

GRAIN PROTEIN AND YIELD RELATIONSHIPS
IN WINTER WHEAT

By

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Bachelor of Science in Agriculture

Oklahoma State University

Stillwater, Oklahoma

1984

Submitted to the Faculty of the
Graduate College of the
Oklahoma State University
in partial fulfillment of
the requirements for
the Degree of
MASTER OF SCIENCE
December, 1986

Thesis
1986
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ACKNOWLEDGMENTS

Sincere appreciation is extended to my major adviser, Dr. Edward L. Smith, for his encouragement and assistance during the initiation of this study. Special appreciation is also extended to Dr. Lewis H. Edwards who accepted the responsibility of major adviser in the absence of Dr. Smith. Appreciation is also extended to the other members of my advisory committee, Dr. Robert L. Westerman and Dr. Richard C. Johnson, for their advice and assistance throughout the course of this study.

Special thanks to Dr. Ram C. Sharma for his assistance in conducting the statistical analyses. Appreciation is also extended to Dr. Donald C. Abbott and Connie Shelton for their assistance in the quality testing.

I am grateful to the Agronomy Department of Oklahoma State University for the facilities and financial support made available for this study. Special thanks to the small grains and soil fertility research teams and the North Central Research Station personnel for their assistance in planting, fertilizer application, and harvesting the thesis material.

I would like to extend a special thanks to my friends and family for their patience, understanding, and support throughout the course of my graduate training.

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CHAPTER I

INTRODUCTION

Chapters II and III of this thesis are separate and complete manuscripts to be submitted to Crop Science for publication. The format of each manuscript conforms to the style of Crop Science.

CHAPTER II

Stability for Grain Protein and Yield in Winter Wheat

ABSTRACT

Grain protein is an important quality trait for hard red winter wheat, Triticum aestivum (L.). Selection for increased grain protein in higher yielding genotypes can be difficult due to a negative correlation which usually exists between grain protein and yield. Forty winter wheat genotypes were grown at six locations in Oklahoma during 1985 to determine the stability of grain protein and yield. Two stability parameters, the linear regression coefficient and deviations from regression, were estimated for each entry using the average of all entries in each environment as the index. The genotypes differed significantly for grain protein and yield. Based on the estimates of the stability parameters, 'OK83396', 'OK83398', and 'OK79256' were identified as having high means and stability for both traits. 'Wrangler', 'OK79257', 'OK81306', 'OK83248', and 'Citation' were genotypes with high means and stability for percent grain protein. 'OK83378', 'Siouxland', and 'OK83152' had high means and stability for grain yield. Correlation between grain protein and yield for all 40 genotypes was nega-

tive, but not significant ($r = -0.14$). The results suggest that simultaneous improvement of grain protein and yield are possible, but both traits should be examined in order for selection to be successful.

Additional index words: Triticum aestivum (L.), genotype-environment interaction.

Genotype-environment (GE) interactions are a cause of concern to plant breeders in developing cultivars with improved grain protein or grain yield. Cultivars tend to perform differently when grown in different environments. A wheat, Triticum aestivum (L.), cultivar growing in the Southern Great Plains will be exposed to many different environmental conditions both associated with geographic location and year to year variation in weather. In order for that cultivar to be successful, it must be able to perform consistently well and exhibit stability over a range of environments.

Grain protein is an important quality trait in wheat. Many of the high yielding cultivars grown today tend to have lower grain protein content due to a negative correlation which usually exists between grain protein and yield (2,6). However, in 1954, Middleton et al. reported a group of cultivars which showed an increase in grain protein without the expected low yield (7). These cultivars all had either 'Fronroso' or 'Fronteira' as one parent. Fronroso and Fronteira were developed in Brazil from the same cross. 'Atlas 66', one of the cultivars reported by Middleton et al., has since been widely used in developing cultivars with improved grain protein content.

In 1981, Halloran (5) indicated that it should be possible to select lines which had increased grain protein content without significantly lowering grain yield. In that study Halloran found that grain yield and protein content in an F_4 population of 'Olympic' x Kenya B' were not signifi-

cantly correlated.

In 1984, Guthrie et al. (4) identified several lines which had higher grain protein content and acceptable levels for grain yield. These lines were shown to be desirable for both traits despite a significant negative correlation between grain protein and grain yield.

Comstock and Moll (1) have shown statistically that large genotype-environment interactions can reduce selection progress. A desirable wheat cultivar, therefore, should be stable over environments as well as exhibit good levels of grain protein and grain yield. The objectives of this study were: i) to estimate the stability parameters for grain protein and grain yield, ii) to identify desirable wheat genotypes based on the estimates of the stability parameters, and iii) to study the relationship between grain protein and grain yield for a set of 40 winter wheat genotypes.

MATERIALS AND METHODS

Forty winter wheat genotypes were grown at each of six locations during the 1984-85 growing season. Twenty genotypes were advanced breeding lines from the Oklahoma State University wheat breeding program. The pedigrees for these lines are presented in Table 1. The remaining genotypes were pure line cultivars developed and released by public institutions or private seed companies. The six locations, Stillwater, Lahoma, Altus, Goodwell (irrigated), Goodwell (dryland), and Woodward, represent a range of environmental conditions. The soil types for these six locations are listed in Table 2.

The experiment was conducted using a randomized complete block design with four replications at each location. The plot size was 1.2m by 3.1m. The plots consisted of four rows spaced 31cm apart at Goodwell (irrigated) and Goodwell (dryland). The plots consisted of five rows spaced 24cm apart at all other locations. Phosphorus and potassium fertilizer were applied according to recommendations based on the results of soil tests. The amount of nitrogen fertilizer applied was determined by soil tests and yield goals at each location. The seeding rate was 30g of seed per plot (80.6 kg ha⁻¹). This rate is consistent with standard seeding rates in this region. Only one location, Goodwell (irrigated), received irrigation during the growing season.

Plots were harvested on a whole-plot basis using a Hege combine. Grain yield was measured by weighing the grain from each plot and expressed as kg ha^{-1} . After grain yield was measured, a sample was taken from each plot to use for grain protein determination. The samples were ground, and percent grain protein was determined using the Technicon InfraAnalyzer TM⁴⁰⁰ (10) to determine the near infrared reflectance (NIR) of the sample. Percent grain protein was recorded on a 14% moisture basis.

Standard analyses of variance were used to test the significance of genotype, environment, and GE interaction. The significant GE interaction was broken down into two components, heterogeneity between regressions and a remainder component, according to the procedure outlined by Perkins and Jinks (9). Perkins and Jinks suggested that if only the heterogeneity between regressions component is significant, the GE interactions for each entry can be predicted from linear regression within the limits of the sampling error. If only the remainder component is significant, there is either no relationship or no simple relationship between the GE interactions and the environmental values, therefore, no predictions can be made using linear regression.

Stability parameters were estimated according to the model suggested by Eberhart and Russell (3). The linear regression coefficient (b) for each entry was calculated using the average of the entry over all environments. The deviations from regression (s^2d) were also calculated for each entry.

RESULTS AND DISCUSSION

The results of the analyses of variance conducted for grain protein and yield are shown in Table 3. Highly significant differences were found for environments, genotypes, and GE interactions for both traits. The significance of the GE interactions indicated that the genotypes tended to perform differently relative to each other when grown in varying environments. The GE interaction was broken down into two components, heterogeneity between regressions and a remainder component (Table 3). Both components were statistically significant for grain protein and grain yield when tested against the error mean squares. The heterogeneity between regressions was not significant for grain protein or yield when tested against the remainder. This indicated that both linear regression and deviations from regression are responsible for the GE interaction, and both components should be examined before making predictions of GE interaction for a specific genotype.

Traditionally, a "stable genotype" has been defined as a genotype that performs relatively the same over a range of environments, that is b 1.0. According to this definition, "stable genotypes" tend to perform better under adverse conditions and not as well under favorable conditions when compared to genotypes with a high mean yield. In this

situation, "stability" is usually associated with a mean which is less than the grand mean. In most instances, however, a breeder wants a genotype which has an above average performance in all environments. Based on this information, Eberhart and Russell (3) defined a stable genotype as one which has a unit regression coefficient ($b=1.0$) and no deviations from regression ($s^2d=0$). In our study, we defined a desirable genotype as one with a mean (\bar{x}) greater than the grand mean, $b=1.0$, and $s^2d=0$. With these definitions in mind, a stable genotype would not be desirable if it had a low grain protein or yield. However, a genotype which is not stable does not fit the definition of a desirable genotype, even if that genotype has a high mean grain protein or yield. This definition was used to determine whether any of the 40 genotypes tested could be considered desirable for grain protein and/or grain yield.

Table 4 shows the rank, means, b values, and s^2d values for grain protein and grain yield for 29 of the 40 genotypes which were tested. In addition, Table 4 lists the grand mean and $LSD_{0.05}$ for the 40 genotypes tested. Each of these 29 genotypes was shown to be not stable and/or had a mean which was not significantly higher than the grand mean, for both grain protein and yield. Therefore, these genotypes were considered to be not desirable. Five genotypes had grain yields above 4170 kg ha^{-1} which were significantly higher than the grand mean, but they were considered not stable and therefore were not desirable because of significant s^2d values. The remaining 24 genotypes had mean grain yields of

less than 4170 kg ha^{-1} which were not significantly higher than the grand mean. Eighteen of these 24 genotypes were not stable because of significant s^2_d values in addition to having low grain yields. One genotype, 'Chisholm', had a b value which was significantly higher than 1.0 in addition to an inferior grain yield. Seven genotypes had grain protein values which were greater than 12.9% and thus were significantly higher than the grand mean. However, they were considered not stable and therefore were not desirable because of significant s^2_d values. The remaining 22 genotypes had grain protein means which were less than 12.9% and thus not significantly higher than the grand mean. Of these 22 genotypes, 10 were considered not stable because of significant s^2_d values. Chisholm and 'OK83199' had b values which were significantly lower than 1.0. 'Hawk' had a b value significantly higher than 1.0 and a significant s^2_d value.

Table 5 shows the ranks, means, b values, and s^2_d values for grain protein and grain yield for the remaining eleven genotypes which were evaluated. Also shown are the grand mean and $\text{LSD}_{0.05}$ for all 40 genotypes. Six genotypes, 'OK83396', 'OK83378', 'OK83398', 'Siouxland', 'OK79256', and 'OK83152', were judged to be desirable genotypes for grain yield. OK83396 ranked first for grain yield out of the 40 genotypes in the study. The mean grain yield for OK83396 was 4539 kg ha^{-1} , which was significantly higher than the grand mean (3949 kg ha^{-1}). OK83378 ranked sixth for grain yield with a mean of 4368 kg ha^{-1} . OK83398 ranked seventh

with a mean grain yield of 4352 kg ha^{-1} . Siouxcross had a mean grain yield of 4284 kg ha^{-1} and ranked eighth for that trait. OK79256 ranked tenth in the study for grain yield with a mean of 4245 kg ha^{-1} . OK83152 ranked eleventh and had a mean grain yield of 4233 kg ha^{-1} . Each of the grain yield means for these genotypes was significantly higher than the grand mean. These six genotypes were also considered stable for grain yield as indicated by b values which were not significantly different from 1.0 and s^2_d values which were not significantly different from zero. Four of these genotypes (OK83396, OK83378, OK83398, and OK79256) were related with the same pedigree (Aurora/2*T101). 'OK79257', 'OK81306', 'Wrangler', 'OK83248', and 'Citation' were not considered desirable for grain yield. OK79257 and OK81306 had grain yields of 4246 and 4220 kg ha^{-1} , respectively. These yields were significantly greater than the grand mean. However, these two genotypes were not stable and not desirable because of significant s^2_d values. Wrangler and OK83248 also had significant s^2_d values for grain yield. In addition, the mean grain yields of Wrangler and OK83248 were 3963 and 3885 kg ha^{-1} , respectively, which are not significantly greater than the grand mean. The mean grain yield of Citation, 3548 kg ha^{-1} , was not significantly greater than the grand mean. Therefore, Citation was not desirable for grain yield.

Eight genotypes, OK79256, Wrangler, OK79257, OK81306, OK83398, OK83396, OK83248, and Citation were judged to be desirable for grain protein (Table 5). OK79256 ranked fifth

for grain protein with a mean of 13.2%. This value was significantly higher than the grand mean (12.7%). Wrangler ranked seventh with a grain protein mean of 13.1%. OK79257 ranked eighth in the study for grain protein with a mean of 13.1%. OK81306 ranked 10th in the study with a mean grain protein of 13.0%. OK83398 ranked 11th for grain protein with a mean of 13.0%. OK83396 had a grain protein mean of 12.9% and ranked 13th. OK83248 ranked 15th with a mean grain protein of 12.9%, and Citation ranked 16th with a mean grain protein of 12.9%. Each of these means was significantly higher than the grand mean (12.7%) for grain protein. These eight genotypes also showed stability over the six environments for grain protein. None of these genotypes had significant b values or s^2d values, thus indicating stability. Three genotypes, OK83378, OK83152, and Siouxland, were not desirable for grain protein. OK83152 and Siouxland both had a mean grain yield of 12.6%, which was not significantly greater than the grand mean. In addition, significant s^2d values indicated that each of the three genotypes was not stable. Three genotypes, OK83396, OK83398, and OK79256, were described as desirable genotypes for both grain protein and grain yield. Each of these genotypes showed high means and stability for both traits. The pedigree of all three was Aurora/2*T101.

The correlation coefficient of grain yield with grain protein was negative, but not significant ($r = -0.14$, Table 6). This r value corresponds with the r value of -0.13 which Halloran (5) observed in the F_4 generation of his

study. This nonsignificant correlation between the two traits indicates that selection for high grain yield while maintaining an acceptable level of grain protein is possible, but both traits should be examined in order to make progress through selection. Table 6 also shows the correlation between the regression coefficients ($r = -0.02$) and the deviations from regression ($r = 0.18$) for grain protein and grain yield. Neither of these values were significant, indicating that stability for grain protein and grain yield are not correlated. Despite the lack of correlation between protein and yield means and the lack of correlation between protein and yield stability parameters, OK83396, OK83398, and OK79256 were identified as genotypes which exhibited high means and stability for both grain protein and grain yield.

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Table 1. Pedigrees of 20 advanced lines from Oklahoma State University wheat breeding program.

Selection Number	Pedigree
OK79256	Aurora/2*TAM W-101
OK79257	Aurora/2*TAM W-101
OK81065	TAM W-101/Amigo
OK81306	Payne//TAM W-101/Amigo
OK81322	Payne//TAM W-101/Amigo
OK82282	OK753889/Payne
OK82377	Amigo Sib/2*Newton
OK83152	Vona//Lancota/Plainsman V
OK83175	Lovrin 6/TAM W-101//Vona
OK83199	Chisholm/Payne//Vona
OK83201	Vona//Chisholm/Plainsman V
OK83248	OK77220/TX71A562-6
OK83257	OK77205/TX71A562-6
OK83283	OK748099/Newton
OK83346	Chisholm/Vona
OK83378	Aurora/2*TAM W-101 (Seln. from OK79256)
OK83396	Aurora/2*TAM W-101 (Seln. from OK79257)
OK83398	Aurora/2*TAM W-101 (Seln. from OK79257)
OKM1057	5052/Sam//KS70H208/3/2*Vona
OKM1091	5052/Sam//KS70H208/3/2*Vona

Table 2. Soil types for the six locations.

Location	Soil Type
Altus	Hollister and Tillman clay loams: fine, mixed, thermic Pachic and Typic Paleustoll
Goodwell (dryland and irrigated)	Richfield clay loam: fine, mont- morillonitic, mesic Aridic Argiustoll
Lahoma	Pond Creek silt loam: fine-silty, mixed, thermic Pachic Argiustoll
Stillwater	Kirkland silt loam: fine-silty, mixed, thermic Pachic Argiustoll
Woodward	Carey loam: fine-silty, mixed, thermic Typic Argiustoll

Table 3. Analyses of variance and stability analysis of genotype-environment interaction for grain protein and yield of 40 genotypes evaluated at six locations in 1985.

Source	df	Grain Protein ms	Grain Yield ms
Environment	5	473.33**	142 492 607**
Genotype	39	10.12**	4 087 386**
Genotype-environment	195	0.61**	622 888**
Heterogeneity between regressions	39	0.81**	376 983**
Remainder	156	0.56**	684 365**
Error	702	0.17	151 513

** Significant at the 0.01 level of probability.

Table 4. Rank, means, regression coefficients, and deviations from regression for grain protein, and yield for 29 of 40 genotypes evaluated at 6 locations in 1985.

Entry	Grain yield				Grain protein			
	Rank	\bar{x} (kg/ha)	b	s^2_d ($\times 10^{-3}$)	Rank	\bar{x} (%)	b	s^2_d
OK83201	2	4453	0.9	121**	28	12.3	1.1	0
OK82377	3	4443	1.1	394**	18	12.8	1.1	0.13**
OK81065	4	4440	1.2	87*	20	12.7	1.2	0.06
OK81322	5	4423	1.1	129**	31	12.3	1.0	0
OK82282	13	4170	1.0	133**	29	12.3	0.9	0
Chisholm	14	4069	1.2*	0	32	12.2	0.8*	0
Mustang	15	4042	1.0	129**	27	12.3	0.9	0.03
OK83283	16	4016	0.9	71*	33	12.2	1.0	0.03
Pioneer 2165	17	4014	1.1	57*	12	12.9	1.0	0.07*
OK83175	18	4009	1.1	24	40	11.7	1.0	0.14**
OK83346	19	3989	1.0	90*	26	12.4	0.9	0
Pioneer 2157	20	3980	1.0	285**	19	12.7	0.9	0
Plainsman V	21	3975	0.9	399**	1	14.6	1.1	0.21**
Payne	23	3961	1.0	555**	6	13.1	0.9	0.07*
OK83257	24	3924	1.0	49	34	12.1	1.0	0.06*
Frontiersman	25	3907	0.8	312**	2	14.6	0.9	0.61**
OKM1091	27	3877	1.1	0	36	12.0	1.2	0.23**
Hawk	28	3854	1.1	241**	25	12.4	1.4*	0.07*
Vona	29	3837	1.1	229**	37	11.9	1.0	0.07*
TAM 107	30	3834	1.0	159**	39	11.8	0.9	0.06*
OK83199	31	3788	0.8	260**	24	12.5	0.9*	0
OKM1057	32	3779	1.2	32	35	12.1	1.1	0.09*
TAM W-101	33	3713	1.2	101**	23	12.5	0.9	0.20**
Triumph 64	34	3570	0.8	6	9	13.0	0.8	0.32**
Brule	36	3499	0.8	94**	38	11.8	1.0	0.15**
Brawny	37	3450	1.0	95**	4	13.6	0.9	0.15**
Newton	38	3432	0.9	155**	17	12.8	1.1	0.14**
TAM 105	39	3386	0.9	181**	30	12.3	1.1	0.06
Laverty Seln.	40	2227	0.5	261**	3	13.7	1.2	0.38**
Grand mean		3949				12.7		
LSD _{0.05}		221				0.2		

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

Table 5. Rank, means, regression coefficients, and deviations from regression for grain protein and yield for 11 of 40 genotypes evaluated at six locations in 1985.

Entry	Rank	Grain yield			Grain protein			
		\bar{x} (kg/ha)	b	s^2_d ($\times 10^{-3}$)	Rank	\bar{x} (%)	b	s^2_d
OK83396	1	4539	1.1	48	13	12.9	1.0	0.05
OK83378	6	4368	1.2	23	14	12.9	1.0	0.16**
OK83398	7	4352	1.0	53	11	13.0	1.0	0
Siouxland	8	4284	0.8	8	22	12.6	0.9	0.08*
OK79257	9	4246	1.1	69*	8	13.1	0.9	0
OK79256	10	4245	1.1	21	5	13.2	1.0	0.05
OK83152	11	4233	1.1	0	21	12.6	1.1	0.21**
OK81306	12	4220	0.8	77*	10	13.0	0.9	0
Wrangler	22	3963	1.1	205**	7	13.1	0.9	0.02
OK83248	26	3885	1.0	55*	15	12.9	1.2	0.03
Citation	35	3548	1.0	16	16	12.9	1.0	0
Grand mean		3949				12.7		
LSD _{0.05}		221				0.2		

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

Table 6. Simple correlation coefficients (r) between grain protein and yield means (\bar{x}), regression coefficients (b), and deviations from regression (s^2d).

Traits	Correlation coefficient
Protein \bar{x} vs. yield \bar{x}	-0.14
Protein b vs. yield b	-0.02
Protein s^2d vs. yield s^2d	0.18

CHAPTER III

Effects of Nitrogen Rates and Split Applications on Quality Traits in Wheat

ABSTRACT

A substantial amount of grain protein must be present in hard red winter wheat, Triticum aestivum (L.), in order to insure good bread making quality. Grain protein and yield can be increased by increasing nitrogen fertilizer or by making late spring N fertilizer applications if soil nitrogen is limiting. Two cultivars were grown at one location in 1985 with five N fertilizer rates and four split applications (fall and spring). Yield, test weight, grain protein, flour protein, loaf volume, and mixing time were evaluated for each treatment combination. Significant differences were found between the two cultivars for each of the six characteristics studied. Significant differences due to the different N treatments were found for test weight, grain protein, and flour protein. The N treatment sum of squares was broken down into eight orthogonal comparisons so these characteristics could be better evaluated. None of the comparisons showed significance at the 0.05 level of probability for flour protein. There were significant differences between the check plot and the fall applications of N for test

weight (P 0.05) and between the check and the split N applications for grain protein (P 0.05).

Additional index words: grain yield, test weight, grain protein, flour protein, loaf volume, mixing time, Triticum aestivum (L.)

In the past 20 years, yield of wheat, Triticum aestivum (L.), in the Southern Great Plains has increased substantially. This increase in yield has been accompanied by a decrease in the percent protein of the grain. The decrease in the percent grain protein has caused much concern due to the decrease in bread making quality which is associated with a decrease in grain protein. Recently, much interest has been shown in breeding lines which exhibit elevated grain protein but which still have acceptable levels of yield. The simultaneous improvement of yield and protein has been met with some success (2,3,7). However, few commercially successful high protein wheat cultivars exist in this region.

Schlehuber and Tucker (9) stated that the major factors responsible for variable protein content hence for variable bread quality are, in order of importance, (a) environment or climate, (b) soil, and (c) variety or cultivar. Oswalt and Schlehuber (8) concluded that the combined influence of climate and soil was more than three times as effective as cultivars in producing a change in grain protein content.

McNeal et al. (6) reported that protein content and protein yield for both wheat grain and straw gradually increased with increasing levels of N fertilizer. A significant increase in grain yield due to increased levels of N fertilizer was also observed.

Hucklesby et al. (4) showed that an increase in grain protein and grain yield could be attained through late

spring application of N fertilizer. Grain protein increased with increasing rates of N with each of the three cultivars in the test.

The objectives of this study were: i) to determine the effect of five different rates of N fertilizer on several agronomic and quality characteristics of wheat and ii) to determine the effect of split fall and spring applications of four N rates on several agronomic and quality characteristics of wheat.

MATERIALS AND METHODS

This study was conducted at Lahoma, Oklahoma in 1985. Two hard red winter wheat cultivars, 'TAM 105' and 'Chisholm', were used with nine N rates as ammonium nitrate. The experiment was conducted using a 2 x 9 factorial arrangement of treatments in a randomized complete block design with four replications. The experiment was grown on a Grant silt loam soil (Udic Argiustoll). Soil fertility analysis indicated that 33.6 kg ha^{-1} residual $\text{NO}_3\text{-N}$ was present in the soil. Other nutrient levels were adequate for wheat production.

N fertilizer rates were 45, 90, 135, and 180 kg ha^{-1} applied in the fall; 45, 90, and 135 kg ha^{-1} applied in the fall followed by 45 kg ha^{-1} in the spring; 90 kg ha^{-1} applied in the fall followed by 90 kg ha^{-1} applied in the spring; and an unfertilized check. The fall fertilizer applications were applied surface broadcast and disked in before planting. The spring N applications were applied surface broadcast when the wheat was in the early jointing stage of growth. The crop was planted using a drill planter at a seeding rate of 78.5 kg ha^{-1} . The plot size was 6.1 by 15.2 m with the rows spaced 20.3 cm apart. The fertilizer was applied to the center 4.9 m of each plot, and the center 3.0 m of each plot was harvested using a Gleaner combine.

Yield was determined by weighing the harvested grain

from each plot. Test weight was also determined for each sample. Grain protein was determined using the standard Kjeldahl method (N x 5.7). A 1200 g sample was taken from each plot and milled on a Buhler mill. Flour protein was then determined by the Kjeldahl method (N x 5.7). Loaves were baked using the modified "pup" method. The dough for each loaf was mixed to the optimum mixing time as determined visually and manually by the baker. The optimum amount of water, also determined visually by the baker, was added to each loaf. Two mg of KBrO_3 was added to each sample of dough. Mixing times were determined using the mixograph, a recording dough mixer. The peak on the graph corresponds with the optimum mixing time.

Standard analyses of variance were used to determine the effect of the N fertilizer treatments. Eight meaningful orthogonal comparisons were made for those characteristics which showed significant differences due to N treatments. The comparisons were calculated according to the procedure outlined by Steele and Torrie (10).

RESULTS AND DISCUSSION

The results of the analyses of variance (Table 1) showed highly significant differences for yield, test weight, grain protein, flour protein, loaf volume, and mixing time due to the treatment combinations. The treatment combinations sum of squares were therefore broken down into three components, cultivars, N treatments, and cultivar x N treatment interactions, in order to better evaluate the differences due to the treatment combinations.

Yield

Table 1 showed significant differences for yield due to replications and cultivar x N treatment interaction and highly significant differences for yield due to cultivars. No significant differences due to the N treatments were observed, therefore no comparisons were made among the different N treatments. This lack of significance could be partly caused by the residual $\text{NO}_3\text{-N}$ which was present in the soil before the N fertilizer treatments were applied (33.6 kg ha^{-1}). Table 2 shows the mean yield for each treatment combination. Chisholm had higher yields than TAM 105 at all treatments except 45 kg N ha^{-1} applied in the fall. The highest yield for Chisholm was 2769 kg ha^{-1} for the 90f + 90s N fertilizer treatment. The lowest yield for Chisholm was 1682 kg ha^{-1}

for the 45 kg ha⁻¹ fall application. TAM 105 showed its highest yield (1699 kg ha⁻¹) for the 45 kg ha⁻¹ fall N application. The lowest yield for TAM 105 was with the 45f + 45s N fertilizer treatment. No consistent trend was observed for yield between the cultivars and N treatments, indicating the presence of cultivar x N treatment interactions.

Test Weight

Table 1 showed highly significant differences due to cultivars and significant differences due to N treatments for test weight. Because of the significant differences due to N treatments, the comparisons listed in Table 3 were made in order to further examine the differences due to N treatments. Comparison of the check with fall N applications showed the check had the highest test weight. Application of N fertilizer resulted in reduced test weights. Similar results have been reported by Kosmolak and Crowle (5) for hard red spring wheats and by Dexter et al. (1) for amber durum wheats. None of the other comparisons were significant.

The analyses of variance (Table 1) showed highly significant differences due to cultivars. Chisholm had test weights which were higher in all cases than the test weights for TAM 105 (Table 2). The mean test weight for Chisholm was 74.3 kg hl⁻¹. This mean was significantly higher than the mean test weight for TAM 105 (69.0 kg hl⁻¹). Greater differences were seen between the two cultivars than among the different N treatments for test weight. Test weights ranged from 74.6 kg hl⁻¹ for the 90f + 90s N treatment to

73.7 kg hl⁻¹ for 135 kg N ha⁻¹ with Chisholm. Test weights for TAM 105 ranged from 70.0 kg hl⁻¹ for the check plot to 68.3 kg hl⁻¹ for the 135 and 180 kg N ha⁻¹ N treatments.

Grain Protein

Table 1 shows highly significant differences for grain protein due to cultivars and N treatments. The comparisons used to examine test weight were also used to examine the significance due to N treatments for grain protein (Table 3). The comparison between the check and the split N applications was significant (P 0.05), with the split applications showing higher grain protein content. None of the other comparisons showed significant differences. The fall N applications also had higher grain protein values than the check, but the difference was not significant at the 0.05 level of probability. However, these comparisons indicate an increase in grain protein on the fertilized plots especially for those receiving split applications. This increase in protein content agrees with the results obtained by Kosmolak and Crowle (5). TAM 105 showed higher grain protein percentages than Chisholm for all treatments (Table 2). The mean grain protein of TAM 105 (12.9%) was significantly higher than the mean of Chisholm (11.6%). Percent grain protein for Chisholm ranged from 12.0% for the 90f + 90s N treatment to 11.2% for the check plot. TAM 105 showed a range of grain protein from 13.2% for the 180 kg ha⁻¹ and the 135f + 45s N treatments to 12.6% for the check plot.

Flour Protein

Table 1 shows significant differences for flour protein due to replications and N treatments and highly significant differences due to cultivars. The same comparisons of specific N treatments were made for flour protein as were made for test weight and grain protein (Table 3). None of these comparisons were significant at the 0.05 level of probability. The comparison between the check and the split N applications was significant at the 0.10 level of probability with the split applications showing higher flour protein values. The lack of greater differences among the comparisons could be attributed to the division of the N treatment sum of squares. Also, smaller F values were seen for flour protein than grain protein. Therefore, there was less variation among the N treatments for flour protein than for grain protein. TAM 105 showed higher flour protein content than Chisholm in most cases (Table 2). The mean flour protein for TAM 105 (10.9%) was significantly higher than the mean for Chisholm (10.4%). Flour protein for TAM 105 ranged from 11.2% at the 180 kg ha⁻¹ and 135f + 45s N treatments to 10.6% for the check plot. Chisholm had a range for flour protein from 10.7% for the 90f + 90s N treatment to 10.1% for the 45f + 45s N treatment.

Loaf Volume

Table 1 showed significant differences for loaf volume due to replications and highly significant differences due to cultivars. No differences were observed due to the N treat-

ments, therefore no comparisons were made among specific N treatments. TAM 105 had higher values for loaf volume than Chisholm in all cases (Table 2). Higher loaf volumes usually occur with higher protein. Therefore, because TAM 105 had higher protein than Chisholm, the higher loaf volumes with TAM 105 were expected. The mean loaf volume for TAM 105 was 796.9 cm³. This was significantly higher than the mean loaf volume for Chisholm (728.1 cm³). Loaf volumes for Chisholm ranged from 742.8 cm³ on the 90f + 90s N treatment to 702.2 cm³ on the 45f + 45s N treatment. Loaf volumes for TAM 105 ranged from 817.9 cm³ with 135 kg N ha⁻¹ to 777.9 cm³ with the 45f + 45s N treatment. Although TAM 105 had higher loaf volumes than Chisholm, both cultivars exhibited loaf volumes which were acceptable for bread baking.

Mixing Time

Table 1 shows highly significant differences for mixing time due to cultivars. No significant differences were seen due to N treatments, therefore no comparisons were made among specific N treatments. Chisholm had longer mixing times than TAM 105 (Table 2) in all cases. The mean mixing time for Chisholm was 4.17 min. This was significantly higher than the mean mixing time for TAM 105 (2.60 min). The shorter mixing times exhibited by TAM 105 could be related to the higher protein content. Kosmolak and Crowle (5) reported shorter mixing times at higher levels of protein content in hard red spring wheat. The mixing times for Chisholm ranged from

4.38 min with 90 kg N ha⁻¹ to 3.88 min with 135 kg N ha⁻¹. TAM 105 showed a range of mixing times from 2.74 min with the 90f + 90s N treatment to 2.44 min with 135 kg N ha⁻¹. Despite the range in mixing times between the two cultivars, both would be equally acceptable for bread making.

Summary

Highly significant differences were seen between the two cultivars for yield, test weight, grain protein, flour protein, loaf volume, and mixing time. Significant differences were seen due to N treatments for test weight, grain protein, and flour protein. Significance at the 0.05 level of probability was detected for test weight for the comparison of the check plot with the fall N application. Significant differences (P 0.05) were also detected between the check plot and the split N applications for grain protein. None of the comparisons made for flour protein showed significance (P 0.05). Greater response to the N fertilizer may have been seen if the initial NO₃-N level of the soil had been lower. However, McNeal et al. (6) reported responses to N fertilization on a soil with 44.8 kg ha⁻¹ of residual NO₃-N. For the study conducted by McNeal et al., the check plot yielded 1924 and 1996 kg ha⁻¹ in consecutive years.

The split applications of N showed no advantage over the fall applications. Differences in protein content may have been seen if the spring applications had been made when the wheat was in a later stage of growth. Hucklesby et al. (4)

showed an increase in grain yield and grain protein due to late spring applications of N fertilizer.

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Table 1. Analyses of variance for six agronomic and quality characteristics evaluated over nine N fertilizer treatments and two cultivars.

Source	df	F values					
		Yield	Test Weight	Grain Protein	Flour Protein	Loaf Volume	Mixing Time
Replication	3	3.70*	2.21	2.16	3.23*	7.22**	0.37
Treatment combination	17	4.98**	60.40**	19.20**	3.94**	11.07**	19.70**
(Cultivar)	(1)	48.77**	1003.63**	300.83**	43.15**	166.80**	327.34**
(Nitrogen)	(8)	1.62	2.34*	3.30*	2.33*	1.88	0.64
(Cult x N)	(8)	2.88*	0.65	0.94	0.64	0.79	0.30
Error ms	51	133 635	0.50	0.23	0.22	1 700	0.27
CV, %		20.72	0.98	2.63	2.98	4.30	11.18

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

Table 2. Means for six characteristics of two cultivars at nine N fertilizer treatments.

Cultivar	Nitrogen (kg ha ⁻¹)	Yield (kg ha ⁻¹)	Test weight (kg hl ⁻¹)	Grain Pro (%)	Flour Pro (%)	Loaf volume (cm ³)	Mix time (min)
Chisholm	0	1797	74.5	11.2	10.2	724.4	4.10
	45 (f)	1682	74.2	11.3	10.2	719.3	4.22
	90 (f)	1836	74.5	11.4	10.4	731.4	4.38
	135 (f)	1743	73.7	11.5	10.3	723.2	3.88
	180 (f)	2310	73.9	11.7	10.5	731.6	4.28
	45f + 45s	2239	74.4	11.4	10.1	702.2	4.17
	90f + 45s	2346	74.4	11.8	10.6	738.1	4.08
	135f + 45s	1868	74.2	11.9	10.5	737.9	4.36
	90f + 90s	2769	74.6	12.0	10.7	742.8	4.11
Chisholm mean		2066	74.3	11.6	10.4	728.1	4.17
TAM 105	0	1514	70.0	12.6	10.6	779.3	2.58
	45 (f)	1699	69.1	13.0	10.8	796.5	2.55
	90 (f)	1477	69.1	12.8	10.8	798.3	2.67
	135 (f)	1314	68.3	13.1	10.9	817.9	2.44
	180 (f)	1448	68.3	13.2	11.2	798.3	2.64
	45f + 45s	1311	69.3	12.7	10.7	777.9	2.56
	90f + 45s	1497	68.9	12.8	10.8	795.0	2.64
	135f + 45s	1553	69.2	13.2	11.2	815.4	2.56
	90f + 90s	1362	68.9	13.0	10.9	793.3	2.74
TAM 105 mean		1464	69.0	12.9	10.9	796.9	2.60
LSD _{0.05} (treatment mean)		519	1.00	0.47	0.45	32.37	0.53
LSD _{0.05} (cultivar mean)		173	0.33	0.16	0.15	10.79	0.18

Table 3. Eight orthogonal comparisons for three traits evaluated over nine N fertilizer treatments.

Comparisons	F values#			
	df	Test Weight	Grain Protein	Flour Protein
Fall vs. split	1	4.03	0.58	0.15
Check vs. fall	1	9.41**	2.86	2.07
Check vs. split	1	3.24	4.72*	2.83
90f vs. 45f + 45s	1	0.02	0.05	0.60
135f vs. 90f + 45s	1	3.14	0.01	0.13
180f vs. 135f + 45s	1	2.99	0.05	0.00
180f vs. 90f + 90s	1	3.35	0.07	0.08
135f + 45s vs. 90f + 90s	1	0.01	0.02	0.05

Significant F value (0.05 level of probability) = 4.04

*,** Significant at the 0.05 and 0.01 levels of probability, respectively.

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