Comparative Effects of Wheat Flour Protein, Lipid, and Pentosan Composition in Relation to Baking and Milling Quality[1]

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ABSTRACT

Variation in milling, baking, and dough-handling properties among 58 hard wheat (*Triticum aestivum*) flours was examined in relation to the variation in flour protein and lipid concentrations and composition and to the variation in water-soluble pentosan concentrations. Simple correlations showed no single biochemical component capable of explaining more than 41% of the variation in any given quality parameter. Similarly, no single biochemical component was highly related to all quality attributes. Canonical analyses, a multivariate statistical approach, revealed that the measured biochemical components were able to explain more than 90% of the variation in major quality attributes such as dough-handling and loaf characteristics. Flour protein concentration was found to be the primary factor contributing to variation in both dough strength and loaf characteristics. Once the primary effects of protein concentration were established, flour polar lipid concentrations showed substantial positive contributions to dough handling. Loaf textural features largely were unrelated to protein concentrations; however, glutenin concentrations, water-soluble pentosans, and flour lipids showed positive relationships. Assay of numerous biochemical components together with multivariate approaches may be needed to develop effective predictive models for observed variation in wheat end-use quality.

Understanding the biochemical basis for variation in hard red wheat quality could enable the development of rapid, predictive tests for end-use quality. Rapid biochemical tests capable of predicting wheat quality would enable millers to identify and composite grain samples based on quality potential. Biochemically based predictive tools would allow bakers the opportunity to make adjustments to bakery formulations and equipment settings before flour lots reached the bakery floor. Wheat breeders need to identify which key biochemical components affecting quality are genetically controlled and amenable to alteration through selection. Identification of biochemical components that are highly influenced by environment would assist in the development of wheats with enhanced quality and stability over diverse environmental conditions.

Attempts to explain the biochemical basis for flour quality variation of hard wheats grown in North America are numerous. Orth and Bushuk (1972), Khan et al (1989), and Graybosch et al (1990) have examined the role of flour protein composition as measured by the relative amounts of protein in various solubility classes. The effects of lipid variation in relation to quality were studied by Pomeranz et al (1966), Hoseney et al (1969), and Chung et al (1980). Shogren et al (1987) analyzed the contribution of pentosan composition. In each study, significant relationships were established between quality variation and the biochemical factor of interest. Thus, numerous biochemical components must contribute to quality variation. No single biochemical component, however, has been shown to explain more than a portion of the quality variation observed among large numbers of flour samples. Also, few studies have examined the relative effects of protein, lipid, and pentosan composition in a common set of flour samples.

During the process of baking, wheat flour becomes a complex biological system in which numerous flour biochemical components interact with each other and with added ingredients to determine quality characteristics. A thorough understanding of the biochemical basis for wheat flour quality variation will require

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analysis of all major factors and an understanding of the interaction of such factors. Results of an attempt to understand variation in end-use quality through simultaneous protein, lipid, and pentosan analyses are presented in this article.

MATERIALS AND METHODS

Flour Samples

Flour samples of the hard red winter wheat (HRWW) cultivars Centurk 78, Plainsman V, Red Chief, Scout 66, and Vona were obtained from seed produced at the following locations in 1988: Bushland, TX; Davis, CA; Hays, KS; Hutchinson, KS; Lahoma, OK; Sidney, NE; and Tulelake, CA. Samples from two planting dates (October and March 1988) were obtained from Tulelake. Samples of the hard red spring wheat (HRSW) cultivars Anza, Marshall, and Stoa were obtained from grain harvested in both 1988 and 1989 from plantings at Aberdeen, ID; Davis, CA; and Fargo, ND. The study used 40 HRWW flours and 18 HRSW flours. Samples were selected to provide a wide range in measured milling, dough-handling, and baking parameters.

Quality Parameters

All quality analyses followed AACC (1983) approved methods. Milling properties assayed included test weight (TSTWT, kg/m^3) and flour yield (FLYD). Dough-mixing properties were measured with a National Manufacturing mixograph (Lincoln, NE). Mixing time (MT) was recorded as time, in minutes, to peak dough development. Mixograph peak height (MTPK) was measured as height of the mixograph curve, in millimeters, at peak time. Mixograph tolerance (MTO) was defined as the width, in millimeters, of the mixograph curve 2 min past peak time. Bake mix time (BMT) was determined using a National 100-g mixer; BMT was defined as time, in minutes, required for doughs to reach peak development. Absorption was evaluated from both the mixograph (MABS) and from actual bake absorption (BABS). Dough type (DT) was a measurement of viscoelasticity at peak dough development. DT was rated on a score of 0–9 where 0 = too viscous, 5 = proper viscosity, and 9 = too elastic. A 100-g pup loaf (straight dough procedure) method was used to measure loaf volume (LV), proof height (PHT), and texture (TXT). Texture was rated on a scale of 1–10 where 1 = unacceptable and 10 = excellent.

Biochemical Parameters

All biochemical analyses were performed in duplicate. Flour protein concentration (FP) (12% flour moisture basis) was determined as Kjeldahl ($N \times 5.7$). Flour protein composition was examined through size-exclusion high-performance liquid chromatography (SE-HPLC). SE-HPLC measures the amount of protein in various protein classes; it is not a measure of allelic composition of the numerous flour protein encoding loci. SE-HPLC procedures were modifications of those of Singh et al (1990a,b). Two flour protein fractions were analyzed for each sample. Protein fraction TFP (total flour protein) was obtained by sonication of an 11-mg (constant moisture) flour sample in 1 ml of 2% (w/v) sodium dodecylsulfate (SDS) in 0.05M phosphate buffer, pH 6.9, for 30 sec at a power level of 5W using a Tekmar (Cincinnati, OH) sonic disrupter. After centrifugation, supernatants were collected for analysis. Fraction TFP-SW (total flour protein minus saltwater-soluble proteins) was obtained by sonication of a second 11-mg flour sample in 1 ml of 0.04M NaCl; after centrifugation, pellets were resonicated in 2% SDS in 0.05M phosphate buffer. After a second centrifugation, supernatants were saved for analysis. Solutions containing fractions TFP and TFP-SW were independently applied to a BioRad (Richmond, CA) high-performance liquid chromatograph fitted with a 10-μm Waters Protein-Pak 300SW silica column. Column pore size was 300 Å. Proteins were eluted with 0.5% SDS (w/v) in 0.05M phosphate buffer, pH 6.4. Protein concentrations of peaks identified in each fraction were measured by absorption at 210 nm. Integrated intensities were used to determine percent area of each peak.

As reported by Singh et al (1990a,b), protein of fraction TFP was separated into three peaks: polymers of molecular weight (MW) 100,000, monomers of MW 25,000–100,000, and monomers of MW 25,000. Peaks with identical retention time were found in fraction TFP-SW, although prior sonication in 0.04M NaCl resulted in a loss of protein from both monomer peaks with negligible loss of protein from the polymer peak. For statistical analyses, protein concentrations (expressed as percentage of total extracted protein) of five peaks were determined in the following manner. Total areas of fractions TFP and TFP-SW were normalized using the polymer (MW 100,000) peak common to both. Percent areas of three peaks, designated GLU (glutenin or polymers of MW 100,000), GLI (gliadin or saltwater-insoluble monomers of MW 25,000–100,000), and LMWRES (low-molecular-weight residue or saltwater-insoluble protein monomers of MW 25,000) were obtained from normalized curves of fraction TFP-SW. Areas of two additional peaks, HSW ("heavy" saltwater-soluble monomers of MW 25,000–100,000) and LSW ("light" saltwater-soluble monomers of MW 25,000) were measured as the loss of protein caused by prior extraction with 0.04M NaCl from peaks GLI and LMWRES, respectively. Normalized peak areas of the two monomer peaks of fraction TFP-SW were subtracted from those of fraction TFP to obtain peak areas of HSW and LSW.

Free lipids were extracted from 100 mg of flour with 1 ml of hexane. All organic solvents used in lipid extractions contained 0.002% (w/v) butylated hydroxytoluene. Extractions were conducted with constant shaking at 4° C to ensure uniformity. Samples were centrifuged, and 450 μl of supernatant was collected. Hexane-soluble lipids were separated into three fractions—nonpolar and free fatty acids (PNP), glycolipids (PGL), and phospholipids (PPL)—through silicic acid chromatography (Weber 1979). Hexane supernatants were applied to 500-mg Bond-Elut silica columns (Analytichem International, Harbor City, CA). PNP lipids were eluted with two volumes (1 ml each) of chloroform; glycolipids were collected with three changes of acetone, and phospholipids were eluted with three volumes of methanol. Samples were evaporated to dryness. Fatty acids of each fraction were converted to fatty acid methyl-esters (FAME) as per Morrison and Smith (1964). Lipid content of each of the three fractions (PNP, PGL, and PPL) was determined through quantification of the FAME content by gas chromatography (Morrison et al 1980). Heptadecanoate was used as an internal standard for methylation reactions and gas chromatography. A Hewlett-Packard gas chromatograph fitted with a 30-m Supelco (Bellefonte, PA) SP 2380 cyano-propyl capillary column was used for FAME separations. Results were expressed in terms of percentage of free lipid. Total free lipid (TFL) and total free polar lipid (TFPL) (μg/mg of flour) also were determined. TFPL was calculated as the sum of the amounts of free PGL and PPL.

Water-soluble pentosan concentration was determined using the methods of Hashimoto et al (1987). Results were expressed as micrograms per 100 mg of flour.

Statistical Analysis

SAS (1985) computer programs were used for all statistical computations. Simple correlations were calculated to test significance of relationships among and between quality and biochemical parameters. Canonical analyses (Gittens 1985) were conducted to examine whether combinations of one set of related variables (e.g., biochemical parameters) could effectively account for the observed variation in a second set of variables (e.g., quality attributes). The canonical approach allows the elucidation of relationships in a common data set among two large sets of variables through reduction into a relatively small number of highly correlated, hypothetical canonical variates (cvs). Canonical variates are constructed from linear combinations of a set of variables selected to maximize covariance with the cvs of a second set of variables. The canonical correlation then expresses the overall degree of relationship (response domain) between the two constructed variates. Once the primary effects are estimated through construction of the first cvs, additional orthogonal variates may be constructed to examine underlying relationships (e.g., secon-

dary and tertiary effects, etc.) in the data.

Only cvs with statistically significant correlations ($P = 0.05$) were reported. The extent to which an individual parameter contributed to a cv was determined by the magnitude of its canonical coefficient. A coefficient above 0.5 indicated a relatively strong contribution of a variable to the cv; coefficients of 0.3–0.5 suggested moderate contributions. Coefficients of less than 0.3 were regarded as indicating independence of a variable to construction of the cv. The relative magnitude of the coefficients of individual parameters with the cv was used to interpret and characterize the overall main effects represented by each hypothetical cv.

Independent canonical analyses were conducted to relate variation in biochemical parameters with each of the three major quality attributes: dough handling, represented by quality variables MT, MTPK, BMT, DT, and MTO; loaf characteristics, described by LV, PHT, TXT, and BABS; and milling properties, FLYD and TSTWT.

TABLE I
Means and Ranges of Quality Characteristics of Wheat Samples

Quality Parameter[a]	Mean	Minimum	Maximum
FLYD, %	59.2	43.7	70.8
MT, min	3.5	1.5	7.6
MTPK, mm	52.2	32.0	75.0
MTO, mm	16.5	6.0	28.0
MABS, %	64.8	63.0	67.0
BMT, min	4.1	1.3	10.2
DT, 0–9[b]	4.2	0.5	9.0
BABS, %	61.5	56.9	63.9
LV, cm^3	905	660	1,250
PHT, cm	7.6	6.5	8.3
TXT, 0–10[c]	1.6	0.0	3.6
TSTWT, kg/m^3	760	531	843

[a] FLYD = flour yield; MT = mixograph time to peak; MTPK = height of mixograph peak; MTO = mixograph tolerance; MABS = mixograph absorption; BMT = bake mix time; DT = dough type; BABS = bake absorption; LV = loaf volume; PHT = proof height; TXT = loaf texture; TSTWT = test weight.
[b] Rated on a scale of 0–9 where 0 = too viscous and 9 = too elastic.
[c] Rated on a scale of 0–10 where 1 = unacceptable and 10 = excellent.

TABLE II
Means and Ranges of Biochemical Parameters of Wheat Samples

Biochemical Parameter[a]	Mean	Minimum	Maximum
FP, %	12.2	8.6	16.5
GLU, %	45.5	43.7	47.2
GLI, %	36.5	29.9	41.6
LMWRES, %	6.1	3.5	7.8
HSW, %	7.5	4.1	11.7
LSW, %	4.5	3.0	5.5
PTN, μg/mg	94.7	69.9	130.0
PNP, %	42.6	13.2	68.4
PGL, %	35.2	15.9	54.3
PPL, %	22.2	9.2	44.8
TFL, μg/mg	0.6	0.2	0.9
TFPL, μg/mg	0.3	0.1	0.6

[a] FP = flour protein concentration; GLU = glutenin; GLI = gliadin; LMWRES = low-molecular-weight residue protein; HSW = heavy saltwater-soluble protein; LSW = light saltwater-soluble protein; PTN = water-soluble pentosans, PNP = nonpolar lipids (percentage of free lipid fraction), PGL = glycolipids (percentage of free lipid fraction), PPL = phospholipids (percentage of free lipid fraction), TFL = total free lipid, TFPL = total free polar lipids (glyco- plus phospholipids).

RESULTS AND DISCUSSION

Mean, minimum, and maximum values for all measured quality characteristics and biochemical variables are listed in Tables I and II, respectively. Variation among quality characteristics was extensive; for example, MT ranged from 1.5 to 7.6 min, whereas LV varied from 660 to 1,250 cm^3. Despite a wide range in quality attributes, little variation was observed among samples in the amounts (expressed as percentage of extracted protein) of protein in the GLU SE-HPLC peak. More extensive variation was evident in the GLI peak. Water-soluble pentosans (PTN) and the various lipid fractions displayed a relatively wider range in variation than did any of the SE-HPLC peaks.

Simple linear correlations were used to examine relationships among biochemical parameters (Table III). With the exception of GLU, all SE-HPLC peaks showed significant correlations with FP. The correlations between the lowest MW SE-HPLC peaks, LMWRES and LSW, were negative; remaining significant correlations between SE-HPLC peaks and FP were positive. LMWRES and LSW likely contain nonstorage proteins; it would be expected that an increasing protein deposition within grain would result in increasing concentrations of storage proteins (gliadins and glutenins). In contrast, free lipid attributes and PTN were independent of FP. However, a positive correlation was detected between PTN and GLU, and negative relationships were observed between PTN and GLI. In addition, numerous significant correlations were identified among SE-HPLC peaks and among the various free lipid fractions.

Correlations between biochemical parameters and quality attributes initially were examined through the use of simple linear correlation (Table IV). No measured biochemical parameter showed significant correlations with all quality attributes. Significant relationships most often were observed with LMWRES, LSW, TFL, and TFPL. The largest amount of variation in a given quality parameter estimated by a single biochemical component was 41% ($r = 0.64$, $r^2 = 0.41$; Table IV). Combinations of the biochemical factors were needed to more completely explain the observed variation in quality components. However, the inter-

TABLE III
Matrix of Simple Correlation Coefficients (r)[a] Describing Relationships Among Biochemical Factors

Factor[b]	FP	GLU	GLI	LMWRES	HSW	LSW	PTN	PNP	PGL	PPL	TFL	TFPL
FP	...		0.63	−0.59	−0.42	−0.49						
GLU		...	−0.50		0.28		0.53				0.41	0.33
GLI			...	−0.38	−0.88	−0.52	−0.41			−0.27	−0.34	−0.37
LMWRES				...								
HSW					...	0.32	0.30	−0.34		0.40	0.43	0.50
LSW						...	0.30				−0.25	−0.27
PTN							...				0.38	0.37
PNP								...	−0.76	−0.71	−0.26	−0.68
PGL									...			0.46
PPL										...		0.55
TFL											...	0.87

[a] Only statistically significant (0.05 level) values are listed.
[b] FP = flour protein concentration; GLU = glutenin; GLI = heavy gliadin; LMWRES = light gliadin; HSW = heavy albumin and globulin; LSW = light albumin and globulin; PTN = water-soluble pentosans; PNP = nonpolar lipids (percentage of free lipid fraction); PGL = glycolipids (percentage of free lipid fraction); PPL = phospholipids (percentage of free lipid fraction); TFL = total free lipid; TFPL = total free polar lipids (glyco- and phospholipids).

TABLE IV
Matrix of Simple Correlation Coefficients (r)[a] for Relationships Between Biochemical and Quality Parameters

Biochemical Variable[b]	Quality Parameter[c]											
	FLYD	MT	MTPK	MTO	MABS	BMT	DT	BABS	LV	PHT	TXT	TSTWT
FP		0.27	0.62	0.34	0.40	0.35	0.35	0.39	0.82	0.31		−0.47
GLU	−0.54							0.24		−0.40	0.30	
GLI	0.35		0.64						0.49	0.36		
LMWRES	0.30		−0.57	−0.44	−0.59	−0.29	−0.31	−0.54	−0.45			
HSW	−0.37	0.38	−0.46			0.35	0.34		−0.28	−0.28		
LSW		−0.35	−0.44	−0.45	−0.50	−0.37	−0.31	−0.44	−0.47			
PTN	−0.40		−0.29							−0.29	0.26	
PNP	0.33	−0.37			−0.40	−0.35	−0.23	−0.32				0.39
PGL		0.23										−0.34
PPL		0.31			0.36	0.30	0.28	0.30				
TFL	−0.51	0.44		0.37	0.33	0.45	0.44	0.42		−0.36	0.31	−0.31
TFPL	−0.57	0.55		0.43	0.45	0.56	0.49	0.48			0.30	−0.45

[a] Only statistically significant (0.05 level) values are listed.
[b] FP = flour protein concentration; GLU = glutenin; GLI = gliadin; LMWRES = low-molecular-weight residue protein; LSW = light saltwater-soluble protein; HSW = heavy saltwater-soluble protein; PTN = water-soluble pentosans, PNP = nonpolar lipids (percentage of free lipid fraction), PGL = glycolipids (percentage of free lipid fraction), PPL = phospholipids (percentage of free lipid fraction), TFL = total free lipid, TFPL = total free polar lipids (glyco- and phospholipids).
[c] FLYD = flour yield; MT = mixograph time to peak; MTPK = height of mixograph peak; MTO = mixograph tolerance; MABS = mixograph absorption; BMT = bake mixing time; DT = dough type; BABS = bake absorption; LV = loaf volume; PHT = proof height; TXT = texture; TSTWT = test weight.

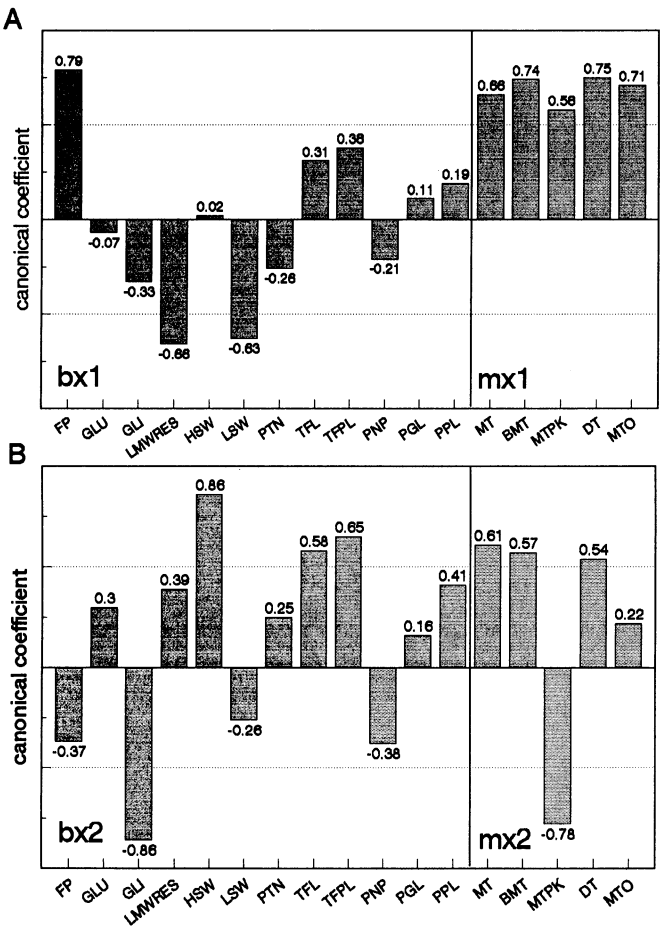

Fig. 1. Canonical analysis, dough-handling properties. **A,** Primary effects. **B,** Secondary effects. FP = flour protein concentration; GLU = glutenin; GLI = gliadin; LMWRES = low-molecular-weight residue protein; HSW = heavy saltwater-soluble protein; LSW = light saltwater-soluble protein; PTN = water-soluble pentosans; TFL = total free lipid; TFPL = total free polar lipids; PNP = nonpolar lipids; PGL = glycolipids; PPL = phospholipids; MT = mixograph time to peak; BMT = bake mixing time; MTPK = height of mixograph peak; DT = dough type; and MTO = mixograph tolerance. bx1 and bx2 = Canonical variates, biochemical parameters; mx1 and mx2 = canonical variates, dough-handling parameters.

related nature of many of both biochemical and quality parameters prevented the application of conventional multiple linear regression approaches (Steel and Torrie 1980). Canonical analysis was selected as an alternative method.

Canonical analysis of biochemical parameters with dough-handling attributes is presented in Figure 1. Primary effects (Fig. 1A) described by the first two cvs, mx1 and bx1, explained 72% of the variation in the variable response domain. A canonical correlation of 0.89 was observed between mx1 and bx1. All dough-handling parameters included in the analysis (MT, BMT, MTPK, DT, and MTO) made strong positive contributions to the cv mx1. The cv mx1, therefore, may be considered a description of overall dough strength. A strong positive contribution to bx1 was detected for FP; moderate positive contributions were noted for TFL and TFPL. Strong negative contributions to bx1 were displayed by LMWRES and LSW. An additional 21% of the variation in the response domain was explained by the second cvs, bx2 and mx2 (Fig. 1B). The canonical correlation of bx2 to mx2 was 0.72. The mx2 variate was considered to reflect dough properties during the hydration process (e.g., time up to and including peak dough development) based on positive contributions of the quality variables MT, BMT, and DT; the negative contribution of MTPK; and the lack of contribution of MTO to the cv. The biochemical factors HSW, TFL, and TFPL and, to a lesser extent, GLU, LMWRES, and PPL showed positive relationships with bx2 and, hence, with dough properties during hydration. GLI showed a strong negative contribution to bx2.

Relationships between loaf characteristics and biochemical factors are described in Figure 2. Seventy-two percent of the variation in the response domain was explained by the first cvs bl1 and lc1 (Fig. 2A). The canonical correlation was 0.88. An additional 21% of the variation was attributed to the second cvs, bl2 and lc2 (Fig. 2B). Bl2 and lc2 were related by a correlation of 0.71. Distinct differences were detected in the response of both loaf characteristics and biochemical variables to the two cvs. The first variate, lc1, was characterized by a high positive contribution of LV and a moderate contribution of BABS. The variables PHT and TXT were essentially unrelated to lc1. The related canonical variate bl1 was dominated by a very strong positive contribution of FP, with additional moderately positive contributions of GLI and TFPL. Strong negative contributions to bl1 were detected for LMWRES and LSW. LV was unrelated to the second cv, lc2, whereas TXT and BABS displayed strong positive contributions, and PHT was characterized by a negative contribution. Strong positive contributions to the corresponding cv bl2 were

found for GLU, HSW, PTN, TFL, and TFPL; GLI and LMWRES displayed moderate negative contributions.

The strong contributions of BABS to both lc1 and lc2 suggest that although a portion of the variation in BABS is dependent on flour protein concentration, additional flour biochemical attributes influence absorption properties. This analysis confirms the primary dependence of loaf volume on flour protein concentration; however, loaf textural features appear to be more highly influenced by flour protein composition (i.e., glutenin concentrations), PTNs, and lipids.

Only the first cvs (bm1 and mp1) explained a statistically significant level of variation (68%) in the response domain of milling properties with biochemical factors. Both FLYD and TSTWT contributed in a strong positive manner to mp1 (Fig. 3). Only one biochemical variable, PNP, displayed a strong positive contribution to bm1; strong negative associations were detected for the variables FP and TFPL; moderate negative contributions were evident for PGL and TFL.

Canonical analyses demonstrated the complex nature of the relationships between flour biochemical factors and variation in end-use quality parameters. No single biochemical component accounted for the majority of variation in any given quality factor. However, variation in FP contributed to a large portion of the variation in dough-handling and loaf characteristics. Once the extent of the variation attributable to FP variation was measured in canonical analyses, the relative importance of additional factors (secondary effects) was revealed.

Variation in glutenin concentration, as determined by SE-HPLC, contributed to variation in flour quality. The results of the present study, however, differed from those of previous investigators. Using simple correlations, Singh et al (1990b) found the relative amount of glutenin protein (equivalent to GLU in this report) to be positively correlated with loaf volume, dough resistance, and mixograph tolerance; in our studies, significant relationships (in the simple correlation analysis) were established only between GLU and TXT and PHT. However, canonical analyses revealed that variation in GLU contributed in a positive manner to both dough-handling and loaf characteristics, once the portion of variation attributable to FP was identified. Despite wide variation in quality parameters, a relatively narrow range in glutenin concentration, 43.70–47.19% (Table II), was found. With such a narrow range of variation, it is unlikely that primary effects could be attributed to GLU. Relative areas of the glutenin peak in materials examined by Singh et al (1990b) ranged from 28.7 to 36.4% of extracted protein. Thus, the materials examined in the present study displayed both a narrower range of variation and a much higher relative amount of glutenin than did the Australian wheats examined by Singh et al (1990b). It is possible that all of the environments sampled in the present study favored relatively high glutenin production. A larger number of genotypes and environments must be examined before this lack of variation in glutenin (as measured by SE-HPLC) in North American hard wheats can be established as a general rule. Whether this is a feature of all North American hard wheats remains to be established; however, subsequent experiments in our laboratory have found significant variation in GLU content only in the presence of wheat-rye chromosomal translocations. Dhaliwal and MacRitchie (1990) also have noted a negative effect of wheat-rye translocations on glutenin protein concentrations.

Simple correlations revealed numerous significant relationships (r values) between the remaining SE-HPLC peaks analyzed and quality parameters. GLI displayed significant positive contributions to FP, LV, and MTPK. Significant correlations between gliadin fractions and loaf volumes of U.S. hard wheats also have been detected by Hoseney et al (1969) and Khan et al (1989). In Australian wheats, LV most often correlated with glutenin fractions (Singh et al 1990b). No relationships between GLI and any quality variables related to dough strength were observed with simple correlations. Canonical analyses, however, revealed negative contributions of GLI to dough strength and loaf texture and positive contributions to LV. LSW and LMWRES, nongluten

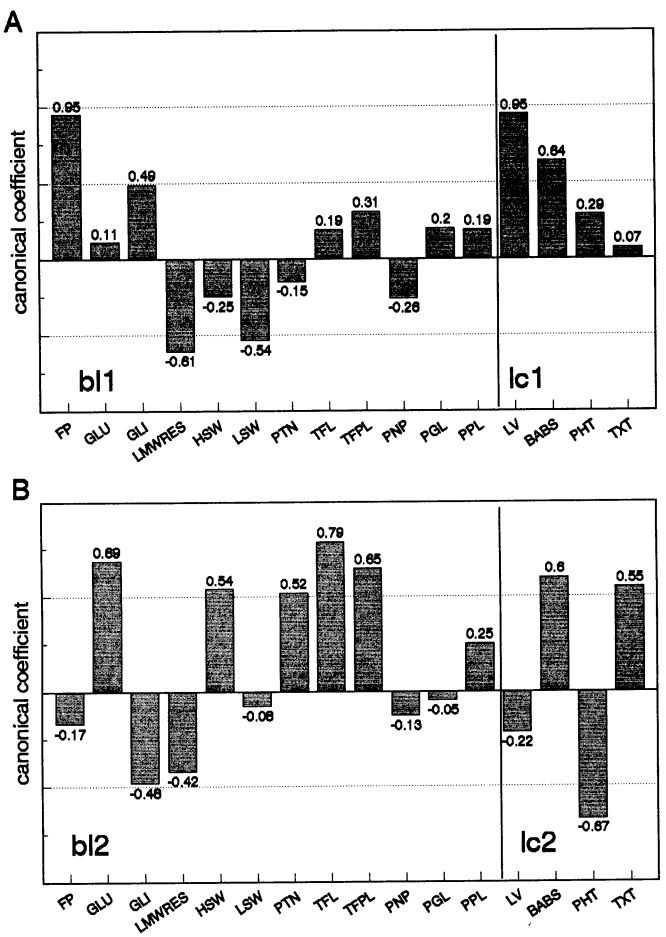

Fig. 2. Canonical analysis, loaf characteristics. **A,** Primary effects. **B,** Secondary effects. FP = flour protein concentration; GLU = glutenin; GLI = gliadin; LMWRES = low-molecular weight residue protein; HSW = heavy salt water soluble protein; LSW = light salt water soluble protein; PTN = water-soluble pentosans; TFL = total free lipid; TFPL = total free polar lipids; PNP = nonpolar lipids; PGL = glycolipids; PPL = phospholipids; LV = loaf volume; BABS = bake absorption; PHT = proof height; and TXT = texture. bl1 and bl2 = Canonical variates, biochemical parameters; lc1 and lc2 = canonical variates, loaf properties.

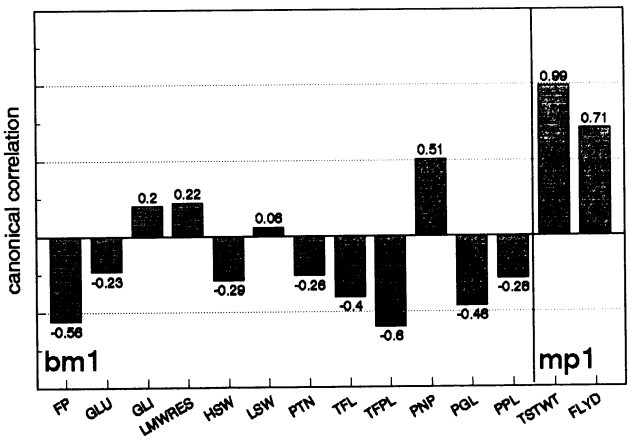

Fig. 3. Canonical analysis, milling characteristics. FP = flour protein concentration; GLU = glutenin; GLI = gliadin; LMWRES = low-molecular weight residue protein; HSW = heavy salt water soluble protein; LSW = light salt water soluble protein; PTN = water-soluble pentosans; TFL = total free lipid; TFPL = total free polar lipids; PNP = nonpolar lipids; PGL = glycolipids; PPL = phospholipids; TSTWT = test weight; FLYD = flour yield. bm1 = Canonical variate, biochemical parameters; mp1 = canonical variate, milling properties.

proteins of MW less than 17,000 (Singh et al 1990b), generally were negatively associated with quality attributes; such relationships also were detected by Singh et al (1990b). Thus, SE-HPLC analysis of flour protein is a useful tool for wheat quality prediction; however, the fractions displaying the largest variation, and those with the strongest relationships to quality parameters, might differ as a function of the environmental origin, or genetic backgrounds, of the wheats in question.

TFL and TFPL were found to be more highly related (in simple correlations) to MT and BMT than were measures of FP or flour composition (SE-HPLC peaks). Positive contributions of TFL and TFPL to both dough-handling and loaf characteristics were confirmed by canonical analyses. Significant relationships between TFPL and dough strength parameters also were established by Chung et al (1980) for U.S.-grown wheats and by Panozzo et al (1990) for Australian wheats, although, in the latter report, results were inconsistent over growing seasons. Reported relationships between TFPL and LV tend to be less uniform. Significant relationships have been reported by Chung et al (1980), Bekes et al (1986), and Panozzo et al (1990), whereas Larsen et al (1989) found flour glycolipids (a component of TFPL) to be a useful predictor of LV only in the absence of strong FP-LV relationships. The highly significant FP-LV correlations detected in the present study also may have prevented the establishment, in the simple correlation analysis, of TFL and TFPL-LV relationships. Canonical analysis (Fig. 2), however, did uncover a slight positive relationship between TFPL and LV and significant contributions of TFL and TFPL to BABS and TXT.

In the simple correlation analysis, variation in PTN was found to contribute little to variation in quality parameters, even though extensive PTN variation was detected. Again, canonical analysis was able to detect contributions of PTN to quality not identified in simple correlation analysis. A positive role of PTN was established for both TXT and BABS; however, this might be a consequence of a positive association of PTN and GLU (Table III). Numerous quality-related roles for pentosans, especially relating to absorption, have been suggested (Shogren et al 1987, Izydorczyk et al 1991). The results of the present investigation confirm the contribution of PTN to absorption properties.

The American baking industry has voiced concern over a perceived decline in the quality of U.S. hard wheats (Cox et al 1989). Loaf textural features of recently released varieties have been a subject of extensive criticism (Wheat Quality Council 1988). To our knowledge, little information is available describing the biochemical basis of loaf textural variation. Canonical analysis revealed strong positive associations of GLU, HSW, PTN, TFL, and TFPL with TXT, once the strong LV-FP relationship was estimated. Hopefully, future experimentation will more fully elucidate the role of these biochemical components in relation to loaf texture.

CONCLUSIONS

The low r values describing relationships between individual flour biochemical factors and quality aspects suggest that biochemically based models for the prediction of certain wheat flour quality parameters will be possible only through measurement of numerous compounds and the use of multivariate statistical approaches. Results of the canonical analyses, however, indicate that quite accurate models could be constructed for further evaluation, provided key biochemical components can be measured simultaneously. More than 90% of the variation in overall dough-handling properties and loaf characteristics could be explained through canonical analyses. Canonical analyses allow the examination of the intercorrelated flour biochemical variables and can aid in the identification of biochemical components that would be of low importance in the prediction of flour quality. Furthermore, canonical analysis reduces numerous variables to a few, more easily managed main effects. Canonical analysis also will allow the development of predictive models (Gittens 1985). Development and testing of broadly based models will require examination of more numerous flour samples, gathered from both a large number of wheat genotypes and growing environments. However, the use of canonical analysis demonstrates that significant amounts of variation in quality parameters can be explained through simultaneous analyses of flour protein, lipid, and pentosan components.

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