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SOFT WHEAT PRODUCTS

Association of Sugar-Snap Cookie Quality with High Molecular Weight Glutenin Alleles in Soft White Spring Wheats[1]

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ABSTRACT

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High molecular weight glutenins (HMW-*Glu*) affect the quality of leaven breads produced from wheat (*Triticum aestivum* L.) flour. However, effects of these proteins on pastry quality are poorly understood. Sugar-snap cookie quality was compared to HMW-*Glu* alleles of soft white spring wheat breeding lines and cultivars from multiple trials over four years at Aberdeen, ID. Sugar-snap cookie quality was affected less by the composition of the flour protein than by the quantity of flour protein. Individual alleles did not have significant effects on cookie diameter, except for the 13+19 allele of the *Glu*-1B locus, which was associated with smaller cookie diameters. The glutenin strength of alleles at the three HMW-*Glu* loci was estimated using a glutenin rank sum (GRS) derived from previously published research. The glutenin strength (GRS score) of cultivars and breeding lines was negatively correlated to cookie diameter ($b = 0.02$ cm unit^{-1}; $P < 0.05$). The negative correlation between GRS score and cookie diameter was greatest in the year with the lowest average flour protein content and least in the year with the highest average protein content. The effect of allelic variation was probably masked in the years with high average protein content due to the overriding effects of total protein content. Selection for cultivars with low GRS scores may produce cultivars with better and more predictable sugar-snap cookie quality.

Quality of pastry wheat (*Triticum aestivum* L.) can be assessed through indirect tests such as alkaline water retention or particle size index, or directly by baking test products such as standardized cookies, crackers, sponge cakes, or udon noodles (Hoseney et al 1988). The protein content of a soft wheat flour is also used as a predictor of the flour quality (Finney et al 1987). Phenotypic correlation of protein percentage and pastry quality is strongly negative. However, the genotypic correlation between a cultivar's flour protein and pastry quality is generally poor within a population of improved soft wheat cultivars. Patterson and Allan (1981) identified genotypes with quite high protein content and good pastry characteristics. Strength of the gluten developed by a flour's protein is negatively associated with pastry quality, as measured by sugar-snap cookies. Alveograph dough strength (P value) has been found to be negatively correlated to cookie quality and could be used to predict residual effects from a simple linear model of flour protein content estimation of cookie spread (Bettge et al 1989). The composition of the flour protein, therefore, may determine, in part, the intrinsic pastry quality of a cultivar.

The high molecular weight glutenin alleles (HMW-*Glu*) are a class of genes that can influence gluten strength. Three homeoallelic loci for HMW-*Glu* are located on chromosomes 1A, 1B, and 1D (respectively *Glu*-1A, *Glu*-1B, and *Glu*-1D). Each locus is complex, conferring zero to two distinct proteins (Graybosch 1992). Allelic variation is noted by numbering each HMW-*Glu* sequentially, based on mobility in sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) (Payne 1987).

The effect of HMW-*Glu* alleles on end-use quality of soft or pastry-type wheats has had little attention previously. However, the HMW-*Glu* allelic variation in hard wheats can significantly influence bread-baking quality (Payne 1987). Cressey et al (1987), for example, compared two allelic variants for the *Glu*-1D locus, 2+12 and 5+10, and found an average of 5% greater loaf volume in cultivars with the 5+10 allele than in cultivars with the 2+12 allele. Payne et al (1984) summarized previous work on the general effects of HMW-*Glu* loci on bread wheat quality. At the *Glu*-1A locus, the null allele is inferior to the 2* and 1 allele, with the 2* and 1 alleles approximately equal in effect (null < 2* = 1). The alleles of the *Glu*-1B locus with known effects on bread quality are: (in order of increasing favorable effects) 6+8 < 7 < 7+9 < 17+18 = 13+16 = 7+8. The third locus, *Glu*-1D, has two common alleles, 2+12 and 5+10, of which 5+10 is the more favorable for bread quality. The alternate alleles at the *Glu*-1D locus 3+12 and 4+12 have been found to be less favorable for bread quality than either the 2+12 or 5+10 alleles. Payne et al

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(1987) assigned each allele a bread-baking quality score; better alleles had higher scores. Cultivars were assigned a glutenin quality score by summing scores for alleles at the three HMW-*Glu* loci. Cultivars with higher glutenin quality scores tend to have better alveograph dough strength (P. N. Fox and E. Souza, *unpublished data*), stronger mixograph types, and larger loaf volumes (Payne 1987). Lookhart et al (1993) surveyed the HMW-*Glu* of the most widely grown wheats in the United States, based on the 1984 USDA survey. Most hard red winter and hard red spring wheats had high glutenin quality scores. Soft red winter wheats had variable quality scores. Graybosch (1992) also cataloged the HMW-*Glu* loci of U.S. red wheats; the distribution of alleles was not strikingly different between the soft red and the hard red winter wheats of this survey. Lookhart et al (1993) found that soft white winter wheats, with the exception of Daws, had very low glutenin quality scores.

Pastry wheats require weak gluten strength for superior quality, particularly under conditions causing higher protein contents (drought or disease stress). Therefore, HMW-*Glu* alleles that cause development of strong gluten should be detrimental to pastry quality. Environmental variation for flour protein percentage cannot be completely eliminated through cultivar or production improvements. Therefore, it would be desirable to identify genes that cause pastry quality to deteriorate when flour protein contents rise. Selection against such genes, once identified, should improve the quality stability of resulting soft wheats. This article examines the relationships between HMW-*Glu* loci and sugar-snap cookie quality variation in 51 soft white spring wheats.

TABLE I
Pedigrees and High Molecular Weight Glutenin Profiles of Soft White Spring Wheat Breeding Lines and Cultivars Grown at Aberdeen, ID, 1982–1990

Name	Pedigree	*Glu*-1A	*Glu*-1B	*Glu*-1D
Bliss	Hyslop/Fielder	Null	7	2+12
Centennial	Cowbird.s/2*Sterling	Null	13+16	2+12
Dirkwin	Twin/Triple Dirk	2*	6+8/7+9[a]	2+12
Edwall	Potam 70/Fielder	Null	7+9	2+12
Fielder	4*Yt54A//Nrn10/Bvr/3/2*Y50/4/Nrn10/Bvr//Baart/Onas	Null	13+19	2+12
Fieldwin	4*Yt54A//Nrn10/Bvr/3/2*Y50/4/Nrn10/Bvr//Baart/Onas	Null	13+19	2+12
Federation	Purplestraw/Yandilla	1	13+19	5+10
ID71006	Cowbird.s/2*Sterling	Null	13+19	2+12
ID71027	Sterling/3/Mochis 73/Pavon.s//Sterling	1	13+19	5+10
ID71042	Neelkant/A773249S-8-2-1	Null	7+9	2+12
ID71055	Bluebird 2/2*Fielder//Seri	2*	13+19	2+12
ID71086	Sterling//Cocaraque 75/Hork.s/3/2*Sterling	Null	13+19	2+12
ID71171	Sterling/3/Bluebird.s//Protor.s/Huac.s/4/Sterling	1	13+19	2+12
ID71202	Tonichi.s/2*Sterling	Null	7+9	2+12
ID71208	Tonichi.s/2*Sterling	1	13+19	2+12
ID71210	Tonichi.s/2*Sterling	2*	13+19	2+12
ID71218	A81579S/4/Tonichi.s/3/Fielder/Zaragoza.s//Fielder	Null	13+19	2+12
ID71219	A81580S//Tonichi.s/A75117S-9300-4	Null	13+19	2+12
ID71240	Treasure.s/Tonichi.s	1	7+9	5+10
ID71244	A75120-2214-1-1/Caldwell	2*	7+8	2+12
ID71252	Tonichi.s/2*Sterling	Null	13+19	2+12
ID71260	Tonichi.s/2*Sterling	Null	13+19	2+12/5+10[b]
ID71320	A771064S-4/A78106S-1	2*	6+8	3+12
ID71353	A71182S-3/Treasure.s	Null	6+8	3+12
ID71363	A771064S-4//'76 IRN#1315/Fieldwin	Null	13+19	2+12
ID71377	A77217S-3/4/Fielder/Zaragoza.s//Fielder	Null	13+19	2+12
ID71419	IDO182/Fieldwin	Null	7+8	2+12
ID71441	IDO183-35/A77182S-3	Null	6+8	2+12
IDO285-52s	IDO182/Fieldwin	2*	6+8	2+12
IDO394	Tonichi.s/3/Fielder/Zaragoza 75//Fielder	1	7+9/13+19[b]	2+12
IDO405	IDO228/3/Fielder/Zaragoza 75//Fielder	Null	13+19	2+12
IDO406	Fielder/Zaragoza 75//Fielder/3/IDO150	2*	13+19	5+10
IDO407	IDO182/Fieldwin	Null	6+8	2+12
IDO408	IDO232/A75120S-2214-1-1	Null	6+8	2+12
IDO409	Treasure/Treasure.s	2*	7+9	2+12
IDO410	Tonichi.s/2*Sterling	1	13+19	5+10
IDO415	Sterling/Bliss	2*	13+19	2+12
IDO417	IDO182/Fieldwin	2*	6+8	2+12
IDO428	IDO182/Fieldwin	2*	6+8	2+12
IDO429	IDO182/Fieldwin	2*	6+8	2+12
IDO442	A7940S-5//Cowbird.s/Sterling	Null	13+19	2+12
IDO449	IDO232/Sterling	Null	13+19	2+12
IDO458	Owens/Neelkant/Owens	Null	6+8	2+12
OR487570	Emu.s/TJB 84	2*	7+8	5+10
Owens	IDO45/6/2*IDO46/5/A653552/3/IDO20 //PI227196/A63166S-A-2-8/4/Gaines/Lemhi 53	Null	7+8	2+12
Penawawa	Potam 70/Fielder	Null	7+9	5+10
Sprite	Western Plant Breeders private cultivar	Null	17+18	3+12
Treasure	Bluebird 2/4/Springfield*7/3/As/Fr//A63167S-A-1-50-45-5/5/IDO46/II8156	2*	6+8	2+12
Treasure Sib	Bluebird 2/4/Springfield*7/3/As/Fr//A63167S-A-1-50-45-5/5/IDO46/II8156	2*	6+8	2+12
Wakanz	Tifton 3725/Walladay//K7400195/Authur 71/3/K806645	Null	7+9	5+10
Whitebird	Owens//A6596S-A-21-1/Fielder	Null	7+8	2+12
WA7496	K7400315/Potam 70	2*	7+9	2+12

[a]Cultivar or breeding line is a mixture of two alleles at the designated locus.
[b]Breeding line or cultivar is heterogeneous for HMW-glutenin profile.

MATERIALS AND METHODS

Genotypes and Field Trials

Fifty-one soft white spring wheats were grown in irrigated field trials at Aberdeen, ID, from 1987 to 1990, from two types of germ plasm: 1) breeding lines from the Aberdeen breeding program with limited or no previous baking-quality evaluations (genotypes with the prefix *ID71* or *IDO* in Table I); and 2) advanced breeding lines and cultivars adapted to the Pacific Northwest (OR48270, WA7497, and named genotypes in Table I). These genotypes will be hereafter referred to collectively as cultivars. The cultivars were grown as part of the Aberdeen breeding program and were organized into multiple trials with 30–51 entries. All entries had been grown each year in the same field of 2 ha or less, although not necessarily in the same trial. The two exceptions were OR48270 and Sprite, which were added to testing in 1988. Trials were organized into randomized complete block trials with two to four replicates. The experimental unit for trials was a 4-m^2 plot of a single cultivar. All named cultivars and breeding lines with an *IDO* prefix appeared in more than one trial per year. In each of the four years, trials were planted within a day of each other, during the last week of March to the second week of April, using a seeding rate of ~80 kg ha^{-1}. Nitrate fertilizers were applied before planting, based on soil tests and a target yield goal of 8,000 kg ha^{-1} (Brown 1987). Trials were irrigated using sprinklers to replace the estimated loss of soil moisture due to transpiration of the crop. Field management and timing management practices generally matched local commercial production practices.

Bake evaluations were made on a 400-g seed sample composite of two replicates of each cultivar from each trial in each year. Samples were first tempered using standard methods (method 26-10A, AACC 1983) and then milled using a Brabender Quadramat Senior mill (method 26-21A). The milling yield of a sample was expressed as the percent of the total grain weight extracted as patent flour. Flour protein was determined using a Dickey-John near-infrared analyzer (method 39-10A), calibrated by Kjeldahl evaluations of total nitrogen content, and corrected to 12% moisture. Sugar-snap cookie quality was evaluated by standard tests (method 10-52). The average diameter for two cookies was measured for each cultivar in each trial-year combination.

HMW-*Glu* Composition

The HMW-*Glu* genotype of each cultivar was determined by SDS-PAGE. Proteins were extracted from samples using a β-mercapto-ethanol extraction (Ng and Bushuk 1987). Proteins were extracted from a single seed of a plant grown in a greenhouse, and based on visual selection, confirmed to be true-to-type for the cultivar A 5-g sample of seed of each cultivar was also extracted. Seed for the bulk lot was obtained from the 1988 plots, which had been rogued to remove visual off-types. The bulk sample was ground using a Wiley mill. An aliquot (0.4 g) of whole grain flour was extracted. Paired samples of each cultivar were placed together on a SDS-PAGE gel for resolution of the HMW-*Glu* profiles (Ng and Bushuk 1987). If the single seed deviated in profile from the bulk flour lot, it was assumed that the cultivar was heterogeneous for HMW-*Glu* profile. Alleles for each of the three loci were determined for cultivars by comparing them to standard cultivars that were run on each gel with the experimental lines. The standard cultivars and respective glutenin profiles were: Hillsdale (1, 6+8, 2+12); Argee (2*, 7+9, 5+10); and McNair 2203 (1, 7+8, 3+12) (Graybosch 1992).

Statistical Analysis

The mean performance of each cultivar was estimated within each year. The mean performance of each cultivar was based on fitting a least-squares solution for experiments and cultivars that estimated what the mean quality of a cultivar would be if they all were grown together in the same trials each year (Rodgers et al 1983). Model experiments were analogous to blocks of an incomplete block design. Within-field error was partitioned in the model based on the between-trial (analogous to between-block error) variance of named cultivars and *IDO* prefix lines that appeared in multiple trials within a field. Two types of prediction models were used to estimate quality performance of cultivars based on HMW-*Glu* composition. The first model (I) tested the association of quality traits with individual alleles at the three HMW-*Glu* loci through a series of preplanned contrasts. Contrasts were made within and across years (1987–1990). The error-mean-square term for contrasts was the mean-square term for cultivars nested within allele classes.

The second model (II) assumed that alleles that conferred stronger gluten in hard wheats would also restrict the spread in cookie diameter of soft wheat. Therefore, the best alleles for bread baking would be the worst for pastry quality. Cultivars were assigned a glutenin rank score (GRS) score that summed the negative effects of the three HMW-*Glu* loci. Payne et al (1987) used a similar scoring system to predict bread quality. The expanded scale, relative to Payne et al (1987), was used to facilitate the use of regression models for prediction of cookie diameter. For *Glu*-1A, the Null allele was given a rank of 1 and the 2* and 1 alleles were given a rank of 4. At the *Glu*-1B locus, the alleles were ranked as: 6+8 (1); 7 and 7+9 (2); 7+8 (3); 17, 13+16, and 13+19 (4). At *Glu*-1D locus, alleles were ranked as: 2+12 and 3+12 (1) and 5+10 (4). Cultivars heterogeneous for alleles were given a rank at the heterogeneous locus that was the average of the ranks for the two alleles. To correct for the effects of total protein content, a model was also fit using flour protein as a covariate. The Model II analysis was repeated without cultivars carrying the 13+19 allele (to ensure that the prediction models were not simply fitting the effects of a single detrimental allele (13+19 at *Glu*-1B)).

RESULTS

Model I, Allele Effects

In soft wheat cultivars selected for pastry quality, the largest factor determining cookie diameter is total flour protein content. Sixty percent of the variation in cookie diameter could be estimated in the reduced model of trial year and flour protein percentage, with 15% variation attributable to the negative regression slope of flour protein on cookie diameter (data not shown). The individual effects of the alleles (Model I) at each locus were nonsignificant, with the exception of the *Glu*-1B allele 13+19. Cultivars carrying the 13+19 allele had an average of 0.01 cm smaller corrected cookie diameter than did cultivars with alternate alleles ($P < 0.01$). The 6+8 allele at the *Glu*-1B locus was present in cultivars with an average milling yield 17.5 g Kg^{-1} higher than that of cultivars with alternate alleles ($P < 0.05$). Similarly, the milling yield associated with the 5+10 allele was poorer than that of cultivars carrying alternate alleles for the *Glu*-1D locus ($P < 0.05$).

Model II, GRS Score Predictions

The effect of individual HMW-*Glu* alleles on cookie diameter was small. However, pooling the effects of the three loci through rank summation (GRS score) predicted variation in cookie quality in the Model II analysis. The cookie diameter of cultivars averaged across four years of testing declined 0.02 cm per GRS unit ($P < 0.05$) (Table II). The amount that the protein-corrected cookie diameter declined was similar to that of the uncorrected diameter. Combining the GRS score with flour protein percentage improved the prediction of cookie diameter over that of the reduced model of GRS score only ($R^2 = 0.27$ vs. 0.09, Table II). When cultivars carrying the 13+19 allele were excluded from the prediction model, the prediction of cookie diameter improved ($R^2 = 0.46$ without 13+19). The GRS score was independent of the protein percentage. The correlation coefficient between GRS score and the average flour protein content of cultivars was nonsignificant ($P < 0.25$). The GRS score was not able to predict flour protein content (Table II) or flour yield (data not shown).

The GRS score was not uniform across years in its ability to predict sugar-snap cookie diameter. The prediction slope varied

TABLE II
Model II Prediction Slopes of Quality Parameters in Soft White Spring Wheat from Rank Summaries of Three High Molecular Weight Glutenin-Loci

Regression Model	Predictor	Cookie Diameter, cm unit^{-1}				
		1987–1990	1987	1988	1989	1990
A) All data	GRS	−0.02*[a]	−0.03*	−0.03*	−0.04**	NS
		(0.09)[b]	(0.12)	(0.12)	(0.15)	
B) 13+19 allele[c] excluded	GRS	−0.03*	−0.04*	−0.03*	−0.06**	NS
		(0.11)	(0.18)	(0.19)	(0.25)	
C) All data	GRS	−0.02**	−0.03*	−0.03*	−0.04**	NS
	Protein	−0.014 cm g^{-1}**	−0.013 cm g^{-1}*	−0.013 cm g^{-1}*	−0.016 cm g^{-1}**	−0.010 cm g^{-1}**
		(0.27)	(0.28)	(0.26)	(0.30)	(0.24)
D) 13+19 allele excluded	GRS	−0.03**	−0.03**	−0.03**	−0.05**	NS
	Protein, per kg	−0.015 cm g^{-1}**	−0.019 cm g^{-1}**	−0.014 cm g^{-1}**	−0.018 cm g^{-1}*	−0.012 cm g^{-1}**
		(0.46)	(0.50)	(0.42)	(0.41)	(0.38)

[a]*, ** = Response significant at the 95 and 99% confidence interval, respectively.
[b]Values in parenthesis are coefficients of determination (R^2) for the regression model.
[c]All cultivars carrying the 13+19 allele at the *Glu*-B locus were excluded from the regression.

from nonsignificant in 1990 to −0.04 cm unit^{-1} in 1989 (Table II). The GRS score was more predictive in years of low average protein content than in years of high average protein content. The highest average flour protein content (101 g kg^{-1}) was that for 1990, when the prediction model using GRS score was nonsignificant. The lowest protein content (92 g kg^{-1}) was that for 1989, when the GRS score prediction model had the highest coefficient of determination ($R^2 = 0.15$). The interaction of GRS with flour protein content was nonsignificant across all years ($P < 0.13$) and within each year ($P < 0.21$–0.91). Therefore, the regression coefficients of GRS with cookie diameter is consistent across protein levels. However, in years with high protein content, the larger protein content effects and within-field variability probably obscured the smaller GRS association.

DISCUSSION

Hard wheat quality is determined by the strength of the gluten developed from a flour's storage proteins. Allelic protein variation should have larger effects on quality in leavened bread than it would in a pastry product, where quality is largely determined by carbohydrate factors and low flour protein content. Prime determinants of sugar-snap cookie quality are grain hardness and flour protein content (Hoseney et al 1988). Individual effects of alleles at a locus were not an important determinant for sugar-snap cookie quality (with the exception of the 13+19 allele). From this it can be concluded that total protein content is more important for sugar-snap cookie quality than is the composition of that protein. However, in environments like the one for 1990, which conferred higher protein content, the effect of protein percentage in deforming sugar-snap cookie diameter was more marked and protein composition played even less of a role.

The effects of glutenin alleles were more apparent when all alleles were summed in a joint index than when individual alleles were considered. Lookhart et al (1993) found that most soft white winter wheats of the Pacific Northwest had relatively low glutenin allele scores (corresponding to weak gluten strength). By contrast, most of the bread wheats had high glutenin scores (corresponding to high glutenin strength). This may indicate that pastry quality selection during the breeding process effective accumulates weak HMW-*Glu*. Both Lookhart et al (1993) and Graybosch (1992) found that the soft red winter wheats unlike the soft white winter wheats were quite variable for HMW-*Glu* alleles. Many of them had strong glutenin alleles such as the *Glu*-1D allele 5+10. It is unlikely that the soft wheat breeders in the Eastern United States are any less vigilant than their counterparts in the Western States about quality selection . However, the effects of the HMW-*Glu* alleles may not be as pronounced in the Eastern environment as in that of the West.

Most of the genotypes represented in this study are progeny of crosses planned to incorporate stripe rust (*Puccinia striiformis*, Westend) resistances in Sterling and Fieldwin types of SWS wheats. The stripe rust resistance sources were mainly from the International Maize and Wheat Improvement Center (CIMMYT) and were unselected for pastry quality. Some of the HMW-*Glu* effects may be related to linkage disequilibrium (residual association of genetic factors despite intermating) between the HMW-*Glu* alleles and poor pastry quality factors in the CIMMYT germ plasm. However, the GRS score probably measures the true effects of HMW-*Glu* alleles because: 1) the linkage disequilibrium is probably small for alleles at all three loci across a broad range of crosses, using a minimum of 10 different stripe rust resistance sources; and 2) the genetic background of the SWS germ plasm used in this study is fairly uniform.

The results of this survey indicate that using a joint index (GRS score) may assist breeders in selecting wheats with good sugar-snap cookie quality across a broad range of protein levels. From a practical standpoint, it may be most efficient to use HMW-*Glu* profiles as method of parental selection to avoid combinations that have no possibility of producing progeny with low GRS scores. Breeders selecting wheats that will be used solely for soft wheat products should select lines with low GRS scores. This should produce soft wheats with reliable pastry quality across environments. Bassett et al (1989) found a partial support of this point in a genotype by environment interaction study of soft white winter wheat quality. The cookie diameter of Daws had the least predictability ($R^2 = 0.29$) across environments, while Nugaines had the most predictable ($R^2 = 0.53$). Based on ratings of Lookhart et al (1993), Daws had the highest glutenin strength score, and Nugaines had the lowest. The milling industry uses grain protein content as a measure of quality when it buys grain for milling; lower grain protein levels are preferred for pastry flours. The effects of the gluten alleles were most pronounced in environments with low protein contents. Therefore, selection to a low GRS score may also minimize unsatisfactory quality performance in low protein grain lots.

The results of the Model II analysis are associations rather than measurements of causal effects. Therefore, the results should be confirmed through mating and selection studies. The effect of HMW-*Glu* alleles may be of lesser or greater importance in other pastry preparations. Determination of the impact of these alleles on pastry products in general will require additional research.

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Amino Acid Content and Protein Biological Evaluation of 12 Mexican Varieties of Rice

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ABSTRACT

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Protein efficiency ratio (PER) and amino acid content were determined in brown and polished samples of 12 varieties of Mexican rice. All samples of the polished rice presented lysine as the limiting amino acid with a chemical score ranging from 46 to 57. The amino acid content of the brown rice samples was similar to that of the polished rice samples for each variety. Again, the limiting amino acid was lysine, except in Sinaloa A-80 and CICA-6, which presented isoleucine as the limiting amino acid. The protein quality of the brown and the polished rice samples was similar for each variety. Only Sinaloa A-80 and CICA-6 brown rice samples presented a PER lower than that of their corresponding polished rice samples. The adjusted PER for the polished rice samples ranged from 2.23 (CICA-6) to 1.30 (Cárdenas A-80). The adjusted PER for the brown rice samples ranged from 2.20 (Morelos A-83) to 1.47 (Cárdenas A-80). According to these results, the varieties that showed the best protein quality were CICA-6, Morelos A-83, and Navolato A-71 (polished samples). In addition, Navolato A-71 (polished samples) presented the highest protein content (11.6%, db). Thus, Navolato A-71 was the best variety of the Mexican rices studied and could have an important nutritional impact if its consumption becomes generalized.

Rice, corn, and wheat are the most consumed cereals in the world. Rice has the lowest protein content, but its protein quality is the best. Lysine is the limiting amino acid in the three cereals (Rosenberg and Culik 1957, MacLean et al 1979, Saunders 1979). The high protein quality of rice is due to its high gluteline-to-prolamine ratio (Huebner et al 1990). Gluteline has better quality than prolamine because of its higher lysine content (Padhye and Salunkhe 1979).

On the other hand, cereals differ greatly in their protein contents due to the environmental conditions, soil composition, genetic improvements, and the use of nitrogen fertilizers (Nishizawa et al 1977, Pérez et al 1990). It has been possible to increase the protein content in corn and wheat using genetic manipulation, but this is always associated with a decrease of protein quality. However, in genetic manipulation of rice, quality is maintained or only slightly decreased (Bressani et al 1971a, Nishizawa et al 1977, Murata et al 1978, Roxas et al 1979, Pereira et al 1981). Different rice varieties cultivated in Mexico have protein contents of 6.9–11.6% (Sotelo et al 1990). Thus, the main goal of the present work was to determine the amino acid composition and the protein quality of 12 Mexican varieties of rice.

MATERIALS AND METHODS

Twelve varieties of rice were studied: 11 were provided by the Instituto Nacional de Investigaciones Agrícolas, Programa de Arroz, Zona Sur Zacatepec Morelos, México; one was obtained

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