ANALYSIS OF THE QUALITY TRAITS OF A BÁNKÚTI 1201 POPULATION

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Summary

The old Hungarian variety *Bánkúti 1201* possesses excellent technological quality parameters despite the fact that it bears the high molecular weight (HMW) subunits 2+12 on chromosome 1D. Lines from the *Bánkúti 1201* population were selected carrying different alleles at the *Glu-A1* and *Glu-B1* loci. The analyses of different lines indicate that the HMW glutenin subunit composition is more closely correlated with properties characteristic of protein quality than with protein quantity. In various lines of *Bánkúti 1201* the correlation between the HMW glutenin subunits and the quality traits was stronger if the alleles of the *Glu-A1* and *Glu-B1* loci were considered together.

Index words: wheat, population, breadmaking quality, HMW glutenins

Introduction

Bánkúti 1201, registered in 1931, was perhaps the most famous and most successful variety in the history of Hungarian wheat breeding. It was of outstanding importance among the winter wheat varieties known collectively today as the old Hungarian varieties, and it was used by wheat breeders both in Hungary and in the neighbouring countries to create lines and varieties with excellent breadmaking quality. The variety was bred by farm manager László Baross from a cross between the winter wheat variety *Bánkúti 5*, selected from the landrace *Tiszavidéki*, and the Canadian spring wheat variety *Marquis* (Lelley and Rajháthy, 1955). Baross was aiming at developing a winter variety with breadmaking quality similar to that of *Marquis*, but adapted to the climatic conditions of Hungary (Rapaics, 1934). An interesting aspect of this combination is that the pedigrees of both parents include elements arising from the famous wheats, the "Proles Hungarica", once grown along the north-eastern boundaries of the Carpathians: on the one side the variety *Red Fife* included in the pedigree of *Marquis*, and on the other the landrace *Tiszavidéki*, originating from seed imported after the great drought of 1863, both had their origin in the Galicia region (Kosutány, 1906; Mándy, 1971).

Bánkúti 1201 has outstandingly good breadmaking quality. Its flour has high protein and gluten contents and in most cases is classified in categories A_2-A_1 on the basis of its farinograph index. As it was taken off the list of state registered varieties

in 1973, after 42 years, it is now only to be found in gene banks or in the variety collections of breeding institutes.

Scientists interested in the breadmaking quality of wheat have long endeavoured to discover first phenotypic and later biochemical markers which would make it possible to classify genotypes unambiguously independently of environmental effects. Although the HMW glutenins make up only 10 % of the total gluten and only 1 % of the whole endosperm (Pomeranz, 1988), they are nevertheless of fundamental significance in determining the rheological properties of the dough.

Genes coding for HMW subunits are to be found on the long arms of chromosomes belonging to homoelogous group 1 (Payne et al., 1980; 1982) and are designated as *Glu-A1*, *Glu-B1* and *Glu-D1*. A number of allelic variants may occur at all three loci. In experiments carried out by Payne et al. (1987) subunits 1 and 2* at locus *Glu-A1* had a favourable influence on protein quality. By contrast, Khan et al. (1989) found that although the gluten content and the water uptake increased in genotypes bearing the 2* allele, the dough development time became shorter. The presence of subunit 9, coded by locus *Glu-B1*, shortened the dough development time and increased loaf volume, farinograph water absorption and gluten content (Khan et al., 1989). According to Payne et al. (1984) and Lorenzo et al. (1987) the HMW glutenin subunit pair 7+8 had a favourable influence on breadmaking quality. The allele coding the subunit combination 5+10 at locus *Glu-D1* had a better effect on breadmaking quality than the 2+12 allele (Payne et al., 1987; Ng and Bushuk, 1988; Khan et al., 1989; Dong et al., 1991; Hamer et al., 1992).

In preliminary experiments it was found that the *Bánkúti 1201* population maintained in Martonvásár was heterogeneous as regards the HMW glutenin subunit composition coded by chromosomes 1A and 1B (1 and 2*; 7+8 and 7+9 respectively), and carried the 2+12 allele at the *Glu-D1* locus (Bedő et al., 1995). It is thus a special property of the variety that it has excellent breadmaking quality despite the fact that, judging by its HMW glutenin subunit composition, it should be classified as of only medium quality. In the course of the present studies the population was divided into lines homogeneous as regards their HMW glutenin subunit composition, after which the quality parameters of each line were tested.

Materials and methods

In order to test the *Bánkúti 1201* population maintained by the Agricultural Research Institute of the Hungarian Academy of Sciences a field experiment was set up in the wheat breeding nursery in Martonvásár. The population was divided into lines by means of spike selection in 1993. The spike progeny lines were sown in two-row plots for three years (1993-1995). The plots were 2 m in length, with a row distance of 20 cm. In all three years spike selection was carried out and the HMW glutenin subunit compositions of the lines were checked by means of SDS-polyacrylamide gel electrophoresis. Heterogeneous progeny lines were eliminated

from the experiment. On the basis of three years of experiments the data of 90 lines were processed.

The lines were characterised using the following parameters:

- protein content, using a Tecator Kjeltec 1035 Analyzer. The data are given on a dry matter basis, using a factor of N×5.7;
- wet and dry gluten content, determined from flour according to the ICC 137/1 standard;
- gluten index, according to the ICC 155 standard;
- gluten spread, according to the MSZ 6369/5-87 Hungarian standard;
- sodium dodecyl sulphate sedimentation volume (hereafter: SDS value) analysed with an automatic Soltek SDS System.

The whole wheat flour for the protein content determination and the SDS test was ground using a Perten Laboratory Mill type 3100, while the flour required for the gluten tests was milled using a Brabender Junior mill.

The first step in the statistical evaluation was analysis of variance to check the significance of differences in breadmaking quality between the lines. In the course of the analysis the replications were given by the different years and the error factor by the line × year interaction (Sváb, 1981). After proving the statistical significance of the treatment effect the mean data of the three years were used to carry out further analysis of variance on the significance of differences between the breadmaking properties of the various HMW glutenin subunit composition groups (hereafter: groups). When the properties were found to differ significantly on the basis of the *F* test, the *t* test was applied to check the significance of deviations between the mean values. Correlation coefficients between various quality traits and the HMW glutenin subunits were calculated.

Results and discussion

On the basis of HMW glutenin subunit composition four different types were found to be present in the 90 lines selected from the *Bánkúti 1201* population maintained in Martonvásár. All the lines examined were found to contain the region responsible for the formation of the 2+12 subunit combination on the 1D chromosome. Of the subunits coded by the *Glu-A1* locus the majority of the lines (more than 95 %) contained subunit 2*. Many of the lines (68.9 %) contained the DNA sequence responsible for the synthesis of HMW glutenin subunits 7+9 on chromosome 1B. This means that the subunit composition occurring most frequently in the lines examined was 2*; 7+9; 2+12.

Three years of data were then used to analyse differences in breadmaking quality between the lines within the population. The differences observed were analysed by means of variance analysis. The treatment effect was significant for all the quality traits, so the mean data of the three years were used in further calculations. The groups formed on the basis of HMW glutenin subunit composition and their quality traits are presented in Table 1.

Table 1. HMW glutenin subunit composition and quality traits of the *Bánkúti 1201* lines examined

HMW subunit			Line		Protein	Wet	Dry	Gluten	Gluten	SDS
Glu-A1	Glu-B1	Glu-D1	No.	%	%	gluten %	gluten %	index	spread	value
2*	**7+9**	**2+12**	55	61.1	15.58	40.49	13.68	70.28	6.17	71.18
2*	**7+8**	**2+12**	22	24.4	15.75	40.23	13.73	83.78	4.85	77.88
1	**7+9**	**2+12**	7	7.8	15.43	41.94	14.04	58.36	7.76	67.52
1	**7+8**	**2+12**	6	6.7	15.76	41.85	13.93	63.18	6.92	68.50

As the groups formed on the basis of HMW glutenin subunit composition contained different numbers of lines the method devised by Sváb (1981) for this case was applied to analyse the data. The homogeneity of variance of the individual groups was tested in the first step using Bartlett's test, the results of which are presented in Table 2.

Table 2. χ^2 values of Bartlett's test for various quality traits

	Protein content	Wet gluten content	Dry gluten content	Gluten index	Gluten spread	SDS value	$\chi^2_{1\%}$ critical	$\chi^2_{99\%}$ critical
Total	0.16	2.83	1.06	0.85	4.48	5.45	11.30	0.12
2*;7+9;2+12	51.49	46.47	55.83	50.28	41.33	55.72	76.20	
2*;7+8;2+12	23.07	30.24	21.94	26.42	31.01	25.46	38.90	
1;7+9;2+12	6.17	3.49	3.10	4.88	9.91	1.15	16.80	
1;7+8;2+12	5.27	5.79	5.13	4.42	3.73	3.67	15.10	

On the basis of Bartlett's test it can be concluded at the P=2 % level of probability that for all the quality traits the deviations of the individual groups do not differ significantly from each other. In the second step the statistical analysis of the differences between the individual groups was carried out using analysis of variance, including the data of all the groups, as justified by the results of Bartlett's test. The results are presented in Table 3.

Table 3. Analysis of variance of the groups for each quality trait

Factor	SQ	FG	MQ	F
Protein content				
Total	20.487	89		
Between groups	0.834	3	0.278	1.217
Within groups	19.653	86	0.229	
Wet gluten content				
Total	346.110	89		
Between groups	25.661	3	8.554	2.296
Within groups	320.449	86	3.726	
Dry gluten content				
Total	29.005	89		
Between groups	1.055	3	0.352	1.082
Within groups	27.950	86	0.325	
Gluten index				
Total	14715.980	89		
Between groups	4981.216	3	1660.405	14.669***
Within groups	9734.764	86	113.195	
Gluten spread				
Total	193.329	89		
Between groups	57.520	3	19.173	12.141***
Within groups	135.808	86	1.579	
SDS value				
Total	3082.079	89		
Between groups	999.696	3	333.232	13.762***
Within groups	2082.384	86	24.214	

According to the results of the *F* test no significant difference could be demonstrated between the groups for traits connected with the protein quantity (protein, wet gluten and dry gluten contents), while the presence of significant differences was proved for traits linked with protein quality (gluten index, gluten spread, SDS value).

Taking the results of the *F* test as the basis, the *t* test was then used to check whether the differences between the group means were statistically significant. The results of these calculations are presented in Table 4.

Table 4. *t* test on the quality traits

Group	t value		
	2*;7+8;2+12	1;7+9;2+12	1;7+8;2+12
Gluten index			
2*;7+9;2+12	-5.03***	2.79**	1.55
2*;7+8;2+12		5.51***	4.20***
1;7+9;2+12			-0.81
Gluten spread			
2*;7+9;2+12	4.17***	-3.15**	-1.38
2*;7+8;2+12		-5.34***	-3.57**
1;7+9;2+12			1.21
SDS value			
2*;7+9;2+12	-5.39***	1.85	1.27
2*;7+8;2+12		4.85***	4.14***
1;7+9;2+12			-0.36

In several cases the *t* test carried out for mean value pairs indicated the presence of strongly significant differences. For all three traits statistically significant differences were found for the group pairs 2*; 7+9; 2+12 - 2*; 7+8; 2+12, 2*; 7+8; 2+12 - 1; 7+9; 2+12 and 2*; 7+8; 2+12 - 1; 7+8; 2+12. The gluten index and gluten spread were significantly different in the group pair 2*; 7+9; 2+12 - 1; 7+9; 2+12, though the mean SDS values of these two groups were statistically equal. No significant differences were exhibited for any of the quality traits by the means of the 2*; 7+9; 2+12 - 1; 7+8; 2+12 and 1; 7+9; 2+12 - 1; 7+8; 2+12 group pairs.

A joint examination of the means of all the groups indicated that the gluten structure of the group containing the HMW glutenin subunit combination 2*; 7+8; 2+12 was significantly stronger than that of the other groups, since it exhibited the greatest gluten index and SDS value and the smallest gluten spread. The group with the worst gluten type was 1; 7+9; 2+12, though this did not differ significantly from the 1; 7+8; 2+12 group. The 2*; 7+9; 2+12 group was intermediate between these two types.

After comparing the mean values of the groups the correlations between quality traits and the HMW glutenin subunit composition in the individual *Bánkúti 1201* lines were analysed. The effect of the subunits coded by loci *Glu-A1* and *Glu-B1* were calculated first separately and then together. In the course of the joint analysis the groups were ranked according to the results of analysis of variance, after which a value corresponding to the order was allotted to each group. The group with the weakest gluten was allotted a value of 1 and that with the strongest gluten a value of 4. The Pearson's correlation coefficients obtained are presented in Table 5.

Table 5. Correlations between the HMW glutenin subunit composition and the quality traits

Quality trait	Glu-A1	Glu-B1	GluA1 + Glu-B1
Protein content	0.036	0.183	0.140
Wet gluten content	-0.266*	-0.018	-0.248*
Dry gluten content	-0.183	0.044	-0.137
Gluten index	0.373***	0.378***	0.554***
Gluten spread	-0.379***	-0.335***	-0.534***
SDS value	0.308**	0.404***	0.511***

Correlation calculations confirmed the results of analysis of variance; in other words, the HMW glutenin subunit composition was found to be more closely correlated with properties characteristic of protein quality than with those associated with protein quantity. A separate analysis of the effect of proteins coded by loci *Glu-A1* and *Glu-B1* indicated that the correlation was strongly significant, but loose, while the effect of the proteins coded by both loci was similar in magnitude. Thus, in contrast to observations by Payne et al. (1987), the two protein subunits coded by the *Glu-A1* locus had different effects on breadmaking quality. The 7+8 HMW glutenin subunit pair coded by chromosome 1B, however, was found to have a positive influence on gluten quality parameters, as reported by Payne et al. (1984) and Lorenzo et al. (1987). When the effects of the subunits on the properties studied were analysed together, it could be seen that the correlation between the HMW glutenin subunits and the quality traits was strengthened when the alleles of both loci were considered. The gluten index and the SDS value exhibited a strongly significant, moderate, positive correlation with the HMW glutenin subunit composition, while the gluten spread showed a similarly strong, but negative correlation.

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