v**: Compair[967]; CS 2D-2M 3/8[967]; Various addition, substitution and translocation lines with **Yr8**[967]. 2M[967]. **su**: Chinese Spring 2M(2A)[967].

SR35

Sr35[957] locus: 3AL[957] syn: SrTm1[1522]

bin: 3AL8 0.85-1.00. **i**: Marquis*5/G2919[10876]. **v, tv**: Tetraploid and hexaploid derivatives of *T. monococcum*[957]. **dv**: DV92 **Sr21**[10876]; G2919 **Sr21**[10876]; *T. monococcum* C69. 69 Selection[957]; G2919[957]. **ma**: **Sr35** was mapped to a 5.1 cM interval between *XBF483299* and *XCJ656351* in diploid wheat[10712]; Mapped in diploid wheat to a 2.2-3.1 cM region between *XBF483299* and *XCJ656351* and corresponding to a 174 bp region in *Brachypodium*[10876]. **c**: **Sr35** is a CC-NBS-LRR gene[10988].

Sr35 was postulated in 21 accessions of *T. monococcum* subsp. *monococcum*[11288].

SR36

Sr36[939] locus: 2BS[939] syn: SrTt1[949]

i: **Sr36**/8*LMPG[685]. **v**: Arthur[939]; Arthur 71[1324]; Flemink[1324]; GK Kincso[235]; Gouritz[1324]; Idaed 59; Maris Fundin[70]; Mengavi[949]; SST 101[1324]; SST 107[785]; Timvera[949]; *T. timopheevii* derivatives[949]; Zaragoza[785];

Others[572, 10609]. **v2**: Bass **Sr26**[1450]; Combination III ***Sr9e***[939]; Timson **Sr5 Sr6**[939]. **tv**: *T. Timopheevii*[949]. **ma**: *Xgwm42* – 0.8 cM – **Sr36**/*Xstm773-2-2B*/*Xgwm31-2B*/*Xwmc477-2B*[10609]; *Xgwm319-2B* – 0.9 cM – **Sr36**/*Xstm773-2-2B*/*Xwmc477-2B*[10609]; *Xgwm429-2B* – 0.8 cM – **Sr36**/*Xstm773-2*/*Xgwm319*/*Xwmc477-2B*[10824]; *Xgwm319-2B* – 0.9 cM – **Sr36**/*Xstm773-2*/*Xwmc477-2B*[10824]; Of four markers *Xwmc477-2B* was the best, but it is not a perfect marker[10845].

SR37

Sr37[939] locus: 4BL[939] syn: SrTt2[949]

v, tv: *T. timopheevii* and derivatives[484, 949]; Line W[949].

SR38

Sr38[62] locus: 2AS[62]. 6M^{v} = 2MS-6MS.6ML or 2MS-6ML.6MS[0009]

Derived from *Ae. ventricosa*.

i: RL 6081 = Thatcher + **Lr37**. This line will carry additional genes from Thatcher. **v**: CDS Stanley[11579]; Mace[11579]; Moisson derivatives Mx12 and Mx22[0213]; VPM1[62]; SY Mattis[11579]. v2 Jagger ***Sr7a***[11420]. **ma**: The 2NS translocated segment carrying **Sr38** replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682* to *XksuH9*; PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682*[10073].

Sr38 is linked with **Lr37** and **Yr17**. See Reaction to *P. triticina* **Lr37** and *P. striiformis tritici* **Yr17**. SCAR markers SC-372 and SC-385 were developed in [10796].

SR39

Sr39[646] locus: 2B[651]

Derived from *Ae. speltoides*. = 2SL-2SS#2.2SL#2[11037].

v: RL 5711[646, 651]. **tv**: Amphiploid RL 5347 = *Ae. speltoides*/*T. monococcum*[651]. **ma**: **Sr39** is closely linked with **Lr35**[651]; A SCAR marker was developed[9923].

Lines with shortened alien segments are reported in [10741]. Although **Sr39** produces similar responses to **Sr32**, also derived from *Ae. speltoides*, recombination studies based on three crosses showed independent inheritance[646]. **Sr39** segregated independently of **Lr13**[651]. **Sr39** may be present in DAS15 in combination with **Sr47**. A Ti2BL.2BS-2SS-2BS translocation[10872] separated from **Sr47** in DAS15 could contain **Sr39** – see *SrAEs7t*.

Further lines with shortened segments are described in [11037] along with tightly linked co-dominant STS markers.

SR40

Sr40[302] locus: 2BS[302]. = T2BL/2G#2S[389]

Derived from *T. araraticum*.

i: RL 6087 = RL 6071*7/PGR 6126; RL 6088 = RL 6071*7/PGR 6195[302]. **tv**: *T. araraticum* PGR 6126[302]; PGR 6195[302]. **ma**: *Xwmc661-2B* – 6.4 cM – **Sr40** – 0.7 cM – *Xwmc344-2B* – 2.0 cM – *Xwmc477-2B*[10825]; *Xwmc661-2B* – 7.8 cM – **Sr40** – 2.5 cM – *Xwmc474-2B* – 1.0 cM – *Xwmc477-2B*[10825].

SR41

Sr41[1215] locus: 4D[1215]

v: WDR-B1[1214]. **v2**: Waldron **Sr5** (heterogeneous) **Sr11** (heterogeneous)[1215].

SR42

Sr42[938] locus: 6DS[938]

v: PI 595667[11087]. **v2**: Norin 40 **Sr54**[938]; PI 410954 **Sr24**[11087]. **ma**: *Xcfd49-6D* – 5.5 cM – *Xbarc183-6D* – 0.5 cM – **Sr42**/*FSD_RSA* – 11.8 cM – *Xbarc301-6D*; *Xcfd6D* – 5.9 cM – **Sr42** – 46.9 cM – *Xcfd13-6D*[10952]; *Xcfa49-6D* – **Sr42**/*IBW31561*/*IBW30767* – *FSDRSA*[11087].

The likelihood that **Sr42** is the same as **SrTmp** and *SrSha7* (see below) is discussed in [11035] where Blouk#1, Coni#1, Niini#1, Phunye#1, Ripper and Tinkio1 were shown to carry a gene, or closely linked genes, on chromosome 6DS. If they are the same, this list would be enlarged to include Digalu, Gambo, Koshan 09 and Morvarid[11035]. Nearest markers *Xbarc183-6D* and *Xcfd49-6D* but not in consistent order[11035]. **Sr42** co-locates with **SrCad**, *SrNini, SrSh7* and **SrTmp**. Three haplotypes were identified in [11087]: C-C-T, AC Cadillac, Peace, PI 595667; T*-C-T, Norin 40, Eagle 10, Ember, Guard, Ripper, Shield; T-C-T, Triumph 64, CnSSrTMP64, Blouk, Digalu, Pfunye, Robin, PI 410954. A genetic analysis of six lines, Blouk, Coni, Niini, Pfuneye, Ripper and Tinkio, is reported in [11132]. All had single genes with linkage to *Xcfd49-6D* ranging from 3.9 – 12.5 cM and the genes were not clearly distinguished from **Sr42** or **SrTmp**[11132].

A resistance allele at the SR42 locus, possibly **SrTmp** or a new allele, was identified in South African cultivars Komati, Koonop, Limpopo and SST387[11725]. This gene was likely derived from Betta[11725].

SR43

Sr43 locus: 7DS-7el$_2$S.7el$_2$L[11076]. 7D. 7DL = T7DL-7Ae#2L.7Ae#2S[389, 657]

Derived from *Th. elongatum*.

tr: KS10-2[653]. 7D = T7DS.7Ae#2L[389, 657]. **v**: KS23-9[653]; KS24-1[653]; KS24-2[653].

Derivatives RWG33 and RWG34 with shortened alien segments were reported in [11076]. c: **Sr43** isolated from RWG34 encoded a protein kinase fused to 2 domains of unknown function[11631]. **Sr43** confers higher resistance at low temperature[11631].

SR44

Sr44[389] locus: T7DS-7J#1L.7J#S 7J#1L[389]

Derived from *Th. intermedium*.

v: Line 86.187 TA5657[939]; Several 7A-7Ji#1L translocations[89]. T7DL.7J#1S[11011]; TA5657[11011]. 7J#2, 7J#2S. **su**: Group 7 alien substitution lines with 7J#1 and 7J#1S[939]. **ad**: TAF2 = L1[169].

SR45

Sr45[894] locus: 1D[897]. 1DS[894] syn: SrD[934], SrX

v: 87M66-2-1[894]; 87M66-5- 6[897]; Thatcher + **Lr21**, RL5406[894, 934]; Various backcross derivatives developed at PBI Cobbitty[1461]. **dv**: *Ae. tauschii* RL5289[894, 934]. **su**: CS1D5406[11134]. **ma**: *Xgwm106-1D*/*BE44426* – 1.82 cM – **Sr45** – 0.39 cM – *csssu45/Af45*[11134]. **c**:. **Sr45** encodes a 1,230 aa CC-NBS-LRR protein[11213]. NCBI LN883757.

Tests of natural and induced mutants of *P. graminis* f. sp. *tritici* indicated that **Sr45** had identical specificity to **Sr21**[934]. One race distinguishing **Sr45** and **Sr21** is reported in [11134]. Cloning of both SR45 and SR21 showed that the genes were different.

SR46

Sr46[10538] locus: 2DS[10538]

bin: 2DS5-0.47-1.00. **v**: L-18913/Meering selections R9.3[10538]; R11.4[10538]; R14.2[10538]. **v2**: L-18913 = Synthetic Langdon/*Ae. tauschii* var. *meyeri* AUS 18913 ***Sr9e***[10538]. **dv**: *Ae. tauschii* var. *meyeri* AUS18913[10538] = Clae 25[11268]; *Ae. tauschii* TA1703[11268]. **ma**: Co-segregation with RFLP *Xpsr649-2DS* at both the diploid and hexaploid levels[10538]; A PCR-based marker, *csSC46* was developed from a BAC clone containing *Xpsr649*[10538]. *Xgwm210-2D* – 3.9 cM – **Sr46** – 5.6 cM – *Xcfd36-2D* – 0.3 cM – *Xwmc111-2D*[11268]. madv: Flanked by *Xgwm1099-2D* and *Xbarc297-2D*[11405]. **c**: Cloned by AgRenSeq and map-based methods **Sr46** has a CC-NBS-LRR structure[11405]. GenBank MG851023.

Sr46 was more effective at higher temperatures in laboratory tests[11268].

SR47

Sr47[10549] locus: 2BS[10872]. 2B = 2BL-2SL-2BL.2BS[10549]

Derived from *Ae. speltoides*.

tv: DAS15[10549]; RWG35[10872]; RWG36[10872]; RWG37[10872].
2B=2BL-2SL-2BL.2BS. **v**: RWG35[10872]. STS marker *Xrwgs38* was diagnostic for the **Sr47** segment in DAS35 and DAS36[11319].
2B=2BL-2SL-2BL.2BS **v**: RWG36[10872].
al: *Ae. speltoides* PI 369590[10549]. **ma**: Located in the interval *Xgwm47-2B* – *Xgpw4165-2B*[10872].

Further markers were used to identify the introgressions in RWG25, RWG26, and RWG27[10872]. STS marker *Xrwgs38* was diagnostic for the **Sr47** segment in DAS35 and DAS36[11319]. Further chromosome engineering on DAS15 showed that the alien segment carried two resistance genes. The gene on 2BL was considered to be **Sr47** based on low infection type. The second gene located in 2BS produced a low infection type similar to **Sr39** and was located in a similar position to that gene[10872].

SR48

Sr48[10564] locus: 2DS[11653]. 2AL[10564, 10565] syn: SrAn1[10565]

bin: 2AL1-0.85-1.00[10564]. **v**: Arina[10511, 10564, 10565]. **v2**: Arina **Sr56** AUS 91457[10851]. **ma**: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – **Yr1** – 16.5 cM – **Sr48**[10564]; **Sr48** is considerably distal to the most distal of published markers, all of which are proximal to **Yr1**; *sun_KASP239* – 0.9 cm – SR48 – 3.5 cM – *Xxib59-2D*[11653].

The revised chromosome location was attributed to a chromosome 2A-2D translocation that explained the earlier reported linkage between SR48 and YR1.

SR49

Sr49[10704] locus: 5BL[10704]

v: Mahmoudi AUS 28011[10704]. **ma**: *sun479* – 0.9 cM – **Sr49** – 1.5 cM – *sun209* – 0.5 cM – *Xwmc471-5BL*[10704].

SR50

Sr50[10745] locus: 1DS[10745] syn: SrR[377]

ad: CS + Imperial 1R[377]. **v**: Line T6-1 AUS 91434[10745]. T1DL.1RS-DR.A1[11316]. **al**: *S. cereale* cv. Imperial. **ma**: Line T6-1 retains the rye marker AW2-5[10745]. **c**: GenBank KT725812, 3,508 bp. **Sr50** encodes a CC-NBS-LRR protein homologous to the barley *Mla* gene[11316]. GenBank KT725812.

In rye **Sr50** may be allelic with **Sr31**; however in wheat they can be regarded as separate loci **Sr50** is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye[10745].

SR51

Sr51[10803]

Homoeologous group 3[10803]; $3S^{S}S$[10803]

3A (3AL.$3S^{S}$S)[10803]. **v**: TA5619[10803].
3B (3BL.$3S^{S}$S)[10803]. **v**: TA5620[10803].
3D (3DL.$3S^{S}$S)[10803]. **v**: TA5621[10803].
3D (3DS-$3S^{S}$S.$3S^{S}$L)[10803]. **v**: TA5622[10803].
al: *Ae. searsii* TA2355[10803]. **ma**: $3S^{S}$-specific markers are provided in [10803].

SR52

Sr52[10774] locus: 6A (6AS.6V#3L)[10774]

v: TA5617[10775]. **ma**: 6V3-specific EST-STSmarkers are given in [10775].

The seedling response conferred by **Sr52** is temperature-sensitive.

SR53

Sr53[10789] locus: 5D

Derived from *Ae. geniculata* 5D[10789].

T5DS.5DL-5MgL-5DL[10789]. **v**: TA5630 (U6154-124)[10789].
T5DL-5MgL.5MgS[10789]. **v**: TA5625 (U6200-64)[10789].
T5DL-5MgL.5MgS[10789]. **v**: TA5643 (U6200-117)[10789].
al: *Ae. geniculata* TA10437[10789]. **ma**: Closest markers: *BE443102/Mbo1* and *BE442600*/*Mse1*[10789].

The three translocation lines are re-engineered derivatives of TA5599 (5DL-5MgL.5MgS[10789]).

SR54

Sr54[10816] locus: 2DL[10816]

v2: Norin 40 **Sr42**[10816]. **ma**: *Xcfd-283-2D* – 8.1 cM – **Sr54**/linkage block of 18 markers – 15.8 cM – *Xwmc167-2D*[10816].

The possibility of a large alien linkage block was supported by the fact that many of the associated markers were null[10816].

SR55

Sr55[10847] locus: 4DL

Adult plant resistance 4DL[10678, 10847].

bin: Distal to break point 0.56 FL[10678]. **i**: RL6077=Thatcher*6/PI 250413[10678, 10847]. **v**: Chapingo 48[11070]. **ma**: Pleiotropic of closely linked with **Lr67** and **Yr46** and associated with *Xgwm165-4D* and *Xgwm192-4DL*[10678, 10847]. **c**: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices[11070].

Sr55 is pleiotropic or closely linked with **Lr67**, **Yr46**, **Pm46** and **Ltn3**.

SR56

Sr56[10851] locus: 5BL[10565, 10851] syn: QSr.Sun-5BL

Adult plant resistance [*QSr.sun-5BL*[10565]].

bin: 5BL160-0.79-1.00. **v**: AF533[10851]. **v2**: Arina **Sr48** AUS 91457[138]. **ma**: *Xsun209* (SSR) – 2.6 cM – **Sr56** – 1.2 cM – *Xsun320* (STS from *wPt-7665*)[10851].

In the earlier QTL analysis of an Arina/Forno population *QSr.sun-5BL* accounted for 12% of the PVE[10565]. In the present study of an Arina/Yitpi RIL population stem rust response segregated as a single gene. The response phenotype was 40-50 MS-S.

SR57

Sr57[10861] locus: 7DS[10861]

Adult plant resistance.

bin: 7DS4. **su**: Lalbahadur(Perula7D) GID 5348503 and GID 5348496[10648, 10861]. **v**: Chinese Spring[10861]; Wheat accessions with **Pm38**/**Lr34**/**Yr18**, see Reaction to *Blumeria graminis*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia triticina*, Leaf tip necrosis. **ma**: See Reaction to *Puccinia triticina*. **c**: Putative ABC transporter[10648].

Further evidence for the effects of this gene on stem rust response can be found in ▶[299, 10565, 10733, 10863, 10864, 10865, 10866].

SR58

Sr58[10965] locus: 1BL[10965]

v: **Lr46** Deletion Mutant 109 (GID 5349718)[10965]; **Lr46** Deletion Mutant 111 (GID 5349716)[10965]. **su**: Lalbahadur(Pavon 1B) (GID 519245)[10965].

SR59

Sr59[11066] locus: 2D(T2DS.2RL)[11066]

Derived from *Secale cereale* 2D (T2DS.2RL)[11066].

v: TA5094[11066]. **su**: SLU238 (2R(2D))[11066]. **al**: VT828041 (6X triticale)[11066]. **ma**: Three rye-based KASP markers identified lines with **Sr59**[11066].

SR60

Sr60[11208] locus: 5A^{m}S[11208]

dv: PI 277130[11385]; PI 277131-2[11385]; PI 277135[11385]; PI 306540[11385]; PI 306545[11385]; PI 306547[11385]; PI 428158[11385]; PI 435001[11385]. dv2: PI 306540 **Sr21 SrTm4** ***SrTm5***[11208]. **v**: PI 689563, PI 306540/Kronos/2/UC1361/4UC12014-36[11385]. **ma**: *Pinb-5A^{m}S* … *GH724575/DK22976/CA5012332* – 0.25 cM – **Sr60**/*LRRK123.1* – 0.19 cM – *CJ942731/CJ884584*[11208]; *GH724575* – 1.56 cM – **Sr60**/*LRRK123.1* – 0.52 cM – *FD475316*[11208]. *Sr60F2R2*[11385]. **c**: **Sr60** from *T. monococcum* PI 306540 encodes a 724 amino acid protein with two putative kinase domains designated *Wheat Tandem Kinase 2* (*WTK2*)[11208, 11385]. GenBank MK629715[11385]. The gene is orthologous to *T. aestivum* gene *TraesCS5A02G005400*[11385].

Sr60 in UC12014-36+**Sr60** (PI 689563) is linked with puroindoline genes for grain softness that were also introgressed from the diploid parent[11385].

SR61

Sr61[11397] locus: *SrB* [11337]. 6A = T6AS.6AL-6Ae#1-6Ae#3[19018]; 6Ae#3[11338]

Derived from *Th. ponticum* 11397}.

v: AGG91586WHEA **Sr26**[11397]. **su**: W3757 = SA8123[11337], a (6Ae#3(6D) line[11338]. **ma**: *SrB* was recombined with a 6Ae#1 segment possessing **Sr26**. Marker *sunKASP_225*[11336] was diagnostic for the recombined line AGG91586WHEA[11338]. **v2**: AGG91586WHEA **Sr26**[11397]. **c**: Encodes a 880 amino acid NLR protein; GenBank MN531844[11528].

The recombinant AGG91586WHEA was produced after crossing the shortened 6Ae#1 recombinant WA-5 (AUS91436) carrying **Sr26** with SA8123. A separate line carrying **Sr61** alone is currently being selected for **Ph1** homozygosity.

SR62

Sr62[11524] locus: 1BS = T1S^{Sh}S.1S^{Sh}L-1BL[11524] syn: Sr1644-1Sh[11519]

v: Zahir*4/*Ae. sharonensis* AS_1644, JIC DPRM0081[11524]. **ma**: Mapped in *Ae sharonensis* to a 480 kb interval on chr arm 1^{Sh}S[11519]. **c**: Cloned from *Ae. sharonensis* and validated in transformed wheat. **Sr62** is tandem kinase with both domains required for function[11524]. **Sr62** has a kinase-pseudokinase (tandem kinase) structure with both components required for resistance function, 740 amino acids[11524]. GenBank MZ826707.
1DS (T1S^{Sh}S.1S^{Sh}L-1DL). **v**: JIC DPRM0092[11524]. **al**: *Ae. sharonensis* AS_1644[11519].

SR63

Sr63[11554] locus: 2AL[11554] syn: QSrGH.cs-2AL[11554]

Adult plant resistance.

tv: GH/M14 RIL49 XXXXX[11554]; GH/M14 RIL188 AUSXXXX[11554]. **tv2**: Glossy Huguenot **Sr58** (syn *QSrGH.cs-1BL*) AUS2499[11554]. **ma**: *IWA200-KASP_32429* – 2.7 cM – **Sr63** – 3.0 cM – *IWB4881*-2AL[11554].

SR64

Sr64[11644]

Derived from *Thinopyrum*.

4D = T4DL.4J^{S}S[10788]. **v**: KS93WGRC27[404]; Mace (PI 651043)[11681].
4D = T4DL.4DS-4J^{S}S[11644]. **i**: Line E*6/rec213 (**Sr64**, **Wsm1**) = GSTR 527[11644] (https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=2158211). **v**: KS08WGGRC50[10788, 11644]. **ma**: KASP markers developed in [11643].

SR65

Sr65[11682] locus: 1AS[11682] syn: SrH2[11682]

v: Hango-2 FLW6-Selection AGG95499WHEA[11682]. **ma**: *KASP_7944/KASP_11804* (2,3 Mb, CS REfSeq 2,1) – 2.6 cM – SR65 – 2.0 cM – *KASP_12147/ASP21832/sunCS_265*[11682]. CHS21_002378110 bp, respectively.

SR66

Sr66[11685] locus: 1DS[11012] syn: SrTA1662[11012]

v: KS05HW14[11405]. **dv**: *Ae. tauschii* TA1662[11012]; TOWWC0017 = TA11134[11685]; TOWWC0033 = TA1582[11685]; TOWWC0104 = TA1658[11685]. **ma**: *Xwmc432-1D* – 4.4 cM – **SrTA1662** – 4.4 cM – *Xwmc222-1D*[11012]. **c**: An **SrTA1662** candidate identified by AgRenSeq encoded a CC-NBS-LRR candidate gene (GenBank MG763911) with 83% homology to **Sr33**[11405]. GenBank MW526949[11612]. **Sr66** is a paralogue of **Sr33**[11685].

SR67

Sr67

v2: KU168-2 **Sr57** = XXXXXX[11687, 11688]. 6AL[11688]. **ma**: Mapping data indicates that **Sr67** (61.80 – 61.80 Mb) is distal to **Sr13** {61.6437} (CS REFSeq v2)[11688].

Consensus maps of many reported genes and QTL for stem rust resistance are provided in [11202].

Temporary designations

Sr1RS^{Amigo} [10845] locus: 1AS (T1AL.1RS)[389, 1624]

v2: Amigo **Sr24**[1464, 10845]. **ma**: *Xscm09-1R*$_{224}$[10845].

This alien segment also carries **Pm17** – see **Pm17**

Sr8155B1[11580] locus: 6AS[11580]

Recessive.

v: Choteau/Mountrail Der. SXD 43 PI 681713[11580]; Marruecos*2/CItr 8155[11580]. **tv**: Alkabo 11580}; Renville[11580]. **tv2**: Grenora **Sr13**[11580]; Munich **Sr13**[11580]. **ma**: Co-segregation with *KASP_6AS_IWB10558*[11580]. Also predicted in durum accessions Belzer, Dilse, Lloyd, Divide and Montrail[11580].

Sr10171[10936] locus: 7DS[10936]

v: Genetic stock to be designated[10936]. **dv**: *Ae. tauschii* TA10171[10936]. **ma**: **Sr10171** – 0.9 cM – *Xgdm88*/*Xwmc827-7D* – 1.9 cM – *Xcfd30-7D*[10936].

Sr10187[10936, 11181] locus: 6DS[10936] syn: SrTA10187[11181]

v: Genetic stock to be designated[10936]. **dv**: *Ae. tauschii* TA10187[10936]. **ma**: *Xcfd49-6D* – 1.9 cM – **Sr10187** – 13.6 cM – *Xbarc173-6D*[10936]; *6DS0027* – 0.2 cM – **Sr10187** – 0.2 cM – *6DS00273*[11181]; **Sr10187** – 0.2 cM – *6DS0039*[11181].

Sr10526[11249] locus: 6DS[11249]

v: CItr 105026[11249]. **ma**: *IWB36391*/*IWB34477* – 2.9 cM – *Sr15026* – 3.0 cM – *IWA4000*[11249]; *IWB36391* – 0.4 cM – *IWB262* – 2.6 cM – *Sr15026* – 1.3 cM – *IWB49086*[11249].

Sr10526 was detected with races QFCSC and TTTTF. When the same DH and RIL populations were tested with race TRTTF there was evidence for complementary resistance genes on chromosomes 6DS and 6AS, one of which was **Sr10526**. When the populations were tested in the field in Kenya with Ug99 races *QSr.abr-6AS.1* (R^2 = 0.1 – 0.3) was detected[11249].

SrA[323]

v: SW55-1[323]; SW56-1[323]. **v2**: SW33-5 ***Sr9a*** **Sr13**[323]; SW54-3 ***Sr9d*** **Sr13**[323].

SrAes7t[10872] locus: 2BS = T2B.2BS-2SS-2BS[10872]

v: Line 0797[10872]. **ma**: **Sr39**#50s[10741, 10872].

SrAes7t may be identical to **Sr39**[10872].

SrCad[10733] locus: 6DS[10733]

v: AC Cadillac[10733]; AC Crystal[10733]; AC Foremost[10733]; AC Karma[10733]; AC Taber[10733]; AC2000[10733]; Peace[10733]; 5700[10733]. **ma**: Lines with **Bt10**[10733]; *Xcfd49-6D* – 7.7 cM – **SrCad** – 1.5 cM – FSD_RSA/**Bt10** – 14.1 cM – *Xbarc301-6D* – 0.8 cM – *Xbarc173-6D*[10733]; *Xcfd49-6D* – 7.2 cM – **SrCad** – 1.8 cM – FSD-RSA/**Bt10** – 14 cM – *Xcfd75-6D*[10733].

SrND643[11092] locus: 4AL[11092]

bin: 4AL4-0.8-1.00. **v**: Kenya Sunbird[11092]; Kenya Tai[11092]; ND643/2*Weebill1 GID6302736[11092]. **tv**: ND643[11092]. **ma**: *Xwmc776-4A* – 2.9 cM – *Xgwm350-4A* – 0.5 cM – **SrND643** – 4.1 cM – *Xwmc219-4A*[11092].

SrPan3161[11722] locus: 4DS[11722]

v: Tugela[11722]. **v2**: PAN 3161 **Sr57**/**Lr34**[11722]. **ma**: RHT-D1 – 12.8 cM – *Xwmc-720-4D* 1.8 cM – *SRPan3161* – 1.8 cM – *Xgpc8038Xwmc52*/*Xgpc7414*/*Xcfd23*/*Xpsp3103-4D*[11722].

SrPI94701[11780] locus: 5BL[11780]

tv: PI 94701[11780]. **ma**: Mapped to a 0.17 cM region flanked by *pku69124* and *pku69228* and corresponding to 1.04 and 2.15 Mb in the Svevo REfSeq 1.0 and CSRefSeq 2 genomes[11780].

SrPI410966[11180] locus: 2BS[10825, 11180]

v: PI 410966[11180].

The marker profile for this gene was very similar to that of a line with **Sr36**[10825, 11180]. Specificity tests were not reported.

SrTA10276-2V[11395] locus: 2V[11395]

ad: TA7753[11395]. **al**: *D. villosum* TA10276[11395].

SrTm4[11111] locus: 2A^{m}L[11111]

Reccessive.

dv: Monogenic line TmS4-260[11673]. dv2: *T. monococcum* PI 306540 **Sr21** ***Sr22b*** **Sr60**[11111, 11673]. bin/contig: IWGS_2AL_contig6401556. **ma**: BQ461276 – 1.6 cM – **SrTm4** – 0.5 cM – DR732348/*Xgwm526*/*Xgdm93-2A*[11111]. Mapped to a 0.06 cM interval – 763.67 – 763.67 Mb in CS RefSeq 2.1[11673]. A 593 kb inversion within the candidate region was completely associated with resistance[11673].

SrTm4 was postulated in several *T. monococcum* accessions originating from the Balkans region – all had the inversion[11673].

SrTmp[1230] locus: 6DS

SrSha7[11057]; *SrA2K*[11691]; *QSr.nc*.6D[11691].

v: AGS2000[11691]; Bai-Yu-Bao[564]; Beijing 9[564]; Beijing 11[564]; Digalu[11057, 11132]; Ember[11152]; Fertodi 293[977]; Guard-1[11152]; Kenya Robin[11057, 11152]; KS91WGRC11 {M22059}. Martonvasari 5[977]; Mironovska = Mironovskaya 808[68, 977]; Morvarid[11132]; Nung-Ta 139[564]; Overland[11152]; Parker[977]; Ripper[11132]; Shield[11152]; Trison[1230]; Triumph 64[841, 977, 1230]; Xuzhou 14[564]; Yen-An 15[564]. **v2**: Beijing 10 **Sr5**[564]; PI 177906 ***Sr7b*** **Sr28**[11419]; MD01W28-08-11 **Sr31**[11691]. **ma**: **SrTmp** – 3.1 cM – *IWB49086*[11419].

The possibility of this gene being present in a number of South African cultivars, including Betta = Klein Impacto, is discussed in [10941].

SrWld[1230]

v2: Prospect **Sr11**[197].

SrZdar[67] locus: 1B[67]

v: Zdar[67].

Th. ponticum-derived, stem rust resistant line WTT34 with a T5DS.5DL-Th chromosome pair is reported in [11783].

Additional temporary designations are listed in [1230]. Genotype lists:[323, 970, 10270, 10511, 10697].

ungrouped

Sr9e_h1

Haplotypes *_h1* and *_h2* code for proteins with several amino acid differences[11747].

v: Vernstein[11747]. **tv**: CI 7778[11747].

Sr9e_h2

Haplotypes *_h1* and *_h2* code for proteins with several amino acid differences[11747].

tv: Kronos and other lines with ***Sr9e***[11747].

3.20.2 Suppressor of genes for resistance to *Puccinia graminis*

A suppressor of stem rust resistance in cv. Canthatch was known from the 1980s based on the response of an extracted tetraploid and aneuploid derivatives of Canthach as well as mutation analysis (11410, 11411) and references therein.

SUSR-1

SuSr-D1[11411] locus: 7DL[11417, 100001]

v: Canthatch CTH-K RL5451[11411]; Columbus[11417]; Katepwa[11417]. Other Canadian Thatcher derivatives[11417]. **ma**: Localised to a 1.3 cM genetic interval flanked by *Xkwh239* and *Xkwh281*[11412]. **c**: *TraesCS7D01G526100*. Encodes a mutant form of *TaMed15b.D*, a subunit of the Medicator complex[11412].

Additional temporary designations are listed in [1230] Genotype lists:[323, 970, 10270, 10511, 10697].

Complex genotypes
AC Taber: **Sr2**, ***Sr9b***, **Sr11**, **Sr12**[9905].
Centurk: **Sr5**[979], **Sr6**[979], ***Sr8a***, ***Sr9a***[979], **Sr17**[979].
Chris: **Sr5**[679, 1371], ***Sr7a***[1371], ***Sr9g***[1371], **Sr12**[1371].
Egret: **Sr5**[939], ***Sr8a***[939], ***Sr9b***[939], **Sr12**[939].
FKN: **Sr2**, **Sr6**, ***Sr7a***, ***Sr8a***[791], ***Sr9b***[791].
H-44: **Sr2**, ***Sr7b***[677], ***Sr9d***[677], **Sr17**.
Hartog: **Sr2**[127], ***Sr8a***, ***Sr9g***, **Sr12**[939].
Hope: **Sr2**[677], ***Sr7b***[677], ***Sr9d***[677], **Sr17**.
Kenya Plume: **Sr2**[1370], **Sr5**[1370], **Sr6**[1370], ***Sr7a***[1370], ***Sr9b***[1370], **Sr12**[1370] **Sr17**[1370].
Khapstein: **Sr2**, ***Sr7a***, **Sr13**[674], **Sr14**[674].
Lawrence: **Sr2**, ***Sr7b***[939], ***Sr9d***, **Sr17**.
Lerma Rojo 64: **Sr2**, **Sr6**, ***Sr7b***[979], ***Sr9a***[979].
Madden: **Sr2**, ***Sr9b***, **Sr11**, **Sr13**[842].
Manitou: **Sr5**[679], **Sr6**[679], ***Sr7a***, ***Sr9g***[965], **Sr12**[939].
Mendos: ***Sr7a***[939], **Sr11**[879], **Sr17**, **Sr36**.
Pasqua: **Sr5**, **Sr6**, ***Sr7a***, ***Sr9b***, **Sr12**. Gene **Lr34** acted as an enhancer of APR[9905].
PI 362698: **Sr5**, ***Sr8a***, **Sr12**, *Sr15?*, **Sr16**[11347].
PI 60599: ***Sr7a***[689], ***Sr8a***, ***Sr9b***, **Sr10**.
Redman: **Sr2**, ***Sr7b***[939], ***Sr9d***[939], **Sr17**.
Reliance: **Sr5**[1308], **Sr16**[1238], **Sr18**, **Sr20**.
Renown: **Sr2**, ***Sr7b***[939], ***Sr9d***[939], **Sr17**.
Roblin: **Sr5**, *Sr7a?*, **Sr11**, **Sr12** Selkirk: **Sr2**[499], **Sr6**[468], ***Sr7b***[499], **Sr17**, **Sr23**[950].
Thatcher: **Sr5**[1308], ***Sr9g***[965], **Sr12**[939], **Sr16**[1308].
Timgalen: **Sr5** (heterogeneous)[1555], **Sr6**[1555], ***Sr8a***, **Sr36**.
WW15 = Anza = Karamu = T4: **Sr5**[939], ***Sr8a***[939], ***Sr9b***[939], **Sr12**[939].

QTL

Arina / Forno: *Qsr.sun-5BL*[10565]; resistance contributed by Arina, associated with *Xglk356-5B*, R^2=11-12%[10565]. *Qsr.sun-7DS*[10565]; resistance contributed by Forno, associated with markers *XcsLV34* and *Xswm10* diagnostic for **Lr34**/**Yr18**[10565].

Avocet S / Pavon 76: RIL population of lines lacking **Sr26**:Five QTLs, *QSr.cim-3B* (**Sr2**), *QSr.cim-1B* (**Lr46**/**Yr29**/**Pm39** region) and *QSr.cim-3D* (R^2=0.2) from Pavon 76; *QSr.cim-4B* and *QSr.cim-5A* from Avocet S[10975].

Carberry (Resistant in Canada) / AC Cadillac (Resistant in Canada and Kenya): DH population: QTLs effective in Kenya were located in chromosomes 2B, 5B, 7B and 7D, those effective in Canada were on 3B (**Sr2**), 5A and 5B; those effective in Kenya and Canada were on 4B and 6D (**Sr2**); both parents had **Lr34**/**Sr51**[11040]

HD2009 / WL711: RILs: Three of several QTLs gave consistent effects across environments, viz. *QSr.sun-3BS*, R^2= 0.09-0.15, probably **Sr2**, *QSr.sun-5DL*, R^2= 0.2-0.44, probably **Sr30**, and *QSr.sun-7A*, R^2= 0.07-0.13, nearest marker *wPT-4515*[10632].

PBW343 (S) / Muu (I): RIL population:4 consistent QTLs were identified, *QSr.cim-2BS*, *QSr.cim- 3BS*(**Sr2**) and *Sr.cim-7AS* from Muu, and *QSr.cim-5BL* from PBW343[11019].

RL6071 / RL6058(R): RIL population: RL6058, a Tc backcross line with **Lr34**/**Sr57** is more resistant than Tc. Enhancement of resistance in both Kenya and North America was attributed to a QTL in the region *wPt5044* **–** *Xgwm-2B* in chromosome 2BL[10902].

Spark / Rialto: DH population: Sr5 and **Sr31** were derived from Rialto and *QDr.sun-3BS* (*Xgwm1034-3B* – *BS00010945* region and *QSR.sun-5A* (*Xgwm445-5A* – *Xgwm205-5A* region) were derived from Spark[11231].

3.21 Reaction to *Puccinia striiformis* Westend.

Disease: Stripe rust, yellow rust.

3.21.1 Designated genes for resistance to stripe rust

YR1

Yr1[851] locus: 2AL[940]. 2A[877, 1610] syn: L[1622]

bin: 2AL1-0.85-1.00[10564]. **i**: AVS+Yr1[970]. **v**: Chinese 166[851]; Corin[230]; Dalee[83]; Durin[1459]; E2025[1267]; E7700[1267]; E8594[1267]; Feng-Kang 13[1610]; Heines 110[604]; Maris Ranger[1459]; Maris Templar[1459]; Odra[73]; Ritmo[10038]. **v2**: Argent ***Yr3a Yr4a*** **Yr6**[1067]; Avocet (UK) **Yr2 Yr6**[1459]; Bounty **Yr13**[1459]; Fenman **Yr2**[1459]; Galahad **Yr2** (heterogeneous) **Yr14**[1459]; Galahad **Yr14**[83]; Kraka **Yr32**[10038]; Ibis **Yr2**[604]; Longbow **Yr2 Yr6**[83]; Mardler **Yr2** ***Yr3a Yr4a*** **Yr13**[604, 1459]; Maris Templar ***Yr3a Yr4a***[604]; Marksman (heterogeneous) **Yr2 Yr13**[1459]; Mithras **Yr2 Yr6**[1459]; Nudif TP1 ***Yr3a***[1431]; Nudif TP3 ***Yr3c***[1431]; Nudif TP250 **Yr6**[1431]; Regina **Yr2**[73]; Rothwell Perdix **Yr2**[604]; Savannah **Yr2 Yr3 Yr9 Yr32**[10032]; Sportsman **Yr13**[1459]; Stetson **Yr9**[83]; Sylvia **Yr2**[1430]; Tadorna **Yr2**[1431]; Virtue **Yr13**[83, 1459]. **ma**: *Xgwm382-2AL* – 0.6 cM – *Xgwm311-2AL* – 2.6 cM – *Xfba8a-2AL* – 1.3 cM – *Xstm673acag* – 1.1 cM – **Yr1** – 16.5 cM – **Sr48**[10564].

A report[1267] that Kalyansona and Nadadores carried **Yr1** is not correct.

YR2

Yr2[851] locus: 7B[184, 186, 746] syn: U[1622]

Recessive[1351].

v: Derius[230]; Flevina[1431]; Hana; HD2329[1352]; Kalyansona[1351, 1352]; Laketch[50]; Leda[1430]; Manella[1431]; Merlin[1622]; Odra[71]; PBW54[1352]; PBW120[1352]; Slavia[71, 73]; Soissonais Desprez[851]; WG377[1352]; WH147[1352]; WL711[1352]; WL1562[1352]. **v2**: Avocet (U.K.) **Yr1 Yr6**[1459]; Brigand **Yr14**[83]; Cleo ***Yr3c***[1457]; Cleo ***Yr3c*** **Yr14**[1431]; Fenman **Yr1**[1459]; Flamingo **Yr6**[1430]; Flevina **Yr7**[1430]; Galahad (heterogeneous) **Yr1 Yr14**[1459]; Garant **Yr7**[230]; Hardi **Yr7**[230]; Heines Kolben **Yr6**[611]; Heines Peko **Yr6 Yr25**[746]; Heines VII **Yr25**[851]; Ibis **Yr1**[604]; Lely **Yr7**[1430]; Liberator ***Yr3c***[1431]; Longbow **Yr1 Yr6**[83]; Mardler **Yr1** ***Yr3a Yr4a*** **Yr13**[1459]; Maris Beacon ***Yr3b Yr4b***[1459]; Maris Huntsman ***Yr3a Yr4a*** **Yr13**[604]; Maris Nimrod **Yr13**[1459]; Marksman **Yr1** (heterogeneous) **Yr13**[1459]; Mithras **Yr1 Yr6**[1459]; Nautica **Yr9**[1430]; Norman **Yr6**[83]; Rapier **Yr4**[83]; Rothwell

Perdix **Yr1**[604]; Sonalika **YrA**[1352]; Stella **Yr3**[1430]; Sylvia **Yr1**[1430]; Tadorna **Yr1**[1431]; Viginta ***Yr3a Yr4a***[71, 73]; Wizard (heterogeneous) **Yr14**[1459]; Yamhill ***Yr3a Yr4a***; Zdar ***Yr4a***[73].

Yr2 originally referred to a gene in Heines VII conferring resistance to European pathotypes. However, Heines VII possesses at least additional resistance gene, **Yr25**[1351] that can be detected with a geographically wider range of pathogen isolates. **Yr2** is present in Kalyansona[1351] and a range of spring wheats distributed by CIMMYT.

YR3

Yr3

Undesignated allele.

v: Enkoy[50], **v**: Vilmorin 23; Staring[1430], **v2**: Minister **Yr2**[1430], **v2**: Savannah **Yr1 Yr2 Yr9 Yr32**[10016], **v2**: Senat **Yr32**[10016], **v2**: Stella **Yr2**[1430]

Yr3a[851] locus: 1B[184, 185]. 2B[10370]. 5BL[11235]

i: Taichung 29*6/Vilmorin 23[10370]. **v**: Bon Fermier[1431]; Nudif TP1[1431]; Stephens[182, 184]; Vilmorin 23[10370]. **v2**: Argent **Yr1** ***Yr4a*** **Yr6**[1067]; Cappelle-Desprez ***Yr4a***[851]; Druchamp ***Yr4a***; Hobbit ***Yr4a*** **Yr14**[604]; Kinsman ***Yr4a*** **Yr6**[604]; Mardler **Yr1 Yr2** ***Yr4a*** **Yr13**[1459]; Maris Huntsman **Yr2** ***Yr4a*** **Yr13**[604]; Maris Freeman ***Yr4a*** **Yr6**[604]; Maris Ranger ***Yr4a*** **Yr6**[604]; Nord Desprez ***Yr4a***[182, 184]; Top ***Yr4a***[230]; Viginta **Yr2** ***Yr4a***; Yamhill **Yr2** ***Yr4a***[182]; Zdar ***Yr4a***[71, 73]. **ma**: **Yr3** (**YrV23**) – *Xwmc356-2B*, 9.4 cM[10370].

Yr3b[851]

Chen and Line[182] found that a second gene in Hybrid 46 – presumably this gene was not located at the **Yr3** locus.

v2: Hybrid 46 ***Yr4b***[851].

Yr3c[851] locus: 1B[184]

v: Minister[182, 184, 851]. **v2**: Cleo **Yr2**[1430]; Maris Beacon **Yr2** ***Yr4b***[1459].

Undesignated allele. v: Enkoy[50]; Vilmorin 23; Staring[1430]. v2: Minister **Yr2**[1430]; Savannah **Yr1 Yr2 Yr9 Yr32**[10016]; Senat **Yr32**[10016]; Stella **Yr2**[1430].

YR4

Yr4 locus: 3BS syn: YrRub

bin: 3BS3 - 0.87 - 1.00[10720], **v**: Avalon[10720], **v**: Bolac, **v**: Emu S[10720], **v**: Kenya Kubangu[50], **v**: Rubric AUS33333[10720], **v2**: Avalon **Yr14**[83], **v2**: Rapier **Yr2 Yr14**[83], **ma**: **Yr4** - 2.9 cM - *Xcfb3530-3B* - 2.4 cM - *Xbarc75-3B*[10720]

Yr4a[851] locus: 6B[184, 185]

v: Vilmorin 23[184]. **v2**: Argent **Yr1** ***Yr3a*** **Yr6**[1067]; Cappelle-Desprez ***Yr3a***[851]; Druchamp ***Yr3a***[182]; Hobbit ***Yr3a*** **Yr14**[604]; Huntsman **Yr2** ***Yr3a*** **Yr13**[604]; Kinsman ***Yr3a*** **Yr6**[604]; Maris Ranger ***Yr3a*** **Yr6**[604]; Maris Freeman ***Yr3a*** **Yr6**[604]; Mardler **Yr1 Yr2** ***Yr3a*** **Yr13**[1459]; Nord Desprez ***Yr3a***[182]; Top ***Yr3a***[230]; Viginta **Yr2** ***Yr3a***[71, 73]; Yamhill **Yr2** ***Yr3a***; Zdar ***Yr3a***[71, 73].

Yr4b[851] locus: 6B[184]

v: Avalon[1160]; Opal[1431]; Staring[1430]. **v2**: Hybrid 46 ***Yr3b***; Maris Beacon **Yr2** ***Yr3b***[1160, 1459]; Nudif TP12 ***Yr3c***[1431]; Stella **Yr2**[1430]. Undesignated allele. [**YrRub**[10720]]. 3BS[10720]. **bin**: 3BS3-0.87-1.00[10720]. **v**: Avalon[10720]; Bolac; Emu S[10720]; Kenya Kubangu[50]; Rubric AUS33333[10720]. **v2**: Avalon **Yr14**[83]; Rapier **Yr2 Yr14**[83]. **ma**: **Yr4** – 2.9 cM – *Xcfb3530-3B* – 2.4 cM – *Xbarc75-3B*[10720].

The conclusion that **YrRub** is **Yr4** is based on specificity similarities and the presence of the $Xcfb3530_{150}$ and $Xbarc75_{132}$ alleles in the five genotypes listed above. The 3BS location is not consistent with that listed for ***Yr4a*** and ***Yr4b***.

YR5

Allelism with YR7 and *YRSP* (*Sr5b*) is reported in ▶[10759] but cloning indicated that YR5 and ***YrSP*** are not allelic with **Yr7**[11351].

Yr5[877] locus: 2BL

i:AVS+Yr5[970], **i**:Lemhi+Yr5[11153], **v**:By 33[03102], **v**:E5557[1267], **v**:E8510[1267], **v**:*T. spelta album*[877], **v**:Seven spelt accessions from Europe and Iran[640], **ma**:GrainGenes **gene** locus link close' target=_blank>Yr5 - 10.5 & 13.3 cM - GrainGenes **microsatellite** marker link close' target=_blank>*Xgwm501-2B*[03102], **ma**:Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers *Xwgp17-2B* / *Xwgp19-2B* and *Xwgp26-2B*[10096], **ma**:*Xwgp17-2B* was later converted into a simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker[10097], **ma**:Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310[10435], **ma**:GrainGenes **microsatellite** marker link close' target=_blank>*Xwmc175-2B* - 1.1 cM - *YrSTS-7* / *8* - 0.3 cM - GrainGenes **gene** locus link close' target=_blank>Yr5 - 0.4 cM - GrainGenes **microsatellite** marker link close' target=_blank>*Xbarc349-2B*[10826], **ma**:GrainGenes **microsatellite** marker link close' target=_blank>*Xwmc175-2B* ? 4.6 CM ? GrainGenes **gene** locus link close' target=_blank>YR5 / *TaAffrx.65234.1.S2-at* / *Ta.28038* ? 0.7 cM ? *S23M41-310* / *STS:S23M41-275*[11153]

Yr5a[11351] locus: 2BL[34] syn: Yr5[877].

Allelic with **Yr7** and ***YrSp***[10759]

i: AVS+Yr5[970]; Lemhi+Yr5[11153]. **v**: By 33[03102]; E5557[1267]; E8510[1267]; *T. spelta album*[877]; Seven spelt accessions from Europe and Iran[640]. **ma**: **Yr5** – 10.5 & 13.3 cM – *Xgwm501-2B*[03102]; Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers *Xwgp17-2B*, *Xwgp19-2B* and *Xwgp26-2B*[10096]; *Xwgp17-2B* was later converted into a simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker[10097]; Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310[10435]; *Xwmc175-2B* – 1.1 cM – *YrSTS-7/8* – 0.3 cM – **Yr5** – 0.4 cM – *Xbarc349-2B*[10826]; *Xwmc175-2B* – 4.6 cM – YR5/*TaAffrx.65234.1.S2-at/Ta.28038* – 0.7 cM – *S23M41-310/STS:S23M41-275*[11153]. Accurate prediction of ***Yr5a*** was achieved with markers *IWA4096*, *IWA 6121* and *IWA7850* for which primer sequences are available in Cereals DB[11286]. **c**: ***Yr5a*** (Genbank MN273772) along with **Yr7** and ***Yr5b*** has a BED-LRR structure lacking a CC-domain[11351].

Yr5b[11351] locus: 2B[10018, 10352] syn: YrSP[10018], YrSp[10352]

bin: 2BL-C-0.5. **i**: Cx1 = Avocet S*4/Spaldings Prolific[10018]; Taichung*6/Spaldings Prolific[10352]. **v2**: Spaldings Prolific **Yr25**[10018, 10352]. **ma**: ***YrSp*** – *Xwmc-2B*, 12.1 cM[10352]; *IWA638* – 0.6 cM – ***YrSP*** – 1.5 cM – *dp269-2* – 1.9 cM – *Xwmc332-2B*[11091]. **c**: (Genbank MN273773) along with **Yr5** and **Yr7** has a BED-LRR structure lacking a CC-domain[11351]. ***Yr5b*** is a truncated form of **Yr5** but confers a different specificity[11351].

YR6

Yr6[877] locus: 7B[746]. 7BS[331] syn: B[1622]

i: AVS+Yr6[970]. **v**: Austerlitz[230]; Fielder[181]; Heines Kolben[1622]; Koga II[746]; Maris Dove[604]; Recital[230]; Takari[368]. **v2**: Argent **Yr1** ***Yr3a Yr4a***[1067]; Avocet (UK) **Yr1 Yr2**[1459]; Cadenza **Yr7**[11187]; Flamingo **Yr2**[1430]; Heines Peko **Yr2**[746, 877]; Kinsman ***Yr3a Yr4a***[604]; Kolben **Yr2**[611]; Longbow **Yr1 Yr2**[83, 1459]; Maris Freeman ***Yr3a Yr4a***[604]; Maris Ranger ***Yr3a Yr4a***[604]; Mithras **Yr1 Yr2**[1459]; Norman **Yr2**[83, 1459]; Nudif TP241 **Yr7**[1431]; Nudif TP250 **Yr1**[1431]; Orca ***Yr3c***[1431]; Pavon 76 **Yr7**[284]; Penjamo 62 (heterogeneous) **Yr18**[1562]. **tv**: Duilio[192]; Latino[192]; Norba[192]; Quadruro[192]; Rodeo (heterogeneous)[192]. **ma**: *Xgwm577-7B* – **Yr6**, <0.4 cM[11187]; Narrowed to an ~60 kb region including *Xgwm577*[11188]; Given the location of *Xgwm577* the gene location should be 7BL.

YR7

TraesCS2B01G488000

Allelism with *YR5a* and *YRSP* is reported in ▸[10759] but cloning indicated that YR7 is not allelic with *YR5a* and ***YrSP*** (*Sr5b*)[11351].

Yr7[877] locus: 2B[612, 1429]. 2BL[965]

Allelic with ***Yr5a*** and ***YrSp***[10759]

i: AVS+Yr7[970]; Taichung 29*6/Lee[10371]. **v**: Present in many hexaploid wheats with ***Sr9g*** – see ▸[965]; Brock[83]; Lee[877]; Nudif TP257[1431]; PBW12[1352]; Paragon[11351]. Prinqual[230]; Renard[83]; Talent[230]; Tango[230];

Tommy[83]; WL2265[1352]. **v2**: Cadenza **Yr6**[11187]; Donata **Yr9**[1430]; Flevina **Yr2**[1431]; Garant **Yr2**[230]; Hardi **Yr2**[230]; Lely **Yr2**[1430]; Nudif TP241 **Yr6**[1431]; Pakistan 81 = Veery#5 **Yr9**[284]; Pavon 76 **Yr6**[284]; Reichersberg 42 **Yr25**[10]; Thatcher[965]. **tv**: Iumillo[965]; but not present Acme and Kubanka which also carry ***Sr9g***[965]. **ma**: **Yr7** – *Xgwm526-2B*, 5.3 cM[10371]; *Xwmc175A-2B* – **Yr7**, <0.4 cM[11187]. **c**: **Yr7** (Genbank MN273771) along with ***Yr5a*** and ***YrSP*** has a BED-LRR structure lacking a CC-domain[11351].

YR8

Yr8[1217, 1218] locus: 2D = T2D-2M[1218]. = T2DS-2M#1L.2M#1S[389]

Derived from *Ae. comosa*.

i: AVS+Yr8[970]. **tr**: Chromosome 2D-2M translocations in Hobbit Sib and Maris Widgeon[1016]; Compair[1217, 1218]; CS 3D/2M 3/8[967]; See also **Sr34** and ▶[967]. 2A = 2A-2M = T2AS-2M#1L.2M#1S[389] CS 2A/2M 4/2[967]. 2M-1. **su**: CS 2M#1(2A)[967].

YR9

Yr9[878] locus: 1B=1BL.1RS

Derived from *S. cereale*. See also Reaction to *P. graminis*, **Sr31**: Reaction to *P. triticina* **Lr26** 1B=1BL.1RS.

i: AVS+Yr9[970]. **v**: Almus[998]; Aurora[1623]. Chromosome status not specified Baron[83]; Benno[998]; Bezostaya II[998]; Branka[71]; Clement[1430, 1532]; Cougar[0267]; Danubia[68]; GR876[753]; Hammer[83]; Iris[68]; Kavkaz[1623]; Kromerzhizhskaya[1149]; Lyutestsens 15[1149]; Lovrin 10[998]; Lovrin 13[998]; Mildress[1027]; Perseus[998]; Predgornaya[998]; Rawhide (heterogeneous)[0267]; Riebesel 47/51[878, 1623]; Roxana[68]; Sabina[68]; Salmon[998]; Sarhad 82[284]; Selekta[68]; Shtorm[1149]; Skorospelka 35[998]; Sleipner[10038]; Solaris[68]; St 2153/63[997]; Stuart[83]; Veery[986]; Weique[1627]; Winnetou[998]; Weihenstephan 1007/53[1623]. **v2**: Agra **Yr3**[68, 71]; Brigadier **Yr17**[10785]; Donata **Yr7**[1430]; Haven **Yr6**[10038]; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 **Yr18 Yr27**[10160]; Lynx **Yr6 Yr17**[10038]; Nautica **Yr2**[1430]; Pakistan 81 = Veery#5 **Yr7**[284]; Savannah **Yr1 Yr2 Yr3 Yr17**[10016]; Stetson **Yr1**[83]; Sparta **Yr3**[71]. **tv**: Cando*2/Veery, KS91WGRC14[381]. 1R(1B)[997, 1623]. **su**: Burgas 2[998]; Clement[1160]; Lovrin 13[998]; Mildress[998]; Mironovskaja 10[998]; Neuzucht[1623]; Orlando[1623]; Roseana[68]; Saladin[997]; Salzmunder Bartweizen[1623]; St 14/44[998]; Weique[1627]; Wentzel W[1623]; Winnetou[1027]; Zorba[998]; See also ▶[50]. **ma**: Several markers tightly linked with **Yr9** were identified in ▶[377]; **Yr9** – 3.7 cM – *Xgwm582-1BL*[10365].

Stripe rust resistant wheat – *S. africanum* derivatives G17 (substitution line with $1R^a$), L9-15 (1BL, $1RS^a$ and L2-20 (putative cryptic translocations) are reported in ▶[10596].

YR10

TraesCS1B03G0003500, *TraesCS1B03G0003600* (CS RefSeq 2.1)

Yr10[878] locus: 1BS[1002]. 1B[641] syn: YrVav[0262]

TraesCS1B03G0003500, *TraesCS1B03G0003600* (CS RefSeq 2.1)

i: AVS+**Yr10**[970]. **v**: AC Radiant[11167]; Crest[11304]; Jacmar[11145]; Moro[878]; PI 178383[878]; QLD709 = Janz*2/*T. vavilovii*[0262]; *T. spelta* 415[641]; *T. vavilovii* AUS 22498[0262]; 10 Chinese cultivars[11304]. **ma**: A SCAR marker was described in ▶[0261]; QLD709 and *T. spelta* 415, both with white glumes, failed to amplify the SCAR sequence, but both carried unique alleles at the **Gli-B1** and *Xpsp3000-1B* loci[0262]. These differed from the Moro source of **Yr10**. **Yr10** – 1.5 cM – **Gli-B1** – 1.1 cM – *Xpsp3000-1B*[0261]; **Yr10** – 1.2 cM – *Xpsp3000* – 4.0 cM – **Gli-B1**[321]; Cosegregation between a RGA marker *RgaYr10a* and **Yr10** was reported in ▶[0376]. **Yr10**/*Xsdauw79* – 0.2 cM – *Xsdauw78* – 1.0 cM – $\mathbf{Yr10}_{CG}$ – 2.1 cM – *Xsdauw75* – 0.5 cM – *Xpsp3000-1B*[11304]. **c**: **Yr10** has a CC-NBS-LRR structure. GenBank AF149112[11145]. AF149112 ($\mathbf{Yr10}_{CG}$), *TraesCS1B03G0000200*, shown not to be the candidate gene[11304].

YrNAM[11692]

c: A gene named **YrNAM** located 1.2 cM from 'Yr_{CG}', the original allegedly claimed **Yr10**, but with common specificity, encoded an NLR with 5' NAM and 3' ZNF0BED domains[11692]. Yr_{CG} was confirmed as **Yr10** {11763). GenBank OP490604.

YR11

Yr11 syn: R11[1157]

Adult plant resistance.

v: Joss Cambier[606]. **v2**: Heines VII **Yr2 Yr25** see ▸[970].

YR12

Yr12 syn: R12[1157]

Adult plant resistance.

v: Fleurus[1158]; Frontier[1159]; Pride[1157]. **v2**: Armada ***Yr3a Yr4a***[81, 1160]; Mega ***Yr3a Yr4a***[1157, 1160]. **v**: Waggoner ***Yr3a Yr4a*** **Yr6**[1158].

YR13

Yr13 syn: R13[1157]

Adult plant resistance.

v2: Bounty **Yr1** ***Yr3a Yr4a***[1459]; Brigand **Yr2** ***Yr3a Yr4a*** **Yr14**[609]; Copain ***Yr3a Yr4a***[1158]; Gawain **Yr2** ***Yr3a Yr4a*** **Yr14**[81]; Guardian **Yr2**[82]; Hustler **Yr1 Yr2** ***Yr3a Yr4a***[83, 1459]; Kinsman ***Yr3a Yr4a*** **Yr6**[1459]; Mardler **Yr1 Yr2** ***Yr3a Yr4a***[1459]; Maris Huntsman **Yr2** ***Yr3a Yr4a***[83, 604, 1459]; Maris Nimrod **Yr2** ***Yr3a Yr4a***[607, 1157, 1459]; Marksman **Yr1** (heterogeneous) **Yr2** ***Yr3a Yr4a***[1459]; Pageant **Yr2** ***Yr3a Yr4a***[82]; Professor Marchal **Yr2** ***Yr3a Yr4a***[607]; Sportsman **Yr1** ***Yr3a Yr4a***[1459]; Virtue **Yr1** ***Yr3a Yr4a***[83, 1158, 1459].

YR14

Yr14 syn: R14[1157]

Adult plant resistance.

v: Kador[1158]; Score[1157]; Wembley[610]. **v2**: Avalon ***Yr3b Yr4b***[83, 1459]; Brigand **Yr2** ***Yr3a Yr4a*** **Yr13**[83, 609, 1459]; Galahad **Yr1 Yr2** (heterogeneous) ***Yr3a Yr4a***[83, 1459]; Gawain **Yr2** ***Yr3a Yr4a*** **Yr13**[81]; Hobbit ***Yr3a Yr4a***[1157, 1459]; Maris Bilbo ***Yr3a Yr4a*** 1459, 1157}; Moulin **Yr6**[83]; Rapier **Yr2** ***Yr3b Yr4b***[83]; Wizard **Yr2** (heterogeneous) ***Yr3b Yr4b***[83, 1459].

YR15

Yr15[432, 969] locus: 1BS[939], {969|,[0003] syn: YrH52[0003], YrG303[11429], Wtk1[11392]

i: AVS+**Yr15**[970]. **v**: Agrestis[330]; Boston[330]; Clearwhite 515[11392]; Cortez[330]; Expresso[11392]; Legron[330]; Ochre[11240]; Patwin 515[11392]; Seahawk[11392]. Hexaploid derivatives of *T. dicoccoides* G-25[432, 466]; *T. dicoccoides* H52[11429, 0003]; *T. dicoccoides* G303[11429]; V763-2312[969]; V763-254[969]. **tv**: *T. dicoccoides* G-25[431, 432, 466];; D447 derivatives B1, B2, B9, B10[1434]. **ma**: *Xgwm33-1B* – 5 cM – **Yr15**[9904]; *Xgwm33-1B* – 4.5 cM – **Yr15** – 5.6 cM – *UBC199200* – 5.6 cM – **Nor-B1**[110]; Gene order **Yr15** – **Yr24** – *Xgwm11-1B*[10112]; *OPB131420* – 27.1 cM – **Yr15** – 11.0 cM – *Nor-B 1*[1434]; *Xwmc128*/*Xgwm273*/*Xgwm582-1B* – 0.4 cM – **Yr15**/*Xwgp34*/*Xgwm413*/*Xbarc8*[10826]; *Xbarc8-1B* – 3.9 cM – **Yr15** – 2.5 cM – *Xgwm413-1BS*[11173]. *Xbarc8-1B* – 0.26 cM – **R11**/*R5* – 0.51 cM – **Yr15** – 0.26 cM – *Xgwm413-1B*/*R8*[11240]; *Xbarc-8-1B* – 4.2 cM – **Yr15** – 3.5 cM – *Xgwm413-1B*[11348]; *Xbarc8-1B* – 4.1 cM – **Yr15** – 2.5 cM – *Xuhw-1B* – 0.5 cM – *Xgwm413-1B*[11348]. **Yr15** is proximal to **Yr64**; recombinant lines are reported in ▸[11349]; *Xwhu300-1B* – 0.013 cM – *Xwhu273-1B*[11392]; distal … **Yr15** – 9.6 cM – **YrH52** – 1.4 cM – **Nor-B1** – 0.8 cM – *Xgwm264a* – 0.6 cM – *Xgwm18*[3]; *Xgmw273a* – 2.7 cM – **YrH52** – 1.3 cM – *Xgwm413*/**Nor1** … centromere[108]; A line combing combining **Yr15** and **Yr64** is reported in ▸[11618]: gene order $Xbarc8_{239}$ – YR15 – $Xgwm413_{102}$ – YR64 – $Xgwm273_{196}$. **c**: Encodes a putative kinase-pseudokinase protein designated as wheat tandom kinase 1 (TPK1), g-DNA 4,655 bp, 665 amino acids. GenBank MG649384, MG674157[11392], MK188918 (**YrH52**)[11429], and MG18819 (**YrG303**).

YR16

Yr16[1598] locus: 2D[1598]

Adult plant resistance.

v: Bersee[1604]; Cappelle-Desprez[1598].

YR17

Yr17[62] locus: 2AS-6M^{v}.2AS[62]. 6M^{v} = 2MS-6MS.6ML or 2MS-6ML.6MS[0009] syn: YrHy1[11308], YrMm58[11308]

i: AVS+**Yr17**[970]. **v**: Apache[10554]; See **Lr37** (Reaction to *P. triticina*) and **Sr38** (Reaction to *P. graminis*); Arche[0044]; Balthazar[0044]; Bill[10554]; Brigadier[0044]; Caphorn[10554]; CDS Stanley[11579]; Clever[10554]; Clarus[10554]; Cordial[0044]; Corsaire[10554]; Eureka[44]; Hussar[0044]; Huaiyang 1[11308]; Jagger[10973, 11328]; Kris[10283]; Kochu[11267]; Mace[11579]; Mengmai 58[11308]; Milan[11267]; Mutus[11267]; Pernel[44]; Rapsodia[10554]; Renan[10554, 0044]; Rheia[10554]; RL 6081[939]; SY Mattis[11579]. Genotype list in ▶[02105]. **v2**: Brigadier **Yr9**[10785]; Lynx **Yr6 Yr9**; Savannah **Yr1 Yr2 Yr2 Yr32**[10016]. **ma**: **Yr17** was closely linked to the SCAR marker SC-Y15, developed from RAPD marker OP-Y15$_{580}$, and to *Xpsr150-2N*^{v} [0044]; Characterized by null alleles for *Xwmc382-2A* and *Xwmc407-2A* [10283]; SCAR markers SC-372 and SC-385 were developed in ▶[10796].

Although **Yr17** was reported as a seedling-effective gene[62] some researchers report problems in obtaining repeatable seedling responses and prefer to treat this gene as conferring adult plant resistance[11221].The 2NS translocated segment carrying **Yr17** replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682*[10073].

Mundt[11340] noted that many genotypes containing **Yr17** continued to have adult plant resistance to races virulent on the seedlings. These cultivars included Renan, Apache, Jagger, Bobtail and Madsen. However, it was unclear as to whether this represented additional resistance gene(s) in the introduced segment or APR genes at other loci.

The 2N^{V}S segment carries a second high-temperature adult plant resistance gene designated *YrM1225* in AvS+**Yr17** mutant M1225[11706]. Presumably the same gene was mapped to the proximal 19.36 – 33 MB region of the translocation in the Jagger reference genome and two candidate genes were predicted[11760].

YR18

Yr18[1362] locus: 1362}. 7DS[324]. 7D[1362]

TraesCS7D03G0183600

i: AVS+**Yr18**[970]; Thatcher (**Yr7**) near-isogenic lines with **Lr34** including the 13 2-gene combinations reported in ▶[434, 937]. **v**: Jupateco 73R; Lerma Rojo 64[1375]; Libellula[11139]; Nacazari 76[1375]; Strampelli[11139]; Tesia F 79[1375]; Tonichi S 81[1375]; Wheaton 1375}. **v2**: Parula **Yr29**[10281]; Penjamo 62 **Yr6** (heterogeneous)[1375]; Saar **Yr29**[10481]; Wheats with **Lr34** (See **Lr34**); Others[1376]; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Bascribey 95, Seyhan 95 **Yr9 Yr27**[10160]. **ma**: Complete linkage with **Lr34**[937, 1362]; **Ltn**[1361]; and **Bdv1**[1363]; *Xgwm120-7D* – 0.9 cM – **Yr18** – 0.7 cM – *Xgwm295-7D*[10259]. **c**: See **Lr34**; Putative ABC transporter[10648]. This gene is identical to **Lr34**, **Pm38** and **Ltn** and confers stem rust resistance in some genetic backgrounds. Some AVS NILs also have **Yr18**. Forty-three Chinese land varieties predicted to have **Yr18** based on markers had high rust severities. Genetic analyses of four of these landrace (Sichuanyonggang 2, Baikemai, Youmai and Zhangsihuang) indicated the presence of an independent suppressor[11101]. Libellula had an additional 4 QTL and Strampelli had an additional 3 QTL[11139].

Yr18 conferred seedling resistance to leaf rust when transformed into durum wheat {M10114}.

YR19

Yr19[183] locus: 5B[183] syn: YrCom[183]

v2: Compair **Yr8**[183].

YR20

Yr20[183] locus: 6D[183] syn: YrFie[181]

v2: Fielder **Yr6**[183].

YR21

Yr21[183] locus: 1B[183, 10450] syn: YrLem[181]

v: Lemhi[183].

A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei*[10450]. Both genes were mapped relative to RGAP markers. **Yr21** – *YrRpsLem*, 0.3 cM[10450].

YR22

Yr22[183] locus: 4D[183] syn: YrLe1[183]

v2: Lee **Yr7 Yr23**[183].

YR23

Yr23[183] locus: 6D[183] syn: YrLe2[183]

v2: Lee **Yr7 Yr22**[183].

YR24

Yr24[952] locus: 1BS[952] syn: YrCH42

Identical to YR26.

i: AVS+**Yr24**[970]. **v**: Chuanmai 42[10339]; Meering*3/K733/*Ae. tauschii* AUS18911[952]; Neimai 836[11259]. Synthetic 769[10339]. **tv**: Decoy 1[10339]; K733[952]. **ma**: Gene order **Yr15** – **Yr24** – *Xgwm11-1B*[10112]; *Xbarc187-1B* – 2.3 cM – **Yr24** – 1.6 cM – *Xgwm498-1B*[10339].

Yr24 is identical to **Yr26**[10339, 11391].

YR25

Yr25[158] locus: 1D[158]

v: Carina[0010]; Hugenout[0010]; Strubes Dickkopf; TP1295[158]; TP981[158]; Tugela[314]; Tugela-DN[314, 0010]. **v2**: Carstens V **Yr32**[10016]; Heines Peko **Yr2 Yr6**[0010]; Reichersberg 42 **Yr7**[0010]; Spaldings Prolific ***YrSP***[10016].

Yr25 was predicted to be present in Strubes Dickkopf, Heines VII **Yr2**, Heines Peko **Yr2 Yr6**, Reichersberg 42 **Yr7** and Clement **Yr9**[158]. This prediction was confirmed for Heines VII, Heines Peko and Reichersberg 42 but the pathogen culture used in [0010] was not virulent on Clement (**Yr9**) or on Strubes Dickkopf where another, or a different gene, must be present.

YR26

Identical to YR24[10339, 11391].

Yr26[617] locus: 1BL[10544]

The earlier location of 6AS (6AL.6VS)[617] is not corect.1BS[0285].

bin: C-1BL-6-0.32[10544]. **i**: AVS+**Yr26**[970]. **v**: Guinong 22[11098]; Nannong 9918[10544]; Nei 2938[10544]; Nei 4221[10544]; Neimai 9[10544]; Lines R43, R55, R64 and R77[0285]. **tv**: *T. turgidum* Gamma 80-1. **tr**: Yangmai-5[617]. **ma**: **Yr26** – 1.9 cM – *Xgwm11-1B*/*Xgwm18-1B*[0285]; *Xgwm11*/*18-1B* – 1.1 cM – *Xwe171*/*202*/*210-1B* – 0.4 cM – *Xwe177*/*201-1B* – 0.3 cM – *Xwe173-1B* – 1.4 cM – **Yr26** – 6.7 cM – *Xbarc181-1BL* – 3.0 cM – *Xwmc419-1BL*[10544]; *Xgwm11-1B* – 0.9 cM – **Yr26** – 6.3 cM – *Xbarc181*[11350]. Located between KASP markers *WRS435* and *WRS312* in an interval of 0.4 cM[11350].

According to [10554] the markers most closely associated with **Yr26** are actually located in chromosome 1BL.

YR27

Yr27[928] locus: 2BS[928] syn: YrSk[928], QYr.sgi-2B.1[10184, 11232]

TraesKAR2B01G0121530LC. *TraesCSB02G182800*.

i: AVS+**Yr27**[970]. **v**: Avocet 2B (= AvocetS + **QYr.sgi-2B.1**)[11593]. Ciano 79[928]; Inquilab 91[928]; Kauz[928]; McMurachy[928]; Opata 85[928]; PWB343[928]; Selkirk[928]; Webster[928]. **v2**: Attila **Yr27**[928]; Kariega **Yr18**[11593]; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 **Yr9 Yr18**[10160]. **ma**: When analysed as a QTL, variation associated with the **Yr27** locus was associated with RFLP markers *Xcdo152-2B* and *Xcdo405-2B*[928]. A **Yr27**-specific molecular marker was based on Asn 895 found only in **Yr27**[11593].

Many CIMMYT wheat lines[953]. Recombination **Yr31** – **Yr27**, 0.148, **Yr31** – **Lr23**, 0.295[0325]. c: **Yr27** is an allele at the LR13/NE2 locus[11593].

YR28

Yr28[1377] locus: ; *YrAet672* [11664]. 4DS[1377] syn: YrAS2388[10822, 11438]

v: Synthetic = Altar 84/*Ae. tauschii* W-219. Synthetic/Opata 85 SSD population. Genotype lists:[970, 1325]. **dv**: *Ae. tauschii* W-219[1377]; CPI 110672[11664]. **ma**: Close association with *Xmwg634-4DS*[1377]. **c**: **Yr28** has a CC-NBS-LRR structure, alternative splicing in the NBS region and duplicated 3' UTR[11438]. GenBank MK73661 – MK73666[11438].

Yr28 was present in all tested accessions of *Ae. tauschii* ssp. *strangulata* and some accessions of ssp. *tauschii*[11438]. Often suppressed in synthetic and derived wheat backgrounds.

Yr22 was also reported for chromosome 4D, but in the absence of an appropriate single gene stock and the unavailability of avirulent cultures in most laboratories, tests of linkage with **Yr28** are unlikely in the foreseeable future. Partial suppression of resistance in synthetic wheat derivatives carrying **Yr28** was associated with reduced transcript accumulation[11664].

YR29

Yr29[119, 0119] locus: 1BL[0119]

Adult plant resistance[0119].

s: Lalbahadur(Parula 1B)[10281]. **v**: Druchamp[11235]; Kundan[11248]. **v2**: Attila **Yr27**[10281]; Parula **Yr18**[10281]; Pavon F76 **Yr6 Yr7 Yr30**[119]; Quaiu3 **Yr30**[10943]; Saar **Yr18**[10481]; **Yr29** is completely linked with **Lr46**. See **Lr46**[119]. **tv**: Stewart[11542]. **ma**: *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – **Yr29** 2.9 cM – *Xbac17R Xgwm140-1B*[10281]; *Xgwm44-1B* – 3.6 cM – **Yr29** – 2.1 cM – *XtG818/XBac17R … Xgwm140-1B*[10281]; Associated with **Ltn2** and **Lr46**; *QYr.ucw-1BL* was mapped to a 0.24 cM region (332 kb IWGSC RefSeq v1.0 between *ucw.k31* and *csLV46G22*[11386].

Yr29 is a frequent gene in durum wheat (11542and references therein).

YR30

Yr30[0120] locus: 3BS[0120]

Adult plant resistance[0120].

v: Opata 85[0120]; Parula[0120]. **v2**: Inia 66 **YrA**[0120]; Pavon F76 **Yr6 Yr7 Yr29**[0120]; Quaiu3 **Yr29**[10943]; **Yr30** is closely linked with **Sr2** and **Lr27**[0120].

According to [11773] **Yr30** is present in Yaco S, Zhou8425b, Napo 63 and Orofen.

YR31

Yr31[0325] locus: 2BS

v: Pastor[0325]. **ma**: Recombination values: **Yr31** – **Yr27**, 0.148; **Yr31** – **Lr23**, 0.295; **Yr27** – **Lr23**, 0.131[0325]; **Yr31** maps between **Lr12** and **Lr23**[10928].

YR32

Yr32[10016] locus: 2AL[10016] syn: YrCV[1430], YrCv[939]

i: Avocet S*4/Carstens V[970]; Cook*6/Carstens V[970]; CRW380 = Carstens V/3*Avocet S[10016]; Tres/6*/Avocet S[10016]. **v**: Anouska[1430]; Caribo[1430]; Consort[10021, 10023]; Cyrano[1430]; Danis[10023]; Deben[10283]; Hereward[10021, 10022]; Okapi[1430]; Oxbow[10021]; Senat[10016]; Solist[10016]; Stakado[10016]; Toisondor[11144]; Tres[10016]; Vivant[10023]; Wasmo[10016]. **v2**: Carstens V **Yr25**[10016]; Felix **Yr3**[1430]; Kraka **Yr1**[10021, 10038]; Savannah **Yr1 Yr2 Yr3 Yr4 Yr17**[10016]; Senat **Yr3**[10016]; Zdar ***Yr3a Yr4a***[67]. **ma**: *Xwmc198-2A* – 2 cM – **Yr32**[10016].

Yr32 was coincident with one AFLP marker[10016].

YR33

Yr33[10039] locus: 7DL[10039]

More readily detected in seedling tests at elevated temperatures[10336].

v: Batavia[10039]; EGA Gregory; Strezecki. **ma**: Linkage with *Xgwm111-7D* and *Xgwm437-7D*[10039].

YR34

Yr34[10040] locus: 5AL[10040] syn: Syn. Yr48[11266]

v: AUSC[10040]; UC1110/PI 610750 RIL#143[11266]; AUS27492[11720]; WAWHT2046 = AUS91389[10040]. **ma**: *Xgwm410.2-5A* – 8.2 cM – **B1** – 12.2 cM – **Yr34**[10040]; *Xgwm291-5A* – 0.5 cM – **B1** – 1.5 cM – **Yr34**/*Xgwm410.2-5A*/*Xcfa2149-5A*/*KASP_109/KASP_6988*/etc.[11266]; *Xgwm291-5A* – 2.3 cM – **B1** – 0.7 cM – **Yr34**/*Xgwm410.2-5A*/*Xcfa2149-5A*/*KASP_109/KASP_6988*/etc.[11266]. **Yr34** is in a 5AS.5AL-5A^{m}L translocation segment that is present in genotypes Arina*LrFor* and SY Mattis in the Wheat10+ Genome panel[11602]. Associated with 5 markers[11720].

This gene confers a weak seedling resistance (IT 2C to 3C) and a strong adult plant resistance (0 to 10R)[10040] to Australian pathotype 134E16A+, but is not effective against Australian pathotype 110E143A+[10040].

Yr34 is <1cM from the awn inhibitor **B1**[11266].

YR35

Yr35[10203] locus: 6BS[10203]; 6^{S}S.6^{S}L-6BL[11778] syn: YrS8[10204]

v: 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS[10204]. **tv**: According to ▶[11778] **Yr35** originated from *Ae. longissima* or *Ae. sharonensis*. *T. dicoccoides* 479[10204]. **ma**: *Xgwm191-6B* – 18.9 cM – **Yr35** – 3 cM – **Lr53** – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B*[10780].

Genetically associated with **Lr53**.

YR36

Yr36[10138, 10272] locus: 6BS[10138]

Adult plant resistance.

i: Yecora Rojo NIL PI 638740[10138]. **v**: Burnside[11044]; Glencross[11044]; Glupro[10138]; Lilian[11044]; Shumai 1701[11258]; Somerset[11044]; UC1041+**Yr36**[10649]. **itv**: UC1113 NIL PI 638741[10138]. **tv**: RSL#65[623, 10138, 10649]; *T. dicoccoides* FA-15[10138]; *T. dicoccum* PI 415152 {M10058}. **ma**: **Yr36** is between *Xucw74-6B* and *Xucw77-6B* and 3-7 cM proximal to **Nor-B2**[10138]; **Yr36** is closely linked to the high grain protein locus of *T. turgidum* var. *dicoccoides* FA-15[10138]; **Nor-B2** … *Xucw68-6B* – *Xucw69-6B*/*Xbarc101-6B*/**Yr36** – *Xucw66-6B*[10272]; **Yr36** is 2 – 4 cM proximal to **Gpc-B1**[10272]. **c**: ACF33182; **Yr36** encodes wheat kinase-START-1 protein[10649]; WKS1 is absent in almost all modern tetraploid and common wheats[10649]; **Sr36** was shown to reduce the ability of the thylakoidassociated ascorbate peroxidase to detoxify reactive oxygen species[11128].

Although originally described as conferring high temperature adult plant resistance. This gene confers partial resistance in both juvenile and adult plants at temperatures less than 18C[11277].

YR37

Yr37[10139] locus: 2DL[10139]

Derived from *Ae. kotschyi*.

v: Line S14[10139]. **ad**: Line 8078[10139]. **al**: *Ae. kotschyi* 617[10139].

YR38

Yr38[10224] locus: 6A (6AL-6L^{sh}.6S^{sh})[10224] syn: YrS12[10204]

v: nong = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17[10224]; Recombinants with shorter segments – 07M4-39, 07M4-157 and 07M4-175 are reported in ▶[10691]. **al**: *Ae. sharonensis*-174[10224].

YR39

Yr39[10416] locus: 7BL

HTAP resistance 7BL[10416].

v: Alpowa[10416]. **ma**: Closely linked to several RGAP markers[10416].

YR40

Yr40[10328] locus: 5DS(5DL.5DS-T5MS^{G} [10328]

Derived from *Ae. geniculata*.

v: TA 5602[10328]; TA 5603[10328]; TA56501[11553]. **ad**: TA7659[11553]. **al**: *Ae. geniculata* (=*ovata*) ($U^{s}U^{s}M^{g}MM^{g}$) TA10437[10328]. **ma**: Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873*[10328]; Completely linkd with **Lr57**[10328]; CAPS marker *XLr57/Yr40-MAS-CAPS16*[10770].

Line TA5601 carries an estimated 5% of $5M^{g}$; and TA5602, 20%[11553]. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chromosome 5D and that **Yr40** is 12.4 cM proximal to **Lr57**[11553].

YR41

Yr41[10502] locus: 2BS[10228, 10502] syn: YrCN19[10228]

v: AIM[10228]; AIM6[10228]; Chuannong 19[10228, 10502]. **ma**: Complete linkage to a 391 bp allele of *Xgwm410-2BS*[10228]; *Xgwm410-2B* – 0.3 cM – **Yr41**[10502].

YR42

Yr42[10537] locus: 6A = 6AL-6^{Aen}L.6^{Aen}S[10537]

Derived from *Ae. neglecta*.

v: Line 03M119-71A[10537]. **al**: *Ae. neglecta* 155[10537]. Associated with **Lr62**[10537].

YR43

Yr43[10673] locus: 2BL[10673]

v: IDO377s = PI 591045[10673]; Lolo[10673]; many IDO377s derivatives[10673]. **ma**: *Xwms501-2B* – 11.6 cM – *Xwgp110-2B* – 4.4 cM – **Yr43** – 5.5 cM – *Xwgp103-2B* – 12.8 cM – *Xbarc139-2B*[10673].

YR44

Yr44[10673] locus: 2BL[10674] syn: YrZak[10674]

v: Zak = PI 607839[10674]. **ma**: *XSTS7/8*/**Yr5** – 12.7 cM – **Yr44** – 3.9 cM – *Xwgp100* – 1.1 cM – *Xgwm501-2B*[10674].

YR45

Yr45[10677] locus: 3DL[10677]

v: PI 181434[10677]; PI 660056[11024]. **ma**: *Xbarc6-3D* – 0.9 cM – *Xwmc656-3D* – 6.9 cM – *Xwpl18-3D* – 4.8 cM – **Yr45** – 5.8 cM – *Xwp115-3D*[10677].

This gene is highly effective and confers resistance to all North American *Pst* pathotypes.

YR46

Yr46[10678] locus: 4DL[10678]

Adult plant resistance.

bin: Distal to 0.56. **i**: RL6077 = Thatcher*6/PI 250413[10678]. **v**: Chapingo 48[11070]; PI 250413[10678]. **ma**: *Xgwm165-4D*/*Xgwm192-4D* – 0.4 cM – **Yr46**/**Lr67**[10678]. **c**: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices[11070].

Pleiotropic or closely linked with **Sr55** and **Lr67**

YR47

Yr47[10679] locus: 5BS[10679]

bin: 5BS6-0.81-1.00. **v**: AUS28183 = V336[10679]; AUS28187[10679]. **ma**: *Xgwm234-5B* – 10.2 cM – **Lr52** – 3.3 cM – **Yr47** – 9.6 cM – *Xcfb309-5B*[10679]; *Xcfb309-5B* – *Xsun480*/*Xmag705*/*Xfcp552-5B* – 0.4 cM –

Yr47 – 4.3 cM – *icg16c008*/*Xgwm234-5B*[11200]; *Xsun180* – 0.4 cM – **Lr52** – 0.2 cM – **Yr47** – 1.4 cM – *Xgwm234-5B*[11200].

This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of *Pst*. V336 is the original source of **Lr52**.

YR48

Yr48[10705] locus: 5AL[10705] syn: Syn. Yr34[11266], Qyr.ucw-5AL

Adult plant resistance. [**Qyr.ucw-5AL**[10705]].

bin: 5AL23 0.87-1.00. **v**: UC1110 (MR)/PI 610750 (MR): RIL4 GSTR 13504[10705]; RIL167 GSTR 13618[10705]; UC1110/PI 610750 RIL#143[11266]. **ma**: Co-segregated with ***Vrn2***, *BE495011*, *Xcfa2149-5AL*, *Xgpw2181a-5AL*, *Xwmc74-5AL*, and *Xwmc410-5AL*[10705]; *Xwmc727-5AL* – 4.4 cM – **Yr48** – 0.3 cM – *Xwms291-5AL*[10705]. PI 610750 = Synthetic 205 ((Croc 1/*Ae. tauschii*)/Kauz)[10705].

YR49

Yr49[10746] locus: 3DS[10746]

Adult plant resistance.

bin: 3DS6-0.55-1.00). **v**: AvocetS*3/Chuanmai 18 AUS91433[10746]. **v2**: Chuanmai 18 **Yr18**[10746]. **ma**: *Xgps7321-3D*/**Yr49** – 1 cM – *Xgwm161-3D*[10746].

YR50

Yr50[10849] locus: 4BL[10849]

Derived from *Th. intermedium*.

v: CH233[10849]. **ma**: cent … *Xbarc1096-4B* – 8.0 cM – **Yr50** – 7.2 cM – *Xbarc-4B*[10849].

The genetic distance between **Yr50** and **Yr62** was estimated to be 27.1±8.6 cM[11023].

YR51

Yr51[10850] locus: 4AL[10850] syn: YrAW1[10850]

bin: 4AL4-0.80-1.00. **v**: Line 5515 AUS 91456[10850]. **v2**: AUS 278589 **Yr57**[10850]. **ma**: *Xowm45F3R304A* – 1.2 cM – **Yr51** – 2.5 cM – *Xsun104-4A* – 1.8 cM – *Xgwm160-4A*[10850].

YR52

Yr52[10852] locus: 7BL[10852]

Adult plant resistance.

bin: 7BL3-0.86-1.00. **v**: PI 183527[10852]; PI 660057 = Avocet S/PI 183527 F4-41[10853]. **ma**: *Xbarc182-7B* – 1.2 cM – **Yr52** – 1.1 cM – *Xwgp5258* – 5.7 cM – *Xcfa2040-7B*[10852].

YR53

Yr53[10854] locus: 2BL[10854]

bin: 2BL3-0-0.35. **tv**: PI 480148[10854]. **v**: Avocet S/PI 480148 F5-128[10854]. **ma**: *Xwmc441-2B* – 5.6 cM – **Yr53** – 2.7 cM – *XLRRrev/NLRRrev*$_{350}$ – 6.5 cM – *Xwmc149-2B*[10853]; **Yr53** was estimated to be 35 cM distal to **Yr5** based on an F2 allelism test, but on an integrated map this distance was about 20 cM.

YR54

Yr54[10943, 10944, 10945] locus: 2DL[10944]

Adult plant resistance.

v: **Yr54** RIL GID6032209[10944]; **Yr54** RIL GID6032334[10944]. **v2**: Quaiu3**Yr29 Yr30**[10943, 10944]. **ma**: **Yr54** – 0.4 cM – *Xgwm301-2D*[10944].

Yr54 could be the same as *Qyr.tam-2D* in Alcedo[10945].

YR55

Yr55[10953] locus: 2DL[10953]

v: Frelon **Yr17** AUS 38882[10953]. **ma**: *Xmag4089-2D* – 11.4 cM – **Yr55** – 8.4 cM – *Xmag3385-2D*[10953].

YR56

Yr56[10955] locus: 2AS[10955] syn: Qyr.sun-2A[10955]

bin: Tentatively 2AS5-0.78-1.00[10955]. **tv**: AUS 91575[10955]; Wollaroi (AUS 99174)[10955]. **ma**: *Xbarc212-2A* – 3.7 cM – *Xbarc124-2A* – 2.1 cM – *Xsun167-2A* – 5.7 cM – **Yr56** – 7.6 cM – *Xsun168-2A* – 5.0 cM – *Xsun169-2A* – 8.0 cM – *Xgwm512-2A*[10955].

Wollaroi has additional APR QTL[10955].

YR57

Yr57[10963] locus: 3BS[10963] syn: YrAW2[10963]

bin: 3BS8-0.78-1.00. **v**: AUS 91463[10963]. **v2**: AUS 27858 **Yr51**[10963]. **ma**: *sts3B15* – 4.5 cM – *BS00062676* – 2.3 cM – **Yr57** – 2.0 cM – *Xgwm389-3B* – 2.0 cM – *Xbarc75-3B*[10963]; *Bs0006276* – 0.3 cM – **Yr57** – 1.3 cm – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B*[11480].

YR58

Yr58[10964] locus: 3BS[10964] syn: QYr.sun-3BS[10964]

Adult plant resistance.

bin: 3BS7-0.87-1.00. **v**: Sonora W195 AUS 19292 **Yr46** {10964. **ma**: *1121669/3023704* – 3.9 cM – **Yr58** – 4.6 cM – *100016328/123392*[10964].

YR59

Yr59[10966, 10967] locus: 7BL[10966]

Adult plant resistance.

bin: 7BL-0.86-1.00. **v**: Avocet S/PI 178759 F_4-158[10967]; PI 660061; PI 178759[10966]. **ma**: *Xwmc557-7B* – 2.2 cM – *Xwgp5175* – 2.1 cM – **Yr59** – 1.1 cM – *Xbarc32* – 0.5 cM – *Xbarc182-7B*[10966]. **Yr59** can be detected in high temperature seedling tests[10966, 10967]. **Yr59** is a highly effective HTAP resistance gene. Crosses with lines possessing **Yr39**, **Yr52** or **YrZH84** previously reported on chromosome 7BL segregated, indicating that they are at different loci. However, the allelism test data were based on F_2 phenotypes only. The linkage order of these genes is (proximal) **Yr39** – 31.2 cM – **Yr52** – 5.4 cM – *YrPI178759* – 6.0 cM – **YrZH84** (distal).

YR60

Yr60[10968] locus: 4AL[10968]

v: Almop, Avocet*3//Lalbmono 1B*4/Pavon GID 5934039[10968]. **v2**: LB(Pavon1B) **Yr29**[10968]. **ma**: *Xwmc313*/*Xwmc219-4A* – 0.51 cM – **Yr60**/*Xwmc776-4A*[10968].

Yr60 was estimated to be about 10 cM distal to **Yr51**

YR61

Yr61[10970] locus: 7AS[10970] syn: Yrpd34[10970], Yrdp34[10970]

v: Pindong 34[10970]. **ma**: *Xwgp5765b* – 3.9 cM – **Yr61** – 1.9 cM – *Xwp5467* – 12.5 cM – *Xcfa2174*[10970].

YR62

Yr62[11023, 11024] locus: 4BL[11023]

Adult plant resistance.

bin: 4BL5-0.86-1.00. **v**: PI 192252[11023]; PI 660060 = Avocet S/PI 192252 F4-103[11024]. **ma**: *IWA3611-4B* – 0.8 cM – *IWA4041-4B* – 0.8 cM – *IWA2171-4B* – 0.7 cM – *IWA99-4B* – 1.0 cM – *IWA1923-4B* – 1.2 cM – *Xgwm251-4B* – 3.3 cM – **Yr62** – 2.0 cM – *Xgwm192-* – 0.6 cM – *Xgwm495-4B* – 0.7 cM – *Xgwm513-4B*[11023].

The genetic distance between **Yr62** and **Yr50** was estimated to be 27.1±8.6 cM[11023].

YR63

Yr63[11027] locus: 7BS[11027]

bin: 7BS1-0.27-1.00. **v**: AUS 27955[11027]. **ma**: *IWB33120* – 0.9 cM – **Yr63** – 1.5 cM – *IWB52844* – 10.5 cM – *Xwmc606-7B*[11027]. *sun_KASP401* (0.6 Mb, CS RefSeq 2.1) – 2.1 cM – *sunCS_Yr63* – 2.1 cM – *sunKASP_406* (7.4 Mb)[11733].

YR64

Yr64[10967, 11030] locus: 1BS[11030]

bin: 1BS9-0.84-1.00. **v**: PI 660064 = Avocet S/PI 331260[10967]. **tv**: PI 331260[11030]. **ma**: *Xbarc8-1B* – 0.6 cM – *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 3.5 cM – **Yr64** – 2.0 cM – *Xgdm33-1B* – 5.0 cM – *Xgwm498-1B* – 3.9 cM – *Xcfd59-* – 0.4 cM – *Xgwm273-1B* – 3.9 cM – *Xgwm18-1B* – 2.6 cM – *Xbarc137-1B* – centromere[11030]; **Yr64** is distal to **Yr15**; recombinant lines are reported in [11349]. A line combing combining **Yr15** and **Yr64** is reported in [11618]: gene order $Xbarc8_{239}$ – YR15 – $Xgwm413_{102}$ – YR64 – $Xgwm273_{196}$.

YR65

Yr65[11030] locus: 1BS[11030]

bin: 1BS10-0.5-centromere. **v**: AvS/PI 480016 F_7-12[11030]. **tv**: PI 480016[11030]. **ma**: *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 5.5 cM – *Xgdm33-1B* – 4.6 cM – *Xgwm498-1B* – 3.5 cM – *Xbarc187-1B* – 2.8 cM – *Xgwm273-1B* – 3.7 cM – *Xgwm18-1B* – 1.2 cM – **Yr65** – 2.1 cM – *Xgwm11-1B* – 2.1 cM – *Xbarc137-1B* – centromere[11030].

YR66

Yr66[11032] locus: 3DS[11032] syn: YrVL1[11032]

bin: 3DS6-0.55-1.00. **v**: AGG91584WHWA = MSP4543.1[11032]. **v2**: VL Gehun 892 = AGG91586WHEA **Yr67**[11032]. **ma**: *KASP_18087* (3.550 Mb) – 2.1 cM – **Yr66** – 0.6 vM – *KASP_48179*[11032].

YR67

Yr67[11032, 11033] locus: 7BL[11032, 11033] syn: YrC591[11033], YrVL2[11032]

bin: 7BL10-0.78-1.00. **v**: AGG91585WHEA = MSP4543.4[11032]; C306[11032]; C591[11032, 11033]. **v2**: VL Gehun 892 = AGG91586WHEA **Yr66**[11032]. **ma**: *Xbarc32-7B* – 2.2 cM – *Xcfa2040-7B* – 8.0 cM – **Yr67** – 11.7 cM – *SC-P35M48*[11033]; *KASP_37096* (7.170 Mb) – 1.2 cM – **Yr67** – 3.6 CM – *KASP_2239* 7.211 MB)[11032].

YR68

CURATOR'S NOTE: publication could not be located.

Yr68[11051] locus: 4BL[11051]

Adult plant resistance.

bin: 4BL1-0.86-1.00. **i**: AGG91587WHEA1 = csAvYr4BL = Avocet S*5/Undesignated International Nursery ex New Zealand Entry 03.25[11051]. **v**: Undesignated International Nursery ex New Zealand 03.25[11051]. **ma**: *IWB74301* – 0.5 cM – **Yr68**/*IWA4640* – 0.5 cM – *IWB28394*[11051].

YR69

Yr69[11052] locus: 2AS[11052] syn: YrCH86[11052]

Derived from *Thinopyrum ponticum* partial amphiploid Xiaoyan 7430.

bin: 2AS5-0.78-1.00. **v**: CH7086[11052]. **ma**: *Xwmc25-2A* – 2.7 cM – *X2AS33* – 1.9 cM – **Yr69** – 3.2 cM – *Xmag3807-2A*[11052].

Linked with **Yr17**: (F_2 seedling test) 30.0 cM[11052]. No positive evidence for a *Th. ponticum* origin was presented.

YR70

Yr70[11055] locus: 5DS[11055] syn: YrUmb[11055]

Derived from *Ae. geniculata* [*YrUmb*[11055]].

v: IL393-4, *T. durum* cv. WH890/*Ae. umbellulata* Pau 3732//CS Ph^{I}/3/2*WL711[11055]. **al**: *Ae. umbellulata* Pau 3732[11055]. **ma**: **Yr70** – 7.6 cM – *Xgwm190-5D*[11055]; A co-segregating 450 bp *Lr57-Yr40*-CAPS16 marker was present in IL393-4, but not in many Australian wheat cultivars[11055].

Yr70 behaves as an allele of **Yr40** derived from *Ae. geniculata*. The low infection types are also different. The introgression carrying the *Ae. umbellulata* segment replacing terminal chromosome arm 5DS was

9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010*[11552]. Independent mutations indicated that **Yr70** differed from **Lr76**[11552].

YR71

Yr71[11056] locus: 3DL[11056] syn: YrSA3[11056]

Adult plant resistance.

v: AGG91588WHEA, Sunco/Avocet S RIL4667.153.11.1[11056]. **v2**: Sunco **Yr18**[11056]. **ma**: **Yr71** – 1.6 cM – *IWB17207*/*IWB10438*/*IWB23615*/*IWB63653* – 0.5 cM – *IWB57983* – 0.9 cM – *IWB23518* – 2.4 cM – *Xgwm114b-3D* – 5.6 cM – **Sr24**/**Lr24**[11056].

YR72

Yr72[11059] locus: 2BL[11059] syn: YrAW4[11059]

bin: 2BL5-0.59-0.89. **v**: AUS27506[11059]; AUS27894[11059]. **ma**: *Xsun481-2BL* (*wPt-665550*) – 1.8 cM – **Yr72** – 1.2 cM – *IWB12294* – 1.5 cM – *Xsun482-2BL* (*wPt-7161*) – 1.5 cM – *IWB69000*[11059].

YR73

Yr73[11062, 11063, 11064] locus: 3DL[11062, 11064]

Complementary gene involved in the *Yr* specificity.

v2: Avocet R **Yr74**[11063]; Anza = WW15 **Yr74**[11062]; Banks R **Yr74**[11063]; Condor R **Yr74**[11063]; Egret R **Yr74**[11063]; Funo **Yr74**[11062]; Jupateco 73 **Yr74**[11062]; Lerma Rojo-64 **Yr74**[11062]. **ma**: Located and mapped by DarT-Seq markers[11062].

YR74

Yr74[11062, 11063] locus: 5BL[11062]

Complementary gene involved in the **YrA** specificity.

v2: Avocet R **Yr73**[11063]; Anza = WW15 **Yr73**[11062]; Banks R **Yr73**[11063]; Condor R **Yr73**[11063]; Egret R **Yr73**[11063]; Funo **Yr73**[11062]; Jupateco 73 **Yr73**[11062]; Lerma Rojo-64 **Yr73**[11062]. **ma**: Located and mapped by DarT-Seq markers[11062].

The cross Avocet R/Teal used to map **Yr73** and **Yr74** included a 5BL-7BL reciprocal translocation. Susceptible lines carrying the individual genes will be permanently accessioned after screening candidate lines for the Avocet R = Chinese Spring chromosome configuration. The translocated chromosomes are present in Teal and do not involve **Yr74**.

YR75

Yr75[11065] locus: 7AL[11065] syn: YrAxe[11065]

Adult plant resistance.

bin: 7AL16-0.86-0.90. **v**: Axe/Nyabing-3 RIL#5[11065]. **v2**: Axe **Yr29**[11065]. **ma**: *Xcfa2016-7A* – 1.0 cM – **Yr75** – 0.3 cM – *IWB36240*[11065]. *sunKASP_429*/*_428* – 0.1 cM – *sunKASP-427* – 0.4 cM – **Yr75** – 0.3 cM – *sunKASP_430*[11670].

YR76

Yr76[186, 11067] locus: 3AS[11067]. 6D[186] syn: YrTye[186]

bin: 3AS4-0.45-1.00[11067]. **i**: AvS*4/Tyee[11067]. **v**: Tyee Citr 17773[11067]. **v2**: ARS-Amber[11067]; Cara[11067]; Chukar[11067]); Hyak **Yr17** (based on flanking markers)[11067]. **ma**: *Xbarc321-6D* – 6.2 cM – *Xbarc57-6D* – 4.3 cM – *Xwmc11-6D* – 2.6 cM – **Yr76** – 3.4 cM – *Xwmc532-6D* – 6.9 cM – *Xgwm369-6D* – 2.6 cM – *Xbarc12-6D*[11067].

YR77

Yr77[11174] locus: 6DS[11174] syn: Qyr.ucw-6D[11174], QYr.ucw-6D[11174]

Adult plant resistance.

v: PI 322118[11174]; PI 164377[11174]; PI 388095[11174]; PI 520350[11174]; PI 623378[11174]. **ma**: **Yr77** was strongly associated with *IWA167* in the region *Xbarc54-6D* (6DS) – 15.2 cM – *IWA167* (6DS) – 3.9 cM – *Xcfd188-6D* (6DL)[11174].

Among the listed accessions two were from India, one from Pakistan, one from Iran, and one from the USA.

YR78

Yr78[11174] locus: 6BS[11174] syn: Qyr.ucw-6B[11174], QYr.ucw-6B[11174]

Adult plant resistance.

v: Cadenza[11591]; Lancer[11591]; PI 519805[11174]; Spelt PI 190962[11591]; Nine others[11174]. **ma**: The **Yr78** peak fell within a 4.3 cM interval, *IWA7257* – *Xwmc737-6B*[11174]. **Yr78** was mapped to a 0.05 cM interval including the un-assembled **NOR-B2** locus on chromosome 6BS (RefSeq v1.1 0 region between 101,735,482 and 112,897,900 bp)[11591].

According to ◗[11174] **Yr78** is identical to *QYr.wgp-6BS.1* in Stephens[10602] and *QYr.sun-6B* in Janz[10751].

YR79

Yr79[11222] locus: 7BS[11222]

bin: 7BL-0.40-0.45. **v**: PI 182103[11222]; PI 679609, Avocet S/PI 679609 RIL#195[11222]. **ma**: *IWA220* – 2.9 cM – **Yr79** – *Xwmc335-7B* – 0.9 cM – *Xbarc72-7B* – 1.7 cM – *Xgwm297-7B*) – 1.6 cM – *Xgwm333*[11222].

YR80

Yr80[11261] locus: 3BL[11261] syn: YrAW11[11261]

Adult plant resistance.

bin: 3BL2-C-0.22. **v**: AUS27284[11261]. **ma**: *Xgwm3763B* – 15.2 cM – *KASP_5392/KASP_65624* – 3.0 cM – **Yr80** – 4.9 cM – *KASP_53113*[11261].

YR81

Yr81[11262] locus: 6AS[11262] syn: YrAW5[11262]

Adult plant resistance.

v: Aus27430/AvS RIL#16[11262]. **v2**: AUS27430 **Yr29**[11262]. **ma**: *KASP_3077* – 2.7 cM – **Yr81** – 6.4 cM – *Xgwm459-6A* – 1.0 cM – *KASP_11315*[11262].

YR82

Yr82[11322] locus: 3BL[11322]

bin: 3BL7-0.63-1.00. **v2**: AUS27969 = JI 1190592 **Yr29**[11322]. **ma**: *KASP_13376/sunKASP_301* – 0.4 cM – *sunKASP_300* – 2.0 cM – **Yr82** – 2.0 cM – *KASP_8775*[11322].

YR83

Yr83[11396] locus: 6A (T6AL.6RL[11396])

tr: T6AL.6RL C19.3[11396]. **ad**: Wheat + 6R[11396]; Wheat + 6RL[11396]. **su**: CS + 6R(6D)[11396]. **al**: Triticale accession T-701[11396]. **ma**: Deletion mapping indicated that **Yr83** was located in 6RL bin FL 0.73-1.00 containing PCR markers KU.86, TNAC1823, TNAC1826, and TNAC1844[11396].

The only previously designated *Yr* gene derived from *Secale cereale* is **Yr9** from chromosome 1RS.

YR84

Yr84[11585] locus: 1BS[11585]. AvocetS + Yr84[11777] syn: YrPI487260[11585]

v: Ruta*2/PI 487260[11585]. **tv**: *T. dicoccoides* PI 487260[11585]. **ma**: Located at 9.65 – 11.99 Mb YR84 is proximal to YR10 (0-1.4 Mb) and distal to YR15 (98 Mb)[11585] in the Zavitan v2 assembly (11585). Reduced to a 0.5 cM interval (975 Kb, Zavitan seq. v2). **c**: **Yr84** mutations were identified in closely linked head-to-head CNL (GenBank PP841907) and NL (NB-ARC-LR) (GenBank PP841906) genes, both of which were required for resistance[11777].

Yr84 confers resistance to all *Pst* pathotypes thus far tested and is described as incompletely dominant. Other named *YR* loci in chr. 1B are proximal to YR15 or located in arm 1BL. The low infection type is ; (fleck) to ;1 on a 0-4 scale. **Yr84** varies from other permanently named *Yr* genes in the region by location, specificity and dominance.

YR85

Yr85[11616] locus: 1BS[11616] syn: YrTr1[181]

bin: 1BS18 (0.5). **i**: AvSYrTr1NIL[11616]. **v**: Tres CI 017917[11616]. **ma**: *IWA406* – 3.0 cM – *IWA63* – 1.6 cM – *IWA5370* – 2.2 cM – *IWA4349* – 2.0 cM – *IWA2583* – 1.8 cM – YR85 – 1.3 cM – *IWA7480* – 3.0 cM – *Xbarc8* – 5.1 cM – *IWA2197* – 3.1 cM – *Xgwm413* – 7.4 cM – *Xbarc137* – 4.6 cM – *Xwmc626*[11616]; **Rg1** – 1.4 cM – **Yr10** – 7.4 cM – YR85[11616]; **Yr10**/*Xsdauw79* (1.519 Mb, 0-1.4 Mb[a]) – **Yr84** (9.65 – 11.99 Mb[a]) – *IWA2583* (30.675 Mb) – YR85 – *IWA7480* (60.382 Mb) – **Yr15**/*uhw264* (67.695 Mb, 98 Mb[a])[11616]. [a]Values from the Zavitan v2 assembly[11585].

YR86

Yr86[11641] locus: 2AL[11641] syn: YrZM895[11641], QYr.caas-2AL.2[11641]

Adult plant resistance.

v: Liken 4 = Shaaken 4[11641]; Zhongmai 895[11641]. **ma**: Flanked by *Ax-111584166* (703.7 Mb) and *Ax-110429464* (715.3 Mb)[11641]. KASP markers developed in ▶[11641]. Located to a 0.15 cM, 710.3 – 712.6 Mb, interval in a Jimai 22/Zhongmai 895 F_2 population; however, recombination was suppressed in crosses of Zhongmai 895 with Emai 580 and Avocet S due to a 4.1 Mb inversion in the region[11730].

YR87

Yr87[11712] locus: 6B (6B-6S^{sh})[11683, 11684, 11712]

v: Line 6B-RY-32-3-14[11683] = Line 42[11684] = D42[11712] = Genebank accession number to be advised. **al**: *Ae. longissima* AEG-6782-2[11712]; *Ae. sharonensis* AEG-548-4[11712]. **c**: The same NLR gene with a distinctive coiled-coil (CC) domain was cloned from each alien diploid accession[11712].

Development of lines with shortened 6S^{sh} segments is described in ▶[11684].

All 16 EMS-induced mutants in Line D42 were susceptible to both stripe rust and leaf rust[11712].

Sources of additional genes for seedling (designated “12”) and adult resistances (“13”, “14”, “15”) are listed in ▶[1430].

Genotype lists: Chinese common wheats[10369]. European wheats[10579]. U.K. wheats[10697].

Sources of additional genes for seedling (designated 12) and adult resistances (13, 14, 15) are listed in ▶[1430].
Genotype list: Chinese common wheats[10369]. European wheats[10579]. U.K. wheats[10697].

3.21.2 Temporarily designated genes for resistance to stripe rust

North American workers[181, 184, 186] allocated a number of temporary designations to uncatalogued genes detected with North American *P. striiformis* accessions. Druchamp, Yamhill and Stephens were reported to carry '***Yr3a*** or ***Yr4a***' because these genes could not be distinguished with the cultures that were used.

Yr041133[11675] locus: 7BL[11675]

v: Line 041133[11675]. **ma**: *Xicst23* (608.9 Mb, CS RefSeq 1.0) – 0.6 cM – **Yr041133** – *Xicst338* (609.7 Mb)[11675].

YrA

Refers to a phenotype specificity that appears to be controlled by complementary genes[1563].

v: Avocet* (*= heterogeneous); Anza = Karamu = Mexicani =T4 = WW15; Banks*; Condor*; Cocamba; Egret*; Inia 66; Lerma Rojo 64; Lerma Rojo 64A; Nainari 60; Nuri 70; Sanda 73; Sonalika; Zaminder 80. **v2**: Condor selection P44 **Yr6***; Pari 73 **Yr6**; Saric 70 **Yr6**; Yecora 70 **Yr6**[1563]. The complementary genes are now named **Yr73** and **Yr74**.

YrAc[11613] locus: 5DS[11613]

v: *Ae. caudata* derivative PAU16060[11613]. **al**: *Ae. caudata* PAU3556[11613].

YrAlp[10416] locus: 1BS[10416]

v2: Alpowa **Yr39**[10416]. **ma**: **YrAlp** – 15.2 cM – *Xgwm18-1B* – 1.1 cM – *Xgwm11-1B*[10416]; and more closely linked to RGAP markers[10416].

YrAS1676[11672] locus: 1AL[11672]

v: Undesignated selection. **v2**: AS1676 **Yr18**[11672]. **ma**: Located to a 1.7 cM region – 485.3 – 490.2 Mb where it co-segregated with 6 KASP markers[11672]. May be the same as **YrXH-1AL** in Xiaohemai based on common markers[11672].

YrAvS[11007]

v: Avocet R[11007]; Avocet S[11007].

This designation was used to describe an assumed resistance gene in both Avocet R and Avocet S, the latter being the genetic background of the Avocet S near-isogenic lines. AvS NILs with **Yr6**, **Yr7** and **Yr9**, as well as Avocet R, were susceptible to the variant of *Pst* race 6 E0[11007].

YrC142[10667] locus: 1BS[10667]

v: Synthetic CI142 = Gaza/Boy//*Ae. tauschii* 271[10667]. **ma**: Located in the **Yr24**/**Yr26** region close to *Xbarc187-1B* and *Xgwm273-1B*[10667]. Although postulated to be unique this gene is likely **Yr24**/**Yr26**.

YrCf75[11646] locus: 2AL[11646]

Recessive.

v: Changfeng 75[11646]. **ma**: Located in interval 577-638 Mb (CS RefSeq v1.0, flanked by *AX-1110060462* and *AX-111004763*[11646].

YrCK[10220, 10221] locus: 2DS[10220]

Temperature sensitive[10219].

v: Cook **Yr34**[10219, 10220, 10221]; Sunco **Yr34**[10220].

YrCle[186] locus: 4B[186]

v2: Clement **Yr9**[186].

YrCN17[10562, 10686] locus: 1B, 1BL, 1RS[10562, 10686]

Derived from *S. cereale*.

v: Chuannong 17[10686]; CN12[10562]; CN17[10562]; CN18[10562]. **dv**: *S. cereale* R14[10686]. **al**: *S. cereale* L155[10562].

YrD[185] locus: 6A[185]

v: Druchamp[185].

YrDa1[186] locus: 1A[186]

v2: Daws **YrDa2**[186].

YrDa2[186] locus: 5D[186]

v2: Daws **YrDa1**[186].

YrDru[184, 185] locus: 6B[185]. 5B[184]

v: Druchamp[184, 185].

YrDru2[184] locus: 6A[184]

v: Druchamp[184].

YrExp1[10601] locus: 1BL[10601]

v2: Express **YrExp2**[10601]. **ma**: *Xwgp78-1B* – 4.2 cM – **YrExp1** – 3.4 cM – *Xwmc631-1B*[10601].

YrExp2[10601] locus: 5BL[10601]

v2: Express **YrExp1**[10601]. **ma**: *Xgwm639-5B* – 9.2 cM – *Xwgp81-5B* – 1 cM – **YrExp2** – 0.7 cM – *Xwgp82-5B*[10601].

Based on the presence of the nearest flanking markers **YrExp2** was postulated in Expresso, Blanca Grande, Buck Pronto and Jeff/Pronto[10601].

YrF[11156] locus: 2B[11218]. 2BS[11219]

v2: Francolin#1 **Yr29**[11156, 11218, 11219]. **ma**: *Xgwm374-2B* – 2.0 cM – **YrF** – 1.8 cM – *Xwmc474-2B*[11219].

Francolin#1 is also released under the names Ufam and BARI Gom 27[11156].

YrF[11781] locus: 5AS[11781]

bin: 5AS-0.4-0.98[11781]. **v**: Flanders[11781]. **ma**: *Xbarc56-5A* 2.0 cM – **YrF** – 0.6 cM – *AX108925494*[11781].

YrH46[184] locus: 6A[184]

v2: Hybrid 46 ***Yr4b***[184].

Not the same gene as **YrDru2**[184].

YrH62[11303] locus: 1B[11303]

v: Line 03031-1-5 (ex CIMMYT)[11303]. **ma**: *Xgwm273-1B* – 3.7 cM – *Ax-109871410/Ax-109472792/Ax109352427* – 0.3 cM – **YrH62** – 0.8 cM – *Ax-109862469* – 2.1 cM *Xbarc137-1B*[11303].

YrH9020[10979] locus: 2DS[10979]

Derived from *Psathyrostachys huashanica*.

v: H9020-1-6-8-3[10979]. **al**: *Psathyrostachys huashanica* 0503383[10979]. **ma**: *Xgwm102-2D* – 3.8 cM – *Xgwm455-2D* – 5.8 cM – **YrH9020** – 4.4 cM – *Xgwm261-2D* – 2.3 cM – *Xwmc503-2D* – 0.6 cM – *Xcfd53-2D*[10979].

YrHA[11100] locus: 1AL[11100]

v: H901414-121-5-5-9[11100]. **ma**: *Xwmc469-1A* – 3.4 cM – **YrHA** – 4.6 cM – *Xgwm497-1A*[11100].

YrHu[11229] locus: 3AS[11229]

Derived from *Psathyrostachys huashanica*.

bin: H9020-17-25-6-4[11229]. **ma**: *Xcfd79-3A* – 7.2 cM – **YrHu** – 0.7 cM – *BG604577*[11229].

YrHVII[186] locus: 4A[186]

v2: Heines VII **Yr2 Yr25**[186].

YrJ22[11195] locus: 2AL[11195]

v: Jimai 22[11195]. **ma**: *Xgwm382-2AL* – 1.0 cM – **YrJ22** – 7.3 cM – *IWA1348*[11195]; The mapped region was reduced to 0.3 Mb corresponding to 340.5 kb; *H736* – *J22/HJ732* – *H400* (768.7 – 769.0 Mb)[11679].

YrJ44[11696] locus: 6AL[11696] syn: QYr.nwafu-6AL[11696]

v2: Jimai 44 **Yr29**[11696]. **ma**: Mapped to a 3.5 cM interval flanked by AQP markers *AX-109373479* and *AX-109563479*[11696].

YrKK[11034] locus: 2BS[11034]

Adult plant resistance.

bin: 2BS-1. **v**: Kenya Kuku[11034]. **ma**: *Xgwm148-2BS* – 3.2 cM – **YrKK** – 1.8 cM – *Xwmc474-3B*[11034]. Resistance conferred by **YrKK** at the adult stage approached immunity. A slight effect was observed on seedling response[11034].

YrLk[11252] locus: 7BL[11252]

v: Lankao 5[11252]. *Xbrac267-7B* – 4.4 cM – **YrLk** – 3.3 cM – *Xwmc396-7B*[11252].

YrLM168a[11284] locus: 6BL[11284]

Adult plant resistance.

v: *Xwmc756-6B* – 4.6 cM – ***YrLM168a*** – 4.6 cM – *Xbarc146-6B*[11284]. **ma**: *Xwmc756-6B* – 4.6 cM – ***YrLM168a*** – 4.6 cM – *Xbarc146-6B*[11284]. LM168a and LM168b are derivatives of Milan[11284].

YrMin locus: 4A[184]

v: Minister[184].

YrMor[186] locus: 4B[186]

v2: Moro **Yr10**[186]. **ma**: The development of an STS marker, derived from an AFLP fragment, that co-segregates with **YrMor** was reported in [357].

YrMY37 locus: *yrMY37* [11282]. 7BL[11282]

Recessive.

v: Mianmai 37[11282]. **ma**: *Xwmc476-7B* – 1.57 cM – *Xgwm297-7B* – 0.79 cM – **YrMY37** – 0.38 cM – *Xbarc267-7B*[11282].

YrMY41[11271] locus: 1B[11271]

v: Mianmai 41[11271].

A cross with AvS+**Yr26** failed to segregate. Although claimed to be a possible allele of **Yr24**/**Yr26** the gene identified is likely to be the same.

YrND locus: 4A[184]

v2: Nord Desprez ***Yr3a Yr4a***[184]. May be the same as **YrMin**[184].

Yrns-B1[33, 0033] locus: 3BS[33]

v: Lgst.79-74[33]. **ma**: *Xgwm493* (distal) – 21 cM – **Yrns-B1**[33]; As a QTL, **Yrns-B1** was located in a 3 cM interval between *Xgwm493-3B* and *Xgwm1329-3B*[10383].

YrP[11614] locus: 5DS[11614]

v: *Ae. peregrina* derivative PAU16058[11614]. **al**: *Ae. peregrina* PAU3519[11614].

YrP81[10696] locus: 2BS[10696]

v: P81[10696]; Xu29[10696]. **ma**: *Xgwm429-2B* – 1.8 cM – **YrP81** – 4.1 cM – *Xwmc770-2B*[10696].

YrPak[11543] locus: 5BS[11543]

v: PI 1388231[11543]. **ma**: *sunKASP_338* – 3.3 cM – **YrPak** – 3.5 cM – *sumKASP_341*[11543].

PI 1388231 also carried two genes for adult plant resistance, one of which was positive with **Lr46** marker *Lr46_SNP1G22*[11543].

YrR61[10914] locus: 2AS[10914] syn: QYr.uga-2AS[10914]

v: Pioneer 26R61 = PI 612056[10914].

YrR212[10562] locus: 1B, 1BL.1RS

Derived from *S. cereale* 1B, 1BL.1RS[10562].

v: R185[10562]; R205[10562]; R212[10562]. **al**: *S. cereale* R212[10562].

YrS[185] locus: 3B[185]

v: Stephens[185].

YrS2199[10618] locus: 2BL[10618]

bin: 2BL0.89-1.00[10618]. **v**: S2199[10618]. **ma**: *Xgwm120-3B* – 11.0 cM – **YrS2199** – 0.7 cM – *Xdp269-2B*[10618].

YrSD[158, 11085] locus: 5BL

i: Taichung 29*6/Strubes Dickkopf[11085]. **v**: Strubes Dickkopf[11085]. **ma**: *Xwmc640-5B* – 3.6 cM – **YrSD** – 2.4 cM – *Xbarc59-5B* – 3.0 cM – *Xwmc783-5B*[11085].

The authors concluded that this gene was different from **Yr25**, which was located in chromosome 1D[158].

YrSte[184] locus: 2B[184]

v: Stephens[184].

YrSte2 locus: Stephens[184]. 3B[184]

Stephens[184]

YrTr2[186] locus: 3A[186]

v2: Tres **YrTr1**[186].

Yru1[11494] locus: *TuG1812G0500003718*. 5AL[11494]

bin: 5AL10-0.57-0.78. **dv**: *T. urartu* PI 428309[11494]. **ma**: *Xgwm186-5A* – 30.5 cM – **Yru1** – 10.8 cM – *Xgpw7007-5A*, then fine mapped with 82 additional polymorphic markers[11494]. **c**: **Yru1** has as NBS-LRR structure with N-terminal ankyrin and C-terminal WRKY repeats[11494]. GenBank MT018453.

The *Yru* resistance allele was present in a number of *T. urartu* accessions, but not in G1812[11494].

YrV23[10370] locus: 2B[184]

Presumed to be ***Yr3a***.

v: Vilmorin 23[10370]; Vilmorin[184]. Allelic but not the same as **YrSte**[184].

Yrwh2[11150] locus: 3BS[11150]

Recessive.

v: Wuhan 2[11150]. **ma**: *Xwmc540-3B* – 5.9 cM – **Yrwh2** – 10 cM – *Xgwm566-3B*[11150].

YrXH[11729] locus: 1AL[11729] syn: YrXH-1AL[11729]

v: Xiaohemai ZM004745[11729]. **ma**: Located to a 1.5 cM interval – 484.33 – 490.09 Mb, CS RefSeq 1.0[11729].

May be the same as **YrXH-1AL**[11672] based on common markers with ▶[11729].

Yrxy1[10829]

High temperature resistance.

v: Mingxian 169/Xiaoyan 54 F_3-4-14[10829]. **v2**: Xiaoyan 54 **Yrxy2**[10829]. **ma**: *Xbarc49-7AS* – 15.8 cM – **Yrxy1** with closer flanking RGA markers[10829].

Yrxy2[10829]

High temperature resistance.

v: Mingxian 169/Xiaoyan 54 F_3-4-30[10829]. **v2**: Xiaoyan 54 **Yrxy1**[10829]. **ma**: *Xwmc794-2AS* – 4.0 cM – **Yrxy2** – 6.4 cM – *Xbarc5-2AL*[10829].

YrYam[184, 185] locus: 4B[185]

v2: Yamhill **Yr2** ***Yr3a Yr4a***[185].

YrZH22[11563] locus: 4BL[11563]

v: Zhoumai 22[11563]. **ma**: *XWGGB133* – 3.29 cM – *YrGH22* – 2.63 cM – *XWGGB146*[11563].

YrZH22 could not be distinguished from **Yr50** based on map location.

YrZH84[10331] locus: 7BL[10331]

v: Annong 7959[10331]; Zhoumai 11[10331]; Zhoumai 12[10331]. **v2**: Zhou 8425B **Yr9**[10331]. **ma**: *Xwmc276-7B* – 0.6 cM – *Xcfa2040-* – **YrZH84** – 4.8 cM – *Xbarc32-7B*[10331].

3.21.3 Stripe rust QTLs

Seedling resistance in Qinnong 142 to race CYR23 was attributed to genes on chromosomes 1DS and 4AL[11377].

Four QTLs were identified for stripe rust infection in a joint analysis of three datasets from a Fukuhokomugi/Oligoculm doubled haploid population[10060]. Their location, associated marker, percentage variation explained and parent contributing to enhanced resistance at that locus are listed as:. 2DL; *Xgwm349-2D*; 6.5-9.6%; Fukuho[10060]. 3BS; *Xgwm389-3B*; 15.1-24.5%; Oligoculm[10060]. The 3BS QTL may be **Yr30**[10060]. 5BL; *Xwmc415-5B*; 6.4-12.7%; Oligoculm[10060]. 7BL; *Xwmc166-7B*; 2.5-9%; Oligoculm[10060].

According to 11393 *Qyr.osu-5A* is an orthologue of *OsXA21* and confers resistance to multiple pathogens/pests.

Four QTLs were detected in a multiple cross analysis[10283]: Chromosome 2AL (probably **Yr32** in Deben, Kris and Soloist), 2AS (probably **Yr17** in Kris), 2BL (*Xwmc149-2B* – *Xwmc317a-2B* in Deben) and 6BL (*Xwmc397-6B* – *Xwmc105b-6B* in Soloist and Kris).A summary of published QTL locations is provided in [11089]; 49 chromosome regions on 20 of the 21 wheat chromosomes were covered.

Markers associated with many stripe rust resistance genes are summarized in [11254].

QTL

Alcedo (R) / Brigadier (S): DH population: Two major QTLs *QPst.jic-2DL* (R^2 up to 0.36) and *QPst.jic-4BL* (R^2 up to 0.29) for percent infection contributed be Alcedo[10785]. A seedling-expressed QTL was located at the same position in 2DL[10774].

Avocet S / AUS27482: AUS 27482 was shown to have **Yr34** (*YrAW6*) and a second novel gene (*YrAW7*) on chromosome 2B linked to *IWB71684*[11720].

Avocet S / Attila: QTLs were located on chromosomes 2BS (probably **Yr27**), 2BL (a race-specific effect) and 7BL (*XP32/M59* – *Xgwm344-7B*[10586].

Avocet (S) / Chapio (I): F_6RIL population: In Mexico QTLs were located in chromosomes 2BS (**Yr31**), 3BS(**Yr30**) and 7DS(**Yr18**); only the last two were effective in 2009. In China QTLs were located in chromosomes 3BS, 5BL and 7DS. A 3DS QTL was effective in Mexico in 2009 and in China in 2013[11020].

Avocet R (S) / Chilero: **Lr46**/**Yr29**, *QLr.cim-5DS*/*QYr.cim-5DS*, *QYr.cim.6BS* and *QYr.cim-7BL* from Chilero, and *QLR.cim-1DL*/*QYr.cim-1DL* from Avocet R[11306].

Avocet S (S) / Eltan (MR): RIL population: Three QTL for seedling reaction located on chromosome arms 2BS, 4AL and 5BS (minor) and two addition QTL for APR identified on chromosome arms 6AS and 7BL[11560]. A significant increase in the disease response of Eltan was associated with races virulent on Eltan seedlings.

Avocet (S) / Kundan (R): **Yr29** plus *QYr.cim-2AL* flanked by *3064488_30:T>G* (R^2 = 0.05 – 0.09), *QYr.cim-3DS* flanked by *3021242* and *224356* (R^2 = 0.04} and *QYr.cim-5AS* flanked by *3025355_10:T>*;**C** and *1067590* (R^2 = 0.04 – 0.05)[11248].

Avocet S (S) / Napo 63 (R): *Qyrnap.nwafu-2BS* (11283}. 2BS[11283]. bin: 2BS-1-0.53. ma: Mapped to a 5.46 cM interval flanked by KASP markers *90K-AN34* and *90K-AN36*; and by *Xbarc55-2B* and *Xgwm374-2B*[11283].

Avocet (S) / Pastor (I): RIL population: QTL mapped on 1BL (**Yr29**), 2BS(**Yr31**), 5A, 6B and 7AL plus minor QTLs on 1AL, 1B, 3A, 3B, 4D, 6A, 7AS and 7AL[10928].

Avocet S / Pavon 76: QTL identified in 1BL (*Xgwm259*), 3BS (PstAATMseCAC2), 4BL (*Xgwm495*), 6AL (*Xgwm617*), 6BL (PstAAGGMseCGA1)[10443].

Avocet S / PI 182103 (R): RIL population: QTL detected on chromosomes 2AS and 3AL for seedling resistance and 4DL, 5BS and 7BL for APR; *QyrPI182103.wgp-4DL* was designated as **Yr79**[11222].

Avocet S (S) / Qinnong 142 (R): RIL population: Two QTL for seedling resistance to race CYR23 on chromosome arms 1DL and 4AL. These genes were not effective against races used in the field where APR was controlled by QTL on chromosome arms 1BL (*QYrqin.nwafu-1BL*: probably **Yr29**), 6BS (*QYrqin.nwafu-6BS*, possibly **Yr78**); 2AL *QYrqin.nwafu-2AL*) and 2BL (*QYrqin.nwafu-2BL*)[11559].

Avocet S (S) / Qinnong 142 (R): RIL population: Adult plant resistance: *QYrqin.nwafu-1BL* – *AX-95133868* – *AX-94522424*, R^2 = 0.16 – 0.20, likely **Yr29**; *QYrqin.nwafu-2AL*, *AX-94655393* – *AX- 9489521*, R^2 = 0.08 – 0.20; *QYrqin.nwafu-2BL*, *AX-94507002* – *AX-94562871*, R^2 = 0.18 – 0.39; *QYrqin.nwafu-6BS* R^2 = 0.14 – 0.31[11377].

Camp Remy / Michigan Amber: Two QTLs were located on chromosome 2BL (*QYR1,* LOD score 12) and 2AL (*QYR2*, LOD 2.2)[0287]. Four QTLs were scored in the ITMI population. The most effective (*QYR3*, LOD 7.4) on chromosome 2BS was probably **Yr27**, the others were located in 7DS (*QYR4,* LOD 3.4), 5A (*QYR5,* LOD 2.8), 3D (*QYR6,* LOD 2.8) and 6DL(*QYR7,* LOD 2.4)[0287].

Camp Remy / Recital: 217 RILs. Six QTLs for APR were detected over 4 years. *QYr.inra-2BL* (R^2=0.42-0.61) corresponded largely to seedling resistance gene *Rsp* and possibly **Yr7**. The other genes were *Qyr.inra-2AL*, *QYr.inra-2BL*, *QYr.inra-2DS* (perhaps **Yr16**), *QYr.inra-5BL.1* and *QYr.inra-5BL.2*[10279]. Differential reactions of RILs possessing different QTL occurred between old and new *P. striiformis* races[11144].

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chromosomes 2AL, 2BL, 3BS and 5A were from Capo and one on chromosome 3AS was from Arina; the QTL on 2AL, 2BL and 3BS were co-located with QTL for resistance to leaf rust[11449].Claire/Lemhi: DH population: 4 QTLs for APR:*Qyr.niab-2D.1* (at or near **Yr16**, R^2=0.1-0.25, *Qyr.niab2DL.2* (R^2=0.14-0.32), *Qyr.niab-2BL*, and *Qyr.niab-7B* (R^2=0.11-0.13)[10962]. An unknown seedling resistance gene was located in chromosome 3BL[10962].

Chuanmai 42 (variable) / Chuanmai 55 (R): RIL population: Two QTL on chr. 1B and 2A were derived from CH55 and a less effective QTL on Chr 7B was from CH42[11558]. The chr 1B QTL was postulated to be **Yr29**. CH42 carries **Yr24** and CH55 carries the 1BL.1RS (**Yr9**) translocation and 5B.7B reciprocal translocation – neither gene was effective in this study[11558].

Coker 9835 (S) / VA96W-270: RIL population: Adult plant resistance was conferred by *QYr.ar-3BS* (nearest markers *Xbarc147*, *ger9-3p*, *IWA6092*) and *QYr.ar-4BL* (nearest markers *Xbarc163*, *Xcfd39* and several *IWA* markers[11175]. Cultivar Pat had the same haplotype[11175]. USG 3555/Neuse: Three QTL on chromosomes 1AS, 4BL and 7D (not **Yr18**) were derived from USG 3555 and one QTL on chromosome 3A was from Neuse[11142].

Express / Avocet S: RIL population: Relative AUDPC for high temperature APR was controlled by *QYrex.wgp-6AS*, R^2=0.326, interval *Xgwm334-6A* – *Xgwp56-6A*; *QYrex.wgp-3BS*, R^2=0.274, interval *Xgwm299-3B* – *Xwgp66-3B*, *QYrex.wgp.1BL*, R^2=0.094, interval *Xwmc631-1B* – *Xwgp78-1B*[10672]. When rust phenotyping was based on infection type only the 6S and 3BL QTLs were evident[10672].

Druchamp (R) / Michigan Amber (S): Eight QTL for high-temperature adult plant resistance: QTL in chromosomes 1BL (nearest marker *Xgwm131-1B*), 2BL (*IWA7583*), and 5BL (2, *IWA2558* and *IWA6383*) were stable across environments, whereas genes in chromosomes 1BL (*IWA8581*, probably **Yr29**), 1DS (*IWA22668*), 3AL (*IWA6834*) and 6BL {*IWA6420*) were not[11284]. In addition three QTL for all stage resistance were detected on chromosomes 5B (probably **Yr3**, *IWA6271*), 5DL (*IWA8331*) and 6BL (*IWA3297*).

Fukuhokomugi / Oligoculm: Seven QTLs were identified for stripe rust severity in a joint analysis of five datasets from a doubled haploid population[10060]. Their location, associated marker, percentage variation explained, and genotype contributing to enhanced resistance at that locus, are listed as: 3BS; *Xgwm389-3B*; 0.2-4.9%; Oligoculm[10060]. 4BL; *Xgwm538-4B*; 1.8-12.3%; Oligoculm[10060]. 4DL; *Xwmc399-4D*; 2.5-8.0%; Oligoculm[10060] 5BL; *Xwmc415-5B*; 2.4-16.1%; Oligoculm[10060]. 6BS(centromeric); *Xgwm935-6B*; 0.5-3.8%; Oligoculm[10060]. 7BS; *Xgwm935-7B*; 1-5.2%; Oligoculm[10060]. 7DS; *Xgwm295-7D*; 10.7-23.7%; Fukuho[10060]; the 7DS QTL was probably **Yr18**[10060].

Flinor (R) / Mingxian 169 (S): Two independent QTLs for high temperature (24/18C) seedling resistance located in chromosome 5BL, designated *QYr-tem-5B.1* (*Xbarc89* – *Xgwm67*) and *QYr-tem-5B.2* (*Xbarc140n* – *Xwmc235*) and R^2 = 0.37 and 0.33, respectively[10797].

Guanggtoumai (R) / Avocet S (S): RIL population. *QYr.GTM-5DL* accounted for 22 – 44% of the phenotypic variation across three sites (11562).

Guardian / Avocet S: F3 lines. One major QTL, *QPst.jic-1BL* (*Xgwm818-1 – Xgwm259-1B*, R^2 up to 0.45), and two minor resistance QTLs on chromosomes 2D and 4B originating from Guardian[10589]. The major QTL was in the region of **Yr29**.

Jagger (MR) / 2174 (MS): RIL population: *Qyr.osu-2A* (**Yr17**) and *Qyr.osu-5A* (in *Xgwm156-5A* – centromere region) from Jagger and **Yr18** from 2174 (but only in tests in China)[10973].

Kariega / Avocet S: DH population: Two QTLs *QYr.sgi-7D* (probably **Yr18**) and *QYr.sgi.2B.1* accounted for 29 and 30%, respectively, of the phenotypic variation for stripe rust response. The nearest marker to the latter was *Xgwm148-2B*[10184]. These locations were confirmed in a subsequent study; *QYr.sgi-2B.1a* was located within the *wPt5556 – wPt6278* segment[11232].

Kukri (MR) / Janz (MR): DH population: Tested with pre- and post-2003 Australian *Pst* races in several environments. *QYr.sun-7B* (Kukri) and *Qyr.sun-7D* (=**Yr18**)) (Janz) were consistent over environments; *QYr.sun-1B*, *-5B* and *-6B* were detected in most environments and *QYr.sun-3B* was identified in only one season. Two genes, *QYR.sun-1A* from Janz and *QYr.sun-2A* from Kukri, were detected only with pre- and post-2003 races, respectively, and likely contributed to differential responses of these cultivars to the two groups of races[10751].

Luke (R) / Aquileja (R): Two QTLs for high-temperature adult plan resistance, *QYRlu.cau-2BS.1* (distal, flanked by *Xwmc154-2B* and *Xgwm148-2B*, R^2 = 0.366) and *QYrl.cau-2BS.2* (proximal, flanked by *Xgwm148-2B* and *Xbarc167-2B*, R^2 = 0.415) from Luke, and *QYraq.cau-2BL* (flanked by *Xwmc175-2B* and *Xwmc332-2B*, R^2 = 0.615) in Aquileja for stripe number[10582].

Luke (MR) / AQ24788-83 (APR): RIL population: *QYr.cau-2AL* near *IWB4475* (R^2 = 23-40%) from AQ24788-83 and **Yr18** (R^2 = 11.0-14.7%) from Luke (11393).

Mianyang351-15 (R) / Zhengzhou 5389 (R): RIL population: Seven QTL were located on chromosome arms 1BL (**Yr29**), 2AS (**Yr17** or another gene), 2DS, 3AS, 3DS, and 7BL (possibly associated with **Lr68**)[11545].

Mingxian 169 (S) / Centrum (R): RIL population: QTL detected on chromosomes 7BL (*QYrcen.nwafu-7BL*, R^2 = 23.4%, *AX-94556751 – AX-110366788*), 1AL (*QYrcen.nwafu-1AL* (R^2 = 11.2%, *AX-94488258 – AX-94458040*) and 4AL (*QYrcen.nwafu-4BL*, R^2 = 12.6%, *AX-94695204 – AX-94996273*[11365].

Mingxian 169 (S) / Chakwal 86 (R): RIL population: QTL on chromosomes 1BL (**Yr29**), 3BS (not **Yr30**) and 6BS (*QYrcw.nwafu-6BS*) contributed to the high level of APR in Chakwal 86[11371].

Mingxian (S) / P1057: RIL population, and Avocet S (S)/P10057 and Zhengmai 9023 (S)/P10057 F_2:F_3 populations: Two strong QTL located in clustered QTL regions: *Qlrlov.nwafu-2BS* identified by *IAW5377*, *IWA2674*, *IWA5830*, and *Qyrlov.nwafu-3BS* identified by *IWB57990* and *IWB6491*[11279].

Mingxian (S) / P9936 (R): RIL population: *QYr.nwafu-3BS* (probably **Yr30**) and *QYr.nwafu-7BL* flanked by *AX-108819274* and *AX*-11040708 (R^2 = 36.0 – 38.9%; a KASP marker was developed for the latter[11373].

Mingxian 169 / P10090: *QYr.nwafu*-6A (syn *YrP10090* for adult plant resistance reduced stripe rust severity by a mean 14.8%. Located in the chr. 6A centromeric region and flanked by *Ax94460938* and*Ax710585473*, a 3.5 cM region corresponding to physical interval 107.1 – 446.5 Mb[11555].

Mingxian 169 (S) / Qing Shumai (R): RIL population: APR QTL *QYr.cau.6DL*, *Xbarc1121-6D – Xgpw4005-6D* region: positive interaction with **Yr18**[11323].

Mingxian 169 (S) / Toni (R): RIL population: *QYrto.swust-3AS*, *AX-95240191 – AX-9482889091*, R^2 = 0.22 – 0.56: *QYrto.swust-3BS*, *AX-994509749 – AX-94998050*, R^2 = 0.23 – 0.55[11379].

Otane (R) / Tiritea (S): DH population: QTL in 7DS (probably **Yr18**), 5DL (from Otane) and 7BL (Tiritea)[10150]. Interval mapping of 7DS indicated that the presumed **Yr18** was 7 cM from *Xgwm44-7D*[10150].

Pingyuan 50 (R) / Mingxian 169 (S): DH population: APR: *QYrcaas-2BS* (*Xbarc13-2BS*) – *Xbarc230-2BS*, R^2=0.05-0.09), *QYr.caas-5AL*(*Xwmc410-5AL – Xbarc261-5AL*, R^2=0.05-0.2), *QYrcaas-6BS*(*Xgwm361-6BS – Xbarc136-6BS*, R^2=0.05-0.08)[10693].

Pioneer 26R61(R) / AGS2000(S): RIL population: Two QTLs, **QYr.uga-2AS** (R^2=0.56) flanked by *Xbarc124-2A* and *Xgwm359-2A* (also named **YrR61**) and *QYr.uga-6AS* (R^2=0.06)[10914]. Minor QTLs were also on other chromosomes

Renan (R) / Recital (S): RIL population: Tested for AUDPC in 1995/6 and 2005/6 with pathogen isolates avirulent and virulent, respectively, for **Yr17**:*QYr.inra-2AS.2*, (=**Yr17**), R^2=0.45, 1995/6; *QYr.inra-2AS.1*, R^2=0.9, 2005/6; *QYr.inra-2BS*, R^2=0.11 & 0.13, *QYr.inra-3Bcent*, R^2=0.06 in 2005/6; *QYr.inra-6B*, R^2=0.04 &

0.06; from Renan; and *QYr.inra-2AS.1*, R^2=0.09; *QYr.inra-3DS*, R^2=0.08 & 0.12 from Recital. Other QTLs were effective only at certain growth stages[10689].

Soru#1 (R) / Naxos (MR): RIL population: Seedling and field tests detected two moderately effective QTL that were likely **Yr24** and **Yr28** derived from Soru#1[11368]. A KASP marker was developed for **Yr28**.

Stephens / Michigan Amber: Two QTLs for high temperature APR were located in chromosome 6BS; *QYrst.wgp-6BS.1* located in a 3.9 cM region flanked by *Xbarc101-6B* and *Xbarc136-6B* and *QYrst.wgp-6BS.2* located in a 17.5 cM region flanked by *Xgwm132-6B* and *Xgdm113-6B*[10602].

Stephens (I) / Platte (S): RIL population: 13 QTLs were identified across several environments; significant QTL x environment interactions suggested that plant stage specificity, pathogen genotype and temperature as well as host genotype were important in determining rust response[10890].

Stewart (R) / Bansi: Durum, F_5 and F_7 populations: **Yr29** and *QYr-3BL* (r^2 = 0.045); the latter was in the vicinity of **Yr80** with *kIWA6221* as the nearest marker[11542].

Svevo (R) / Zavitan (MS): Tetraploid, RIL population tested in Israel and China. Nine QTL for APR; 8 from Svevo and one from Zavitan, the most effective of which was *QYrsv.swust-1BL.1*[11557]. This QTL overlapped the **Yr29** region and Svevo was positive for the **Yr29** marker.

Thatcher (S) / Hong Qimai (APR): RIL population: *QYr.cau-2AL* near *Xgwm311-2A* and *IWB4475* (R^2 = 47-52%), *Qyr.cau*-4AL (R^2 = 5-7%) and *Qyr.cau-7AL* (R^2 = 9-10%) derived from Hong Mai[11366].

T. monococcum **PAU14087 (R) /** *T. boeoticum* **PAU5088 (R)**: RIL population: One adult plant resistance QTL identified in each parent and named *QYrtm.pau-2A* (in a 3.6 cM interval between *Xwmc407-2A* and *Xwmc170-2A*; R^2 = 0.14) and *QYrtb.pau-5A* (in a 8.9 cM interval between *Xbarc151-5A* and *Xcfd12-5A*; R^2 = 0.24)[10518].

UC1110 (MR) / PI 610750 (MR): RIL population: *QYr.ucw-3BS* ex UC1110, R^2=0.22, associated with *Xgwm522-3B.1*. This marker differs from *Xgwm533-3B.2* that is associated with **Yr30**[10705]; *QYr.ucw-5AL*, R^2=0.1, ex PI 61075 – syn. **Yr48**[10705]; *QYr.ucw-2BS*, R^2=0.045, ex UC1110, located in the centromeric region near *Xwmc474-2BS*[10705], *Qyr.ucw-2AS*, R^2=0.023, ex PI 61725, near *wPt-5839*[10705].

Yaco S (R) / Mingxian 169 (R): Adult plant resistance. *Qyryac.nwafu-2BS* located within a 1.3 cM region flanked by KASP markers *BS00022657_51* and *IACX6411.BobWhite_22503_605* within the 10.4 cM *Xgwm148-2B* – *Xbarc55-2B* region[11241].

Yibinzhuermai (AS1591) / Taichung 29: RIL population: QTL in chromosome arms 5BL, 6AL and 7DS (**Yr18**) derived from Yibinzhuermai; *QYr.YBZR-6AL* was considered new (11759}.

Yr16DH70 (Cappelle Desprez / 2*Palmiet Selection) / Palmiet: DH population: One major effect QTL, *Qyr.ufs-2A*, and three less effective QTLs in 2D (possibly **Yr16**), 5B and 6D were from Yr16DH70, and a minor effect QTL on 4B was from Palmiet[10933].

Kofa (S) / W9262-260D3 (MR): DH population: QTL were identified on chromosomes 5B (APR) and 7B (seedling resistance and APR) in the region of **Yr67**[11689]. Full resistance required the presence of both QTL. The 5B QTL was not detected in field trials in Mexico[11689].

3.21.4 Spike response to stripe rust

Bouvet et al.[11658] identified five QTL controlling stripe rust response in spikes in a UK Magic population; three (on chromosomes 2D, 4D and 5A (possibly **Yr34**)) co-located with previously identified QTL and two (chromosomes 2D and 4A) associated with flowering time. Heritability was lower than that for leaf response.

3.22 Reaction to *Puccinia triticina*

Disease: Brown rust, leaf rust.

3.22.1 Genes for resistance

LR1

Lr1[47] locus: 5D[954]. 5DL[945]. 1B[1409]

i: Centenario/6*Thatcher[317]; Malakoff/6*Prelude[317]; Wichita*4/Malakoff[613]. **v**: Line 87E03-S2B1[10561]; Centenario[317]; Chicora 'S'[143]; Daws (heterogeneous)[1019]; Dirkwin[1019]; Glenlea[976, 1255]; Halle 9H37[74]; Hyslop[1019]; Luke (heterogeneous)[1019]; Malakoff[47]; McDermid[1019]; Mexico 120[933]; Newton[143, 1023, 1024]; Norco[1019]; Shabati Sonora[842]; Sonora 64[842]; Tarsa[842]; Uruguay[954]; Walliday[1019]. **v2**: Blueboy **Lr10**[143]; Blueboy II **Lr10 Lr24**[143]; Erythrospermum 142 and 953 **Lr3**[74]; Laura **Lr10 Lr34**[712]; Norka **Lr20**[1552]; Plainsman V **Lr3**[1024]; Suneca **Lr13**[485]. **dv**: Several *Ae. tauschii* accessions[10191]. **ma**: Co-seg. with *Xpsr567-5D* and *Xglk621-5D* in a Frisal/**Lr1** resistant line. pTAG621 was converted to a diagnostic STS[354]; Terminally located[10189]; In *Ae. tauschii* recombination in the region was 5-10X that in common wheat, gene order *Xpsr567-5D* – **Lr1** – *Xabc718-5D*[10191]; Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat[10408]; A candidate gene for **Lr1**, *Lr1RGA1*, encoding a CC-NBS-LRR protein, cosegregated with **Lr1**[10408]; Co-segregation with RGA567-5[10561]. **c**: **Lr1** is a member of a multigene family (PSR567), has a CC-NBS-LRR structure, and produces a protein of 1,344 aa, EF567063[10561].

LR2

Lr2 locus: 1B[1409]. 2DS[843, 942]

Lr2a[320] syn: Lr2[47]

i: Prelude*6/Webster[320]; Red Bobs*6/Webster[320]; Webster/6*Thatcher RL6016[306]; Wichita*4/Webster[613]. **v**: EurekRRa CI 17738[143]; Festiguay[843]; Webster CI 3780[47]; Common in the Canadian Western Spring Wheat (CWSW) cultivars[11700]. **v2**: Alex **Lr10**[976]; Ck 9835 **Lr9**[10146]; Ck 9663 **Lr2 Lr10**[10146]; Guard *Lr10c*[976]; James **Lr10**[976]; Len **Lr10**[976]; Marshall **Lr10**[976]; Mediterranean W1728 **Lr3**[1369]; Shield **Lr3 Lr10**[198]; Waldron **Lr10**[143]. **ma**: Flanked by KASP markers *kwm1620* (64.455 Mb, CS REFSeq 2.1.) and *kwm1623* (64.760 Mb)[11700].

Lr2b[320] syn: $Lr2^2$ [1409]

i: Prelude*6/Carina[320]; Red Bobs*6/Carina[320]; Thatcher*6/Carina[320]; Wichita/4*Carina[613]. **v**: Carina[613].

Lr2c[320] syn: $Lr2^3$ [1409]

i: Prelude*5/Brevit[320]; Prelude*6/Loros[320]; Red Bobs*6/Brevit[320]; Red Bobs*6/Loros[320]; Thatcher*4/Brevit[320]; Thatcher*6/Loros[320]; Wichita*4/Brevit[613]; Wichita*4/Loros[613]. **v**: Brevit[613]; Loros[317, 1257].

LR3

Lr3[47]

Because **Lr3** appears to be a complex locus[486] Democrat and Democrat/6* Thatcher should be accepted as standards. There is evidence to suggest that the allele in Mentana, and therefore many derivatives, is ***Lr3b***[939]. If this is correct, many genotypes listed under ***Lr3a*** are likely to be ***Lr3b***. Durum cv. Storlom likely carries ***Lr3a*** or ***Lr3b***[10469]. Cv. Camayo was considered to have a closely linked gene, or **Lr3** allele[10469]. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B*. All three Thatcher NILs with named **Lr3** alleles carried the STS marker[10469].

Lr3a[10028] locus: 6B[549]. 6BL[939] syn: Lr3[47]

i: Democrat/6*Thatcher[318]; Wichita*4/Mediterranean[613]. **v**: Belocerkovskaja 289[74]; Bennett[1024]; Democrat[47]; Fertodi 293[74]; Gage[1024]; Hana[68]; Homestead[1024]; Ilyitchovka[75]; Juna[75]; Jubilejne[68]; Kawvale[143]; Lancota[1024]; Mara[68]; Mediterranean[47]; Mediterranean W3732[1369]; Mentana[842]; Mironovskaya 264 & 808[74]; Odra[75]; Osetinskaya[74]; Ottawa[143]; Pawnee[1408]; Ponca[143]; Rannaja 12[74]; Shawnee[143]; Shirahada[842]; Sinvalocho MA[10929]; Skorospelka 3b[74]; Sledkovicova K1004[74]; Viginta[68]; Warrior[143, 1024]; Yubileynaya[75]. **v2**: Amika **Lr26**[76]; Bezostaya 1 **Lr34**[74]; Bowie ***Lr14b***[319]; Erythrospermum 142 & 953 **Lr1**[74]; Istra **Lr26**[76]; Mediterranean W1728 ***Lr2a***[1369]; Plainsman V **Lr1**[1024]; Shield ***Lr2a*** **Lr10**[198]; Solaris **Lr26**[76]; See also ▶69. **tv**: Storlom[10469]. **ma**: Co-segregation with *Xmwg798-6B*[9921, 10469]; cDNA marker TaR16 was completely linked to **Lr3** in a population of 109 gametes[10058]; $UBC840_{540}$ – ***Lr3a***, 6 cM[10263].

Lr3b [486, 10028] syn: Lr3bg[486]

i: Thatcher*6/Bage; RL6094 = Tc*6/T6[307]. **v**: Bage[486]. **v2**: T6 **Lr16**[307].

Durum cv. Storlom likely carries ***Lr3a*** or ***Lr3b***[10469]. Cv. Camayo was considered to have a closely linked gene, or **Lr3** allele[10469]. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B*. All three Thatcher NILs with named **Lr3** alleles carried the STS marker[10469].

Lr3c [486, 10028] syn: Lr3ka[486]

i: Tc*6/Klein Aniversario. **v**: Blava[10345]; CI 13227[11021]; Klein Aniversario[486].

Lr3d [11054]

i: RL6062, Thatcher*6/PI 268316[11054]. **v**: PI 268316[11054].

LR9

Lr9[1408] locus: 6BL = T6BS.6BL-6U#1L[389]. 6B[954, 1296, 1299]

Derived from *Ae. umbellulata*.

i: T47 = Transfer = CS + **Lr9**[1408]; Thatcher*6/Transfer; Wichita*4/Transfer[613]; Lines listed in ▶[10244]. **v**: Abe[143]; Arthur 71[1024, 1320]; Clemson 201[465]; McNair 701 & 2203[143]; PI 468940[1439]; Riley 67[1024, 1320]; Sullivan[1110]; Transfer[1296]. **v2**: Ck 9835 ***Lr2a*** **Lr10**[10146]; Ck 9663 ***Lr2a*** **Lr10**[10146]; Lockett **Lr24**[10146]; Oasis **Lr1**[1109]. **al**: *Ae. umbellulata* TA1851[11630]. **ma**: Co-seg with *XksuD27-6B*[48]; co-seg with *Xmwg684-6B* and STS *Xsfr1*[1272]; **Lr9** – 8 cM – *Xpsr546-6B*[1272]; SCAR markers were developed in ▶[10244]. **c**: Encodes a 1,167-aa protein with an N-terminal tandem kinase domain followed by a von Willebrand factor type A (vWA) domain in the C-terminus[11630]. The ~28.4 Mb translocation at 725.61 Mb replaces a 5.58 Mb wheat segment containing 87 high confidence genes[11630].

Lr9 has the identical sequence and translocation breakpoint to **Lr58**[11630]. The structures of additional translocations are given in ▶[389].

LR10

Lr10[199] locus: 1A[312, 546]. 1AS[939] syn: LrL[31]

i: Exchange/6*Thatcher[306]; Gabo/6*Thatcher[306]; Lee/6*Thatcher[306]; Selkirk/6*Thatcher[306]; Timstein/6*Thatcher[306]. **s**: CS*5/Timstein 1A[939]; CS/7*Kenya Farmer 1A[939]. **v**: Centurk[1024]; Centurk 78[1024]; Concho[143]; Federation[939]; Mayo 52[31]; Mayo 54[31]; Parker[546, 1024]; Rocky[1024]; Scout 66[02101]; Sinton[1256]; Tascosa[143]; TAM-105[55]; Unknown accessions[208]; See also ▶[337]. **v2**: Alex ***Lr2a***[976]; Blueboy **Lr1**[143]; Blueboy II **Lr1** **Lr24**[143]; Ck 9663 ***Lr2a*** **Lr9**[10146]; Era **Lr13**[143]; Exchange **Lr12** **Lr16**[31]; Gabo **Lr23**[31]; Guard ***Lr2a***[976]; James ***Lr2a***[976]; Kenya Farmer **Lr23**[939]; Laura **Lr1** **Lr34**[712]; Lee **Lr23**[31]; Len ***Lr2a***[976]; Marshall ***Lr2a***[976]; Parker 76 **Lr24**[143]; Selkirk ***Lr14a*** **Lr16**[31, 199]; Shield ***Lr2a*** **Lr3**[198]; Timstein **Lr23**[31]; Waldron ***Lr2a***[143]; Warden **Lr16**[31]. **tv**: Altar 82[10760]; Russello[10760]. **ma**: *Xcdo426-1A* – 5.1 cM – **Lr10**[1058]; **Lr10** – 8 cM – **Glu-A3**[355]; cosegregation with *Xsfr1(Lrk10-1A)* and *Xsfrp1(Lrk10-1A)*[1270]; complete linkage with *Xsfr1(Lrk10-1A)*, which encodes a protein kinase[639]. **c**: **Lr10** was cloned – it has a CC-NBS-LRR structure, syn, *T10rga1* GenBank AY270157[10442]; A second CC-NBS-LRR gene, *RGA2*, is required for expression of **Lr10** in tetraploid and hexaploid wheats[10760].

Lrk10

A receptor-like kinase. The locus *Xsfr1(Lrk10)-1A*, detected by the probe **Lrk10**, is completely linked with **Lr10** in chromosome 1AS[356]. The gene encodes a receptor-like kinase with extracellular and kinase domains[0297]. Using probe pLrk10-A, developed from the extracellular domain, 6 homologues were found in chromosomes 1A (1), 1B (3) and 1D (2) as well as group 1 chromosomes of *T. monococcum*, *Ae. tauschii* and barley[0294, 0296]. Probes based on the kinase domain identified further homologues in chromosomes 3AS and 3BS as well as the corresponding regions in rice and maize[0294]. Both orthologous and paralogous evolution were suggested.

LR11

Lr11[1409] locus: 2DS[11074]. 2A[1409] syn: LrBP2[11074]

i: Thatcher*6/Hussar[306]; Wichita*4/Hussar[613]. **v**: Bulgaria 88[142]; Hart[1024]; Hazen[49]; Hussar[1409]; Panola[10830]; Pioneer 2850; Pocahontas[10146]; Saluda[10146, 10699]. **v2**: Buck Poncho **Lr10**[11074]; Ck9803 **Lr18**[10595]; FFR 524 **Lr18**[10595]; Jamestown **Lr18**[10830]; Karl 92 **Lr3 Lr10**[02101]; Oasis **Lr9**[143]; Pioneer 2684 **Lr18**[10595]; SS520 **Lr18**[10595]. **ma**: **Lr11** – 0.3 cM – *SCAR32/35* – 1.6 cM – *Xgwm614-2D*[11074].

LR12

Lr12[326] locus: 4B[312]. 4BL[10951]

Adult plant reaction.

bin: 4BL5-0.86-1.00. **i**: Exchange/6*Thatcher[306]. **v**: Opal[306]. **v2**: AC Domain **Lr10 Lr34**[228]; Caldwell ***Lr14a***[10787]; Chinese Spring **Lr34**[301]; Exchange **Lr10 Lr16**[326]; Sturdy **Lr13**[301]; Unknown accessions[208]. **ma**: *Xgwm251-4B* – 0.9 cM – **Lr12** – 1.9 cM – *Xgwm149-4B*[10951].

Possible commonality with **Lr31**.

LR13

TraesCS2B01G182800[11530, 11531]; also predicted in ▸[11529].

Lr13[326] locus: 2BS[939] syn: LrZH22[11467, 11468], LrLC10[11468]

Although originally described as a gene for adult plant reaction[32, 326], **Lr13** can be detected at the seedling stage especially at high temperatures[939, 1156].

i: Tc*7/Frontana = RL4031[306]; fifteen Thatcher lines with 2-gene combinations[711]. **bin**: 2BS1-0.35-0.75. **v**: This gene is very widespread[939]; Hereward[288]; Hustler[608]; Kinsman[608]; Kenya Plume[1370]; Liaochen 10[11468, 11530]; Manitou[326]; Mardler[608]; Maris Huntsman[608]; Moulin[288]; Napayo[70]; Neepawa[143]; Norman[608]; Pastiche[288]; Polk[143]; Virtue[608]; Zhoumai 22[11467, 11468, 11531]. **v2**: AC Barrie *Lr6*[10178]; Beaver **Lr26**[1032]; BH1146 **Lr34**[268]; Biggar ***Lr14a***[712]; Chris **Lr34**; Columbus **Lr16**[1258]; Cumpas 88 **Lr26**[1373]; Era **Lr1** *0*[143]; Frontana **Lr34**[32, 326, 1374]; Genesis ***Lr14a***[712]; Hartog **Lr1 Lr46**[127]; Hobbit ***Lr17a***[608]; Hobbit Sib ***Lr17a***[1350]; Inia 66 ***Lr14a*** **Lr17**[1373]; Klein Aniversario ***Lr3ka***[32]; Kenyon **Lr16**[300]; Lerma Rojo 64 ***Lr17a*** **Lr34**[1373]; Oasis 86 **Lr19**[1373]; Parula **Lr34 Lr46**[1374]; Suneca **Lr1**[485]; Yecora **Lr1**[1374]. **ma**: *Xpsr912-2B* – 9.1 cM – **Lr13** – 7.9 cM – *Xbcd1709-2B* – 9.8 cM – Cent.[88]; **Lr13** – 10.7 and 10.3 cM – *Xgwm630-2BS*[10463]; *Xbarc163-2B* – 5.1 cM – **Lr13** – 8.7 cM – *Xstm773b-2B*[329]; *Xbarc55-2B* – 1.1 cM – *Xkwh37* – 4.9 cM – **Lr13** – 5.8 cM – *Xgpw1109* – 3.7 cM – *Xbarc18-2B*[11068]; *Xbarc55-2B* – 2.4 cM – **LrZH22** – 4.8 cM – *Xgwm374-2B*[11467]; *Xbarc55-2B* – 2.2 cM – *XCAUT163* – 1.10 cM – **LrLC10** – 0.55 cM – *Lseq22* – 6.05 cM – *Xbarc18-2B*[11468]. **c**: Encodes a CC-NBS-LRR protein {11531; 11532} that is identical to that produced by one of the ***Ne2m*** haplotypes[11531].

GenBank MW756036[11532]. **Lr13** is an allele of the YR27/NE2 locus[11593]. Pleiotropic with the specific ***Ne2m*** allele at the NE2 locus.

LR14

Lr14

Lr14a[319, 964] locus: 7B[964]. 7BL[770] syn: LrLla[10520]

bin: 7BL10-0.78-1.00. **i**: Selkirk/6*Thatcher[319]; Arina LrFor[11549]. **s**: CS*6/Hope 7B[964]. **v**: Aotea[964]; Brigand[608]; Gala[964]; Glenwari[964]; Hofed[964]; Hope[964]; H-44[964]; Lawrence[964]; Redman[964]; Regent[964]; Renown[964]; Spica[964]. **v2**: Biggar **Lr13**[712]; Brambling **Lr23 Lr34**[10563]; Caldwell **Lr12**[10787]; Genesis **Lr13**[712]; Inia 66 **Lr13** ***Lr17a***[939]; Selkirk **Lr10 Lr16**[319]. **tv**: Arcangelo[11015]; Bicre[11015]; Creso[11015]; Colosseo[11015]; Italo[11015]; Lloreta INIA[10520]; Plinio[11015]; Somateria[10520]. **v2**: Forno **Lr34 Lr75**[11549]. **ma**: *Xwmc273-7B* – 13 cM – ***Lr14a*** – 10 cM – *Xgwm344-7B*[10520]; *Xwmc10*/*Xgwm344*/*wPt1085-7B* – 1.1 cM – *wPt4038-HRM* – 0.1 cM – ***Lr14a*** – 1.0 cM – *wPt4140-HRM*[11015].

The **Lr14** region in tetraploid wheat harbours *Qlr.ubo-7B.2*, a gene that confers durable resistance in durums[10734, 10736] and that is present in many Italian, CIMMYT and ICARDA durum cultivars[10736]. The relationship of this gene described as *Lr14c* (reference genotype Creso) in ▸[10735] remains to be determined. Reasons for considering *Lr14c* as a unique allele are given in ▸[10735] but according to ▸[11518]

the gene sequence in Creso is identical to that of ***Lr14a***. In association mapping the presence of *QLr.ubo-7B.2* was predicted with 96% accuracy based on appropriate alleles of *Xcfa2257.2*, *Xgwm344.2* and *Xwmc10* in the distal region of chromosome 7BL[10736]. c: ***Lr14a*** encodes a membrane-localized protein with 12 ankyrin repeats and structural similarity to Ca^{2+}-permeable non-selective cation channels[11549]. GenBank MT 123593.

Based on sequence ***Lr14a*** was identified in a few spelt (e.g. PI 190962) and a few wild emmer accessions[11549].

Lr14b[319]

i: Maria Escobar/6*Thatcher[319]. **v**: Weebill 1[10571]. **v2**: Bowie **Lr3**; CI 13227 **Lr68**[10817]; Maria Escobar **Lr17**[319]; Rafaela **Lr17**[314].

Most accessions with ***Lr14b***, including the Tc NILs probably carry APR gene **Lr68**[10817] which could be the same as *QLr.osu-7BL*[10817]. A marker based on the ***Lr14a*** sequence failed to amplify a product in the Tc+14b NIL[11549].

Lr14ab

i: ***Lr14a***/6*Thatcher//***Lr14b***/6*Thatcher Seln[319].

LR15

Lr15[843] locus: 2DS[843, 942]

i: Thatcher*6/Kenya W1483[306]. **bin**: 2DS1-0.33-0.47. **v**: Kenya W1483[843]. **ma**: *Xgwm4562-2D* – 3.1 cM – **Lr15** – 9.3 cM – *Xgwm102-2D*[11234]; *Xwmc764-2B* – 9.4 cM – **Lr16** – 1.4 cM – *Xwmc661-2B*[11219].

Probably allelic with **Lr2**.

LR16

Lr16[318] locus: 4B[312]. 2BS syn: LrE[31]

The following chromosome locations are consistant with the finding that the first location was based on the use of a Rescue monosomic series. Rescue differs from CS by a 2B-4B translocation[939]. **Lr16** is always asociated with **Sr23**.

i: Exchange/6*Thatcher[306]; RL6096 = Tc*6/T6[307]. **v**: AC Domain[10170]; AC Foremost[10170]; Arapahoe[02101]; Brule[02101]; Ciano 79[1373]; Etoile de Choisy[74]; Imuris 79[1373]; McKenzie[10170]; Millenium[02101]; Papago 86[1373]; Redland[02101]; Vista[02101]; Waxwing[11267]. **v2**: AC Barrie **Lr13**[10178]; Columbus (heterogeneous) **Lr13**[1258]; Exchange **Lr10 Lr12**[31]; Kenyon **Lr13**[300]; Francolin#1 **Lr46**[11219]; Selkirk **Lr10** ***Lr14a***[31]; T6 ***Lr3bg***[307]; Warden **Lr10**[31]. **ma**: Distally located: **Lr16** – *Xwmc764-2*, 1, 9 and 3 cM, respectively, in crosses RL4452/AC Domain, BW278/AC Foremost and HY644/McKenzie[10170, 10189].

A recessive gene *LrCH1539* in accession CH1539, flanked by markers *scau2BS81* (6.227 Mb, CS RefSeq 1.0) and *scau2BS47* (7.006 Mb) was located at the same position as **Lr16** {11680|.

LR17

Lr17[318] syn: Lr17a

v: Santa Fe[10830]

Lr17a[318, 1350] locus: 2A[314]. 2AS[62] syn: Lr17

bin: 2AS-5[10572]. **i**: Klein Lucero/6*Prelude[318]; Klein Lucero/6*Thatcher[318]; Maria Escobar/4*Thatcher[318]. **v**: CDS Stanley[11579]; EAP 26127[314]; Jagger[338, 10146, 10346]; Jupateco[939]; Klein Lucero[318]; Mace[11579].

Santa Fe[10830]; TAM111[10595]; SY Mattis[11579]; Trego[10572]. v2: Fuller **Lr39**[10699]; Inia 66 **Lr13** ***Lr14a***; Jagger **Lr37**[11328]; Lerma Rojo 64 **Lr13 Lr34**[1373]; Maria Escobar ***Lr14b***[318]; Rafaela ***Lr14b***[314]. ma: *Xbarc123-2A* – 4.8 cM – *Xgwm636-2A* – 4.0 cM – ***Lr17a***[10571]; *Xgwm614-2A* – 0.7 cM – ***Lr17a*** – *Xwmc407-2A*[10572]; ***Lr17a*** – 3.7 cM – *Xbarc212-2a*[10795].

Lr17b[1350] locus: 2A[1350] syn: WBR2[615], LrH[970]

v: Brock[260]; Harrier[1350]; Maris Fundin[1350]; Norin 10-Brevor, 14[1350]; Norman[1350]. **v2**: Contra **Lr13**[10345]; Hobbit Sib = Dwarf A **Lr13**[1350]; Kalasz **Lr13**[10345]; Riband **Lr13**[10345]; Sarka **Lr13**[10345]; Tarso **Lr26**[229].

LR18

Lr18[318] locus: 5BL[935]

Derived from *T. timopheevii*. Independently derived lines with **Lr18** possess a unique N band terminally located in chromosome 5BL[1614]. Low seedling responses conferred by **Lr18** are most effective at 15-18C. With increasing temperatures the response becomes less effective and ineffective at 25-27C[935], see also,[1614]. = T5BS.5BL-5G#1L[389].

i: Africa 43/7*Thatcher[318]; Red Egyptian PI 170925/6*Thatcher[318]. **v**: Africa 43[318]; Red Egyptian PI 170925[318];Red Egyptian PI 17016-2c[318]; Sabikei 12[935]; Timvera[935]; Timvera Derivative[935]; Certain WYR accessions[935]; FTF[1614]; Several Sabikei lines including Sabikei 12[1614]. **v2**: Ck9803 **Lr11**[10595]; FFR 524 **Lr11**[10595]; Jamestown **Lr11**[10830]; Pioneer 2684 **Lr11**[10595]; SS520 **Lr11**[10595].

A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to **Lr18**. The claim that **Lr18** and *LrTt2* were different was based on low seedling infection types, but the genetic backgrounds were different[10752].

LR19

Lr19[140] locus: 7DL = T7DS.7DL-7Ae#1L[291, 388, 389, 657, 956, 1323]

Derived from *Th. elongatum*.

i: Agatha = T4 = TC + **Lr19**[956, 1323]; Sears transfer 7D-7Ag no. 1[10255]. **v**: Dobrynya[10821]; Ekada 6[10821]; L503[1346]; L505[10821]; L513[1346]; Mutant 28[598]; Samsar[108]; Sunnan[684]; Pallada[11161]; Volgouralskaya[10821]; See **Sr25**.
7AL Lines I-22 and I-23[10255]. **v2**: Kinelskaya Niva **Lr23**[10821]; Oasis 86 **Lr13**[1373].
7AL **tv**: This translocation was transferred to durum wheat and engineered to produce normally inherited secondary recombinants with smaller alien segments, such as R5-2-10, and tertiary recombinants such as R1[10633]. **ma**: Located in the *Xwg420-7Ag* – *Xmwg2062-7Ag* interval[10255]; RAPD, SCAR and SSR markers co-inciding with, or flanking, **Lr19** in a derivative of Knott's Agatha Mutant 28 (C80.1) were reported in ▶[10379]. **ma**: *Xbg262436* – LR19 – *Xbarc76-7E* – *PSY-E1* – *XBE445653*[11699]. **c**: A candidate sequence, AG15, with a 1,258 amino acid sequence and a CC-NBS-LRR structure was reported in ▶[10575]. The chromosome with **Lr19** in Indis is probably identical to that in Agatha[1162].
7DL = T7DS.7DL-7Ae#1-7DL[388]. **v**: Mutant 235[681].
7AL = T7A-7Ae#1[330]. **v**: Sears' 7A-7Ag No.12[330].
7BL[1163]. **v**: 88M22-149[1163]; 4 further derivatives of 88M22-149[0232].
7AgL[1304] = 7Ae#1L. **su**: Agrus. **ma**: Co-seg with 8 RFLP markers[48]; ***Ep-D1c*** – 0.33 cM – **Lr19**[1587]; cosegregation with ***Ep-D1d***[974]; Prins *et al*[1162] studied 29 deletion mutants in Indis and determined the gene order: *Sd-1* – *Xpsr105-7D* – *Xpsr129-7D* – **Lr19** – **Wsp-D1** – **Sr25** – *Y*; The following gene order for the *Thinopyrum* segment is given in ▶[0101]; Cent – **Sd1** – *Xpsr165-7D* – *Xpsr105-7D* – *Xpsr129-7D* – *XcslH81-1* – *Xwg380-7D* – *Xmwg2062-7D* – **Lr19** – **Wsp-D1** – **Sr25**/*Y*; An STS marker closely linked and distal to **Lr19** was developed from an AFLP[0273].

Although **Lr19** is usually associated with **Sr25**. Sears' transfer 7D-7Ag No. 11 carries neither **Lr19** nor **Sr25**. See **Lr29**.

Knott[681] obtained two mutants (28 and 235) of Agatha possessing **Lr19**, but with reduced levels of yellow pigment in the flour. Marais[890, 892] obtained mutants and recombined lines with intermediate levels of, or no, yellow pigment. It was shown that recombinant line 88M22-149 lacked yellow pigment[1163].

Secondary translocation line I-96 derived from Sears' 7D-7Ag no.1 involved **Lr19** being located in an intercalary segment with low yellow pigment and lacking **Sd1**[10255].

Two T7DS.7DL-7EL-7DL lines: 1-40 lacked *PSE-E1* whereas 9-80 carried it[11699].

Lr19 in lines I-22 and I-23 retaining yellow pigment but lacking **Sd1** was transferred to durum chromosome 7BL[10255]. One of the lines with the shortest 7Ag segment, **Lr19**-I49-299, was used in a further cycle of recombination[10278].

LR20

Lr20[140] locus: 7AL[1305, 1554]

i: Thatcher+**Lr20**. **s**: CS*5/Axminster 7A[1293]. **v**: Axminster[348, 1175, 1305]; Birdproof[1554]; Bonus[1554]; Converse[1554]; Festival[1554]; Kenora[1554]; Kenya W744[1554]; Maris Halberd[608]; Normandie[348, 1554]; Sappo[608]; Sicco[310]; Thew[140, 1552]; Timmo[608]. **v2**: Norka **Lr1**[1554]; See **Pm1** (Reaction to *Blumeria graminis*) & **Sr15** (Reaction to *Puccinia graminis*) with which **Lr20** is always associated. **Lr20** in Sicco appears to differ from that in Sappo, Timmo and Maris Halberd[310]; **Lr20** in Norka (**Lr1**+**Lr20**) may differ from that in Thew[939]. **ma**: Complete cosegregation of several markers including *Xcdo347-7A*, *Xpsr121-7A*, *Xpsr680-7A*, *Xpsr687-7A*, *Xbzh232(Tha)-7A*, *Xrgc607-7A* and *Xsts638-7A* with **Pm1** and **Lr20** was reported in ▶[323]; **Lr20** – *STS638*, 7.1 cM[10263].

LR21

Lr21[1241] locus: 1DL[1241]. 1D[650]. 1DS[448] syn: Lr40[1200, 10415]

i: Thatcher*6/Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289[306]. **v**: Barlow[11093]; Faller[11093]; Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289, RL 5406[648]; Lovitt[10766]; McKenzie[228, 10766]; Prosper[11093]; WGRC2 = TA1649/3* Wichita[299]; WGRC7 = Wichita/TA1649//2*Wichita[299]. **v2**: AC Cora **Lr13**[713]; WGRC16 = TAM107*3/*Ae. tauschii* TA 2460 **Lr39**[220, 10415]. **dv**: *Ae. tauschii* accessions: RL5289 = TA1599[1241]; *Ae. tauschii* TA2460 **Lr39**[220, 10415]; TA1649[299]; TA1691[299]; TA2378[299]; TA2470[299]; TA2483[299]; TA2495[299]; TA2527[299]; TA2528[299]. **ma**: All members of the **Lr21** family carry a STS derivative of *XksuD14-1D* that has a resistance gene analogue structure[299]; *XksuD14-1D* was reported to map 1.8 cM proximal to **Lr21** in▶[375]; **Lr21** – 0 cM – *rgaYr10b* – 0.6 cM – *Xgdm33-1D*[360]; *Xksu-1D* is part of **Lr21**[10420]. **c**: **Lr21** was cloned and shown to have a NBS-LRR structure[10420]. **Lr21**-mediated resistance requires expression of *RAR1, SGT1* and *HSP90*[11274].

A reconstituted effective **Lr21** allele (designated *Lr21-b*) was obtained as a rare (1/5,872) recombinant (accession TA4446) between **Lr21** pseudogenes in common wheat cultivars Fielder and Wichita[10620]. Further haplotype analyses are reported in ▶[10766].

A further spontaneous allele designated *Lr21-tbk* with 'several mutations in exons 2 and 3' leading to three amino acid changes was identified cv. Tobak[11762].

LR22

Lr22 locus: 2DS

Lr22a[1241] locus: 2DS[1241]

Adult plant reaction.

i: Neepawa*6/RL5404, RL4495[10467]; Thatcher*3//Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271[306]; Thatcher*7//Tetra-Canthatch/RL5271, RL 6044[10467]; CH Campala ***Lr22a***[11209]. **v**: Line 98B34-T4B[10467]; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404[311]. **v2**: AC Minto **Lr11** **Lr13**[713]. **dv**: *Ae. squarrosa* var. *strangulata* RL 5271. **ma**: *Xgwm296-2DS* – 2.0 cM – ***Lr22a***[10446]; *Xgwm455-2D* – 1.5 cM – ***Lr22a*** – 2.9 cM – *Xgwm296-2D*[10467]; *Xgwm455-2D* – 0.39 cM – ***Lr22a*** – 1.1 cM – *Xgwm296-2D*[11209]. **c**: GenBank KY064064; NBS-LRR structure encoding an intracellular immune receptor homologous to the *Arabidopsis thaliana* RPM1 protein[11209].

Lr22b[298]

Adult plant reaction.

v: Canthatch[298]; Marquis[970]; Thatcher[298]. This gene will be present in near-isogenic lines based on Thatcher.

LR23

Lr23[948] locus: 2BS[948] syn: LrG[951]

i: Lee FL 310/6*Thatcher[948]. **s**: CS*7/Kenya Farmer 2B[948]; CS*6/Timstein 2B[948]. **v**: BT-Schomburhk[11601]; Cranbrook; Crim[1091]; Hope/Timstein[1091]; I 310678[1091]; I 310685[1091]; I 349162[1091]; IWP94[10569]; K 45973[1091]; K 51070[1091]; Rocta[1091]. **v2**: Gamenya **Lr3**[1552]; Gabo **Lr10**[1552]; Kenya Farmer **Lr10**[1552]; Lee **Lr10**[1552];

Pastor **Lr46**[10928]; Timstein **Lr10**[1552]; Brambling ***Lr14a*** **Lr34**[10563]. **tv**: Altar 84[1058]: Gaza[11601]; Tamoroi[11601]. **ma**: Associated with *Xksu904(Per2)-2B*[90]; SSR and KASP markers were developed in ▶[11601].

A QTL, which is likely to correspond to **Lr23**, was identified in the Opata 85/W-7984 (ITMI) RIL mapping population. The resistance was contributed by W-7974[0090].

LR24

Lr24 locus: 3DL[956, 1389] syn: LrAg[141]

Derived from *Thin. elongatum*. Always present with **Sr24**[956]. See **Sr24** (Reaction to *P. graminis*).

i: Tc+**Lr24** (ex Agent). **v**: Cody[1284]; Cutter[10595]; Jagalene[10595]; McCormick[10595]; Ogallala[10595]; Osage[143]; Payne[1024, 1390]; SST 23[1324]; SST 44 = T4R[1324]; Timpaw[1255]; Torres[128]; Wanken[1255]; Australian genotypes[340]. **v2**: Blueboy II **Lr1** **Lr10**[141]; Fox **Lr10**[141]; Lockett **Lr9**[10146]; Parker 76 **Lr10**[143, 1024]; Siouxland **Lr26**[1283]. **ma**: Co-seg of **Lr24** in Agent with 8 RFLP markers; segment in Sears' 3D-3Ag#1 is shorter than in Agent[48]; Tagged with *Xpsr1203-6B*[1271]; cosegregation with RAPD marker that was converted to a SCAR[231]; Linked with SCAR marker $SCS73_{719}$ earlier thought to tag **Lr19**[10147]. Australian white seeded cultivars with **Lr24** were recombinants derived from Sears' translocation lines 3Ag#3 and 3Ag#14. 1BL[185] = T1BL.1BS-3Ae#1L[600] **v**: Amigo[185, 600, 1463]; Teewon[600]. **ma**: SCAR markers were developed in ▶[10368]. A PCR marker, **Sr24**#12, was confirmed across all sources of **Lr24**[10257]. This source of **Lr24** is also not associated with red seed colour.

LR25

Lr25 locus: 4BS[270, 271, 380, 389]

Derived from *S. cereale* cv. Rosen. Revised to T4BS.4BL-5RL[543] and later to T4BS.4BL-2R#1L.

i: Tc+**Lr25** **Lr48**[10738]. **v**: Transec[273]; Transfed[269]; Always present with **Pm7**. **ma**: Cosegregation with a RAPD[1165].

LR25 is closely linked with LR48[10738].

LR26

Lr26 locus: 1R (1B), T1BL.1RS

Derived from *S. cereale*. See also Reaction to *P. graminis*, **Sr31**; Reaction to *P. striiformis*, **Lr26**. T1BL.1RS.1R (1B).

i: MA1 and MA2 four breakpoint double translocation lines 1RS-1BS-1RS-1BS.1BL in Pavon[84]. **v**: AGS 2000[10595]; Derivatives of Petkus rye – see **Yr9** (Reaction to *P. striiformis*) & **Sr31** (Reaction to *P. graminis*); Bacanora 88[1373]; Cougar[267]; Pioneer 26R61[10595]; Rawhide (heterogeneous)[267]; GR876[753]; Iris[75]; Sabina[75]. **v2**: Beaver **Lr13**[10687]; Cumpas 88 **Lr13**[1373]; Istra **Lr3**[76]; Siouxland **Lr24**[1283]; Solaris **Lr3**[76]; Many wheats with **Lr26** also carry **Lr3**. Amika (heterogeneous) **Lr3**[76]; See also ▶[310]. **tv**: Cando*2/Veery, KS91WGRC14[381]. **ma**: Several markers tightly linked with **Lr26** were identified in ▶[377]. 1BS/1RS recombinants 4.4 cM proximal to **Gli-B1**/**Glu-B3**[0084]. Hanusova *et al.*[492] identified 127 wheats with **Lr26** but only 16 of them were listed.

LR27

Lr27[1367] locus: 3BS[1367] syn: LrGt[1366], A[1058, 1366]

One of two complementary genes; the second gene, **Lr31**, is located in chromosome 4BS[1367]. **Lr27** is present in wheats with **Sr2**, but is not expressed in the absence of the complementary factor[1366]. The following wheats have both **Lr27** and **Lr31**.

s: CS*6/Ciano 3B[1366]; CS*6/Ciano 5B[1366]; CS*6/Hope 3B[1366]. **v**: Gatcher[1366]; Ocoroni 86[1373]. **v2**: Anhuac **Lr13** **Lr17**[1361]; Cocoraque 75 **Lr13** ***Lr17a*** **Lr34**[1361]; Jupateco 73S ***Lr17a***[1361]; SUN 27A **Lr1** ***Lr2a***[1366]; Timgalen **Lr3** (heterogeneous) **Lr10**[1366]. **tv**: Benimichi C2004[10585]; Jupare C2001[10585]. **ma**: Positive association with *XksuG53-3B*[1058].

LR28

Lr28[967] locus: 4AL[967]

Derived from *Ae. speltoides*. = T4AS.4AL-7S#2S[389].

i: CS 2A/2M 4/2[967]; CS 2D/2M 3/8[967]. **v**: Sunland[11069]; Tobak[11717]. **ma**: **Lr28** was tagged using STS primer OPJ-01$_{378}$[1052]; A linked RAPD marker, S421$_{640}$ was converted to a TPSCAR, SCS421$_{570}$[10236]; *Xbarc219-4A* – 2.2 cM – *Xwmc219-4A*[11069].

LR29

Lr29[939] locus: 7DS[939]

Derived from *Th. elongatum*. = T7DL-7Ae#1S[389].

i: Sears' CS 7D/*Ag*#11[939, 1300]; RL6080 = Tc*6/Sears' 7D/Ag#11[316]. **ma**: Co-segregation with two RAPDs[1165].

LR30

Lr30[315] locus: 4AL[315] syn: LrT

Recessive[315].

i: RL 6049 = Thatcher*6/Terenzio[315]. **v2**: Terenzio **Lr34**[315].

LR31

Lr31[1367] locus: 4BL[1367] syn: B[1058, 1366]

One of two complementary genes, the second gene is **Lr27**.

v: Ocoroni 86[1373]. **v2**: Chinese Spring **Lr12 Lr34**[1367]; See **Lr27** for list of wheats with **Lr27 +Lr31**. **tv**: Benimichi C2004[10585]; Jupare C2001[10585]. **ma**: A positive association with *XksuG10-4B*[1058].

Possible commonality with **Lr12**.

LR32

Lr32 locus: 3D[644]. 3DS[645]

i: RL6086 = Tc*7/RL5713/Marquis K[10874]; BW196 = Katepwa*6/RL5713/2*Marquis K[10874]. **v**: Tetra Canthatch/*Ae. tauschii* RL5497-1, RL5713, RL5713/Marquis-K[644]. **dv**: *Ae. tauschii* RL5497-1[644]. **ma**: *Xbcd1278-3D* – 3.6 cM – **Lr32**[48]; *Xcdo395-3D* – 6.9 cM – **Lr32**[48]; *Xbarc128-3D* – 9.1 cM – **Lr32** – *Xwmc43*/*Xbarc235-3D*[10874].

LR33

Lr33[325] locus: 1BL[325]

i: RL6057 = Tc*6/PI 58548[297, 321, 325]. **v**: PI 268454a[297]; PI 58548[297, 325]. **v2**: KU168-2 **Lr34**[11687]; PI 268316 ***Lr2c*** **Lr34**[297]; Others[1322]. **ma**: KASP markers flanking **Lr33** in the centromeric region were identified in [11687].

LR34

Lr34[297, 299] locus: 7DS[324, 1058]. 7D[299] syn: LrT2[321]

TraesCS7D03G0183600

In addition to conferring seedling and adult plant resistance, **Lr34** responds in a complementary manner when combined with either **Lr33** or *LrT3*[321]. In the Thatcher background, **Lr34** is associated with increased resistance to stem rust[299, 321]. Although the resistance gene in the near-isogenic Thatcher line, RL6077, was considered to be **Lr34** on the basis of disease response, leaf tip necrosis and its association with resistance to stripe rust, a cross with RL6058 segregated for two genes. A translocation to another chromosome was suggested[324].

i: Arina + **Lr34**[10648]; Lalbahudar + **Lr34**[10648]; Line 897[321]; Line 920[321]; Selections Jupateco 73R ***Lr17a*** **Lr27** + **Lr31** and Jupateco 73S ***Lr17a*** **Lr27** + **Lr31** and Cocoraque 75 **Lr13** ***Lr17a*** **Lr27** + **Lr31** and

Anhuac 75 **Lr13** ***Lr17a*** **Lr27** + **Lr31**, can be considered near-isogenic for the presence and absence, respectively, of **Lr34**[1361]. **v**: Ardito[10648]; Arina*3/Forno[10380]; Bezostaya[10387, 10648]; Condor[10387, 10648]; Cook[10387]; Forno[10066, 10380, 10387]; Fukuho-Komugi[10387, 10648]; Kavkaz[10648]; Lantian 12[10682]; Libellula[10682]; Otane[10387]; Pegaso[10648]; Penjamo 62[10648]; RL6058 = Tc*6/PI 58548[297]; PI 268454[297]; Strampelli[10682]; Westphal 12[268]; Others[299, 321, 1322, 1376]; See ▶[1362]; 2174[10888]; List of U.S. hard wheats in ▶[10888]; Pedigree charts showing the presence of **Lr34** in various Canadian wheat classes are given in ▶[10889]. **v2**: Anza = WW15 **Lr13** heterogeneous[10648]; Brambling ***Lr14a*** **Lr23**[10563]; BH1146 **Lr13**; Chinese Spring **Lr12 Lr31**[301, 10648]; Chris **Lr13**[10648]; Frontana **Lr13**[1374]; Glenlea **Lr1**[327, 10648]; Jupateco R ***Lr17a***, **Lr27** + **Lr31**[10648]; Lageadinho *LrT3*[321]; Laura **Lr1 Lr10**[712]; Mentana ***Lr3b***[10493, 10648]; Parula **Lr13 Lr46**[1374]; PI 58548 **Lr33**[297, 321]; RL 6059 = Tc*6/Terenzio **Lr33**[297]; RL 6069 = Tc*6/Lageadinho *LrT3*[321]; RL6070 = Tc*5/PI 321999 *LrT3*[321]; RL6050 = Tc*6/Terenzio *LrT3*[321]; Saar **Lr46**[10481]; Sturdy **Lr12 Lr13**[301]; Terenzio **Lr3 Lr30** *LrT3*[321]; Thirteen Thatcher lines with 2-gene combinations[434]. **ma**: Complete linkage with **Ltn** (leaf tip necrosis)[1361], **Yr18** (Reaction to *P. striiformis*)[937, 1362] and **Bdv1** (Reaction to barley yellow dwarf virus) and **Pm38** (Reaction to *B. graminis*)[0090]; association with *Xwg834-7D*[268]; *Xgwm120-7D* – 0.9 cM – **Lr34** – 2.7 cM – *Xgwm295-7D*[10259]; **Lr34** … *XsfrBF473324* – 0.5 cM – *Xsfr.cdo475-7D* – 0.7 cM – *Xswm10-7D*[10387]; A 150 bp allele (b) of STS *csLV34*, derived from wEST *BQ788742* was identified in most wheats with **Lr34**; *CsLV34a* – 0.4 cM – **Lr34**[10387]; STS marker *csLV34* was used to confirm or postulate the presence of **Lr34** in Australian cultivars[10493] and Hungarian materials[10701]; Further markers for **Lr34** and various marker-positive haplotypes that lack leaf rust resistance are described in ▶[10887, 10888]; A gene based (3 bp indel in in exon 11), dominant HRM marker is reported in ▶[11669]. **c**: **Lr34** spans 11,805 bp and produces a 1,401 aa protein that belongs to the drug resistance subfamily of ABC reporters[10648]; GenBank FJ436983[10648]; Further confirmation of the ABC transporter is provided in ▶[10887].

A QTL, which is likely to correspond to **Lr34**, was identified in the Opata 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by Opata 85[0090].

On the basis of leaf tip necrosis and lack of segregation in a diallel, cv. Saar, Simogh, Homa, Parastoo and Cocnoos were considered to have **Lr34**, but each also possessed 2 or 3 additional adult plant resistance factors[10110]. This gene is identical to **Yr18**, **Pm38** and **Ltn** and confers stem rust resistance in some genetic backgrounds.

Lr34 conferred seedling resistance to leaf rust when transformed into durum wheat[11314].

Diagnostic markers based on the gene sequence are reported in ▶[10713]; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry **Lr34**[10713].

LR35

Lr35[651] locus: 2B[651]

Derived from *Ae. speltoides*[651]. Adult plant resistance[651]. = 2BL-2SL-2SS#2.2SL#2[11037].

i: RL6082 = Thatcher*7/RL5711[11037]. **v**: RL5711[651]. **ma**: A. SCAR marker was developed[9923].

Complete cosegregation between **Lr35** and RFLP loci *Xwg996-2B*, *Xpsr540-2B* and *Xbcd260-2B* was observed. The RFLP probe BCD260 was converted to a CAPS and STS marker[0045]. Lines with shortened alien segments are reported in ▶[10741].

Lines with shortened alien segments bearing **Lr35** are described in ▶[10741].

LR36

Lr36 locus: 6BS[292]

Derived from *Ae. speltoides*.

v: CDC Bounty[11253]; Line 2-9-2[292]; Line E84018[292]. **al**: *Ae. speltoides* Popn. 2[292]. **ma**: *Xcfd13-6* – 5.2 cM – **Lr36** – 3.8 cM – *Xgwm88-6B*[11588]. Since **Lr36** is located in an alien segment these markers likely map the boundaries.

LR37

Lr37[62] locus: 2AS[62]. 6M^{v} = 2MS-6MS.6ML or 2MS-6ML.6MS[0009]

Derived from *Ae. ventricosa*. Recessive[667]. **Lr37** can be detected in seedlings at low temperatures (17°C) and is effective in adult plants under field conditions. See also **Sr38** (Reaction to *P. graminis*) and **Yr17** (Reaction to *P. striiformis*).

VPM1 and derivatives: 2AS[62] = 2AL.2AS-2N^{v}S[0213]. **i**: RL 6081 = Tc*/VPM1[939]; RL6081 = Tc*8/VPM1[316]; Various NILs listed in ▶[0213]. **v**: Hyak[21]; Madsen[20]; Rendezvous[62]; VPM1[62]; VPM1 derivatives[939]; see also Reaction to *P. striiformis tritici* **Yr17**.
Moisson derivatives: *Lr*[113]. 2AS = 2AL.2AS-2N^{v}S[113]. **ad**: Moisson + 6N^{v} = 6N^{v}S.6N^{v}L-2N^{v}S or 6N^{v}L.6N^{v}S-2N^{v}S[0009]. **v**: Mx12[0213]; Mx22[0213].
ma: (relevant to both groups of derivatives) PCR primers designed from marker *csVrga1D3*[0183] producing a 383 bp product allows detection of the 2N^{v}S segment[0213].

A resistance gene analog containing an NBS-LRR R gene sequence was isolated from the *Ae. ventricosa* segment carrying **Lr37**[0183].

The 2NS translocated segment carrying **Lr37** replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH-9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682*[10073]. SCAR markers SC-372 and SC-385 were developed in ▶[10796].

LR38

Lr38[392]

Derived from *Th. intermedium*.

1DL = T1DS.1DL-7Ai#2L[389, 390]. **v**: T25[390].
2AL = 2AS.2AL-7Ai#2L[389, 392]. **v**: W49[392] = T33[390].
3DS = 3DL.3DS-7Ai#2L[389, 390]. **v**: T4[390].
5AS = 5AL.5AS-7Ai#2L[389, 390]. **v**: T24[390].
6DL = 6DS.6DL-7Ai#2L[389, 390]. **i**: RL6097 = Thatcher*6/T7[307]. **v**: T7[307, 390].
7Ai#2(7D)[389, 392]; 7Ai#2(7A)[390]. **su**: W52[389, 390].

LR39

Lr39[1200, 02100, 02100] locus: *Lr41* [215]. 2DS[10731, 02100] syn: LrT[11207]

Derived from *Ae. tauschii*[02100].

i: TC*4/Overley, GSTR 447[11498]. **v**: Amour[11086]; Bullet[11086]; Fuller[10595]; KS90WGRC10 = TAM107*3/*Ae. tauschii* TA2460[220]; Overley[10595, 10699]; Postrack[10830]; PostRock[11093]; PBW114/*Ae. tauschii* PAU14195//4*WH542 backcross selections[11207]; TAM112 {11086; TA4186 = TA1675*2/Wichita[02100]; Thunderbolt[02100]; Winterhawk[11086]. **v2**: Fuller ***Lr17a***[10699]; WGRC16=TAM107*3/*Ae. tauschii* TA 2460[220]. **dv**: *Ae. tauschii* PAU14195[11207]; *Ae. tauschii* TA 1675[02100]; *Ae. tauschii* TA2460 **Lr21**[220, 10415]; **Lr21**[220, 10415]. **ma**: 10.7 cM distal to *Xgwm210-2D*[02100]; Four markers, *Xbarc124-2D*, *Xgwm210-2D*, *Xgdm35-2D* and *Xcfd36-2D* were closely linked with the terminally located **Lr39** (formerly **Lr41**), but the gene order was inconsistent and no specific allele was associated with it[10731]; *Xcau96-2D* – 1.6 cM – **LrT** (**Lr39**) – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – *lwT* – 4.1 cM – *Xgdm35-2D*[11207]. **c**: Predicted to encode a wheat tandom kinase (WTK) – two amino acid changes relative to *T. tauschii* AL8/78[11685].

LR40

LR40 Deleted, see LR21.

LR41

LR41 Deleted, see LR39.

Lr41[215]

Deleted, see **Lr39**

LR42

Lr42[218] locus: 1D[218]

AET1Gv20040300

i: TC*4/Century, GSTR 448[11498]; Tc + **Lr42** PI 701841 (J. Kolmer pers. com Feb 2023). **v**: AR93005[10840]; Fannin[10595]; KS93U50 {M22059}. **v2**: KS91WGRC11 **Lr24**[218, 10840]; Quaiu 3 **Lr46**[10943]. **dv**: TA2450[218]. **v**: KS93U50[11599]. **ma**: **Lr42** – 0.8 cM – *Xwmc432-1D* – 1.6 cM – *Xcfd-D1*[10840]. Flanked by *pC43* and pC50 at 8.65 Mb and 8.77 Mb, respectively (Aet 4.0)[11599]. **c**: CC-NB-ARC protein with 920 amono acids[11599]. Marker *Pc50*, 46 kb from LR42 was recommended for MAS although additional gene-based markers were identified[11599].

According to [11599] **Lr42** was present in >1,000 CIMMYT lines.

lr42

c: The **lr42** allele has fewer LRR repeats[11599].

LR43

LR43 Deleted, wrongly based on a gene combination.

Lr43[218]

Deleted, wrongly based on a gene combination

LR44

Lr44[322] locus: 1B[322]

i: RL6147 = Thatcher*6/*T. spelta* 7831[322]. **v**: *T. spelta* 7831[322]; *T. spelta* 7839[322].

LR45

Lr45[958] locus: 2A = T2AS-2R#3S.2R#3L[389, 958]

Derived from *Secale cereale*.

i: RL6144 = Thatcher*7/ST-1[958]. **v**: ST-1[958]; Various Australian backcross derivatives[958].

LR46

Lr46[1364] locus: 1B[1346]. 1BL[0119]

Completely linked with **Yr29**[0119]. Adult plant resistance.

s: Lalbahadur(Pavon 1B) **Lr1**[1364]; Lalbahadur(Parula 1B)[10281]. **v**: Attila[10281]; Kundan[11248]; Siete Cerros[10817]. **v2**: CI 13227 ***Lr3c***; Frontana **Lr13** ***Lr14b*** **Lr34 Lr68**[10817]; Pavon F76 **Lr1 Lr10 Lr13**[119, 1364]; Parula **Lr13 Lr34**[10281]; Parula ***Lr3b*** **Lr13** ***Lr14b*** **Lr34 Lr68**[10817]; Quaiu 3 **Lr42**[10943]; Saar **Lr34**[10481]. **tv**: Present in the following tetraploid wheats in combination with other genes/QTL: Bairds[11600]; Dunkler {M23032}; Heller#1 {M23032}. **ma**: An RFLP marker associated with **Lr46** with a recombination value of about 10% was identified in[0119]; *Xwmc44-1B* – 1.4 cM – *Xbac24prot* – 9.5 cM – **Lr46** – 2.9 cM – *Xbac17R … Xgwm140-1B*[10281]; *Xwmc44-1B* – 3.6 cM – **Lr46** 2.1 cM – *XtG818*/*Xbac17R Xgwm140-1B*[10281]; *XSTS1BL2* – 2.2 cM – **Lr46**/*XSTS1BL9* – 2.2 cM – *XSTS1BL17*[10326]. Associated with **Ltn2** and **Yr29**.

LR47

Lr47[9901] locus: 7AS

Derived from *Ae. speltoides*[9901].

7AS = Ti7AS-7S#1S-7AS.7AL[9901]. **v**: Bionta 2004[10737]. Pavon derivative PI 603918[9901]. Backcross derivatives based on Express, Kern, RS15, Yecora Rojo and UC1041[11721, 0126]. Recombinants with reduced 7S#1 segments[11721]. **c**: **Lr47** was identified as a CNL, which was also present in *Ae. speltoides* accessions T2140002, Y162 and Y397[11721].
7A = T7AS-7S#1S.7S#1L[389]. **v**: CI 17882, CI 17884, CI 17885, KS 90H450[9901].
7AL = Ti7AS.7AL-7S#1L-7AL. **v**: Pavon derivative PI 603919[9901].

ma: **Lr47** was located in the distal one-third of 7AS, 2-10 cM from the centromere and within a 20-30 cM segment[9901]. Complete linkage with several RFLP markers[9901] and PCR specific markers[0126].

KASP markers for detection of **Lr47** are reported in [11544].

LR48

Lr48[0085] locus: 2BS[329, 10842]. 4BS[10738]

Adult plant resistance[0085]. Recessive[0085].

i: CSP44/5*Lal Bahadur AUS91421[0329]. **v2**: CSP44 **Lr34**[0085]; Dove **Lr34**[0329]. **ma**: *Xgwm429b-2B* – 6.1 cM – **Lr48** – 7.3 cM – *Xbarc7-2B*[329]; RAPD markers flanking **Lr48** at 2.7 and 8.6 cM are reported in [10738]; *Xwmc175-2B* – 10.3 cM – **Lr48** – 2.5 cM – *Xwmc332-2B*[10842]; Centromere – 27.5 cM – **Lr48** (est.)[10842]; *Xgwm429b-2B* – 4.2 cM – *Sun563/Sun497* – 0.6 cM – *IWB31002*/*IWB39834*/*IWB3432*/*IWB72894*/**Lr48** – 0.3 cM – *IWB70147* – 2.0 cM – *Xbarc67-2B*[11112]; *Xsun563*/*Xsun497* – 0.6 cM – 5 SNP markers/**Lr48** – 0.3 cM – *IWB70147* – 2.0 cM – *XBARC0-7-2B* – 9.4 cM – **Lr13**[11172].

Lr48 is closely linked with **Lr25**[10738]. Based on haplotype analysis **Lr48** was postulated in 13 Australian Condor relatives[11112]. The suggestion that this gene is present in 13 Australian varieties carrying **Lr48** markers and hence **Lr48**[11172] needs verification.

LR49

Lr49[0085] locus: 2AS[0329]. 4BL[0329]

Adult plant resistance[0085].

i: VL404/5*Lal Bahadur **Lr34**[0329]. **v2**: Tonichi **Lr34**[0329]; VL404 **Lr34**[0085]. **ma**: *Xbarc163-4B* – 8.1 cM – **Lr49** – 10.1 cM – *Xwmc349-4B*[0329]; *Xgwm251-4B* – 8.6 cM – *XsunKASP_21* – 0.4 cM – **Lr49** – 0.6 cM – *XsunKASP_24* – 8.1 cM – *Xwmc349-4B*[11484].

LR50

Lr50[0221] locus: 2BL[0221]

Based on linkage with SSR markers.

v: KS96WGRC36 = TAM*3/TA870[0221]; U2657 = Karl 92*4/TA674[0221]; U3067 = TAM107*4/TA874[0221]; U3193 = TAM107*4/TA874[0221]. **tv**: *T. armeniacum* TA870[0221]; *T. armeniacum* TA145; TA874[0221]; TA870[0221]; TA895[0221]. **ma**: Linked with *Xgwm382-2B* (6.7 cM) and *Xgdm87-2B* (9.4 cM)[0221].

LR51

Lr51[308, 0308] locus: 1BL[0308]

i: Express*7/T1[0308]; Koln*7/T1[308]; UC1037*7/T2[0308]. **v**: Neepawa*6/*Ae. speltoides* F-7, selections 3 and 12[306]; Interstitial translocations T1AS.1AL-1S#F7-12L-1AL[0308] = T1; T1BS.1BL-1S#F7L-1BL[0306]. **al**: *Ae. speltoides* F-7 selections 3 and 12[0306]. **ma**: Linked with RFLP markers *Xmwg710-1B* and *Xaga7-1B*[0308]; A CAPS marker was developed from *XAga7-1B*[0308].

LR52

Lr52[10035] locus: 5BS[10035] syn: LrW[309]

bin: 5BS6-0.81-1.00. **v**: AUS28183 = V336[10679]; AUS18187[10679]; Tc-LrW = RL6107[10035]. **v2**: V618 **Lr33**[309]; V336 **Lr33** *LrB*[309]. **ma**: *Xgwm234-5B* – 10.2 cM – **Lr52** – 3.3 cM – **Yr47** – 9.6 cM – *Xcfb309-5B*[10679]; *Xcfb309-5B* – *Xsun480*/*Xmag705*/*Xfcp552-5B* – 0.4 cM – **Yr47** – 4.3 cM – *icg16c008*/*Xgwm234-5B*[11200]; *Xsun180* – 0.4 cM – **Lr52** – 0.2 cM – **Yr47** – 1.4 cM – *Xgwm234-5B*[11200].

LR53

Lr53[10203] locus: 6BS[10203]; According to [11778] syn: LrS8[10204]

Lr53 originated from *Ae. longissima* or *Ae. sharonensis*; $6^{S}S.6^{S}L$-6BL[11778].

v: 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS[10204]. Yangmai 21 derivative C580 with a reduced alien segment (<6.03 MB). **tv**: *T. dicoccoides* 479[10204]. **ma**: *Xgwm191-6B* – 18.9 cM – **Yr35** – 3 cM – **Lr53** – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B*[10780]. **Lr53** was genetically independent of **Lr36**[10780].

Genetically associated with **Yr35**.

LR54

Lr54[10139] locus: 2DL[10139]

Derived from *Ae. kotschyi*.

v: Line S14[10139]. **ad**: Line 8078[10139]. **al**: *Ae. kotschyi* 617[10139].

LR55

Lr55[10180] locus: 1B (1BL.1H^{t}S[10180]

Derived from *Elymus trachycaulis*[10180].

ad: CS + 1H^{t}[10180]. **v**: KS04WGRC45 = Heyne*3/TA5586.

LR56

Lr56[10224] locus: 6A (6AL-6S^{sh}L.6S^{sh}S)[10224] syn: LrS12[10204]

v: Line 0352 = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17[10224]; Recombinants with shorter segments – 07M4-39, 07M4-157 and 07M4-175 – are reported in ▶[10691]. **al**: *Ae. sharonensis*-174[10224].

LR57

Lr57[10328] locus: 5DS (5DL.5DS-T5MS^{G}[10328]

Derived from *Ae. geniculata*.

v: TA5601[11553]; TA5602[10328]; TA5603[10328]; Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry **Lr13**. **al**: *Ae. geniculata* (=*ovata*) (U^{S}U^{S}M^{G}M^{G} TA10437)[10328]. **ma**: Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873*[10328]; Completely linked with **Yr40**[10328]; CAPS marker *XLr57/Yr40-MAS-CAPS16*[10770].

Line TA5601 carries an estimated 5% of 5M^{g}; and TA5602, 20%[11553]. Genetic analysis of the segment in TA5602 indicated terminal replacement of 9.4 Mb in chr 5D and that **Lr57** is 12.4 cM distal to **Yr40**[11553].

LR58

Lr58[10375] locus: 2BL[10375]

Derived from *Ae. triuncialis* = T2BS.2BL-2^{t}L(0.95).

v: TA5605 = WL711*4/*Ae. triuncialis* TA10438 **Lr13**[10375]. **al**: *Ae. triuncialis* TA10438[10375]. **ma**: TA5605 possesses *Ae. triuncialis* alleles of RFLP markers *XksuH16*, *XksuF11* and *Xbg123* and SSR marker *Xcfd50* in the terminal region of chromosome 2BL[10375]; A codominant STS marker *Xncw-Lr58-1* was based on the sequence of *XksuH16*[10819].

Identical in sequence to **Lr9**[11630]. The differing chromosome location was attributed to radiation treatment[11630].

LR59

Lr59[10399] locus: 1A, probably 1AS alien centric fusion[10399]

Derived from *Ae. triuncialis*.

v: Line 0306[10399] = *Ae. peregrina*-680/2*CS//5*W84-17[10399]. **al**: *Ae. peregrina* (UUSS, 2n=28) 680[10399].

Problems in recovering balanced recombinants are reported in ▶[10762].

Further study of this translocation (Lr59-Full) identified a 1AS.1L^{P}-6S^{P}-6BS structure. Another round of recombination identified the following types: 1AS.1L^{P}-1AL; 1AS.1L^{P}-6S^{P}-6BS; and 1AS.1AL-1L^{P}-6S^{P}-6BS (Line Lr59-151 had the shortest alien segment). Recombinants with 6BS retained the wheat GLI-B2 locus[11499].

LR60

Lr60[10400] locus: 1DS[10400] syn: LrW2[0305]

v: RL6172[0305] = Thatcher*3/V860. **ma**: **Lr60** – 8.4 cM – *Xbarc149-1D*/**Lr21**[10400]; **Lr60** – 13 cM – **Lr21**[10400].

LR61

Lr61[10485] locus: 6BS[10485] syn: LrAW2[11223]

tv: AUS 26579[11224]; AUS 26582[11224]; Guayacan 2[10485]; Guayacan INIA[10485]; PI 244061[11280]. **ma**: **Lr61** – 2.2 cM – *P81/M70*$_{269}$/P87/M75$_{131}$ – 4.6 cM – *P87/M76*$_{149}$ – 21.7 cM – *Xwmc487-6B*[10485]; *sun682* – 0.7 cM – **Lr61**/*sun683/sun684* – 0.2 cM – *sunKASP_60*[11223]; *sun682* – 0.6 cM – **Lr61**/*sun684* – 0.6 cm – *sunKASP_59*[11223].

The designation **LrAW2** was also used for **Lr82**.

LR62

Lr62[10537] locus: 6A = 6AL-6^{Aen}L.6^{Aen}S

Derived from *Ae. neglecta* 6A = 6AL-6^{Aen}L.6^{Aen}S[10537].

v: Line 03M119-71A[10537]. **al**: *Ae. neglecta* 155[10537]. Associated with **Yr42**[10537].

LR63

Lr63[10875] locus: 3AS

Derived from *T. monococcum* 3AS[10875].

i: RL6137 = Thatcher*6/TMR5-J14-12-24[10646, 10875]. **v**: TMR5-J14-12-24[10646]. **dv**: *T. monococcum*[10646]. **ma**: *Xbarc321*/*Xbarc57-3A* – 2.9 cM – **Lr63**[10875].

LR64

Lr64[10550] locus: 6AL[10550]

i: RL 6149 = Thatcher*6/*T. dicoccoides* 8404 *LrX*[10550]. **v**: Tc/RL6149-RIL13, GSTR 451[11399, 11498]. **tv**: *T. dicoccoides* 8404[10550]. **ma**: *Xbarc104-6A* – 13.9 cM – **Lr64** – 21.9 cM – *Xgwm427-6A*[10550]; *K-IWB38521* – 1.0 cM – **Lr64**/*K-IWB59855* – 2.9 cM – *K-IWB72197* – 10 cM – *K-IWB73609*[11399].

The second recessive gene (*LrX*) in RL6149 was located in chromosome 1DS: *K-IWB577* – 11.2 cM – *LrX*/*IWB38437*[11399].

LR65

Lr65[10848] locus: 2AS[10739, 10848] syn: LrAlt[10739]

v: Selection ARK 0;[10848]. **v2**: *T. spelta* Altgold Rotkorn **Lr71**[10739, 10848]. **ma**: **Lr65** – 1.8 cM – *Xbarc212-2A*/*Xwmc382-2A* – 2 cM – *Xgwm636*[10739]; *XE41M57-165* – 3 cM – **Lr65** – 2 cM – *Xbarc124*/*Xbarc222*/*Xgwm614-2A*[10848]; LR65 – 0.5 cM – *Alt-64* – 0.05 cM – *Alt-21* – 1.7 cM – *Xbarc212-2A*[11536]; *AltID-11* – 0.7 cM – **Lr65** – 0.02 cM – *Alt-64* – 1.1 cM – *Alt21*[11536]. *TraesCS2A02G001500* was predicted as the candidate position for LR65[11536]. LR65 was estimated to be about 10 cM from LR17[10848].

Some plants of Altgold Rotkorn possess **Lr71** conferring IT 12C[10848].

LR66

Lr66[10591] locus: 3A[10591]. 3A = 3A-3S^{S} syn: LrS13[10592]

v: Line 07M127-3 = *Ae. speltoides*/5*CS//2*CSph1b mutant/3/2* W84-17/4/CSN3AT3B[10591]. **al**: *Ae. speltoides* Accession 691[10591]. **ma**: Most user-friendly marker, SCAR S15-t3[10591].

LR67

Lr67[10675] locus: 4DL[10675]

Adult plant resistance.

bin: C-0.53[10675]; Distal to 0.56[10678]. **i**: RL6077 = Thatcher*6/PI 250413[10675]. **v**: Chapingo 48[11070]; PI 250413[10676]; Yaqui 53[11070]. v2 NP876 **Lr46**[11441]; Sujata **Lr46**[11440, 11442]. **ma**: *Xcfd71-4D* – 1.5 cM – **Lr67**[10675]; Pleiotrophic with **Yr46**; Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of **Lr67**/**Yr46**[10678]; *Xgwm165-4D*/*Xgwm192-4D* – 0.4 cM – **Yr46**/**Lr67**[10678]. **c**: This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices[11070]; GenBank: coding sequence KR604817.2, 1,545 bp; protein sequence ALL26331.2, 514 amino acids. **Lr67** was predicted in 51 accessions mainly collected in the Indian subcontinent[11448] using the gene-specific marker *SNP1-TM4*[11070].

Lr67 is pleiotropic or closely linked with **Sr55**, **Yr46**, **Pm46** and **Ltn3**.

LR68

Lr68[10817] locus: 7BL[10817]

Adult plant resistance.

v: Arula 1 CIMMYT GID 1847450[10817]; Arula 2 CIMMYT GID 1847422[10817]. **v2**: Arula 1 ***Lr14b*** CIMMYT GID 1847450[10817]; Arula 2 ***Lr14b*** CIMMYT GID 1847422[10817]; Frontana **Lr13** ***Lr14b*** **Lr34 Lr46**[10817]; Parula ***Lr3b*** **Lr13** ***Lr14b*** **Lr34 Lr46**[10817]; Rayon F89 ***Lr14b***[10817]; Sujata **Lr46 Lr67**[11442]; Weebill ***Lr14b***[10817]. **ma**: Close linkage with several markers in chromosome arm 7BL and ***Lr14b*** in the Apav x Arula population. Flanking markers are *Xpsy1-1* and *Xgwm146-7BL* at 0.4 and 0.6 cM. Gamma-irradiation induced deletion stocks of Arula 1 that lack **LrP** but have ***Lr14b*** were identified showing that the two genes are located at different closely linked loci[10817]; *Xwmc232-2B* – 0.2 cM – *Xcfa2257-2B* – 1.1 cM – Cs7BLNLRR – 0.3 cM – *Psy1-1* – 0.5 cM – **Lr68** – 0.6 cM – *Xgwm146-2B*[10817].

Gamma-irradiation induced deletion stocks of Arula 1 lacked **Lr68** but had ***Lr14b*** showing that the two genes are located at different closely linked loci[10817].

LR69

Lr69[10903] locus: 3DL[10903]

v: Toropi-6.3[10903].

LR70

Lr70[10904] locus: 5DS[10904]

v: Yet to be named selection of cross or backcross to Tc[10904]. **v2**: KU3198 *Lrk1*[10904]. **ma**: **Lr70** – 5.6 cM – *Xbarc130-5D* – 1.7 cM – *Xwmc233-5D*[10904].

Lrk1 is possibly **Lr52**[10904].

LR71

Lr71[10911] locus: 1B centromere region not resolved[10911] syn: LrAK12c[10910]

bin: Markers flanking **Lr71** mapped to 1BS10-0.5-cent and 1BL6-cent-0.32. **v**: LrARK12c = *T. spelta* Altgold Rotkorn selection[10910]; Common wheat reference line under increase[10911]. **v2**: *T. spelta* Altgold Rotkorn (heterogeneous) **Lr65**[10910, 10911]. **ma**: *Xgwm11-1B* – 3.3 cM – *Xgwm18-1B* – 1.0 cM – **Lr71** – 1.3 cM – *Xbarc187-1B* – 0.5 cM – *Xbarc137-1B*[10911].

LR72

Lr72[10947] locus: 7BS[10947]

tv: Altar C84 GID 30374[10947]; Atil C2000 GID 6719128. **tv2**: Storlom ***Lr3a***[10947]; Llareta INIA ***Lr14a***[10947]; Jupare **Lr27** + **Lr31**[10947]. **ma**: **Lr72** – 5.5 cM – *Xwmc606-7B*[10947].

LR73

Lr73[10969] locus: 2BS[10969]

v: Morocco[10969]; Several Australian cultivars[10969]. **v2**: Federation LR10[10969]. **ma**: *wPt8760* – 4 cM – **Lr73** – 1.4 cM – *wPt8235*[10969].

LR74

Lr74[11031] locus: 3BS[11031]

Adult plant resistance 3BS[11031].

bin: 3BS8-0.78-0.87. **v**: AGG91583WHEA=BT-Schomburgk Selection[11031]; Spark[11031]. **ma**: *Xcfb5006-3B* – 1.9 cM – **Lr74** – 2.2 cM – *BS00009992* – 2.7 cM – *Xgwm533-3B*[11031].

Tc*3/Caldwell population: a gene for adult plant resistance derived from Caldwell was identified with closest marker *Xcfb5006-3B*; the Tc*2/Caldwell 24-1 parent shared the same T allele at KASP marker *IWB44132* as Spark and BT-Schomburgk Selection[11281].

LR75

Lr75[10066, 11053] locus: 1BS[10066, 11053] syn: Qlr.sfr-1BS[10066]

Adult plant resistance.

bin: 1BS10-0.5-1.00. **v**: ArinaLr75, Arina*2//Forno/Arina#F7NIL85[11053]; C14.20[11053]. **v2**: Forno ***Lr14a*** **Lr34**[11053]. **ma**: *Xgwm604-1B 1.6* – cM – **Lr75** – 2.70 cM – *swm271* – 0.14 cM – *Xgwm11-1B*/*Xgwm18-1B*/*swm294/swm278/swm275*[11053].

LR76

Lr76[11055] locus: 5DS[11055] syn: LrUmb[11055]

Derived from *Ae. umbellulata*.

v: IL 393-4[11055]; *T. durum* cv. WH890/*Ae. umbellulata* Pau 3732//CS Ph^{I}/3/2*WL711, C14.21[11055]. **al**: *Ae. umbellulata* Pau 3732[11055]. **ma**: **Lr76** – 7.6 cM – *Xgwm190-5D*[11055]. **Lr76** behaves as an allele of **Lr57** derived from *Ae. geniculata*. The low infection types are also different. A co-segregating 450 bp *Lr57-Yr40*-CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars[11055]. The introgression carrying the *Ae. umbellulata* segment replacing terminal Chr. 5DS was 9.47 Mb with the break point between *TraesCS5D02G1600* and *TraesCS5G02G20010*[11552]. Independent mutations indicated that **Lr76** and **Yr70** were different genes[11552].

LR77

Lr77[11164] locus: 3BL[11164]

Adult plant resistance.

v: Tc*2/Santa Fe 8-1C.9[11164]; Tc*2/Toropi GSTR 449[11164]. **v2**: Duster ***Lr3a*** **Lr11 Lr34** PI 639233[11164]; Santa Fe ***Lr3a*** **Lr37** PI 641772[11164]. **ma**: *IWB2531* – 3.5 cM – *IWB32805* – 3.5 cM – **Lr77**/*IWB10344* – 0.9 cM – *IWB73555* – 5.3 cM – *IWB12260*[11164].

LR78

Lr78[11212] locus: 5DS[11212] syn: QLr.cdl.5D[11212]

Adult plant resistance.

bin: According to ▶[10125] *Xbarc130* is in bin 5DS2-0.78-1.00 and *Xcfd189* is in bin 5DS1-C-0.63. **v**: Tc*2/Santa Fe GSTR 450[11498]. Tc*3/Toropi 4A212A[11212]. **v2**: Toropi PI 344200[11212]. **ma**: *Xcfd189-5D* – 13.2 cM – *IWA2689* – 2.2 cM – **Lr78** – 8.0 cM – *Xcfa2104-5D*[11212].

A second selection Tc*2/3A12A crossed with Tc segregated for multiple QTL in chromosome arms 1BL (possibly LR46), 3BS and 4BS[11212].

LR79

Lr79[11224] locus: 3BL[11224] syn: LrAW3[11224]

bin: 3BL-0.63-0.90. **tv**: 242/Bansi#149, C18.15[11224]. **tv2**: AUS26582 **Lr61**[11223, 11224]. **ma**: *KASP_31457* – 8.1 cM – *sun770* – 2.9 cM – **Lr79** – 1.8 cM – *sun786*[11224].

Lr79 conferred resistance to Australian common wheat *Pt* races, but not to durum-specific Ethiopian and Californian races[11224].

LR80

Lr80[11464] locus: 2DS[11464] syn: LrH2[11464]

v: Hango-2, FLW6-Selection AGG95499WHEA[11464]. **ma**: *Xgdm35-2D* – 7.5 cM – *Xcau96-2D* – 0.4 cM – **Lr80** – 0.2 cM – *Xbarc124-2D* – 13.2 cM – *Xgwm296-2D*[11464]. *Xcau96-2D* – 4.0 cM – *KASP_17425* – 0.2 cM – **Lr80** – 0.4 cM – *KASP_17148* – 1.0 cM – *Xbarc124-2D*[11464].

LR81

Lr81[11583] locus: 2AS[11583] syn: Lr470121[11583]

bin: 2AS-0.78-1.00. **v**: RIL 92 PI 700925[11583]. **v2**: PI 470121 **Lr34**[11583]. **ma**: *Xwmc827-2A* – 9.4 cM – *Xstars-KASP320* – 0.5 cM – LR81 – 0.2 cM – *Xstars-KASP323* – 5.3 cM – *Xwmc296-2A*[11583].

LR82

Lr82[11586] locus: *LrAW2* [11586]. 2BL[11586]

Recessive.

v: Aus27352[11586]. **ma**: *KASP_22131* – 0.8 cM – **Lr82** – 1.2 cM – *KASP_11333*[11586].

The designation **LrAW2** was also used for **Lr61**.

LR83

Lr83[11638] locus: *LrX* [11399]. 1DS {11399; 11638}

Recessive.

v: PI 701502[11638]. **v2**: RL6149 **Lr60** {11399; 11638}. **ma**: *K-IWB38437* – 1 cM – LR83 – 8.6 cM – 1D_9037237 – 4.7 cM – *K-IWB577*[11638]. LR83/*IWB38437* – 11.2 cM – *K-IWB577*[11399]. Locus order: LR83 – LR60 – LR42 – LR21[11638].

LR84

Lr84[11640] locus: 6BL[11600, 11639]

TRITD6Bv1G225630 (Svevo).

QLr.cim-6BL)[11600]; *QLr.hzau-6BL*[11640]; *TtRPM1-630*[11640]. Adult plant resistance.

tv: Atred#2+6BL[11640]; Atred#2/Bairds RIL 397 GID 7013103[11600, 11640]. **tv2**: Bairds {M11600, 11640}; Dunkler[11639, 11640]; Heller#1[11639, 11640]; Planeta[11640]. **ma**: *IWB8763* – *LRXX* – *IWB10767* (0.9 cM. 131.6 Kb)[11640]. **c**: NBL-LRR structure annotated as an *RPM1*-like gene[11640].

LR85

Lr85[11712] locus: 6B (6B-6S^{sh})[11683, 11684, 11712]

v: Line 6B-RY-32-3-14[11683] = Line 42[11684] = D42[11712] = Genebank accession number to be advised. **al**: *Ae. longissima* AEG-6782-2[11712]; *Ae. sharonensis* AEG-548-4 {11683; 11712}. **c**: The same NLR gene with a distinctive coiled-coil (CC) domain was cloned from each alien diploid accession[11712].

Development of lines with shortened 6S^{sh} segments is described in [11684].

All 16 EMS-induced mutants in Line D42 were susceptible to both leaf rust and stripe rust[11712].

ungrouped

Lr4, Lr5, Lr6, Lr7, Lr8[365]

v: Purdue Selection 3369-61-1-10 = Waban[365]; Not available as separate single-gene lines. Therefore, alleles at these predicted loci were never characterized.

A series of temporary designations for seedling and adult plant resistance genes in six durums is given in [1648].

A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* - 8.9 cM - *Lr* - 2.3 cM - STS $Xtxw_{200}$[10253].

Complex genotypes
AC Domain: **Lr10 Lr16 Lr34**[820].
Alsen: ***Lr2a*** **Lr10 Lr13 Lr23 Lr34**[10223].
Benito: **Lr1** ***Lr2a*** **Lr12 Lr13**[1256].
Buck Manantial: **Lr3 Lr13 Lr16 Lr17** *Lr34?*[300].
Era: **Lr10 Lr13 Lr34**[342].
Grandin: ***Lr2a*** **Lr3 Lr10 Lr13 Lr34**[821].
Mango: **Lr1 Lr13 Lr26 Lr34**[1374].
MN7529: **Lr1** ***Lr2a*** **Lr10 Lr16**[976].
Opata 85: **Lr10 Lr27+Lr31 Lr34**[1058].
Pasqua: **Lr11 Lr13** ***Lr14b*** **Lr30 Lr34**[304].
Prospect: **Lr1** ***Lr2a*** **Lr10 Lr13**[197].
Roblin: **Lr1 Lr10 Lr13 Lr34**[303, 713].
Trap: **Lr1 Lr3 Lr10 Lr13 Lr34**[1374].
AC Splendor: **Lr1 Lr16 Lr34**[10179]
AC Teal: **Lr1 Lr13 Lr16**[821]
Alsen: ***Lr2a*** **Lr19 Lr13 Lr23 Lr34**[10152]
Norm: **Lr1 Lr10 Lr13 Lr16 Lr23 Lr34**[10152, 10223]
Coker 9663 **Lr9 Lr10** ***Lr14a***[10742].
Pioneer 26R61 **Lr13** ***Lr14b*** **Lr26**[10742].

Genotype lists:Australian cultivars[0288]; Chinese cultivars[10682, 0013]; Combinations with **Lr34**[1361]; Cultivars from the former USSR[1380]; Czechoslovakian cultivars[855, 0102]; European cultivars[10345, 10794, 0229, 0260, 0288, 0337]; Indian cultivars[1345, 1365]; Indian Subcontinent[1365]; Mexican cultivars[1373]; U.S.A. cultivars[978, 1219, 10111, 10146, 10152, 0334], French cultivars[10792], see also ▸[970].

3.22.2 Temporary designations

Lr64i#2[11079] syn: 6Ai#2[11079]

v: Tulaikoskaya 5[11079]; Tulaikoskaya 10[11079]; Tulaikoskaya 100[11079].

LrAc[11613] locus: 5DS[11613]

Adult plant resistance.

v: *Ae. caudata* derivative PAU16060[11613]. **al**: *Ae. caudata* PAU3556[11613].

LrAp[11698] locus: 6BL = 6BS.6BL-6U^{P} [11698]

v: WL711 derivative ILpau16061[11698]. **al**: *Ae peregrina* pau3519[11698].

LrBi16[11042, 11082] locus: 7BL[11042]

bin: 7BL-10. **v**: Bimai 16[11042]. **ma**: *Zcfa2257-7B* – 2.8 cM – **LrBi16** – 2.6 cM – *Xgwm344-7B*[11042]; *Xcfa2257-7B* – 2.8 cM – **LrBi16** – 2.5 cM – *Xgwm344-7B*[11082]; A closer AFLP marker could not be converted to a STS/SCAR marker[11082].

Bimai 16 also carries **Lr26** and **LrZH84**[11042]. Allelic with *Lr14c*, but showed different reaction patterns compared to lines with *Lr14c* and **LrFun**[11082].

LrFun[11038] locus: 7BL[11038]

bin: 7BL-10. **v**: Fundulea 90[11038]. **ma**: *Xgwm344-7B* – 4.4 cM – **LrFun** – 5.7 cM – *Xwmc70-7B*[11038].

LrGam6[10929] locus: 2BL[10929]

v2: Sinvalocho MA **Lr3 LrSV1 LrSV2**[10929]. **ma**: *Xbarc-2B* – 0.6 cM – *Xgwm382-2B* – 0.6 cM – **LrGam6** – 17.9 cM – *Xgwm528-2B*[10929].

LrK1[10904] locus: 5BS[10904]

v2: Ku3198 **Lr70**[10904]. **ma**: **LrK1** – 0.6 cM – *Xcfd20*/*Xgwm234-5B*[10904]. **LrK1** could be **Lr52** or an allele[10904].

LrKr1[10233]

v: Thatcher[10233]. **v2**: Kanred **LrKr2**[10233].

LrKr2[10233]

v2: Kanred **LrKr1**[10233].

LrMq1[10233]

v: Marquis[10233].

LrNJ97[11043] locus: 2BL[11043]

v: Neijiang 977671[11043]. **ma**: *Xwmc317-2B* – 4.2 cM – **LrNJ97** – 2.2 cM – *Xbarc159-2B* – 2.3 cM – *Xwmc356-2B*[11043].

LrP[11614] locus: 5DS[11614]

v: *Ae. peregrina* derivative PAU16058[11614]. **al**: *Ae. peregrina* PAU3519[11614].

LrPI209274[11218] locus: 6BS[11280]

tv: PI 209274[11280]. **ma**: *KASP_6BS_IWB39456* – 3.7 cM – **LrPI209274** – 1.0 cM – *KASP_6BS_IWB6117* – 8.1 cM – *Xdupw217-2B*[11280].

This gene may be **Lr53**[11280].

LrPI244061[11280] locus: 2BS[11280]

tv: PI 244061[11280]. **ma**: *LrPI144061* – 11.5 cM – *KASP_2BS_IWB6117*[11280].

This gene might be **Lr13**[11280].

LrPI287263[11280] locus: 6BL[11280]

tv: PI 287263[11280]. **ma**: **LrPI287263** – 2.8 cM – *KASP_6BL_IWB44753* – 2.8 cM – *Xdupw217*[11280].

LrSV1[10929] locus: 2DS[10929]

Adult plant resistance.

v2: Sinvalocho MA **Lr3 LrGam6 LrSV2**[10929]. **ma**: *Xgwm296-2D* – 1.4 cM – **LrSV1** – 7.1 cM – *Xgwm261-2D*[10929].

LrSV2[10929] locus: 3BS[10929]

Adult plant resistance.

v2: Sinvalocho MA **Lr3 LrGam6 LrSV1**[10929]. **ma**: *Xgwm389-3B* – 3.0 cM – **LrSV2**/*Xgwm533-3B* – 4.2 cM – *Xgwm49-3B*[10929].

According to ▶[11334] **LrSV2** acted in a complementary way with *Lrc*-SV2 on chromosome 4BL. These complementary genes were closely linked to the locations of **Lr27** and **Lr31** but were considered to be different genes.

LrTb[820]

Adult plant resistance[820].

v2: AC Taber **Lr13** ***Lr14a***[820].

LrTm[277, 0277]

dv: *T. monococcum*. **ma**: Linked to microsatellite locus *Xgwm136*[277].

LrTr[227, 0227]

v: *Ae. triuncialis* derivatives[227]. **ad**: WL711 BC2F5 addition lines[227]. **al**: *Ae. triuncialis* Acc. 3549[227]. **ma**: Lines with *LtTr* possessed a homologue of *Xgwm368-4B*[227].

LrTt1[10031] locus: 2A[10031] syn: lrTt1[10031]

Reccessive[10031].

v: Line 842 = Saratovskaya*2/*T. timopheevii* spp. *viticulosum*[10031]. **ma**: *Xgwm812-2A* – 1.5 cM – **LrTt1**[10031].

LrVPM[1603] locus: 7DL[1603]. GERMPLASM?

LrWo[10747] locus: 5B[10747]

tv: Wollaroi AUS99174[10747]. **ma**: *Xgwm234-5B* – 7.2 cM – **LrWo** – 20.3 cM – *wPT-1420*[10747].

The relationship of **LrWo** to **Lr52** was not established.

LrZH84[10581] locus: 1BL[10581]

v: Guizhou 98-18[11042]; Tian 95HF2; Xinong 1183-4[11042]; Zhoumai 11[10682]. **v2**: Predgornaia 2 **Lr26**[10581]; Zhou 8425B **Lr26**[10581]. **ma**: *Xbarc8-1B* (cent) – 5.2 cM – *LrZh84* – 3.9 cM – *Xgwm582-1B*[10581].

A series of temporary designations for seedling and adult plant resistance genes in six durums is given in ▶[1648].

A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* – 8.9 cM – *Lr* – 2.3 cM – STS $Xtxw_{200}$[10253].

AC Domain: **Lr10 Lr16 Lr34**[820].
AC Splendor: **Lr1 Lr16 Lr34**[10179]
AC Teal: **Lr1 Lr13 Lr16**[821]
Alsen: ***Lr2a*** **Lr19 Lr13 Lr23 Lr34**[10152]
Alsen: ***Lr2a*** **Lr10 Lr13 Lr23 Lr34**[10223].
Benito: **Lr1** ***Lr2a*** **Lr12 Lr13**[1256].
Buck Manantial: **Lr3 Lr13 Lr16 Lr17** *Lr34?*[300].
Carberry: **Lr21 Lr16 Lr23 Lr34 Lr46**[11567].
Coker 9663: **Lr9 Lr10** ***Lr14a***[10742].
Duster: **Lr34 Lr46 Lr77**[11369].
Estanzuela Benteveo: **Lr13 Lr26 Lr34**[10980].
Estanzuela Pelon: **Lr1** ***Lr17a*** **Lr26 Lr34**[10980].
Estanzuela Tarariras: ***Lr3bg*** **Lr13 Lr34**[10980].
Era: **Lr10 Lr13 Lr34**[342].
Grandin: ***Lr2a*** **Lr3 Lr10 Lr13 Lr34**[821].
INIA Boyero: **Lr13 Lr26 Lr34**[10980].
INIA Churrinche: **Lr10 Lr24**[10980].
INIA Tero: ***Lr17a*** **Lr24**[10980].
Mango: **Lr1 Lr13 Lr26 Lr34**[1374].
MN7529: **Lr1** ***Lr2a*** **Lr10 Lr16**[976].
Norm: **Lr1 Lr10 Lr13 Lr16 Lr23 Lr34**[10152, 10223]
Opata 85: **Lr10 Lr27+Lr31 Lr34**[1058].
Pasqua: **Lr11 Lr13** ***Lr14b*** **Lr30 Lr34**[304].
Pioneer 26R61: **Lr13** ***Lr14b*** **Lr26**[10742].
Prospect: **Lr1** ***Lr2a*** **Lr10 Lr13**[197].
Roblin: **Lr1 Lr10 Lr13 Lr34**[303, 713].
Trap: **Lr1 Lr3 Lr10 Lr13 Lr34**[1374].

Genotype lists: Australian cultivars[0288]; Chinese cultivars[10682, 11310, 0013]; Combinations with **Lr34**[1361]; Cultivars from the former USSR[1380]; Czechoslovakian/Czech cultivars[855, 11717, 0102]; European cultivars[10345, 10794, 0229, 0260, 0288, 0337]; Indian cultivars[1345, 1365]; Indian Subcontinent[1365]; Mexican cultivars[1373]; U.S.A. cultivars[978, 1219, 10111, 10146, 10152, 0334], French cultivars[10792], Croatian cultivars[11135]. Kazakhstan cultivars[11161], see also ▶[970]. See ▶[11178] for review and analysis of leaf rust resistance genes in six durum wheats.

3.22.3 Suppressor of genes for resistance to *P. triticina*

SULR23

SuLr23[1058] locus: Suppressing allele. 2DS[1058]

v: Altar 84/*Ae. tauschii* 219[1058].

suLr23[1058] locus: Non-suppressing allele

v: Opata 85[1058].

See also evidence for specific suppression in ▶[948].

3.22.4 QTLs for reaction to *P. triticina*

Two QTLs, located distally on chromosome arm 1BL and on chromosome 7DS, were mapped for leaf rust severity in a Fukuho-komugi/Oligoculm doubled haploid population[10060]. The resistance on 1BL was contributed by Oligoculm and explained 15% of the variation. The 1BL QTL may correspond to **Lr46** and was associated with marker *Xwmc44-1B*[0460]. The resistance on 7DS was contributed by Fukuho-komugi and explained 41% of the variation. The 7DS QTL corresponds to **Lr34** and was associated with marker *Xgwm295-7D*[10060]. Two major QTL, located on chromosomes 7D and 1BS, for leaf rust resistance were mapped in an Arina/Forno RIL population[10066]. The resistance on 7D was contributed by Forno and explained 32% of the variation. This QTL most likely corresponds to **Lr34**[10066]. The resistance on 1BS (*QLr.sfr-1BS*) was associated with *Xgwm604-1B* and was contributed by Forno[10066]. Additional minor QTLs were identified on chromosome arms 2DL, 3DL, 4BS and 5AL[10066].QTLs for leaf rust resistance were identified in [0050] and were named by the catalogue curators as follows:

QLr.pser-1BL[10743] locus: 1BL[10743] syn: QLr.pser.1BL

bin: 1BL6-0.32[10743], **ma**: Proximal to *Xgwm264.1-1BL*[10743]

Associated with **lm** producing a lesion mimic phenotype in the absence of disease[10743].

QLr.sfr-1B[0050] locus: 1BS[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xpsr949-1B* and *Xgwm18-1B*[0050].

QLr.sfr-2B[0050] locus: 2B[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0050]. **ma**: Associated with *Xpsr924-2B* and *Xglk699-2B*[0050].

QLr.sfr-3A[0050] locus: 3A[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xpsr570-3A* and *Xpsr543-3A*[0050].

QLr.sfr-4B[0050] locus: 4B[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xpsr921-4B* and *Xpsr593-4B*[0050].

QLr.sfr-4D[0050] locus: 4DL[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xglk302-4D* and *Xpsr1101-4D*[0050].

QLr.sfr-5D[0050] locus: 5DL[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer[0050]. **ma**: Associated with *Xpsr906-5D* and *Xpsr580-5D*[0050].

QLr.sfr-7B.1[0050] locus: 7B[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xpsr593-7B* and *Xpsr129-7B*[0050].

QLr.sfr-7B.2[0050]

v: Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno[0050]. **ma**: Associated with *Xglk750-7B* and *Xmwg710-7B*[0050].

Review of QTL in hexaploid wheat[11442].

Association mapping in durum wheat indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (**Lr13**, **Lr23** region), 3B, 5A, 5B, 6B, 7A, and 7B (see **Lr14**[10736].

Historical review of leaf rust work in Canada[18053].

QTL

AGS 2038 (R) / UG111729 (MR): RIL population. Seedling and adult plant resistance was controlled by several QTL, the most important of which was designated *QLr.ags-1AL* spanned by *IWB20487* and *IWA4022*[11507].

Avocet S / Attila: At least two additive genes for slow rusting[10586]. In addition to **Lr46** there were small effects on chromosomes 2BS, 2BL and 7BL[10586].

Avocet R (S) / Chilero: **Lr46**/**Yr29** and *QLr.cim-5DS*/*QYr.cim-5DS*, from Chilero, and *QLR.cim-1DL*/*QYr.cim-1DL* from Avocet R[11306].

Avocet / Kundan: RIL population: **Lr29** (flanked by *10902272* and *02414*, R^2 = 0.5 -0.65), *QLR.cim-2BL* flanked by *1237388* and *1081780_35C>T* from Avocet and *QLr.cim-2DS* flanked by *1237388* and *1081780_35C>T* from Kundan[11248].

Avocet / Pastor: RIL population: QTLs mapped on 1BL (**Lr46**, 2BS, 5A, 6B and 7BL plus minor QTLs on 1B, 2A and 2D[10928].

Avocet S / Pavon 76: QTL identified included: 1BL (*PstAFAMseCAC1&2*), 4BL (*Xgwm368*), 6AL (*Xgwm617*), 6BL (*PstAGGMseCGA1*)[10443].

Beaver / Soissons: DH population: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B(1BL.1RS), 4BS (proximal to *Xbarc20-4B*) and 5AS (*QTLBvr5AS*, proximal to *Xbarc10-5A*) and in the vicinity of *wPt-8756* and *wPt-1931* [10687].

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chr. 2AL, 2BL, 2BS and 3BS, were from Capo and one on 5BLwas from Arina; the QTL on 2AL, 2BL and 3BS were co-located with QTL for resistance to stripe rust[11449].

CI 13227 (R) / Lakin (MS): DH population: Adult plant resistance conferred by *QLR.hwwg-2DS* (R^2 = 0.11 – 0.26), *QLr,hwwg-7BL* (R^2 = 0.08-0.19, likely **Lr68**), and *QLr.hwwg-7AL* from CI 13227, and *QLr.hwwg-3BS* from Lakin[11311].

CI 13227 (R) / Suwon (S): SSD population[10211]. Two QTLs for slow leaf rusting, located on chromosomes 2B and 7BL, were mapped for final severity, area under disease progress curve, and infection rate in a *QLr.osu-2B* was associated with microsatellite markers *Xbarc18-2B* and *Xbarc167-2B* (R^2 = 9-18%). *QLr.osu-7BL* was associated with microsatellite marker *Xbarc182-7B* (R^2 = 12-15%)[10211]. CI 13227 constributed the resistant alleles for both QTLs. *QLrid.ocu-2D*, linked to *Xgwm261-2D*, affected the duration of infection[10211]. However, Thatcher backcross derivatives of CI 13227 appeared to have ***Lr3c*** and **Lr46**[11021].

Libellula / Huixianhong: RIL population: Six QTL on chromosome arms 1AS, 1AL, 1BL (**Lr34**), 3AL, 4BL and 7DL were detected in a least two of seven environments, the most effective of which was identified as **Lr34**[11757].

Mianyang351-15 (R) / Zhengzhou 5389 (R): RIL population: four QTL were located on chromosome arms 1BL (**Lr46**), 2AS (**Yr37**), 2DS, and 7BL (**Lr68**)[11545].

Ning7840 / Clark: RIL population: *QLr.hwwg-5AS* from Ning 7840; *QLr.hwwg-6AS* from Clark, flanked by *barc23-6A* and *IWA3321*; *Qlr.hwwg3BS.1* from Clark, flanked by *IWA4654* and *IWA1702*; possibly **Lr74**; and *QLr.hwwg-7DS*/**Lr34** from Ning 7840[11278].

TA 4152-60 (MR) / ND495 (MR): DH population: Five QTLs for APR were identified in the field, viz. *QLr.fcu-3AL* (R^2 = 0.18), *QLr.fcu-3BL* (R^2 = 0.19), *QLr.fcu-5BL* (R = 0.07), and *QLr.fcu-6BL* (R^2 = 0.12) from TA 4152-60 and *QLr.fcu-4DL* (R^2 = 0.13) from ND495[10757]. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS[10757].

Thatcher*3 / Americano 44d: RIL population: QTL for adult plant resistance identified on chromosomes 3AS (*QLr.cdl-3A*), 3DS (*QLr.cdl-3DS*) and 6DS (*QLr.cdl-6D*); both the 3AS and 3DS QTLs were required for expression of resistance[11296].

26R61 (S) / AGS 2000 (R): RIL population. A single QTL (*QLr.uga-2BS*) flanked by *wPt-666389* and *wPt-2600* on chromosome arm 2BS was designated *LrA2K*[11507]. *LrA2K* – 2.9 cM – *Xwmc770-2B*[11507].

Atred#1 / Dunkler: RIL population: Four QTL for APR, including **Lr46**, *QLr.cim-5BL* and *QLR.cim-6BL* from Dunkler and *QLr.cim-2Bc* from Atred#1[11639].

Atred#1 / Heller#1: RIL population: Four QTL for APR, including **Lr46**, *QLr.cim-5BL* and *QLR.cim-6BL* from Dunkler and *QLr.cim-2Bc* from Atred#1[11639].

Bairds (R) / Atred#1: RIL population: Four QTL for APR, including **Lr46**, *QLr.cim-5BL* and *QLR.cim-6BL* from Bairds and *QLr.cim-2Bc* from Atred#1[11600].

Colosseo / Lloyd: A major QTL, *QLr.ubo-7B.2*, for seedling and adult plant resistance from Colosseo, was located between *Xgwm344.2-7B* and DART 378059, bin: 7BL 10-0.78-1.00[10600].

TA4152-60 / ND 495: DH population: Four QTLs for APR, *QLr.fcu-3AL*(*Xcfa2183-3AL* – *Xgwm666-3AL*, R^2=0.18), *Qlr.fcu-3BL*(*Xbarc164-3BL* – *Xfcp544-3BL*, R^2=0.19), *Qlr.fcu5BL*, and *Qlr.fcu-6BL*(*Xbarc5-6BL* – *Xgwm469.2-6BL*, R^2=0.12) were from TA4152-60 and *Xlr.fcu-4DL* (*Xgdm61-4DL* – *Xcfa2173-4DL*, R^2=0.13) was from ND495[10717]. The 3AL QTL conferred seedling resistance to all 3 races, and the 3BL gene gave race-specific seedling resistance to one race. *Xlr.fcu-3BL* was effective only in the presence of an allele associated with *Xgwm359-5DS*[10717].

3.23 Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici-repentis*)

Disease: Tan spot, yellow leaf spot. Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, Ptr ToxA, Ptr ToxB and Ptr ToxC have been identified (see ▶[10153]). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved. A review is provided in ▶[10690].

Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in ▶[10153].

3.23.1 Insensitivity to tan spot toxin (necrosis)

TSN1

Tsn1

Sensitive to Ptr ToxA.

v: Bobwhite[10458]; Cheyenne[10458, 0007]; Glenlea[10458]; Grandin[10458]; Hope[10458, 0007]; Jagger[0007]; Katepwa[10458]; ND2709[10458]; ND495[0007]; Sumai 3[10458]; Timstein[10458, 0007]. **v2**: Kulm **Tsc1**[346, 10030, 10458]; Trenton **Tsc1**[0315]. **dv**: Two *Ae. speltoides* accessions[10756]. **tv**: Langdon[10458]; Some *T. dicoccoides* accessions[10756]. **ma**: *Xbcd183-5B* – 1.2 cM – **Tsn1**/*Xbcd1030-5B* – 2.4 cM – *Xrz575-5B*[10688]. **c**: **Tsn1** has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA[10756]. Tsn-ToxA interaction has a major role in SNB development in both common and durum wheat whereas it has a variable role in tanspot development in bread wheat and is not a significant factor for tanspot development in durum wheat[11204].

tsn1[346, 10207] locus: 5BL[346]

Insensitivity (disease resistance) is recessive[346]. **Tsr1**[10508], see Resistance to tanspot.

v: AC Barrie[10153]; AC Cadillac[10153]; AC Elsa[10153]; Atlas 66[10458]; BR34[10458, 0007]; CEP17[0007]; Chinese Spring[10458, 0007]; Erik[7, 10030, 10458]; IA807[0007]; IA905[7]; Laura[10153]; ND688[10458]; Opata 85[10458]; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122[346, 10207, 10458]; Synthetic W-7984 = Altar 84/*Ae. tauschii* CI 18[10458, 0007]. **tv**: Altar 84[0007]; D87450[0007]; *T. dicoccoides* Israel A[10506]. **ma**: *Xbcd1030-5B* – 5.7 cM – **tsn1** – 16.5 cM – *Xwg583-5B*[346]; **tsn1** – 3.7 cM – *Xbcd1030-5B*[0007]; *Xfgcg7-5B* – 0.4 cM – **Tsn1**/*Xfcg17-5B* – 0.2 cM – *Xfcg9-5B*[10207]; *Xfcg17-5B* – 0.2 cM – **Tsn1** – 0.6 cM – *Xfcg9-5B*[10207]; *Xfcp1-5B* and *Xfcp2-5B* delineated **Tsn1** to an interval of about 1 cM[10337]; **Tsn1** was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1*/*XBE425878*/*Xfcc1*/*XBE443610*[10413].

According to ▶[10376] the same dominant allele, presumably **tsn1**, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

Ptr ToxA is functionally identical to *S. nodorum* ToxA but has two predicted amino acid differences[10459]. See Reaction to *Phaeosphaeria nodorum*. Australian cultivars with **tsn1** and **Tsn1** are listed in ▶[10540].

TSN2

Tsn2[10344] locus: 3BL[10344]

Conditions resistance to race 3[10344]

sutv: LDN(DIC-3B)[10344]. **tv**: *T. turgidum* no. 283, PI 352519[10344]; *T. dicoccoides* Israel-A[10344]. **ma**: Identified as a QTL in region *Xgwm285-3B* – *Xwmc366.2-3B* (R^2=91%)[10344]; Also classified as a single gene: *Xgwm285-3B* – 2.1 cM – **tsn2** –.2 cM – *Xwmc366.2-3B*[10344].

In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected by 4-5 genes[10030].

3.23.2 Insensitivity to tan spot toxin (chlorosis)

TSC1

Tsc1[344] locus: 1AS[344]

Sensitivity to Ptr ToxC[344].

v: 6B365[0315]; Louise[11751]; LMPG-6[11751]; Opata 85[344]. **v2**: Kulm **Tsn1**[0315]; Trenton **Tsn1**[0315]. **ma**: **Gli-A1** – 5.7 cM – **Tsc1** – 11.7 cM – *XksuD14-1A*[0315]; Mapped to a 2.4 cM region spanning184 kb (CS RefSeq 2.1) in the Penawawa/PI 626523 RIL population[11751].

According to ▶[10376] the same allele, presumably **tsc1**, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN2137 in crosses with 6B-365.

tsc1[344] syn: QTsc.ndsu-1A[9924]

Insensitivity is recessive.

v: Chinese Spring[11751]; Katepwa[315]; Opata 85[344]; Penawawa[11751]; PI 62673[11751]; Synthetic W-7984[315].

TSR1

Tsr1 locus: 5BL syn: tsn1 See: Insensitivity to tanspot toxin

Resistance is recessive.

v: Genetic stocks that do not have **Tsn1** and other genes that respond to toxins produced by the pathogen.

The gene in Erik was allellic with resistance in a diverse set of genotypes including spelt and durum derivatives[10557].

TSC2

Tsc2 locus: 2BS[10015]

Sensitive to Ptr ToxB[10015].

bin: 2BS3-0.84-1.00. **v**: Aronde[11750]; Katepwa[10871]; Maris Dove[11750]; Synthetic W-7984[10015]; Thatcher[11750]. **tv**: Altar 84[11750]; Altar 84[11750].

tsc2 locus: Insensitivity allele[10015]

v: Chinese Spring[11750]; Lynx[11750]. Opata 85; Salamouni[10871]. **tv**: Altar 84 {10871; Langdon[11750]. **ma**: *Xmag681-2B*/*XTC339813* – 2.7 cM – *Tsc*/*XBE444541* – 0.6 cM – *XBE517745*[10871]; An *XBE444541* EST-STS co-segregating marker for **Tsc2** was developed and lines with **tsc2** produced a 505 bp fragment whereas those with **Tsc2** produced a 340 bp band[10871]. Mapped to a 1.921 Mb region (23.106 – 25.027 Mb)[11750].

TSR2

Tsr2 locus: 3BL[10344] syn: tsn2[10344]

Resistance is recessive. Confers resistance to race 3[10344].

sutv: LDN (DIC-3B)[10344]. **tv**: *T. dicoccoides* Israel-A[10344]. **tv2**: *T. turgidum* no. 283, PI 352519 **Tsr5**[10344]. **ma**: Identified as a QTL in region *Xgwm285-3B* – *Xwmc366.2-3B* (R^2 = 91%)[10344]; also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsr2* – 15.2 cM – *Xwmc366.2-3B*[10344].

TSR3

Tsr3 locus: 3D[10394]. 3DS[10419] syn: tsn3[10394]

v: XX41 = [Langdon/*Ae. tauschii* CI 00017][10394]; XX45[10394]; XX110[10394]. **dv**: *Ae. tauschii* CI 00017[10394]. **ma**: *Xgwm2a* – **tsn3**, 15.3 cM, 14.4 cM and 9.5 cM in CS/XX41, CS/XX45 and CS/XX110, respectively[10419]. Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant – all three were hemizygous-effective[10394]. The genes were given different temporary designations[10394, 10419], but all will be considered to have a common gene until they are shown to be different.

TSR4

Tsr4 locus: 3A[10350] syn: tsn4[10350]

Resistance is recessive. Resistance to race 1 (culture ASC1a)[10350].

v: Salamouni[10350].

TSR5

Tsr5 locus: 3BL[10509] syn: tsn[10509]

tv2: *T. turgidum* no. 283, PI 352519 **Tsr2**[10509]. **ma**: **Tsr5** – 8.3 cM – *Xgwm285-3B* – 2.7 cM – **Tsr2**[10509].

TSR6

Tsr6[10668] locus: 2BS[10668]

Resistance is recessive.

v: ND-735[10668]. **ma**: *Xwmc382-2B* – 15.3 cM – *wPt-0289* – 4.6 cM – **Tsr6** – 18.7 cM – *Xwmc-2B*[10668]. According to ▶[10668] **Tsr6** should be identical to **tsc2** (see Insensitivity to tan spot toxin (chlorosis)).

TSR7

Tsr7[11363] locus: 3BL[11362, 11363] syn: QTs.zhl-3B[11362]

Dominant.

v: Br34[11363]; Penawawa[11363]. **sutv**: Linked STARP markers were developed[11363]. **ma**: Linked STARP markers were developed[11363].

Tsr7 conferred resistance to race 1 (isolate Pti2), race 2 (isolate 86-124), race 3 (isolate 331-9), and race 5 (isolate DW5)[11362]. Temporary designations

TsrAri[10765] locus: 3A

Recessive 3A[10765].

v: Arina[10765]; Heines VII[10765]; Zenith[10765].

TsrHar[10590] locus: 3B[10590]

v: Dashen[10590]; HAR 604[10590]; HAR 2562[10590].

Effective against races ASC1a (race 1) and DW-16[10590].

ungrouped

QTsc.ndsu-1A[9924] locus: 1AS[344] syn: Tsc1[344]

Resistance is likely recessive[344]

v: Synthetic W7984[344]. **ma**: Association with **Gli-A1**[344, 0264, 0040].

QTsc.ndsu-1A, or a closely associated gene, confers insensitivity to Ptr ToxC, see ▶[0315]. Inoculation with purified toxin Ptr ToxC was used to map this locus. *QTsc.ndsu-1A* confers resistance in both seedlings and adult plants.

QTsc.ndsu-4A locus: 4AL[0090]

v: Opata 85/Synthetic W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984[0090]; In W-7976/Trenton resistance was contributed by W-7976[0264]. **ma**: Association with *Xksu916(Oxo2)-4A*

and *Xksu915(14-3-3a)-4A* [0090]; In W-7976/Trenton there was association with *Xwg622-4A* [0264]; Minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants[0264].

'ITMI population': In addition to **tsc2** which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (*Xksu916(Oxo)-4AS*, W-7948) accounted for 20% of the phenotypic variation[10015].

QTL analyses of durum crosses infected with various isolates of race 4 (lacking in Ptr Tox 1, 2 and 3) detected QTL on chromosomes 1A (2 QTL), 4B (3 QTL) and 5A (1 QTL)[11649].

A QTL analysis of 4 durum crosses identified 12 QTL on chromosomes 1B, 2B (2), 3A (3), 5A (5) and 7A[11481].

QTL
Salamouni / Katepwa: RIL population: variation at the **Tsc2** locus explained 54% of the variation in response to race DW5[10871].

Louise / Penawawa: RIL population: *QTs.zhl-1A*, located at interval 0-6.0 cM and likely **Tsc1**; *QTs.zhl-2D*, located at 144.0-152.0 cM; **QTs.zhl-3B**, located at 72.0-78.0; and *QTs.zhl-5A* located at 154-160 cM[11362].

QTL
Batavia (S) / Ernie (R): DH population tested over three years. Four (1A(Ernie), 7A, 2BS, 3BS (Batavia)), five (2BS, 5BL(E), 3D, 6A, 7D(B)) and four (2BS, 5BL(E), 1A, 6A(B),) QTL accounted for most of the variation in each year. The greatest effect across years was the QTL on chromosome 2BS (R^2=0.382, 0.298 and 0.362, respectively). This QTL was validated in four additional populations[10782].

Grandin (S) / BR34 (R): RIL population: QTL in 1BS, *QTs.fcu-1BS*, (13-29% of variation depending on race) and 3BL, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses[10248].

TA4152-60 (R) / ND495 (S): DH population: Five QTLs for resistance, all from TA4152-60[10580], viz., *QTs.fcu-2AS* and *QTs.fcu-5BL.1* conferring resistance to all races used, *QTs.fcu-5AL* conferring resistance to races 1, 2 and 5, *QTs.fcu-5B.2* conferring resistance to races 1 and 2, and *QTs.fcu-4AL* conferring resistance to race 3.

WH542 (R) / HD29 (S): RIL population: SIM indicated QTL on chromosomes 1B, 3AS, 3BL, 5B and 6BS, but only two were confirmed by CIM, *Qts.ksu-3AS* flanked by *Xbarc45-3A* and *Xbarc86-3A* (LOD 5,4, R^2 = 0.23) and *Qts.ksu-5BL* (probably **Tsn1**) flanked by *Xgwm499-5B* and *Xest.stsbe968-5B* (LOD 6,5, R^2 = 0.27)[10552].

Wangshuibai / Ning 7840: RIL population: Race 1: *QTs.ksu-1AS*, R^2=0.39 (nearest marker *Xcfa2153-1A* and *QTs.ksu-2BS*, R^2=0.04) (nearest marker *Xbarc2-2B* [10753].

3.24 Reaction to *Rhizoctonia* spp.

Cause of Rhizoctonia root rot.

ROT1

Rot1 [10761]

v: Scarlet-Rz1[10761].

Scarlet-Rz1 was produced by mutagenesis[10761].

3.25 Reaction to *Sitobion avenae*

English grain aphid.

SA1

Sa1 [10877] locus: 6AL [10877] syn: RA-1 [10877]

tv: C273[10877]. **ma**: *Xwmc179-6A* – 3.37 cM – **Sa1** – 4.73 cM – *Xwmc580-6A* [10877].

3.26 Reaction to *Sitodiplosis mosellana* (Gehin) (orange blossom wheat midge)

Insect pest: Orange blossom wheat midge, Wheat midge. This pest should not be confused with *Contarinia tritici*, the yellow blossom wheat midge.

SM1

Sm1[218, 0218] locus: 2B[218]

v: Augusta[218, 11137]; Blueboy[218]; Caldwell[218]; CDC Landmark[11579]; Clark[218]; FL302[218]; Glencross[11044]; Goodeye[11044]; Howell[218]; Knox 62[218]; Mono[218]; Paragon[11579]; Robigus[11137]; Seneca[218]; Skalmeje[11137]. Unity[11579]. **ma**: Linked to a SCAR marker[223]; **Sm1** was mapped to a 2.5 cM interval on chromosome 2BS flanked proximally by AFLP-derived SCAR marker *WM1* and distally by SSR *Xgwm210-2B*[10291]; A combination of *2BS-5344126_kwm707* and *2BS-6229175_kwm693* appeared to be predictive of **Sm1** but there was variation between sources[11137]. KASP marker developed in [11579]. **c**: Gene candidate with NB-ARC-LRR-kinase-MSP structure[11579].

QTL

Henong 215 (R) / Yanyou (S) and 6218 (S) / Jimai 24 (R): selected RIL populations: Several QTL identified: *QSm.hbau-4A.2* with LOD scores 5.58 – 29.22 and PVE 24.4 – 44.8% were mapped to a 4.9 Mb interval; nearest markers *AX-109543456*, *AX-108942696* and *AX-110928325*[11425].

Reeder I / Conan: RIL population: *QSm.mst-1A*, flanked by *Xwmc59-1A* and *Xbarc1022-1A* was the most effective and constant QTL for reduced larval infection over two years (R^2=0.17 and 0.34)[10841]. RILs with this QTL in three genetic backgrounds had reduced infestations of 42%[10841].

3.27 Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Insect pest: Greenbug

GB1

Gb1[1514] locus: 1AS[11731] syn: gb1[222]

Recessive. CI 9058[222]; Dickinson Selection 28A[222].

Located in the region 13.3 – 14.2 Mb[11731].

GB2

Gb2[1313, 1514] locus: 1A[554]. = T1AL.1R#2S[389]

Derived from *Secale cereale*.

v: Amigo CI 17609[1313]; Century[0008]; TAM107[0008]; TAM200[0008]; TAM202[8]. **ma**: 2.7 cM proximal to **Sec1** in 1RS, but co-segregated with *Sec-1P*[10167]; Within the 1R segment: **Gb6** – 15.8 cM – **Gb2** – 11.4 cM – *XIA294*[10764].

GB3

Gb3[624, 1514] locus: 7D[554]. 7DL[0319]

Resistance in Largo and derivatives was controlled by multiallelic complementary genes[783]. **Gb3** was postulated to be one of the loci concerned.

bin: 7DL3 0.82-1.00. **v**: Largo CI 17895[622]; TAM110[0319]; TAM112[194, 10764]; TXGBE373[0319]. **al**: Insave rye. **tv**: *Ae. tauschii* PI 268210[10907]. **ma**: Completely associated with 2AFLP markers[0319]. These were also present in germplasm line KS89WGRC4, implying the likely presence of **Gb3** or a closely linked resistance gene[0319]; *Xgwm037-7D* – 0.4 cM – **Gb3**/*Xwmc634-7D* – 0.8 cM – *Xbarc76-7D*[10169]; *H1067J6-R* – 0.7 cM – **Gb3** – 0.4 cM – *H1009B3-F*[10907]. **Gb3** – **Gb8** 15+-1.35 cM[11378].

GB4

Gb4[523, 1514] locus: 7DL[10267]

v: CI 17959[903].

Gb4 is either closely linked or allelic to **Gb3**[10267].

GB5

Gb5[1514, 1515] locus: 7S#1L(7A)[391]; T7S#1L.7S#1S-7S[389]

tr: CI 17883; CI 17884; CI 17885[1515]; UCRBW98-1 and UCRBW98-2 (PI 603919 has a shortened alien segment[11515]. **ma**: KASP markers are reported in ▶[11516].

GB6

Gb6 locus: 1A = T1AL.1R#2S[1151]

Derived from *Secale cereale*.

v: GRS1201[1152]; GRS1202[1152]; GRS1203[1152]; GRS1204[1152]; GRS1205[1152]; N96L9970[10764]; see also **Pm17** (Reaction to *Blumeria graminis*). **su**: Tx4386[1150]. **ad**: Tx4333[1150]. **al**: Insave rye. **ma**: Within the 1R segment: **Gb6** – 15.8 cM – **Gb2** – 11.4 cM – *XIA294*[10764].

GB7

Gb7[10169] locus: 7DL[10169]

v: Synthetic W7984[10169]. **tv**: *Ae. tauschii* TA1651[10169]. **ma**: *Xwg420-7D* – 2.1 cM – **Gb7** – 13.4 cM – *Xwmc671-7D*[10169]. KASP markers developed {M23026}; KASP markers developed[11633].

GB8

Gb8[11378] locus: 7DL[11378] syn: Gb595379-1[11378].

bin: 7DL3-0.82-1.00. **v**: PI 595379-1[11378]. **ma**: *Xbarc11-7D* – 10.41 cM – **Gb8**/*Xstars508* (596.4 Mb) – 7.4 cM – *Xwmc824-7D* – 4.8 cM – *Xgwm428-7D*[11378]. **Gb3** – **Gb8** 15+-1.35 cM[11378].

GB9

Gb9[11726] locus: 7DL[11726] syn: Gb76364[11726]

v: PI 703387, CWI 76364[11726]. **dv**: *Ae. tauschii* Wx1027 (CIMMYT)[11726]. **ma**: Mapped to a 0.6 Mb interval – *Stars-KASP872* (599.8 Mb; CS RefSeq 2.1) 0.6 cM – **Gb9** – 0.5 cM and *Stars-KASP881* (600.5 Mb)[11726]. **Gb9** – **Gb3**, 14.9 cM[11726]. **Gb9** – **Gb8**, 16.3 cM[11726].

Temporary designations

Gba[10267] locus: 7DL[10267]

v: TA4152L94 = CETA/*Ae. tauschii* Wx1027[10267]. **ma**: *Xwmc671-7D* – 34.3 cM – **Gba** – 20.7 cM – *Xbarc53-7D*[10267].

Gbb[10267] locus: 7DL[10267]

v: TA452L24 = CROC 1/*Ae. tauschii* Wx224[10267]. **ma**: *Xwmc671-7D* – 5.4 cM – **Gbb** – 20.2 cM – *Xbarc53-7D*[10267].

Gbc[10267] locus: 7DL[10267]

v: TA4063.1 = 68111/Rugby//Ward//*Ae. tauschii* TA2477[10289]. **ma**: *Xgwm671-7D* – 13.7 cM – **Gbc** – 17.9 cM – *Xgdm150-7D*[10267].

Gbd[10267]

v: TA4064.1 = Altar 84/*Ae. tauschii* TA2841[10267]. **ma**: *Xgwm671-7D* – 7.9 cM – **Gbd** – 1.9 cM – *Xwmc157-7D*[10267].

Gbx1[10267] locus: 7DL[10267] syn: Gbx[10267]

v: KS89WGRC4 = Wichita/TA1695//2*Wichita[10267]. **dv**: *Ae. Tauschii* TA1695[10267]. **ma**: *Xwmc157-7D* – 2.7 cM – *Xgdm150-7D*[10267].

Gbx2[10267] syn: Gbx[10267]

v: W7984[10267]. **ma**: **Gbx2** was located 8.8 cM from **Gb3**[10267].

Gby[10192] locus: 7A[10192]

v: Sando's Selection 4040[10192]. **ma**: *Xpsr119-7A*/*Xbcd98-7A* – 5.8 cM – **Gby** – 3.8 cM – *Xpr1B-7°*[10192].

Gbz[10171] locus: 7DL[10171]

v: KSU97-85-3[10171]. **tv**: *Ae. tauschii* TA1675[10171]. **ma**: *Xgdm46-7DL* – 9.5 cM – *Xwmc157-7D*/**Gb3**/**Gbz** – 5.1 cM – *Xbarc53-7D*[10171]; *Xwmc671-7D* – 3.9 cM – **Gbz**/*Xwmc157-7D* – 5.1 cM – *Xbarc53*[10267].

QGb.unlp-6A

for antixenosis was associated with *Xgwm1009-6A* and *Xgwm1185-6A* in a CS/CS(Synthetic 6A) DH population[10216].

Antibiosis was associated with several markers, including ***Rc3*** (7DS) in chromosome 7D[10167].

3.28 Reaction to Soil-Borne Cereal Mosaic Virus

Syn.: Soilborne wheat mosaic. Vectored to the roots by the fungus, *Polymyxa graminis*

SBM1

Sbm1[10614] locus: 5DL[10614] syn: SbmCz1[10132]

v: Cadenza[10132]; Claire[11138]; Moulin[11138]; Tonic[10614]; Tremie[11138]. **v2**: Cadenza **Sbm2**[11500]. **ma**: *Xbarc110-5D* – 14.7 cM – **Sbm1** – 2.1 cM – *Xwmc765-5D* – 3.1 cM – *Xbarc144-5D*/*Xwmc443-5D*/*RRES01-5D*[10614]; Caps marker RRESO1 was developed from an AFLP fragment[10614]; *E37M49* – 9.0 cM – **Sbm1** – 1.0 cM – *Xgwm469-5D* – 2.0 cM – *Xwmc765-5D*. Resistant varieties carried 152 or 154 bp alleles at *Xgwm469-5D*[11138]; all susceptible genotypes had a null allele[11138].

Sbm1 was identified in a DH population of Avalon (S)/Cadenza (R)[10132].

SBM2

Sbm2[11500] locus: 2BS[11500]

v: Xi19[11500]. **v2**: Cadenza **Sbm1**[11500].

Temporary designations

SbmTmr1[10683] locus: 5D[10683]

v: TAM 107-R7[10683].

Sbmwm1[11435]

v: Heyne[11435]. 5D[11435]. **ma**: *Xgwm272-5D* – 20.2 cM – *Sbwm1* – 2.2 cM – *wsnp_CAP11_c209_198467* – 0.7 cM – *wsnp_JD_c4438_5568170* – 8.7 cM – *Xgwm469*[11435].

Sbm1 and **Sbmwm1** are likely the same gene.

SBWMV[10685] locus: 5D[10685]

v: KS96WGRC40[10685]. **dv**: *Ae. tauschii* TA2397[10685]. **ma**: *Xcfd010-5DL* – 9.5 cM – **SBWMV** – 11.1 cM – *Xbarc144-5D*[10685].

QSbv.ksu-5D

This major QTL (R^2=0.38) was found in Karl 92*2/TA4152-4[10273]; the resistance was contributed by Karl 92.

3.29 Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)

Disease: eyespot, strawbreaker footrot.

PCH1

Pch1 locus: 7DL[708, 1603]. 7D[591, 592] syn: Pch[261]

s: Courtot*/Roazon 7D[592]; Hobbit Sib*/VPM1 7D[591]. **v**: *Ae ventricosa* derivative[261]; Coda[10513]; H-93-70[236, 1521]; Hyak[21]; Madsen[20]; Rendezvous[1603]; Roazon[591]; 5L 219[1521]. 7A[0224]. **tv**: Five recombinant lines[0224]. **al**: *Ae. ventricosa*[261]. **ma**: **Pch1** was linked to **Ep-D1** and mapped 2 cM from microsatellite marker *XustSSR2001-7D*[10070]; ***Ep-d1b*** was a more reliable marker than the STS for selecting **Pch1**[10238]; Leonard et al.[10513] predicted that **Ep-D1** might encode an oligopeptidase B, and by comparative genetics, developed

primers to a wheat oligopeptidase B-encoding wheat EST *BU1003257*. Complete linkage occurred for a derived STS marker *Xorw1* and **Pch1** in a Coda/Brundage RIL population and the marker identified the presence or absence of **Pch1** among 44 wheat accessions[10513]. **Pch1** is closely linked with **Ep-V1**[973]. Delibes *et al*.[236] concluded that **Pch1** was not located in chromosome 7D whereas Law *et al*.[776] found that H-93-70 possessed a unique allele, ***Ep-D1b***, in common with VPM1 and its derivatives. Eyespot resistance and ***Ep-A1b*** in chromosome 7A were genetically associated[704].

PCH2

Pch2[228] locus: 7A[704]. 7AL[228, 229]

s: CS*/Cappelle Desprez 7A[228, 704]. **v**: Cappelle Desprez[228, 704]. **ma**: *Xcdo347-7A* (distal) – 11 cM – **Pch2** – 18.8 cM – *Xwg380-7A* (proximal)[229].

According to ▶[0380], this gene is not effective at the adult plant stage. Instead, the adult resistance of Cappelle-Desprez was controlled by a gene on chromosome 5A with the possibility of two less effective genes on 1A and 2B.

PCH3

Pch3[616]

ad: CS + 4V[1050].

Temporary designation

Pch_{Dv}[618] locus: 4VL[618]

ad: Wheat + 4V[618]. **su**: Wheat 4VL (4D), Yangmai 5[618]. **ma**: Distally located; Cent … *Xcdo949-4V* – 16 cM – **Pch_{Dv}** – 17 cM – *Xbcd588-4V*[618].

ungrouped

QPch.jic-5A [10771]

bin: 5AL-6 0.68-0.78. **ma**: Closely associated with *Xgwm639-5AL* [10771].

3.30 Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Disease: Bunt, dwarf smut, stinking smut.

BT1

Bt1 locus: 2B[1310] syn: M1[135]

s: CS*7/White Federation 38[1304]. **v**: Albit[129]; Banner Berkeley[129]; Federation 41[137]; Regal[129]; Sherman[137]; White Federation 38[1166]; White Odessa[137]. **v2**: Columbia **Bt6**[1005]; Hussar **Bt2**[135]; Hyslop **Bt4**[733]; Martin **Bt7**[135]; McDermid **Bt4**[734]; Odessa **Bt7**[137]; Tyee **Bt4**[22].

Markers report for Bt1

primary reference 999215

PI 554101 is the proposed line by Goates (2012). Genetic analysis has identified the gene at chromosome 2B at the position 755.889.858-772.760.826 bp. (Christensen and Borgen 2023A). Several lines have been well tested for having Bt1 without other Bt-genes and can be used as alternatives, including Starke II Bt1 NIL (selection in NGB11503), 'Albit' (CItr 8275), and 'PG3540' (Agrologica breeding line). For spring wheat trials, 'M83-1531' (PI 554108) can be used.

Investigation of recombination events in the Starke II NIL / Starke II / Albit triplet together with a comparison of haplotypes for all Bt1 postulated lines in our mapping population across an interval extending the GWAS interval at 2B allowed identification of the 11,043,031bp interval 799,983,180 – 811,026,211bp. Other references 129 137 1310 999216 999217 999218 999219 999220 999221.

marker	allele	chr	position	assembly
AX-158609666	**A**	**2B**	**799,983,180 bp**	**TG25K Gregor/DKC**
Excalibur_c48404_59	C	2B	799,991,797 bp	RefSeq v2.1
wsnp_Ex_c15646_23969140	A	2B	789,869,194 bp	RefSeq v2.1
BS00065302_51	G	2B	800,405,470 bp	RefSeq v2.1
AX-94890379	G	2B	800,409,495 bp	TG25K Gregor/DKC
BS00083998_51	G	2B	800,879,575 bp	TG25K Gregor/DKC
Ra_c105904_187	*C*	*2B*	*800,881,187 bp*	*RefSeq v2.1*
Ra_c105904_1191	*G*	*2B*	*800,882,423 bp*	*RefSeq v2.1*
AX-158610188	*A*	*2B*	*801,265,942 bp*	*TG25K Gregor/DKC*
AX-94808568	*G*	*2B*	*803,272,878 bp*	*TG25K Gregor/DKC*
AX-158562114	C	2B	803,471,810 bp	TG25K Gregor/DKC
Kukri_c49784_86	A	2B	804,811,318 bp	RefSeq v2.1
Excalibur_rep_c106698_235	A	2B	806,010,015 bp	RefSeq v2.1
BS00065264_51	G	2B	806,046,215 bp	RefSeq v2.1
Excalibur_c25043_357	*A*	*2B*	*808,464,426 bp*	*RefSeq v2.1*
Kukri_c900_1334	T	2B	809,152,228 bp	RefSeq v2.1
AX-95017900	**G**	**2B**	**811,026,211 bp**	**TG25K Gregor/DKC**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 11,043,031 bp

BT2

Bt2 syn: H129

v: Canus137; Seln 110211693; Seln 209211693; Selection PS60-1-1075551; Selection 1403137. **v2**: Hussar **Bt1**135.

BT3

Bt3 locus: 1A999202

v: Florence202, 203; Ridit152, 1000, 1395.

Markers report for Bt3

primary reference 999202

Initially known as the Florence factor. Ridit is a selection from a Florence x Turkey cross and is used as the Bt3 differential line. Mapped by BOKU in Blizzard/Bonneville. Chromosome 1A - 492.81 - 515.55 Mbp. Other references 999208 999209.

marker	allele	chr	position	assembly
wsnp_Ku_c21316_31053745	**T**	**1A**	**499,646,938 bp**	**RefSeq v2.1**
CAP12_c1906_217	T	1A	405,363,751 bp	RefSeq v2.1
RAC875_rep_c112044_340	C	1A	500,312,849 bp	RefSeq v2.1
TA003955-1138	A	1A	406,073,088 bp	RefSeq v2.1
BS00094553_51	A	1A	502,463,023 bp	RefSeq v2.1
Kukri_rep_c117029_125	C	1A	502,472,121 bp	RefSeq v2.1
RAC875_c29540_1109	A	1A	505,761,810 bp	RefSeq v2.1
wsnp_Ex_rep_c108951_91954190	G	1A	505,764,279 bp	RefSeq v2.1
BS00021728_51	C	1A	505,766,553 bp	TG25K Gregor/DKC
RAC875_c37545_289	G	1A	506,799,443 bp	RefSeq v2.1
Kukri_c29039_315	T	1A	507,186,655 bp	RefSeq v2.1
wsnp_Ku_c10292_17066821	T	1A	508,358,564 bp	RefSeq v2.1
wsnp_Ku_c1642_3232242	**T**	**1A**	**508,582,099 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 8,935,161 bp

BT4

Bt4 locus: 1B[1005, 1274, 1285] syn: T[136]

v: Bison[1285]; CI15588[11693]; Kaw[1285]; Nebred[1285]; Omaha[1285]; Oveson[1235]; Tres (heterogeneous)[23]; Turkey 1558[137]; Turkey 2578[137]. **v2**: Hyslop **Bt1**[733]; McDermid **Bt1**[734]; Oro **Bt7**[137]; Turkey 3055 **Bt7**[137]; Tyee **Bt1**[22]. Since **Bt4** and **Bt6** are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of **Bt4**, and Rio should be used as the source of **Bt6**.

BT5

Bt5 locus: 1B[1001]

v: Hohenheimer[397]; Selection R60-3432[551].

Markers report for Bt5

primary reference 999202

Markers in this interval correctly identifies 59 (61) out of 64 lines postulated to have Bt5, yielding a 92 (95) % identification rate. 15 out of 165 lines not postulated to have Bt5 were incorrectly identified as having Bt5, giving a false positive rate of 9 %. 10 + crosses done in 2022 between Bt5 donors and lines with good marker contrast in the interval. Other references 999210 999211 999212.

marker	allele	chr	position	assembly
BS00022473_51	**C**	**1B**	**118,731,183 bp**	**RefSeq v2.1**
Ra_c455_283	T	1B	123,383,762 bp	RefSeq v2.1
RAC875_c60360_389	C	1B	126,093,027 bp	RefSeq v2.1
BS00093740_51	G	1B	127,088,890 bp	RefSeq v2.1
BS00010992_51	T	1B	129,534,002 bp	RefSeq v2.1
BS00073034_51	C	1B	142,999,000 bp	RefSeq v2.1
BS00063574_51	T	1B	151,195,722 bp	RefSeq v2.1
wsnp_BE637864B_Ta_1_1	G	1B	206,017,979 bp	RefSeq v2.1
BS00068512_51	T	1B	159,323,844 bp	RefSeq v2.1
BS00068246_51	G	1B	162,804,916 bp	RefSeq v2.1
BS00022218_51	G	1B	163,104,223 bp	RefSeq v2.1
BS00066165_51	G	1B	164,434,808 bp	RefSeq v2.1
BS00022317_51	A	1B	224,277,236 bp	RefSeq v2.1
AX-109342634	A	1B	265,108,595 bp	TG25K Gregor/DKC
AX-110385663	C	1B	283,934,501 bp	TG25K Gregor/DKC
Excalibur_c6497_535	**G**	**1B**	**284,939,075 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 166,207,892 bp

BT6

Bt6 locus: 1B[1005] syn: R[1418]

v: Rio[1418]; Turkey 10095 & 10097[53]. **v2**: Columbia **Bt1**[1005].

Since **Bt4** and **Bt6** are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of **Bt4**, and Rio should be used as the source of **Bt6**. [T[136]].

BT7

Bt7 locus: 2D[1000] syn: M2[1275]

s: CS*7/Cheyenne 2D[1000]. **v**: Baart[1275]; Cheyenne[1000]; Federation[1275]; Gallipoli[1000]; Onas[1275]; Ranee[1000]; Selection 1833[556]; Seln500-77[11693]. **v2**: CI 7090 **Bt9**[1000]; Martin **Bt1**[137]; Odessa **Bt1**[137]; Oro **Bt4**[1000]; Turkey 3055 **Bt4**[1000].

Markers report for Bt7

primary reference 999235

Initially known as the Martin gene number 2. Selection 50077 / PI 554100 uses as differential. Mapped by monosomic analysis to chromosome 2D. The GWAS gave 45 significant markers on 2A, 2B and 2D. Markers are working very well. “Perfect” detection rate. Low false positive rate. Other references 137 551 1310 999206 999232 999236.

marker	allele	chr	position	assembly
BS00110411_51	**C**	**2D**	**618,996,780 bp**	**RefSeq v2.1**
RAC875_c30919_311	G	2D	621,068,206 bp	RefSeq v2.1
RAC875_rep_c114621_200	C	2D	752,946,446 bp	RefSeq v2.1
wsnp_Ex_c42970_49408712	A	2D	622,542,240 bp	RefSeq v2.1
wsnp_RFL_Contig4402_5154408	**A**	**2D**	**623,541,443 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 4,544,663 bp

BT8

Bt8[1558]

v: HY476[10181]; M822161[11693]; PI 178210[1558]; Yayla 305[1558].

BT9

Bt9[1006, 999202] locus: 6D[999202]. 6DL[11299]

v: PI 166910[1006]; PI 166921[1006]; PI 167822[1006]; PI 554099[11299]; Selection M69-2073[551]; M90387[11693]. **v2**: CI 7090 **Bt7**[1000]; Jeff **Bt10**[1436]; PI 178383 **Bt10**[1006]; Ranger **Bt10**[1438].

Not clearly differentiated from **Bt11**[11693].

Markers report for Bt9

primary reference [999234]

R. J. Metzger found a resistance gene in the line C.I. 7090 / PI 57143 that was different from B1-Bt8 and hence named Bt9. C.I. 7090 / PI 57143 also contains Bt7. The Bt9 differential line is R63-6968 / PI 554099 which is a selection from the cross Elgin / PI 178383. Bt9 was first mapped to the distal end of 6DL in a biparental population of 91 double haploid (DH) lines. The parents were PI 554099 (National Small Grains Collection, Aberdeen, Idaho, USA), carrying resistance gene Bt9, and common bunt susceptible-wheat cv. Cortez (Wiersum Plant Breeding, Winschoten, The Netherlands). (Steffan et al. 2017)

Markers correctly identifies 84% of lines postulated to have Bt9 alone or in combination with other genes. For lines postulated to have Bt9 alone the hit rate is 98%. The false positive rate is 5%. Some notable lines supposed to have Bt9 that does not match the markers are the Bt11 source Dimenit / PI 166910, Malkesi / PI 178201 and Ark / CItr 15286. Other references [999203] [999204] [999205].

marker	allele	chr	position	assembly
BS00022206_51	**A**	**6D**	**490,336,397 bp**	**RefSeq v2.1**
wsnp_JG_c5646_2148382	C	6D	490,706,861 bp	RefSeq v2.1
wsnp_JG_c5646_2148296	*C*	*6D*	*490,706,775 bp*	*RefSeq v2.1*
Kukri_rep_c107605_164	*T*	*6D*	*490,707,682 bp*	*RefSeq v2.1*
wsnp_CAP8_rep_c4586_2232878	*C*	*6D*	*490,708,624 bp*	*RefSeq v2.1*
wsnp_CAP7_c1735_859875	*G*	*6D*	*490,708,625 bp*	*RefSeq v2.1*
AX-94589700	A	6D	490,830,504 bp	TG25K Gregor/DKC
RAC875_c484_1063	**A**	**6D**	**491,341,666 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 1,005,269 bp

BT10

Bt10[1004, 10181] locus: 6DS[10721] syn: QCbt.spa-6D {M11298}

i: BW553 = Neepawa*6//Red Bobs/PI 178383[10475]. **v**: AC2000[10181]; AC Cadillac[10181]; AC Carma[10181]; AC Crystal[10181]; AC Foremost[10181]; AC Taber[10181]; AC Vista[10181]; Fairview[1183]; M822102[11693]; PI 116301[1004]; PI 116306[1004]; PI 554118[11299]; Selection M69-2094[551]. **v2**: Jeff **Bt9**[1436]; PI 178383 **Bt9**[1000]; Ranger **Bt9**[1438]; Others[128, 239]. **ma**: **Bt10** was completely linked with a 590 bp fragment produced by UBC primer 196[239]; RAPD – 1.5 cM – **Bt10**[763]; **Bt10**/*FSD_RSA* – 19.3 cM – *Xgwm469-6D* – 1.8 cM – *Xwmc749-6D*. The RAPD fragment was sequenced and converted to a diagnostic PCR marker for **Bt10** in [0128].

Present in lines with **SrCad**[10733].

Markers report for Bt10

primary reference 999222

'R63-6982' (PI 554118) is the proposed differential line by Goates (2012). Bt10 was first associated with a position at chromosome 6D by Laroche et al (2000). We have confirmed the association with 6D at the position 1.769.916-3.642.206 bp (Christensen and Borgen 2023D). 'Starke II NIL-Bt10' (selection in NGB11506), 'M83-1621' (PI 554109), Tillexus and Tillstop can be used as alternatives for Bt10. For spring wheat trials, M83-1621 (PI 554109) and 'H86-706' (PI 542432), can be used. Other references 1004 10997 999223 999224 999225 999226 999227 999228 999229.

marker	allele	chr	position	assembly
GENE-3775_326	**T**	**6D**	**1,769,966 bp**	**RefSeq v2.1**
RAC875_c7178_404	C	6D	2,087,623 bp	TG25K Gregor/DKC
wsnp_Ku_c19587_29102203	G	6D	2,152,048 bp	RefSeq v2.1
CAP7_c1208_150	T	6D	2,253,027 bp	RefSeq v2.1
wsnp_Ex_c14439_22426200	C	6D	2,388,914 bp	RefSeq v2.1
TA002853-0110-w	A	6D	2,391,362 bp	RefSeq v2.1
Kukri_c55362_75	A	6D	2,470,346 bp	RefSeq v2.1
AX-108746724	C	6D	2,818,635 bp	TG25K Gregor/DKC
Excalibur_c7731_2743	A	6D	3,118,642 bp	RefSeq v2.1
AX-158531240	C	6D	3,140,478 bp	TG25K Gregor/DKC
BS00011513_51	**A**	**6D**	**3,642,156 bp**	**TG25K Gregor/DKC**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* — interval 1,872,190 bp

BT11

Bt11 10997 locus: 3B 11297; 6DL 11693 syn: QBt.ifa-6DL 11693

v: M822123 = PI 554119 10997, 11693; Elgin/PI 166910 10997, 11693. **ma**: May be associated with *Xbarc180*, *Xwmc623*, *Xwmc808* and *Xgwm285* 11297; Located between 492.6 and 495.2 Mbp, CS RefSeq 2.1 11693. Not clearly differentiated from **Bt9** 11693.

BT12

Bt12 10997 locus: 7DS 11469 syn: QBt.ifa-7DS 11469

v: PI 119333 10997. **ma**: Associated with 13 markers in a distally located physical region of ~4.3 Mbp 11469. Validated KASP markers were derived from *IWB61302* and *IWB50978* 11469. Although appearing to be proximal to *QDB.ui-7*DS 11182 the genes were not clearly distinguished.

Markers report for Bt12

primary reference 999202

Added to the differential set by Blair Goates The differential line for Bt12 is PI119333 Has been mapped to the 7DS interval 6.5–10.8 Mbp by BOKU Seven markers for use in MAS found. Other references 999213 999214.

marker	allele	chr	position	assembly
Excalibur_c46904_84	**C**	**7D**	**5,559,572 bp**	**RefSeq v2.1**
BS00108793_51	T	7D	5,736,446 bp	RefSeq v2.1
Kukri_c80931_147	A	7D	7,432,654 bp	RefSeq v2.1
TA003860-0782	G	7D	7,804,232 bp	TG25K Gregor/DKC
RAC875_c99892_81	C	7D	8,535,542 bp	RefSeq v2.1
wsnp_JD_c2734_3667052	A	7D	8,603,151 bp	RefSeq v2.1
Ra_c11887_1826	G	7D	8,604,313 bp	RefSeq v2.1
Ra_c9123_2016	G	7D	9,639,081 bp	RefSeq v2.1
IAAV9104	C	7D	9,642,443 bp	RefSeq v2.1
wsnp_Ex_c410_810250	C	7D	9,645,128 bp	RefSeq v2.1
D_F5XZDLF02H192C_184	T	7D	11,023,286 bp	RefSeq v2.1
D_contig78519_72	A	7D	11,032,679 bp	RefSeq v2.1
RFL_Contig1323_544	G	7D	11,141,495 bp	RefSeq v2.1
RAC875_c41169_68	**T**	**7A**	**10,698,871 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 5,139,299 bp

BT13

Bt13 10997

v: Thule III 10997; PI 181463 10997.

Markers report for Bt13

primary reference 999230

1192 wheat lines were phenotyped using a design described in Borgen et al (2018) and genotyped using TG25k SNP markers in different trials in the LIVESEED, BOOST and DIVERSILIENCE projects. Each line was postulated to have or not have Bt13 based on phenotypic data and information about the pedigree. Our mapping population has strong population structure regarding Bt13 because Thule III is a direct parent of most of the 64 lines postulated to have Bt13. For this reason there are a many sporadic significant markers scattered across chromosomes.

At chromosome 7D in the interval 6,820,874 – 11,141,495 bp we have what appears to be the correct signal. The marker at 7A, which is the most significant of all, was investigated further and was found to placed at 7D by linkage analysis in the BOKU Bt12 mapping population. Furthermore, a BLAST against RefSeq 2.1 had 7D 8,602,319 bp as a possible (and very likely) location. The likelihood that the 7D signal is the correct one is strengthened by this placement of the most significant marker in the middle of it. Other references 999213 999231 999232.

marker	allele	chr	position	assembly
TA001746-1415	*G*	*7D*	*6,820,874 bp*	*TG25K Gregor/DKC*
AX-158595238	*T*	*7D*	*6,939,438 bp*	*TG25K Gregor/DKC*
Kukri_c80931_147	*A*	*7D*	*7,432,654 bp*	*RefSeq v2.1*
IAAV9104	*C*	*7D*	*9,642,443 bp*	*RefSeq v2.1*
AX-111707392	*T*	*7D*	*11,139,971 bp*	*TG25K Gregor/DKC*
RFL_Contig1323_544	*G*	*7D*	*11,141,495 bp*	*RefSeq v2.1*
AX-158555104	**C**	**7D**	**5,005,482 bp**	**TG25K Gregor/DKC**
AX-94804328	C	7D	5,410,853 bp	TG25K Gregor/DKC
Kukri_c37227_579	A	7D	5,411,236 bp	RefSeq v2.1
AX-95237430	G	7D	5,450,099 bp	TG25K Gregor/DKC
Ra_c30952_531	T	7D	5,542,839 bp	RefSeq v2.1
AX-158544378	T	7D	5,661,151 bp	TG25K Gregor/DKC
AX-94708419	G	7D	6,366,823 bp	TG25K Gregor/DKC
TA001746-1415	G	7D	6,820,874 bp	TG25K Gregor/DKC
AX-158595238	T	7D	6,939,438 bp	TG25K Gregor/DKC
Kukri_c80931_147	A	7D	7,432,654 bp	RefSeq v2.1
IAAV9104	**C**	**7D**	**9,642,443 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 4,636,961 bp

BT14

Bt14 10997

tv: Doubbi CI 13711 10997.

BT15

Bt15 10997

tv: Carleton CI 12064 10997.

Temporary designation

Btp 10997

v: PI 173437 10997.

ungrouped

BtZ 100000, 999233

v: Kalininskaya 27 100000,**v**: Nemchinovskaya 25 100000

Markers report for BtZ primary reference [999233]

marker	allele	chr	position	assembly
RAC875_rep_c118305_446	*C*	*6D*	*4,243,619 bp*	*RefSeq v2.1*
Excalibur_c7731_2743	*G*	*6D*	*3,118,642 bp*	*RefSeq v2.1*
AX-158531240	*T*	*6D*	*3,140,478 bp*	*TG25K Gregor/DKC*
Kukri_c73802_205	*A*	*6D*	*4,572,453 bp*	*RefSeq v2.1*
wsnp_CAP12_c720_382116	**G**	**6D**	**3,444,503 bp**	**RefSeq v2.1**
BS00065960_51	C	6D	4,454,205 bp	RefSeq v2.1
Kukri_c73802_205	**A**	**6D**	**4,572,453 bp**	**RefSeq v2.1**

MAS flank markers=**BOLD**, markers for MAS=ROMAN, GWAS markers=*ITALIC* interval 1,127,950 bp

QTL

Blizzard (R) / 8405-JC3C (S): DH population. Resistance and markers *Xgwm374-1BS*, *Xgwm364-1BS* and *Xbarc128-1BS* were within a 3.9 cM interval[10783].

Carberry / AC Cadillac: AC Cadillac contributed QTL **QCbt.spa-6D** (**Bt10**) on chromosome 6D (markers *XwPt-1695*, *XwPt-672044*, and *XwPt-5114*). Carberry contributed *QCbt.spa-1B* (*XwPt743523*), *QCbt.spa-4B* (*XwPt 744434 – Xwmc617*), *QCbt.spa-4D* (*XwPt-9747*), *QCbt.spa-5B* (*XtPt-3719*), and *QCbt.spa-7D* (*Xwmc273-7D*)[11298].

Idaho 444 (R) / Rio Blanco S: RIL population: Three QTL for dwarf bunt resistance: *QDB.ui-7DS* (R^2 = 0.3-0.6), *QDB.ui-1A* (R^2 = 0.11-0.15) and *QDB.ui-2B* (R^2 = 0.06). Two PCR-based markers were developed for the *wPt-2565* sequence on chromosome 7DS[11182].

IDO835 (R) / Moreland (S): DH population: **Q**.*DB.ui-6DL* (PVE 0.53, **Bt9** region) and **Q**.*DB.ui-7AL* (PVE 0.38)[11400].

Trintella / Piko: DH population: One major gene in the chromosome 1BS centromere region, nearest marker *Xgwm273-1B*[11003]. Smaller QTL effects were detected on chromosomes 7A, 7B and 5B in different years. Additional QTL are listed in [18099].

3.31 Reaction to *Tilletia indica* Mitra

Disease: Karnal bunt.

KB1

Kb1[394]

v: Chris[394]. **v2**: CMH77.308 **Kb2**[394].

KB2

Kb2[394]

v: PF7 113[394]. v CMH77. 308 **Kb1**[394]; Shanghai #8 **Kb4**[394].

KB3

Kb3[394]

v: Amsel[394].

KB4

Kb4[394]

v: Shanghai #8 **Kb2**[394].

KB5

Kb5[394]

Recessive[394]

v2: Pigeon **Kb6**[394].

KB6

Kb6[394]

Recessive[394]

v2: Pigeon **Kb5**[394].

ungrouped

Qkb.cnl-3B[9956]

ma: Located in the interval *XATPase-3B* – *Xcdo1164-3B*.

Qkb.cnl-5A.1[9956]

ma: Located in the interval *Xmwg2112-5A* – *Xcdo20-5A*.

Qkb.cnl-5A.2[9956]

ma: Located in the interval *Xabg391-5A* – *Xfba351-5A*.

Qkb.ksu-4BL.1

WL711/HD29 (R): RILs: R^2 = 0.25, associated with *Xgwm538-4B*[10498]. WH542/W485 (R) RILs: R^2 = 0.15, *Xgwm6-4BL* – *Xwmc349-4BL* interval[10499].

Qkb.ksu-5BL.1

WH542/HD29 (R): RILs: R^2 = 0.19, *Xgdm116-5BL* – *Xwmc235-5BL*[10499].

Qkb.ksu-6BS.1

WH542/HD29 (R): RILs: R^2 = 0.13, *Xwmc105-6BS* – *Xgwm88-6BS*[10499].

3.32 Reaction to *Ustilago tritici* (Pers.) Rostrup

Disease: Loose smut.

UT1

Ut1[1073]

v: Florence/Aurore[1073]; Renfrew[1073]; Red Bobs[1074].

UT2

Ut2[1073]

v: Kota[1073]; Little Club[1073].

UT3

Ut3[1074]

v: Carma[1074].

UT4

Ut4[1074] locus: 7B[11168] syn: QUt.spa-7B[11168]

v: 9340-CP[11168]; Glenlea[11168]; TD1[11168]; Thatcher/Regent[1074].

UT5

Ut5[10940, 11164] locus: 5BL[10940] syn: Ut-Fore[10940], Ut-X[11164]

v: Foremost[10940]. **ma**: *Xgpw5029* – 2.8 cM – **Ut5** – 1.3 cM – *Xbarc232-5b*[10940]. See **Ut-x**.

Race T10 was used for analysis[10940].

UT6

Ut6[10040, 11168, 11169] locus: 5BL[11169] syn: QUt.spa-5B[11168]

v: AC Foremost[11169]; AC Karma[10040]; AC Vista[11168]; Chinese Spring[11169]; Glenlea[11169]; HY320[11169]; Oasis[11169]. **ma**: *Xgpw5029-5B* – 2.8 cM – **Ut6** – 2.8 cM – *Xbarc232-5B*[11169].

UT7

Ut7[11168] locus: 7A[11168] syn: QUt.spa.7A[11168]

v: SC8021V2[11168].

UT8

Ut8[11168] locus: 3A[11168] syn: QUt.spa-3A[11168]

v: 9340-SP[11168]; Glenlea[11168].

UT9

Ut9[11168] locus: 6B[11168] syn: QUt.spa-6B[11168]

v: SC8021V2[11168].

UT10

Ut10[11168] locus: 6D[11168] syn: QUt.sps-6D[11168]

v: SC80-21V2[11168].

UT11

Ut11[11406] locus: 7BS[11406]

v: DH line TD14XDIA*B0075, CN 120264[11406]; Sonop, TD-14[11406]. **ma**: Co-segregation with *BS00022562_51, Excabibur_C3489_182* and *Kukri_rep_c71778_644* at 0.43, 1.20 and 1.25 Mbp[11406].

Ut11 conferred resistance to race T2 but not T9 and T39; resistance to those races (and race T2) was conferred by *QUt.mrc-5B*[11406].

Temporary designations

Ut-x[1164, 11164]

v: Biggar BSR[11164]. **ma**: *Xcrc4-2B* – 14 cM – **Ut-x** – 10 cM – *Xabc153-2B.2*[11164]; *Xcrc4-2B.2* (Syn. *Xcrc4.2*) is a SCAR.

UtBW278[11729] locus: 5BS[11729]

v: BW728[11729]. **ma**: Mapped to a region close to **Utd1**[11729].

Identified in a BW278/AC Foremost cross with a *Ustilago tritici* isolate virelent to AC Foremost[11729].

Utd1[10684] locus: 5BS[10684]

tv: D93213[10684]; P9163-BJ08*B[10684]; VIR 51658[10684]. **ma**: SCAR – 3.2 cM – **Utd1** – 5.9 cM – *Xgwm234-5B*[10684].

Resistance to race 19 was associated with chromosome 6A of Cadet, Kota, Thatcher and TD18[0208]. In the case of Cadet, resistance was localized to 6AS[0208].

3.33 Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)

WSSMV is soil-borne and vectored by the fungus *Polymyxa graminis*. This virus has some sequence similarity to Wheat Yellow Mosaic virus[10285]. Wheat streak mosaic disease can also be caused by Triticum mosaic virus, which is also known as High Plains Wheat mosaic virus. Low rates of seed borne transmission of WSSMV are reported.

WSS1

Wss1[10271] locus: 4D(4DL.4VS)[10271]

Derived from *Haynaldia villosa*. T4VS.4DL[10271].

tr: NAU413[10271]. **su**: Yangmai#5 4V(4D)[10271].

A number of secondary translocations were induced, the smallest of which was NAU421 (FL 0.78-1.00)[11488].

QTL
Geneva (R) / Augusta (S): 79% of the variation between these accessions was associated with markers *Xbcd1095-2D* and *Xcdo373-2D* located 12.4 cM apart in chromosome 2DL[0131].

3.34 Reaction to wheat streak mosaic virus

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to [10226] WSMV may also be see-borne. At least some sources of resistance to WSMV are also effective against Triticum mosaic virus.

WSM1

Wsm1[379, 440] locus: 4D = T4DL.4J^{S}S[389, 391]; T4DL.4DS-4JSS[10788]

Derived from *Th. intermedium*.

i: Karl*4/CI 17884 = PI 583794 = KS93WGRC27[440]; Line E*6/rec213 (**Sr64**, **Wsm1**) = GSTR 527[11644] (https://npgsweb.ars-grin.gov/gringlobal/accessiondetail?id=2158211). **v**: CA74[10971]; CI 17766 = B-6-37-1[391, 800, 1543]; CI 17884[391]; S90H445[391]; KS90H450[391]; CI 17883[389]; Mace PI 651043[11006, 11179, 11643]; KS03HW12[11006]; KS08WGGRC50[10788]. **ad**: CI 17881[391]; CI 17886[391]. **su**: CI 15092[391]; CI 17882[391]; CI 17885[391]. **ma**: **Wsm1** co-segregated with a STS amplified by the primer set STSJ15[1456]; KASP markers developed in [11643].

Wsm1 is located in 4J^{S}S (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885 and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*).

Wsm1 also confers resistance to Triticum Mosaic Virus[10788]. **Wsm1** confers resistance at temperatures below 19C[11179].

WSM2

Wsm2[10802, 10898] locus: 3BS[10802]

v: Clara CL PI 1665948[11329]; CO960293-2[10802]; Oakley CL PI 670190[11329]; RonL[10898]; Snowmass[10802]. **ma**: **Wsm2** – 5.2 cM – *XSTS3B-55*[10802]; *Xbarc102-3B* – 1.6 cM – **Wsm2**[10802]; *Xgwm389-3B* – 30.8 cM – **Wsm2** – 45.2 cM – *Xgwm566-3B*[10898]; *Xbarc87-3B* – 4.4 cM – **Wsm2** – 3.9 cM – *Xbarc102-3B*[10982]; Eight SNP markers were mapped within 1 cM of **Wsm2**[11329]. KASP markers were developed from some of these SNP[11330]; Mapped to a 4.0 Mb region in distal arm 3BS carrying 142 candidate genes, six of which were differentially expressed in Snowmass relative to susceptible Antero[11654].

Wsm2 confers resistance at temperatures below 19C[10802]. Allele *Xbarc102-3B*$_{219}$ was the best predictor for **Wsm2**[10982].

WSM3

Wsm3[10775] locus: 7B[10775]. 7B (7BS.7S#3L)[10775]. TBS.7S#3L[10775]

v: KS12WGGRC5 TA5624[10775].

Wsm3 was also effective against Triticum mosaic virus at 18C[10775]. For a review of WSMV see [11656].

3.35 Reaction to *Xanthomonas campestris* pv. *undulosa*

Disease: Bacterial leaf streak

Bls1[244]

v2: Pavon **Bls2**[244]; Mochis T88 **Bls3 Bls4**[244]; Angostura F88 **Bls5**[244].

Bls2[244]

v2: Pavon **Bls1**[244].

Bls3[244]

v2: Mochis T88 **Bls1** *Bls 4*[244].

Bls4[244]

v2: Mochis T88 **Bls1** **Bls3**[244].

Bls5[244]

v2: Turnco F88[244]; Angostura F88 **Bls1**[244].

3.36 Resistance to colonization by *Eriophyes tulipae* (*Aceria tulipae*)

Eriophyes tulipae is the vector of wheat streak mosaic virus (WSMV) and the wheat spot mosaic agent (WSpM).

CMC1

Cmc1[1467] locus: 6DS[1576]

i: Norsa*5/**Cmc1**[10166]. **v**: *Ae. squarrosa* CI4/Novamichurinka (= AC PGR 16635)[1467]; Norstar derivative[222].

CMC2

Cmc2[1573] locus: 6A = T6AS.6Ae#2S[389]. 5B = T5BL.6Ae#2S[389]. 6D[1575]

Derived from *Th. elongatum*. = T6DL.6Ae#2S[389, 1575].

i: Norstar*5/**Cmc2**[10166]. **v**: 875-94-2[389]. **tr**: Rescue Derivative[1575]. **su**: Cadet 6Ae#2(6A)[1575]; Cadet 6Ae#2(6D)[1574]; Rescue 6Ae#2(6A)[1574]; Rescue 6Ae#2(6B)[1574]; Rescue 6Ae#2 (6D). **ad**: Cadet + mono-6Ae#2[1574]; Rescue + 6Ae#2[1574].

CMC3

Cmc3[222, 0222] locus: 1A = 1AL.1RS

Derived from *Secale cereale*.

i: Norstar*5/**Cmc3**[10166]. Need to confirm relationship of 1RS segment in Amigo and Salmon as this NIL was derived from KS80H4200 a Chinese Spring Salmon line[10166]. **v**: Amigo; TAM107[222]. **v2**: KS96GRC40 **Cmc4**[222]. **ma**: Wheat lines with the 1RS segment and hence **Cmc3** can be selected with the rye-specific SSR *Xscm09-1R*[222].

CMC4

Cmc4[222, 0222] locus: 6DS[222]

v2: KS96WRC40 **Cmc3**[222]. **v**: TAM112[11612]; TAM115[11612]; TAM204[11612]. **dv**: *Ae. tauschii* accession[222]; *Ae. tauschii* TA1618 (11612}. **ma**: *XksuG8-6D* – 6.4 cM – **Cmc4** – 4.1 cM – *Xgdm141-6D*[222].

3.37 Reaction to Wheat Yellow Mosaic Virus

WYMV is soil-borne and vectored by the fungus *Polymyxa graminis*. This virus has some sequence similarity to Wheat Spindle Streak Mosaic[10258], another bymovirus.

Temporary designations

Ymlb[10750] locus: 2DL[10750]

v: Ibis[10750]; Jagger[10750]; KS 831957[10750]; Madsen[10750]; Yumechikara[10750]. **ma**: *Xwmc181-2D* – 12.4 cM – **Ymlb** – 2.0 cM – *Xcfd16-2D* – 2.0 cM – *Xwmc41-2D* – 3.1 cM – *Xcfd168-2D*[10750].

The relationship of **Ymlb** to a previously mapped gene in 2DL for resistance to WYMV and WSSMV in Yangfu 9311[10258] and a Geneva derivative[0131] was not established.

YmYF[10258] locus: 2DL[10258]

v: Yangfu 931[10258]. **ma**: *Xpsp3039-2D*/*Xwmc181-2D* – 0.7 cM – *Xwmc41-3D* – 8.1 cM – *Xgwm349-2D*[10258].

QYm.nau-2D[11186] locus: 2DL[11186] syn: Q.Ymym[11660]

bin: 2DL9-0.76-1.00. **v**: Fielder[11645]; Yining Xiaomai[11186]. **ma**: *Xwmc41-2D* – 3.7 cM – *2SNP86.2* – 0.4 cM – *QYm.nau-2D* – 1.0 cM – *2EST784*[11186].

According to [11645] *QYm.nau-2D* is a natural alien translocation from an *Aegilops* species and several subsequent wheat haplotypes arose from rare recombination events. This QTL is present in a wide range of cultivars from Europe, USA, Japan, and China[11645].

QTL

Xifeng(R) / Zhen 9523(S): RIL population: Three QTLs, *Qym.njuy5A.1* (R^2 = 0.26-0.54), *Ym.njau-3B.1* (R^2 = 0.03-0.01) and *QYm.njau-7B.1* (R^2 = 0.03-0.05 in some trials). The chromosome 5A gene was closely associated with *Xwmc415.1*, *CINAU152* and *CINAU153* and was phenotyped as a single Mendelian gene[11073]

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