

Correlation between high molecular weight gluten subunits composition and bread-making quality in Brazilian wheat

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ABSTRACT

Bread-making quality is one of the most important targets in the genetic improvement of wheat. Although extensive analyses of quality traits such as farinography, sodium dodecyl sulfate (SDS) sedimentation, alveography, and baking are made in breeding programs, these analyses require high amounts of seeds which are obtained only in late generations. In this experiment the statistical correlations between the high molecular weight subunit of glutenin and bread-making quality measured by alveograph, farinograph and SDS sedimentation were evaluated. Seventeen wheat genotypes were grown under the same conditions, each producing about 1 kg of seeds for the evaluations. The high molecular weight (HMW) glutenin subunits were analyzed by SDS-PAGE. Statistical correlations were highly significant between HMW glutenin subunits and alveograph and SDS sedimentation. These results indicate the possibility of manipulating major genes for wheat seed quality by coupling traditional breeding with non-destructive single seed analysis. Only half seed is necessary to perform the SDS-PAGE analysis. Therefore, the other half seed can be planted to generate the progeny. Seed yield and SDS sedimentation were statistically correlated, indicating the possibility of simultaneous selection for both traits.

INTRODUCTION

Bread-making quality is one of the most important targets in the genetic improvement of wheat. Although extensive analyses of quality traits such as farinography, SDS sedimentation, alveography, and baking are made in breeding programs, these analyses require high amounts of seeds which are obtained only in the late generations. The analysis for determining bread-making quality is generally considered as being

for complex traits, making difficult the simultaneous selection with seed yield.

The association of high molecular weight (HMW) glutenin subunits to SDS sedimentation values as an indicator of bread-making quality has been demonstrated by Payne *et al.* (1981). The HMW glutenin subunits are coded by genes at the Glu-A1, Glu-B1 and Glu-D1 loci in chromosomes 1A, 1B and 1D, respectively (Payne *et al.*, 1980, 1982, 1988). Lawrence and Shepherd (1980) have determined extensive variability in wheat cultivars produced by allelic variation at each locus.

Payne *et al.* (1987) have assigned a score of each HMW glutenin subunit which permitted a statistical evaluation of the amount of variation in bread-making quality attributable to the HMW glutenin subunits. For

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British- and Spanish-grown wheat cultivars, 47 and 68%, respectively, of the variation in quality is directly related to Glu-1 score (Payne *et al.*, 1987, 1988). For Canadian-grown wheat, 59-69% of the variation in bread-making quality is directly related to this score (Lukow *et al.*, 1989).

The utilization of this methodology has more advantages: a) only half seed is necessary to separate HMW glutenin subunits in SDS-PAGE analysis. Therefore, the other half seed can be planted to generate the progeny (Bhagwat and Bhatia, 1988). Thus, the F₂ and F₃ generations can be analyzed; b) it is independent of wheat-growing conditions, especially protein content and alpha amylase activity; c) it allows us to consider bread-making quality a single characteristic, and select simultaneously the seed yield and bread-making quality.

The Brazilian cultivated wheat is primarily used for baking. Bread-making quality evaluation is recent in Brazilian genetic improvement programs. In the present study, the objective was to evaluate the statistical correlations between the HMW glutenin subunits and bread-making quality measured by alveography, farinography and SDS sedimentation in some genotypes at the end of genetic improvement programs.

MATERIAL AND METHODS

Genetic material

Seventeen wheat genotypes were included in this study. These genotypes were composed of four cultivars recommended for cultivation in Minas Gerais, seven lines originated from EMBRAPA/CPAC (Planaltina, DF), four lines originated from EMBRAPA/CNPT (Passo Fundo, RS), one line originated from IAPAR (Londrina, PR) and one line introduced by international assay.

These genotypes were cultivated under the same uniform conditions, yielding the seeds for the evaluations.

Electrophoresis

Total protein was extracted from a segment of one sample of kernel of each cultivar and fractionated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) using 10% w/v polyacrylamide gel as described by Payne *et al.* (1980, 1982). The numbering system for the HMW glutenin subunits (Table I) was used previously (Lukow *et al.*, 1989). Genotypes containing wheat-rye translocation were

Table I - Qualitative scores for HMW glutenin single subunits or pairs of subunits¹.

Score	Chromosome		
	1A	1B	1D
4	-	-	5 + 10
3	1	17 + 18	-
3	2*	7 + 8	-
3	-	13 + 16	-
2	-	7 + 9	2 + 12
2	-	-	3 + 12
1	N	7	4 + 12
1	-	6 + 8	-
1	-	20	-
Without information	-	21	2.2
Without information	-	22	2 + 11
Without information	-	13 + 19	2 + 10

¹Adapted from Payne (1987) and Lukow *et al.* (1989).

N is absence of chromosome 1A band.

corrected in this score: less 3 points to scores 8-10, 2 points to scores 5-7 and one point to scores 3-4.

Quality analysis

After the milling, the flour was analyzed for quality tests:

- Protein content: two grams of each genotype was used to determine the protein content, utilizing the Kjeldahl method.

- Alveography: using 250 g of flour of each genotype, alveography was made in Chopin alveograph, obtaining the "W" value (baking strength index or deformation energy of dough), "P" value (tenacity, or maximum pressure, expressing the dough resistance to deformation), "L" (dough stability to disruption) and "G" (inflating index).

- SDS sedimentation: 7 g of whole wheat flour was placed in a test tube with 20 ml SDS, shaken for one minute and the test tubes rested in a plane surface for 20 min. After this time, the sedimented volume at the bottom of the test tube was determined.

The results were submitted to statistical analysis to estimate the single correlations (Pearson's correlations). These correlations were submitted to *t*-statistics, given by $t = r \sqrt{n-2} / \sqrt{1-r^2}$, with *n*-2 degrees of freedom.

RESULTS AND DISCUSSION

The HMW glutenin subunits composition of the genotypes, determined by SDS-PAGE, permitted the calculation of Glu-1 score for all genotypes. Figure 1 shows the electrophoresis gel. The Glu-1 score of these

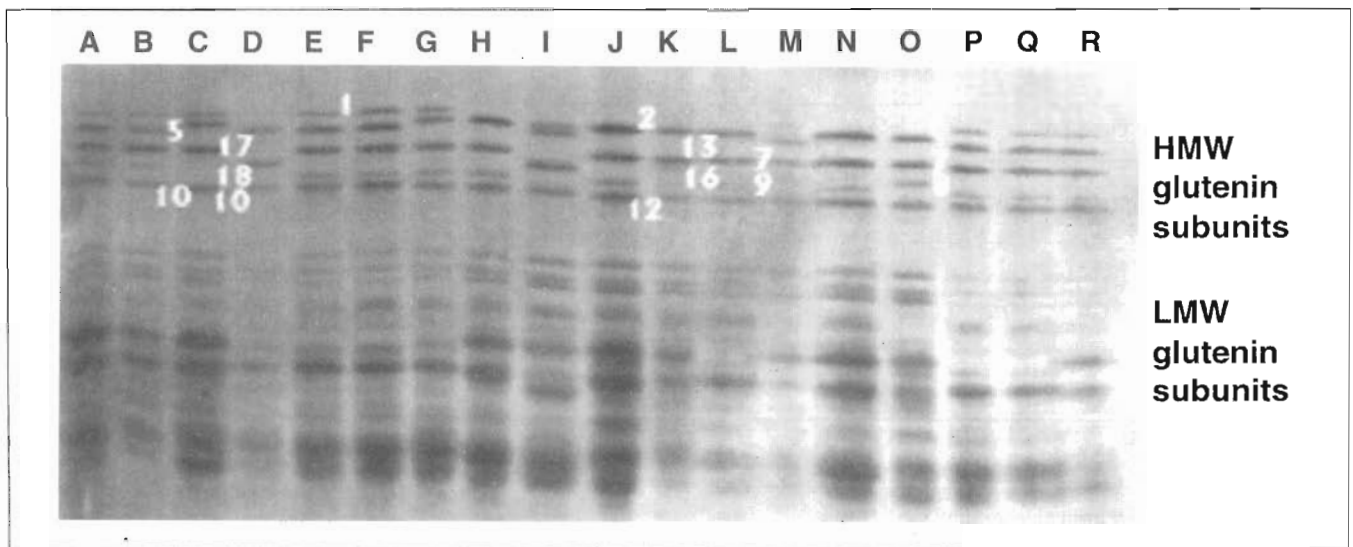


Figure 1 - SDS-PAGE electrophoresis gel for HMW glutenins. A = ANAHUAC, B = PF 89481, C = CPAC 89137, D = BR 10, E = PF 87949, F = NL 459, G = IAPAR 8745, H = PF 89490, I = BR 30 (tester), J = CPAC 8932, K = CPAC 89128, L = CPAC 89194, M = CPAC 89223, N = PF 87950, O = CPAC 8947, P = BR 33, Q = BR 26, R = CPAC 8909. The numbers indicate the amount of bands on the left.

genotypes and the results of the quality analysis are presented in Table II.

In general, bread-making quality of the evaluated wheat was low, as shown in the alveography, farinography and SDS sedimentation. This demonstrates that bread-making quality is insufficiently observed in the first generation of breeding programs. The seed yield was high, considering Brazilian wheat.

The Spearman's correlations (Table III) showed a statistically significant correlation between the Glu-1

score and baking strength ("W"), SDS sedimentation and seed yield. Therefore, this score will be utilized for an important trait in selection for bread-making quality in the first generation of the breeding programs, when quantities of seeds necessary for the conventional test are not available. Only half seed is necessary to perform the SDS-PAGE analysis. Therefore, the other half can be planted to generate the progeny. This test can be considered a non-destructive test for bread-making quality.

Table II - Characterization of wheat genotypes evaluated for yield and bread-making quality, and HMW glutenin subunit scores.

Genotype	Yield (kg/ha)	Flour Prot.	"W" ¹	S-SDS ²	Sta. ³ (min)	ADT ³ (min)	Abs. ³ (%)	HMW gluteninin			Score Glu-1
								AA	BB	DD	
CPAC 8909	5.059	8.70	153	8.2	4.1	3.1	55.7	1	7	5 + 10	8
CPAC 8932	5.400	9.23	152	9.0	4.0	3.5	58.8	N	7 + 9	2 + 12	5
CPAC 8947	5.152	9.44	149	9.2	3.3	2.7	58.9	N	7 + 8	2 + 12	6
CPAC 89128	5.147	9.20	142	9.8	4.6	3.5	57.2	N	13 + 16	2 + 12	6 - 2 = 4*
CPAC 89137	#	9.33	111	8.2	3.1	2.2	59.3	1	7	2 + 12	6
CPAC 89194	4.949	10.50	148	8.6	3.1	3.0	61.2	N	7 + 9	2 + 12	5 - 2 = 3*
CPAC 89223	5.711	9.88	253	13.0	3.5	2.5	57.0	1	7 + 8	5 + 10	10
PF 87949	5.022	9.92	105	9.4	3.0	2.5	58.8	1	7 + 9	5 + 10	9
PF 87950	5.124	9.51	128	8.8	4.0	3.0	59.0	N	7 + 9	2 + 12	5
PF 89481	5.900	10.14	127	10.6	3.5	3.9	58.4	1	7 + 8	5 + 10	10 - 3 = 7*
PF 89490	4.961	9.14	135	9.6	4.2	2.8	61.8	N	7 + 9	2 + 12	5 - 2 = 3*
NL 459	5.738	9.95	171	10.2	3.2	2.0	58.7	1	7 + 9	5 + 10	9
IAPAR 8745	5.615	9.72	125	9.2	2.9	3.5	59.5	1	7 + 9	2 + 12	7
ANAHUAC	5.714	10.20	185	12.4	7.7	4.2	55.8	1	7 + 8	5 + 10	10
BR 10	5.382	9.31	116	8.0	4.0	2.8	58.4	N	17 + 18	5 + 10	8 - 3 = 5*
BR 26	4.968	9.66	128	9.0	3.8	3.0	57.9	1	7 + 9	5 + 10	9 - 3 = 6*
BR 33	5.544	11.62	169	10.6	3.3	3.0	60.8	1	7 + 9	5 + 10	9

¹Bread strength obtained from alveography.

²Sedimentation with sodium dodecyl sulfate.

³Sta. = Stability; ADT = average development time; Abs. = water absorption obtained from farinography.

*Scores revised for wheat/rye translocation as indicated in Material and Methods.

#The line CPAC 89137 could not have yield evaluated. The correlations for yield were made in 16 genotypes.

Table III - Single correlations between characteristics related with bread-making quality in wheat.

	Glu-1	Flour Prot.	"W" ¹	S-SDS ²	Sta. ³	ADT ³	Abs. ³	Yield
Glu-1	1.00	0.38	0.51*	0.63**	-0.14	-0.07	-0.50*	0.60*
Flour Prot.		1.00	0.21	0.44	-0.13	0.08	0.35	0.42
"W"			1.00	0.77**	-0.06	-0.11	-0.31	0.45
S-SDS				1.00	-0.18	0.16	-0.29	0.64**
Sta.					1.00	-0.37	0.33	-0.06
ADT						1.00	-0.29	0.26
Abs.							1.00	-0.25
Yield.								1.00

Degrees of freedom = 16.

*P < 0.05.

**P < 0.01.

¹Bread strength obtained from alveography.

²Sedimentation with sodium dodecyl sulfate.

³Sta. = Stability; ADT = average development time; Abs. = water absorption obtained from farinography.

Bread-making quality is a complex trait influenced by the environment. However, using HMW glutenin subunits, it is possible to evaluate the bread-making quality potential of wheat genotypes, enabling the manipulation in the first generation of breeding programs. Thus, bread-making quality could be considered as controlled by major genes, making the selection of favorable alleles, or eliminating the undesirable ones.

In addition, seed yield and SDS sedimentation were positively correlated, which indicates the possibility of simultaneous selection for both traits.

Commonly, there is a tendency towards using only the subunits coded by genome D (2 + 12 and 5 + 10) as molecular markers for the potential bread-making quality in wheat. The subunit 2 + 12 was correlated with poor bread-making quality potential and subunit 5 + 10 was correlated with high bread-making quality potential. The results obtained in this work demonstrate, as suggested by Campbell *et al.* (1987), the significance of the interaction between subunits coded by chromosome 1A, 1B and 1D in bread-making quality of wheat. In the genotypes tested, approximately one half presented subunit 2 + 12 and one half presented subunit 5 + 10, but the scores for each group varied from 3 to 10. Considering only the subunit coded by chromosome 1D, no correlation was found.

All the genotypes used in this work are going through the final phases of productivity and adaptability in order to be released as a new cultivar; therefore, they may be considered as a sample of the genotypes that will be released as new cultivars. On the other hand, almost all genotypes presented low bread-making quality. Conventional bread-making quality tests cannot be performed during the early generations in

breeding programs because they demand large amounts of seeds, and the tests are destructive, which means that only one sample of the seeds that will be planted is tested. The same seeds that are tested cannot be planted. Due to this factor, during the segregating generations, the bread-making quality of the genotypes cannot be tested. The results of this study demonstrate that the selection assisted by the HMW glutenin standard can be utilized during these segregating generations, because since the correlation between the Glu-1 score and the sedimentation test with SDS with the production was positive, it is

possible to select genotypes with high yield and good bread-making quality at the same time. Since only half of the grain of wheat is enough for protein determination, the same seed tested can be planted and originate the progeny. This enables the selection of wheat genotypes for bread-making quality, indirectly through the HMW glutenin standard in segregating generations in breeding programs. Using this strategy of selection in segregating generations increases the probability that the genotypes at the end of the selection cycles present, not only high yield, but also good bread-making quality.

The production of a new wheat cultivar demands a lot of effort, and it is costly and time-consuming. The new cultivar needs to be accepted and be planted in a large area to compensate this work. This will only be made possible if not only the cultivar presents high yield but also presents good flour quality, because wheat cultivars, even high yielding ones but with low flour quality, are not competitive in the market.

With this work we hope to contribute more and more to the use of the selection of flour quality in segregating generations of wheat breeding programs, enabling the cultivars that reach the productivity and adaptability phase tests to present good flour quality and therefore to be more competitive in the market.

CONCLUSION

This work utilized a few number of genotypes, but these results showed low bread-making quality in genotypes that are in the final part of breeding programs, indicating the non-observance of bread-making

quality in these programs. However, the statistical correlations between bread-making quality and HMW glutenin subunits enabled the selection in the beginning of the breeding programs for those traits.

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RESUMO

Qualidade de panificação é um dos principais alvos do melhoramento genético do trigo. Embora em programas de melhoramento sejam realizadas diversas análises de qualidade de panificação, tais como farinografia, sedimentação com dodecil sulfato de sódio (SDS), alveografia e panificação, estas requerem grandes quantidades de sementes, que somente são obtidas em gerações avançadas. Neste experimento foi avaliada a correlação estatística entre subunidades de gluteninas de alto peso molecular e a qualidade de panificação, medida por alveografia, farinografia e sedimentação com dodecil sulfato de sódio. Dezesete genótipos de trigo foram cultivados sob as mesmas condições, produzindo cada um cerca de um quilograma de sementes para as avaliações. As gluteninas de alto peso molecular foram analisadas por SDS-PAGE. As correlações estatísticas foram altamente significativas entre subunidades de gluteninas de alto peso molecular, com alveografia e sedimentação com SDS. Estes resultados indicam a possibilidade de manipular genes maiores para qualidade de panificação, juntando o melhoramento convencional com análise não destrutiva de uma única semente. Apenas metade da semente é necessária para realizar a análise em gel SDS-PAGE. A outra metade da semente pode ser plantada para gerar a progênie. Produção de grãos e sedimentação com SDS foram estatisticamente correlacionadas, indicando a possibilidade de seleção simultânea para ambas as características.

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