GENETICS STUDIES OF PROTEIN IN WHEAT

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1975

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1978

Submitted to the faculty of the
Graduate College of the
Oklahoma State University
in partial fulfillment of
the requirements for
the Degree of
DOCTOR OF PHILOSOPHY
July, 1982

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ACKNOWLEDGMENTS

To my mother Zahra, my wife Ladan, and my daughter Layla, I wish to express my deepest gratitude for their sacrifices, encouragement, and understanding which made this endeavor possible.

Sincere appreciation is expressed to my major adviser, Dr. Lewis H. Edwards for his inspiration, guidance, counsel, and assistance throughout this study. Gratitude is also expressed to the other members of my committee, Dr. Edward L. Smith, Dr. Robert D. Morrison, and Dr. Robert L. Reed for their valuable advice and assistance in preparation of this manuscript.

Special gratitude is expressed to Dr. P. L. Claypool for his assistance in conducting the statistical analysis of the data and to Dr. Donald C. Abbott for his valuable assistance in conducting the protein analysis.

Special thanks is extended to Mr. Robert L. Heister, Mrs. Linda H. Franzmann, Miss Teresa E. James, Mr. Randy D. Dinkins, Mr. Tunya Kunta, and other members of the soybean research team for their assistance in planting and harvesting the thesis study.

Appreciation is extended to Mrs. Melanie B. Bayles for typing the final copy of this manuscript.

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CHAPTER I

INTRODUCTION

Triticum aestivum L. em Thell is the second largest grain crop in the United States and the most widely cultivated of all cereals in the world. Approximately one and a half billion people or 35 percent of the world's population rely on wheat as their principal food and main source of protein. The percentage is more pronounced at lower economic levels of the population in less developed countries where there is a lack of animal proteins in the human diet. Wheat, like other cereal grains, is generally low in grain protein content and inadequate for human nutritional needs, so the necessity of improving the protein content and its quality is urgent.

High levels of grain protein depend on many factors and are the end product of a complex series of biochemical and physiological processes. Grain protein may be increased by the application of nitrogen fertilizer, by conventional breeding programs or by induced mutation for higher protein. However, genetic manipulation and improvement seems to be vitally important.

The second chapter deals with the mutation induction for grain protein. This study was initiated in 1972;

treatment and selection procedures as well as advanced data are discussed. Protein data of the mutant lines tested under different environments in the advanced generations are also presented.

In the third chapter an evaluation of the genetic potential of the mutant lines when backcrossed to their mother line, based on broad-sense heritability estimates, is reported. Information related to the simple phenotypic correlation between grain protein and yield, tiller number, and height is also presented.

Information related to the genetic control of protein and the association between this trait and yield and yield-related characters is presented in Chapter IV. Broad-sense as well as narrow-sense heritability estimates are calculated for grain protein. Also studied are the simple phenotypic correlations between grain protein and other characters.

Chapters II, III, and IV will be presented in a form acceptable to the Crop Science Society of America.[1] Chapter V is a general summary of the three experiments.

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[1]Handbook and Style Manual for ASA, CSSA and SSSA publications, 1976.

CHAPTER II

Mutation Induction for Grain Protein in Wheat[1]

ABSTRACT

The seed of a pure line of wheat (Triticum aestivum L. em Thell) was treated with 0.5% ethylmethanesulfonate solution in 1972 to produce mutations for grain protein. Treated seed, along with checks, was sown in the field as the M_1 generation. Selections for high protein were practiced in the M_2, M_3, and M_4 generations. Thirty-seven lines were selected and studied in a yield nursery in the M_5 and M_6 generations. Ten lines that were relatively high in protein percent and protein yield were selected and planted as the M_7 generation. Selected lines along with the mother line and checks were studied in a randomized complete block design with six replications at the North Central Agronomy Research Station, Lahoma, Oklahoma, during the 1978-1979 crop season. The characters investigated were grain protein and protein yield.

Analyses of variance indicated the significant differences (P=0.01) due to varieties and lines for protein

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[1]To be submitted for publication.

and protein yield. Four lines LA7626305, LA7627378, LA7627390, and LA7627610 revealed a significantly higher grain protein and higher protein yield than their mother line. Mutations for protein yield were evidently produced in these lines. Other mutations may have been produced for higher protein percentage and/or higher protein yield.

Additional index words: Ethylmethanesulfonate (EMS), Protein Yield, Mutant, Mutation.

Wheat (Triticum aestivum L. em Thell) is generally low in grain protein and inadequate for human nutritional needs. Grain protein may be increased by the application of nitrogen fertilizer (4), by conventional breeding programs, or by induced mutation for higher protein. Genetic variability can be accomplished by chemical mutagens as well as by radiation. Prakken (5) stated that the most effective chemicals are several derivatives of sulfonic acid, notably ethylmethanesulfonate (EMS). Siddiqui (6) stated that allohexaploidy of bread wheat presents many opportunities for the induction of mutations for useful agronomic traits. The result of a study on improvement of quality and yield of wheat by mutation induction indicates that the protein content of wheat can be increased without any reduction in yield (3). However, favorable results are not always easy to achieve by mutagenic treatment since the desired mutant trait may be governed by a gene located on the same chromosome as other genes that give rise to undesirable characteristics (7).

The objective of this study was to produce mutation for grain protein in a pure line of winter wheat.

MATERIALS AND METHODS

In the fall of 1972 the seed of a pure line of wheat (5*KAW//DS28A/PNC) was treated with 0.5% ethylmethanesulfonate solution (EMS), (KH_2PO_4) buffer solution at pH 7, for 24 hours with aeration. The temperature during treatment was 20° C. After treatment, the seed was washed with distilled water and dried to remove excess surface moisture. Treated seed, along with checks, was sown in the field in rows 3 meters long and 30 centimeters apart as the M_1 generation.

Individual spikes were bagged during flowering to avoid any cross pollination. Each spike was harvested and threshed separately. The M_2 generation consisted of 3,040 rows, each row traced to one M_1 spike. Every M_2 plant was harvested separately. Because of lack of seed, protein analysis was not conducted on every M_2 plant. However, for every row, which contained approximately 20 M_2 plants, a sample of seed was taken (10 seeds from each plant of that row) and composited. Protein analysis was conducted on the composite sample from each M_2 plant row. Ten to 20 plants from each high protein row were selected and planted for the next generation.

The M_3 generation was grown as plant rows from putative mutants of the M_2 generation in 1974-1975. The M_3 generation consisted of 1,786 plant rows. Individual rows were harvested and protein was run on a row basis. Ten high

protein lines out of each 100 plant rows were selected and planted for the next generation.

The M_4 generation was grown as progeny rows in 1975-1976. Each row traced back to one M_2 plant and one M_3 plant progeny. In this generation individual rows were harvested and protein was run on bulk seed from the row.

Those lines that were high in protein in both the M_3 and M_4 generations were selected for the M_5 generation and were grown in a yield nursery in 1976-1977. The M_5 generation consisted of 37 lines grown in a randomized complete block design with four replications. The plots were 3 meters long and 60 centimeters wide. In the 1977-1978 crop season, these 37 lines were evaluated in a yield nursery at two locations as the M_6 generation. Ten lines that were relatively high in protein percent and protein yield were selected and planted as the M_7 generation. The mother line and four high protein varieties were included as checks. The field experiment involved a randomized complete block design with six replications. The plots were 3 meters long and 30 centimeters wide.

Protein content was determined for all material used in this study by the Udy dye-binding method (1). Protein yield was calculated on the basis of grain protein percent and grain yield using the following formula:

Protein Yield = Grain Yield X Protein Percent

RESULTS AND DISCUSSION

Analyses of variance for grain protein for the putative mutant lines and their mother line were conducted for the M_5 and the M_6 gereations separately, and then for years and locations combined (Table 1). Significant differences (P=.Ø1) due to lines for protein indicated that considerable genetic variability has been achieved through mutation induction. Highly significant genotype X year interaction was detected when two years' and three locations' data were combined (Table 1). Diehl et al. (2) reported highly significant effects of years and genotype X year for grain protein. This reveals differential responses of the lines for grain protein over the years and variability of protein content under the influence of environmental factors. The data (Table 2) for mean protein of the putative mutant lines and their mother line in the M_5 and M_6 generations and over years and locations showed that the mother line (5*KAW//DS28A/PNC) was the lowest in protein content in comparison with the putative mutant lines that were derived from it. The least significant difference (LSD) was used for the comparison of the averages. In the M_5 generation, LA7627558, LA7627355, LA7626993 and LA7627610 were in the highest group. LA7626301 and LA7627310 were the only two lines that were not significantly different from the mother line (5*KAW//DS28A/PNC). In the M_6 generation, LA7626993, LA7627558, LA7627355, LA7627610, LA7626476, and LA7627390

were in the highest group. LA7626301, LA7627310, and LA7626313 were not significantly different from the mother line at Lahoma. At Stillwater, LA7627355, LA7627610, LA7626993, LA7626476, and LA7390 were in the highest group. Only 27 lines revealed significant differences (P=.05) from the mother line (5*KAW//DS28A/PNC) at this location. Over years and locations LA7627355, LA7627558, LA7626993, LA7627610, LA7626476, LA7627390, and LA7626230 were in the highest group, and LA7626301, LA7627310, and LA7626313 were not significantly different from the mother line.

Most of the mutant lines were low yielding compared to their mother line. These results agree with the findings of Stubbe (8) who reported a reduced yield of mutants with high protein. The reduction in yield may be explained either by the possibility that the mutant gene(s) govern yield of the plant as well as protein or else more than one mutation has occurred in these lines.

The selected lines along with the mother line and checks were examinied for protein yield. Significant differences (P=.01) due to varieties and lines for protein percentage and protein yield in the M_7 generation were observed (Table 3). Means for protein percentage and protein yield are presented in Table 4. Mutant line LA7627355 and 'Atlas 66' with 17.2% had the highest protein content and were significantly (P=.01) different from all other lines and checks. Four lines (LA7626993, LA7627610, LA7626305, LA7627390) revealed comparable protein content to

'Flex', and were not significantly different from it. 'Plainsman V' (ck) was not significantly different from LA7626993, LA7627610, LA7626305, LA7627390, LA7627558, and LA7627378. Plainsman V had the highest protein yield and was significantly different (P=.05) from 'Lancota'. Lancota, which was second in protein yield, was significantly higher than the lines and other checks. All mutant lines except LA7626993 revealed comparable protein yield to Flex and were not significantly different from it. Mutants LA7627610, LA7627378, LA7626459, anmd LA7627274 revealed a significantly higher protein yield than Atlas 66.

Four lines (LA7626305, LA7627378, LA7627390, LA7627610) revealed a significantly higher protein percentage and higher protein yield than their mother line (5*KAW//DS28A/PNC). Mutations for protein yield were evidently produced in these lines. The other lines, however, were either higher in protein percentage or higher in protein yield.

The present study showed the presence of genetic variability for protein that was accomplished by mutation induction. The protein content of some of these mutant lines was comparable to Atlas 66, Flex, and Plainsman V. It should be possible to use these high protein mutants as a genetic source for increasing the protein content in existing conventional breeding programs.

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Table 1. Mean squares from analyses of variance of protein percentage for 37 putative mutant lines and their mother line.

Source of Variation	df	1977 Lahoma	1978 Lahoma	1978 Stillwater	2 Yrs. 3 Loc.
Entry	37	5.87**	2.35**	1.82**	7.91**
Year-Loc	2	----	----	----	8.43ns
Entry X Year-Loc	74	----	----	----	1.07**

**Significant at the .01 level of probability.

Table 2. Average grain protein of thirty-seven mutant lines and their mother line at 3 locations for 2 years.

Line	1977 (M_5)	1978 (M_6)		2 Years &
	Lahoma	Lahoma	Stillwater	3 Locations
LA7627558	19.0	17.3	17.4	17.9
LA7627355	18.5	17.3	18.3	18.0
LA7626993	18.4	17.7	17.6	17.9
LA7627610	18.2	17.3	18.0	17.8
LA7626476	17.9	17.1	17.5	17.5
LA7626230	17.7	16.8	17.0	17.2
LA7627390	17.6	17.1	17.5	17.4
LA7626310	17.6	16.5	16.7	16.9
LA7627378	17.4	16.4	16.7	16.8
LA7626451	17.2	16.0	16.5	16.5
LA7626535	16.8	15.9	16.0	16.2
LA7627313	16.8	16.7	16.9	16.8
LA7627357	16.7	16.5	16.8	16.7
LA7626450	16.7	15.6	16.5	16.3
LA7627472	16.7	16.0	16.4	16.4
LA7627273	16.7	16.5	16.9	16.7
LA7626419	16.6	16.8	16.1	16.5
LA7627554	16.6	16.2	16.1	16.3
LA7627407	16.5	16.1	16.9	16.5
LA7626459	16.5	15.5	15.8	15.8
LA7627231	16.4	16.8	16.4	16.5
LA7626458	16.4	15.7	16.5	16.2
LA7627229	16.3	15.9	16.4	16.2
LA7626418	16.3	15.3	15.9	15.8
LA7626793	16.3	14.8	16.1	15.7
LA7627064	16.1	15.7	16.6	16.1
LA7627043	15.7	15.6	16.3	15.9
LA7627274	15.7	15.8	17.1	15.9
LA7626621	15.7	15.8	16.4	16.0
LA7626691	15.6	15.3	15.9	15.6
LA7627312	15.5	16.4	17.1	16.4
LA7627414	15.5	15.9	16.5	16.0
LA7626333	15.4	16.5	16.8	16.2
LA7626305	14.9	16.1	16.6	15.9
LA7626313	14.9	15.0	16.0	15.3
LA7627310	14.4	15.1	15.6	14.9
LA7626301	14.3	15.0	16.0	15.1
5*KAW//DS28A/PNC (Mother line)	13.8	14.6	15.3	14.5
LSD .05	1.0	0.9	0.9	0.9

Table 3. Mean squares from analyses of variance of protein percentage and protein yield for selected lines and their mother line.

Source of Variation	df	Protein Percentage	Protein Yield
Entry	14	4.44**	17933.36**

**Significant at .Ø1 level of probability.

Table 4. Average protein percentage and protein yield of fifteen wheat varieties and lines.

Variety	Protein Percentage	Protein Yield Kg/ha
LA7627355	17.2**	389
LA7626993	16.5**	362**
LA7627610	16.5**	420*
LA7626305	16.5**	406*
LA7627390	16.4**	405*
LA7627558	16.3**	392**
LA7627378	16.2**	420*
LA7626621	15.1	402**
LA7626459	15.0	424**
LA7627274	14.6	427**
5*KAW//DS28A/PNC (Mother line)	14.8**	355
Atlas 66	17.2**	367**
Flex	16.7**	425**
Plainsman V	16.4**	561**
Lancota	15.1	513**

LSD .05 (Protein) = .34
LSD .05 (Protein Yield) = 39
LDS .01 (Protein) = .45
LSD .01 (Protein Yield) = 52
*, ** Significantly different from mother line (5*KAW//D28A/PNC) at P = 0.05 and P =0.01, respectively.

CHAPTER III

Inheritance of Grain Protein in Wheat Mutants[1]

ABSTRACT

The parents, F_1 and F_2 populations were derived from backcrossing five mutant lines to their mother line. These lines were derived by mutation induction of a pure line of wheat (Triticum aestivum L. em Thell) with ethylmethanesulfonate (EMS). The planting arrangements was a completely randomized design, and the experimental units were individual plants. Tests were conducted at the Agronomy Research Station, Stillwater, Oklahoma, and at the North Central Agronomy Research Station, Lahoma, Oklahoma, during the 1980-1981 crop season.

Protein content, grain yield, tiller number, and height were the characters investigated. To determine the inheritance of grain protein in wheat mutants, broad-sense heritability estimates were calculated for all crosses. Also studied were simple phenotypic correlations between grain protein and other characters.

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[1]To be submitted for publication.

Broad-sense heritability estimates ranged from .00 to .70. Mutant lines "LA7626993", "LA7627610", and "LA7627558" showed medium to high heritability estimates in their corresponding crosses (.58 and .70; .43 and .50; .42 and .44 at Stillwater and Lahoma, respectively), indicating that these mutants may be a gentic source for high protein. Positive as well as negative associations between grain protein and grain yield, tiller number, and height were found. Most of the negative correlations were not statistically significant. LA7626993, showed the highest heritability estimates, positive correlations between grain protein and tiller number at both locations, and positive correlation between grain protein and grain yield at one location when backcrossed to the mother line. The present study showed and confirmed the presence of genetic variability for protein induced by mutation in mutant lines.

Additional index words: Ethylethanesulfate, Mutant line, Broad-sense heritability, phenotypic correlation.

The necessity of improving the protein content in wheat (Triticum aestivum L. em Thell) has been stressed by a number of plant breeders, and development of high protein varieties is one of the main aims of most breeding programs. The nutritional value of wheat depends to a large extent on the quality and quantity of its protein content. Grain protein content in wheat has been shown to be heritable (4, 11).

Recently, there has been remarkable progress in the use of induced mutation as a supplementary approach to the conventional breeding programs. Papa et al. (7), Rawlings et al. (9), and Williams and Hanway (13) reported increased genetic variation for quantitative characters in soybeans as a result of irradiation. Khan (6) obtained an increase in protein content of wheat without any reduction in yield as a result of mutation induction. In contrast, Hiraiwa et al. (5) reported the mutant lines with higher protein content were generally lower in yield than the control variety.

The study reported herein was conducted to obtain additional evidence that mutations(s) for protein had been produced, and to obtain information about inheritance of protein mutation(s). Simple phenotypic correlations between grain protein and other characters were also studied.

MATERIALS AND METHODS

The material for this study consisted of five populations; each with parental, F_1, and F_2 subpopulations. The populations were derived by crossing five putative mutant lines to their original parent. These lines were derived by mutation induction of a pure line of wheat with ethylmethanesulfonate.

In the fall of 1972 the seed of a pure line of wheat (5*KAW//DS28A/PNC) was treated with 0.5% ethylmethanesulfonate sulution (EMS) , (KH_2PO_4) buffer solution at pH 7, for 24 hours with aeration. The temperature during treatment was 20°C. After treatment, the seed was washed with distilled water and dried to remove excess surface moisture. Treated seed, along with checks, was sown in the field in rows 3 meters long and 30 centimeters apart as the M_1 generation.

Individual spikes were bagged during flowering to avoid any cross pollination. Each spike was harvested and threshed separately. The M_2 generation consisted of 3,040 rows, each row traced to one M_1 spike. Every M_2 plant was harvested separately. Because of the lack of seed, protein analysis was not conducted on every M_2 plant. However, from every row, which contained approximately 20 M_2 plants, a sample of seed was taken (10 seeds from each plant of that row) and composited. Protein analysis was conducted on the composite sample for each M_2 plant row. Ten to 20 plants

from each high protein row were selected and planted for the next generation.

The M_3 generation was grown as plant rows from putative mutants of the M_2 generation in 1974-1975. The M_3 generation consisted of 1,786 plant rows. Individual rows were harvested and protein was run on a row basis. Ten high protein lines out of each 100 plant rows were selected and planted for the next generation.

The M_4 generation was grown as progeny rows in 1975-1976. Each row traced back to one M_2 plant and one M_3 plant progeny. In this generation, individual rows were harvested and protein was run on bulk seed from the row.

Those lines that were high in protein in both M_3 and M_4 generations were selected for the M_5 generation and were grown in a yield nursery in 1976-1977. The M_5 generation consisted of 37 lines grown in a randomized complete block design with four replications. The plots were 3 meters long and 60 centimeters wide.

In the 1977-1978 crop season, these 37 lines were evaluated in a yield nursery at two locations as the M_6 generations. Protein analysis in the M_2, M_3, M_4, M_5, and M_6 generations were done by Udy dye-binding method (1).

Five mutant lines with highest protein content over years and locations were selected and backcrossed to the mother line with no reciprocal crosses. The populations were designated as follows: P_1 = mother line, P_2 = mutant line, $F_1 = P_1 \times P_2$, $F_2 = F_1$ selfed. Seedlings of the

parents, F_1, and F_2 were started in flats in the greenhouse on October 16, 1980. After seedling emergence, flats were placed outside for one week, and the plants were transplanted to the field on November 20 and 21, 1980, at the Stillwater and Lahoma Agronomy Research Stations. The soil was Bethany silt loam at Stillwater and Pond Creek silt loam at Lahoma. The planting arrangement was a completely randomized design, and the experimental units were individual plants. Each cross consisted of four populations with each population composed of the same number of experimental units as follows:

Population	Number of Plants	
	Stillwater	Lahoma
P_1	14	9
P_2	14	9
F_1	14	9
F_2	14	9

Rows were 3 m long and 30 cm apart. Eight test plants were spaced 30 cm apart within each row. Triticale seeds were planted at the ends of each row to minimize border effects. To insure optimum growth conditions at the Stillwater Agronomy Research Station 90 mm of water in addition to rainfall was provided during the growing season. Two malathion applications were made on March 4 and March 26, 1981, to control greenbugs (Schizaphis graminum Rondani). After harvest heavy infestations of Angoumois grain moth

(Sitotroga cereallella) occurred in several samples. All samples with a sign of infestation were discarded, and data collection continued on an unequal number of plants in each population. All mesurements were made on an individual plant basis, and the following data were collected:

Grain yield. Total weight in grams of the seed from each plant.

Grain protein content. Estimated by the Technicon Infra Alyzer TM400 (12) on the dry weight basis using the near infrared reflectance (NIR) characteristics of the sample.

Tiller number. Total number of tillers with a fertile spike for each plant at the time of threshing.

Height. Corresponded to the distance in centimeters from the soil surface to the tips of spikes, excluding the awn.

Broad-sense heritabilities, h^2_{bs}, were estimated by the method described by Burton (2) as:

$$\hat{h}^2_{bs} = \frac{Var(X)F_2 - \{Var(X)P_1 + Var(X)P_2 + Var(X)F_1\}/3}{Var(X)F_2}$$

where $Var(X)F_2$, $Var(X)P_1$, $Var(X)P_2$, and $Var(X)F_1$ represent the variance of character (X) in F_2, P_1, P_2, and F_1 generations, respectively. The simple phenotypic (rp) correlations between grain protein and other characters were calculated as:

$$r_p = \frac{Cov(X,Y)F_2}{\{Var(X)F_2 \cdot Var(Y)F_2\}^{1/2}}$$

where $Cov(X,Y)F_2$ represents the covariance between character X and Y in the F_2 and $Var(X)F_2$ and $Var(Y)F_2$ represents the variance of X and Y in the F_2 generation.

RESULTS AND DISCUSSION

Grain protein of the five selected mutant lines and their mother line in the M_5 and M_6 generations are presented in Table 1. Protein level of the mother line (5*KAW//DS28A/PNC) was significantly (P=Ø.Ø1) lower than each of the mutant lines in each of the tests.

Parental means and standard errors for protein as well as variances in the M_7 generation are presented in Table 2. The mother line (5*KAW//DS28A/PNC) was the lowest in protein content in comparison with the mutant lines. At Lahoma, all lines had significantly higher protein content than the mother line. At Stillwater, however, only two lines 'LA7626476' and 'LA7627558' exhibited significantly (P=Ø.Ø1) higher protein level than the mother line. This could be attributed to the lower number of samples from which data were taken at this location. Mean protein contents were not consistent over locations and are due to the genotype x environment interactions. The protein levels at Stillwater were higher than at Lahoma. This may be attributed to the better growing conditions at this location.

Heritability Estimates

Broad-sense heritability estimates are presented in Table 3. At Stillwater, these estimates ranged from .ØØ to .7Ø while they ranged from .17 to .58 at Lahoma. The rank for heritability estimate for the crosses was similar

across locations. Mutant line LA7626993 showed the highest heritiability estimate and LA7627355 the lowest heritability estimate when they were backcrossed to their mother line at both locations. This indicates that selection should be effective toward improving protein content in the cross involving LA7626993. At Stillwater, a negative heritability estimate was calculated in the cross between the mother line and LA7627355 and was set at 0.00 in accordance with acceptable procedure. This negative value may be attributed to the high variance for protein in LA7627355 and the relatively low corresponding variance within F_2 plants. Diehl et al. (3) stated that the magnitude of environmental variances in non-segregating spaced plants can exceed segregating progeny variances for a quantitative trait such as protein. Medium to relatively high heritability estimates for protein in three crosses in which mutant lines LA7626993, LA762761Ø, and LA627558 (.58 and .7Ø; .43 and .5Ø; .42 and .44 respectively) were involved indicate the promising values of these mutant lines as a genetic source for high protein. In general, these heritability estimates indicate that progress can be expected when using these lines in our breeding programs for high protein variety.

Correlations

Estimates of the simple phenotypic correlations are presented in Table 4. Positive associations as well as

negative associations between grain protein and grain yield were observed. At Stillwater, the range was from -.70 to -.04. A range of -.82 to +.25 was observed at Lahoma. These figures agree with the findings of others who reported negative correlations (4, 11) as well as positive correlations (10) between these two traits. In general, most of the negative correlations were not statistically significant, suggesting that selection for high protein and high yield should be possible in some of these crosses. Two positive but not significant correlations were found at Lahoma in the crosses in which mutant lines LA7626993 and LA7627558 were involved. These two lines also were shown to have the highest heritability estimates for protein in their corresponding crosses. This indicates that promising recombinants progenies of these two crosses should be isolated as parents for further backcrosses.

Positive and negative correlations between grain protein and tiller number were observed at both locations. At Stillwater, the range was from -.64 to +.05. A range of -.57 to +.44 was observed at Lahoma. In the cross between the mother line and LA7626993 positive but not significant correlations between grain protein and tiller number were observed at both locations. This cross also exhibited a positive relationship between grain protein and yield at Lahoma. This suggests that in this cross there would be chance of improving grain protein by selecting for tiller

number. A highly significnat negative association between these two traits was observed in cross involving LA7627610. A negative correlation between grain protein and yield was also observed in this cross, indicating the direct association between grain yield and tiller number in this cross.

Correlations between grain protein and plant height ranged from -.57 to +.48, but none of them were significant. Stuber et al. (11) reported a negative correlation, and Gill and Brar (4) reported a positive correlation between grain protein and height. Our results agree with the finding of Pepe and Heiner (8) that plant height did not influence grain protein significantly.

The present study showed and confirmed the presence of genetic variability for protein induced by mutation in lines. Heritability estimates of .58 to .70, .43 to .50, and .42 to .44 in crosses in which mutant lines LA7626993, LA7627610, and LA7627558 were involved indicate the value and effectiveness of using these lines as a genetic source for high protein. Negative and positive associations between grain protein and grain yield, tiller number, and height were observed. Most of the negative correlations between grain protein and yield were not statistically significant and generally low in magnitude, indicating the possibility of selection for high protein and high yield. Mutant line LA7626993 with high heritability estimates (.58 and .70) for protein and positive association between grain

protein and grain yield at one location and positive associations between grain protein and tiller number at both locations seems to be the most promising and suitable line to be used in breeding programs for high protein varieties.

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Table 1. Average grain protein percent of five selected mutant lines and their mother line at three locations for 2 years.

Line	1977 (M_5)	1978 (M_6)		
	Lahoma	Lahoma	Stillwater	2 years and 3 locations
LA7626476	17.9	17.1	17.5	17.5
LA7626993	18.4	17.7	17.6	17.9
LA7627355	18.5	17.3	18.3	18.0
LA7627558	19.0	17.3	17.4	17.9
LA762761Ø	18.2	17.3	18.0	17.8
5*KAW//DS28A/PNC (Mother line)	13.8	14.6	15.3	14.5
	LSD.Ø5=1.0 LSD.Ø1=1.4	LSD.Ø5=Ø.9 LSD.Ø1=1.2	LSD.Ø5=Ø.9 LSD.Ø1=1.2	LSD.Ø5=Ø.9 LSD.Ø1=1.2

Table 2. Parental means and variance for protein in the M_7 generation.

Cross	Stillwater Mean of protein	Lahoma Mean of protein
LA7626476	20.85**±1.86	17.06*±1.43
LA7626993	18.79±.76	17.25**±.38
LA7627355	18.65±1.74	16.35*±.76
LA7627558	20.65**±1.15	18.08**±.76
LA762761Ø	19.55±2.18	16.42*±.91
5*KAW//DS28A/PNC (Mother line)	18.54±.87	15.57±.64

*, ** Significantly different from mother line (5*KAW//DS28A/PNC) at p = Ø.Ø5 and Ø.Ø1, respectively.

Table 3. Estimates of heritability in Broad-sense (h^2_{bs}) for protein in five wheat crosses.

Cross	Stillwater h_2 Broad-sense	Lahoma h_2 Broad-sense
5*KAW//DS28A/PNC X LA7626476	.20	.40
5*KAW//DS28A/PNC X LA7626993	.70	.58
5*KAW//DS28A/PNC X LA7627355	.00	.17
5*KAW//DS28A/PNC X LA7627558	.44	.42
5*KAW//DS28A/PNC X LA7627610	.50	.43

Table 4. Simple phenotypic correlation between protein and other characters in five wheat crosses.

Cross	Stillwater			Lahoma		
	Grain yield	Tiller number	Height	Grain yield	Tiller number	Height
5*KAW//DS28A/PNC X LA7626476	-0.50	-.13	.02	-.82**	-.57	-.57
5*KAW//DS28A/PNC X LA6726993	-.60	.05	-.33	.25	.44	-.22
5*KAW//DS28A/PNC X LA7627355	-.04	-.18	-.17	-.20	-.10	.28
5*KAW//DS28A/PNC X LA7627558	-.50	-.55	-.26	.11	-.09	.48
5*KAW//DS28A/PNC X LA6727610	-.70**	-.64**	-.07	-.22	-.16	-.09

*, ** Significant at P=0.05 and 0.01, respectively.

CHAPTER IV

Inheritance of Grain Protein and Its Relationship With Yield and Yield-Related Traits in Wheat[1]

ABSTRACT

The parental, F_1, F_2, BC_1, and BC_2 populations under study were derived from three wheat (Triticum aestivum L. em Thell) cultivars and one mutant line. These materials were evaluated in a space-planted, completely randomized design during the 1980-1981 crop season at the Agronomy Research Station, Stillwater, Oklahoma and at the North Central Agronomy Research Station, Lahoma, Oklahoma.

The objectives of this study were to estimate heritability for grain protein and simple phenotypic correlations between grain protein and yield and yield-related characters. All measurements were made on an individual plant basis. The characters studied were: tiller number, kernels/spike, kernel weight, grain yield, and grain protein content.

Heritability estimates for protein ranged from .28 to

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[1]To be submitted for publication.

1.00. Estimates of additive and non-additive gene action indicated that additive gene action was larger for grain protein. Narrow-sense heritability estimates were in general higher than broad-sense estimates. This was attributed to sampling error or differential responses of the F_2 and backcrosses to the environment or both. On the basis of gene action and heritability estimates, we concluded that the crosses Vona X Atlas 66, Vona X LA7627558, and Plainsman V X Atlas 66 populations should produce superior selections for grain protein.

Negative associations between grain protein and yield were observed for all crosses except Plainsman V X LA7627558 at Stillwater. At Stillwater, the range in r values was from -.71 to +.35. A range of -.14 to -.57 was observed at Lahoma. Correlations between grain protein and kernel weight was negative for all crosses and at both locations. They ranged from -.09 to -.84 at Stillwater and from -.19 to -.81 at Lahoma. Positive and negative correlations between grain protein and tiller number were observed at both locations, but none of them were statistically significant. They ranged from -.68 to +.28 at Stillwater and from -.49 to +.22 at Lahoma. Low to medium negative correlations (-.14 to -.61) as well as positive (+.19, +.38) correlations between grain protein and kernels/spike were found at both locations.

The present study showed the presence of genetic

variability for protein. The presence of additive gene action indicates that selection should be effective for improving protein content in these materials. Since most of the negative correlations were not statistically significant and were low in magnitude, simultaneous selection for high protein and high yield should be possible.

Additional index words: Broad-sense heritability, Narrow-sense heritability, Additive variance, Nonadditive variance, Phenotypic correlation, Mutation.

The rapidly increasing population in the world demands the development and utilization of higher yielding and better quality plant protein sources. Wheat (Triticum aestivum L. em Thell) supplies a major portion of the protein needs for the less developed countries. Schlehuber and Tucker (15) listed, in the order of importance, environment or climate, soil, and genotype as the major factors responsible for grain protein content. Genetic manipulation, however, seems to be the principal and most powerful factor contributing to protein increase. Grain protein content in wheat has been shown to be heritable (2,7,17). Heritability estimates of medium to high for protein (7,9,17) indicate the presence of genetic variability for this trait. The presence of additive gene action (2) suggests that rapid progress by selection would be effective for increasing protein content. Cowley and Wells (3) found that the protein content in the wheat cultivar 'Hand' is controlled by a single dominant gene named PrHand. Hanold et al. (9) studied F_2, F_3, and F_4 generations of the crosses of 'Atlas 66' X 'Wichita' and Atlas 66 X 'Comanche' concluded that protein content may be controlled by a few major genes. Johnson et al. (11) observed transgressive segregation for higher protein in the cross 'Nap Hal' X Atlas 66. Stuber et al. (17) reported polygenic control for protein in wheat.

Generally, an increase in grain protein content is useful when it is combined with a high yield capacity.

Negative associations between grain protein and yield (7,9,17) as well as positive associations (16) have been reported. Johnson et al. (12) and Middleton (14) obtained progenies with high grain yield and high protein. Eckebil et al. (6) suggested that since many negative correlations between yield and grain protein have not been statistically significant and r^2 values are low, simultaneous selection for higher yield and high grain protein may be possible.

The objectives of this study were to estimate heritability for grain protein in six wheat crosses. Also studied were the simple phenotypic correlations between grain protein and yield and yield-related characters.

MATERIALS AND METHODS

Six crosses, each consisting of the parental, F_1, F_2, BC_1, and BC_2 populations, were the basic set of materials used in this study. The populations were derived by crossing Atlas 66, 'Plainsman V', and 'Vona', and one mutant line, 'LA7627558', in all combinations with no reciprocal crosses. The populations were designated as follows: P_1 = parent, P_2 = parent, F_1 = P_1 X P_2, F_2 = F_1 selfed, BC_1 = Backcross of F_1 to P_1, BC_2 = Backcross of F_1 to P_2.

Atlas 66 was developed by the North Carolina Agricultural Experimental Station from a cross involving the South American cultivar 'Frondoso'. It is a source of high grain protein. Atlas 66 is not adapted to Oklahoma environmental conditions. Plainsman V was developed by a private seed company in Kansas. It exhibits both high grain protein and high yield and is adapted to Oklahoma environmental conditions. Vona was released by Colorado State University. It is low to medium in grain protein and well adapted to Oklahoma environmental conditions. LA7627558 is an Oklahoma mutant line that was selected from an ethylmethanesulfonate (EMS) treated experimental line 5*KAW//DS28A/PNC. It is high in grain protein and is adapted to Oklahoma environmental conditions. The parents, F_1, F_2, BC_1, and BC_2 were planted in flats in the greenhouse on October 16, 1980. After seedling emergence, flats were placed outside for one week, and the plants were

transplanted to the field on November 20 and 21, 1980, at the Stillwater and Lahoma Agronomy Research Stations. The soil was Bethany silt loam at Stillwater and Pond Creek silt loam at Lahoma. The planting arrangement was a completely randomized design and the experimental units were individual plants. Each cross consisted of six populations with each population composed of the same number of experimental units as follows:

Population	Number of Plants	
	Stillwater	Lahoma
P_1	20	13
P_2	20	13
F_1	20	13
F_2	20	13
BC_1	20	13
BC_2	20	13

Rows were 3 meters long and 30 cm apart. Eight test plants were spaced 30 cm apart within each row. Triticale seeds were planted at the ends of each row to minimize border effects. To insure optimum growth conditions at the Stillwater Agronomy Research Station, 90 mm of water in addition to rainfall was provided during the growing season. Two malathion applications were made on March 4, and March 26, 1981, to control greenbugs (Schizaphis graminum Rondani). After harvest, heavy infestations of Angoumois grain moth (Sitotroga cerealella) occurred in several

samples. All samples with infestation were discarded and data collection continued on an unequal number of plants in each population. All measurements were made on an individual plant basis and the following data were collected:

Tiller number - Total number of tillers with a fertile spike for each plant at the time of threshing.

Kernels/spike - Determined indirectly by dividing the yield (in grams) of individual plants by the randomly selected 50-kernel weight multiplied by fifty to get the total number of seeds, then by dividing total number of seeds by the number of tillers.

Kernel weight - The weight in grams of 50 randomly selected kernels, expressed as 1000-kernel weight.

Grain yield - Total weight in grams of the seeds from each plant.

Grain protein content - Estimated by the Technicon Infra Alyzer TM^{400} (20) on the dry weight basis using the near infrared reflectance (NIR) characteristics of the sample.

Heritability estimates for protein were calculated using the following methods. Broad-sense heritabilities, h^2_{bs}, were estimated by the method described by Burton (1) as:

$$\hat{h}^2_{bs} = \frac{Var(X)F_2 - \{Var(X)P_1 + Var(X)P_2 + Var(X)F_1\}/3}{Var(X)F_2}$$

where $Var(X)F_2$, $Var(x)P_1$, $Var(X)P_2$, and $Var(X)F_1$ represent the variance of character (X) in F_2, P_1, P_2, and F_1

generations, respectively. Narrow-sense heritabilities, h^2_{ns}, were estimated by the method described by Warner (19) as:

$$\hat{h}^2_{ns} = \frac{2\text{Var}(X)F_2 - \{\text{Var}(X)BC_1 + \text{Var}(X)BC_2\}}{\text{Var}(X)F_2}$$

where $\text{Var}(X)F_2$, $\text{Var}(X)BC_1$, and $\text{Var}(X)BC_2$ represent the variance of character (X) in F_2, BC_1, and BC_2 generations, respectively. Additive and nonadditive variances were estimated as:

$$\hat{\sigma}^2_A\{X) = 2\ \text{Var}(X)F_2 - [\text{Var}(X)BC_1 + \text{Var}(X)BC_2]$$

$$\hat{\sigma}^2_{NA}(X) = \text{Var}(X)F_2 - \hat{\sigma}^2_A(X)$$

where $\hat{\sigma}^2_A(X)$ represents an estimate of the additive genetic variance of character (X), and $\hat{\sigma}^2_{NA}(X)$ denotes an estimate of the nonadditive variance of the same character. The simple phenotypic (rp) correlations between grain protein and yield, and grain protein and other yield-related traits were calculated as:

$$r_p = \frac{\text{Cov}(X,Y)F_2}{\{\text{Var}(X)F_2 \cdot \text{Var}(Y)F_2\}^{1/2}}$$

where $\text{Cov}(X,Y)F_2$ represents the covariance between character X and Y in the F_2 and $\text{Var}(X)F_2$ and $\text{Var}(Y)F_2$ represents the variance of X and Y in the F_2 generation.

RESULTS AND DISCUSSION

Parental means and standard errors for the five characters studied are presented in Table 1. Mean protein contents were not consistent over locations due to genotype X environment interactions. The mean protein percentage for each cultivar was higher at Stillwater than Lahoma. At Stillwater, Atlas 66 had the highest protein content followed by Plainsman V, LA7627558, and Vona. Atlas 66 was dropped from the test at Lahoma because of insect damage. Plainsman V had the highest protein at Lahoma followed by LA7627558 and Vona. The variation among plants is also given. Variability for protein was greater in parents with high protein content than with low protein content. Stuber et al. (18) found the greatest variation for protein in the high protein variety Atlas 66. This indicates that changes in environment have more effect on grain protein production in high protein varieties than in low protein ones.

Heritability and Gene Action

Broad-sense heritability estimates as well as narrow-sense estimates are presented in Table 2. Broad-sense estimates ranged from .28 to .69 at Stillwater while they ranged from .45 to .58 at Lahoma. Narrow-sense heritability estimates were high at both locations and ranged from .69 to 1.ØØ (heritability estimates greater than the theoretical limit, i.e., 1.ØØ, may be interpreted as one). Narrow-sense

heritability estimates of .68 to .82 were also reported by Stuber et al. (17). Because heritability estimates are influenced by the populations used, method of estimate, unit of measurement, and the environmnetal conditions during the test, a wide range of heritability estimates for protein has been reported in wheat. Estimates made in this study indicate the existence of genetic variabilities for protein in the populations used. The high narrow-sense heritability estimates indicate the effectiveness of selection for higher grain protein in these populations. Broad-sense heritability estimates were smaller than the narrow-sense estimates in all crosses and at both locations. In calculating the broad-sense heritabilities, the genetically uniform populations, namely parents and F_1, were used to estimate the environmental variation. If the environmental variations for these genetically uniform populations were larger than the environmental variation of the F_2, then the heritability would have been underestimated. Diehl et al. (5) stated that the magnitude of environmental variances in non-segregating spaced plants can exceed segregating progeny variances for a quantitative trait such as protein. Hanson (8) pointed out that estimates of environmental variability are not entirely reliable when they are based on data from spaced plants. Excessively high narrow-sense heritability estimates may be associated with several causes, namely sampling error or differential responses of the F_2 and backcrosses to the environment. Because the environmental

components of variance of the F_2 and of the two backcrosses are assumed to be equal (19), the additive genetic variance would have been overestimated and the nonadditive genetic variation would have been underestimated if the environmental variation of the backcross was less than that of F_2. The difference between broad-sense and narrow-sense heritability estimates in the same population is due to the unequal environmental influences in the generations used in calculating each of the heritability estimates. Additive as well as nonadditive variances for protein were calculated (Table 3). At Stillwater, additive variances ranged from 1.41 to 9.84 while they ranged from 1.10 to 4.00 at Lahoma. Non-additive variances were low and ranged from -3.22 to .86 at both locations. Additive variances were consistently higher than nonadditive variances in all populations. It suggests the effectiveness of selection for this trait. Nonadditive variances were low in magnitude and less important than additive variances. On the basis of gene action and heritability estimates, the Vona X Atlas 66, Vona X LA7627558, and Plainsman V X Atlas 66 populations may supply the best opportunities for superior selections.

Correlations

Simple phenotypic correlations between protein and yield, and yield-related characters were calculated for all crosses (Table 4). Negative associations between grain

protein and grain yield were observed for all crosses except Plainsman V X LA7627558 at Stillwater. At Stillwater, the range was from -.71 to +.35. Two negative significant correlations were observed in crosses involving Atlas 66 and the other high protein parents, Plainsman V and LA7627558. This indicates that selection for high protein and high yield in these crosses would be difficult. A range of -.14 to -.57 was observed at Lahoma. At each location, crosses between Plainsman V and Vona showed a small negative correlation between grain protein and yield. This may be attributed to the high yielding ability of these two cultivars and contributions of gene or genes for protein from the low protein parent Vona that are absent in Plainsman V, the high protein parent. These results agree with findings of others who reported a negative correlation (7, 9, 17) and Shebeski (16) who reported a positive correlation between grain protein and yield. An inverse relationship between grain protein and yield appears to be the result of interaction between source and sink. In some wheat cultivars an increase in sink size, which results in higher grain yield, occurs at the expense of lower protein content. Johnson et al. (10) found that the high grain protein of the Atlas 66 - derived lines results from more efficient translocation of nitrogen from the plant to its grain. Croy and Hagman (4) also reported the differential translocation and transporting of reduced nitrogen as the basis for a high grain protein in wheat.

Correlations between grain protein and kernel weight were negative for all crosses and at both locations. They ranged from -.09 to -.84 at Stillwater and from -.19 to -.81 at Lahoma. Two highly significant correlations (significant at P=0.01) were observed in crosses involving LA7627558. This indicates that simulataneous improvements of these two traits may not be possible in these populations. The low kernel weight of LA7627558 may be responsible for the negative relation between grain protein and kernel weight in these crosses. At Stillwater, the smallest negative correlation was found in the cross Plainsman V X LA7627558. This cross also exhibited a positive relationship between grain protein and yield. At Lahoma, Plainsman V X Vona exhibited the smallest negative correlation. This cross also showed a small negative correlation between grain protein and yield. Because percent grain protein is a ratio of protein to protein plus non-protein materials in the kernel, mainly starch, factors that affect either of the components will change protein percentage. Gill and Brar (7) obtained a highly significant negative association between grain protein and 100-kernel weight. They suggested that an increase in the plumpness of grain adds to the grain weight and to the carbohydrate/protein ratio that in turn results in a decrease in grain protein.

Positive and negative correlations between grain protein and tiller number were observed at both locations,

but none of them were statistically significant. At Stillwater they ranged from -.68 to +.28. A range of -.49 to +.22 was observed at Lahoma. The largest positive correlation appeared in the cross Plainsman V X LA7627558. This cross also exhibited positive relationship between grain protein and yield and grain protein and seeds/spike.

Low to medium negative correlations (-.14 to -.61) as well as positive (+.19, +.38) correlations between grain protein and kernels/spike were found at both locations. The largest negative correlation obtained in the cross Plainsman V X Atlas 66 may be responsible for the significant negative protein-yield relation at this cross. McNeal and Davis (13) and Stuber et al. (18) reported that the protein content of the grain in the top one-third of the head was approximately 60% less than that found in the center and lower portion. So, an increase in number of seeds per spike might result in lower grain protein content. The largest positive correlation was found in the cross Plainsman V X LA7627558. This cross also exhibited a positive relationship between grain protein and yield.

The present study showed the presence of genetic variability for protein. Heritability estimates ranging from .28 to 1.00 and the presence of additive gene action indicate that selection should be effective toward improving protein content in these materials. Negative phenotypic correlations between grain protein and yield and grain protein and yield-related characters as well as positive

associations were observed. Negative associations between grain protein and yield were observed for all crosses except Plainsman V X LA7627558 at Stillwater. Two negative significant correlations were observed in crosses involving Atlas 66 and the other high protein parents, Plainsman V and LA7627558. Correlations between grain protein and kernel weight were negative for all crosses and at both locations. Two highly significant correlations were observed in crosses involving LA7627558. Positive and negative correlations between grain protein and tiller number were observed at both locations, but none of them were significant. The largest positive correlation (.28) occurred in the cross Plainsman V X LA7627558. Low to medium negative correlations (-.14 to -.61) as well as positive (.19, .38) correlations between grain protein and kernels/spike were found at both locations. The largest negative correlation occurred in the cross Plainsman V X Atlas 66. This cross showed a significant negative protein-yield relation. The largest positive correlation was found in the cross Plainsman V X LA7627558. This cross also exhibited positive relationships between grain protein and yield and grain protein and tiller number. Since most of the negative correlations were not statistically significant and were low in magnitude, simultaneous selection for high protein and high yield should be possible.

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Table 1. Parental means and standard errors for the five characters studied.

Variety	Protein percentage	Tiller number	Kernels/ spike	Kernel weight	Grain yield
Atlas 66	23.2 ± 1.4[a] - - - -	5.9 ± 2.4 - - - -	32.2 ± 11.0 - - - -	22.5 ± 6.0 - - - -	4.21 ± 2.5 - - - -
LA7627558	20.0 ± 1.0 18.2 ± 1.1	10.5 ± 2.3 8.3 ± 2.8	23.5 ± 6.4 23.7 ± 3.5	26.6 ± 3.1 27.5 ± 2.8	6.5 ± 2.1 5.9 ± 2.1
Plainsman V	21.4 ± 1.3 19.5 ± 1.6	7.8 ± 2.2 8.4 ± 2.4	31.1 ± 4.1 27.7 ± 3.9	27.4 ± 3.4 28.9 ± 2.7	6.6 ± 2.2 6.7 ± 2.3
Vona	16.5 ± .7 14.8 ± .6	10.1 ± 3.5 9.7 ± 2.0	33.8 ± 4.7 33.9 ± 3.5	28.5 ± 2.3 29.4 ± 2.1	8.7 ± 2.2 9.6 ± 2.1

[a]The upper value in each pair is the mean at Stillwater, and the lower value in each pair is the mean at Lahoma, respectively.

Table 2. Estimates of heritability in the Broad-sense (h^2_{bs}) and Narrow sense (h^2_{ns}) for protein in six wheat crosses.

Cross	Stillwater		Lahoma	
	h^2 Broad-sense	h^2 Narrow-sense	h^2 Broad-sense	h^2 Narrow-sense
Plainsman V X Vona	.28	.69	.45	1.20†
Plainsman V X Atlas 66	.61	.96	-	-
Plainsman V X LA7627558	.64	.76	.45	1.46†
Vona X Atlas 66	.68	1.49†	-	-
Vona X LA7627558	.69	1.07†	.58	.95
Atlas 66 X LA7627558	.29	.80	-	-

† Values >1 which may be interpreted as 1.

Table 3. Estimates of additive and nonadditive variance for protein in six wheat crosses.

Cross	Stillwater		Lahoma	
	Additive variance	Nonadditive variance	Additive variance	Nonadditive variance
Plainsman V X Vona	1.41	.62	2.98	-.49†
Plainsman V X Atlas 66	5.07	.18	-	-
Plainsman V X LA76227558	2.73	.86	4.00	-1.27†
Vona X Atlas 66	9.84	-3.22†	-	-
Vona X LA7627558	4.57	-.30†	1.10	.05
Atlas 66 X LA7627558	2.07	.53	-	-

† Negative values which may be interpreted as 0.

Table 4. Simple phenotypic correlation between protein and yield, and yield-related characters in six wheat crosses.

Cross	Stillwater				Lahoma			
	Grain yield	Kernel weight	Tiller number	Kernels/ spike	Grain yield	Kernel weight	Tiller Number	Kernels/ spike
Plainsman V X Vona	-.08	-.12	-.08	-.14	-.14	-.19	.22	-.26
Plainsman V X Atlas 66	-.58*	-.49	.20	-.61*	-	-	-	-
Plainsman V X LA7627558	.35	-.09	.28	.38	-.53	-.81**	-.20	-.27
Vona X Atlas 66	-.41	-.51	-.12	-.48	-	-	-	-
Vona X LA7627558	-.38	-.84**	.04	-.39	-.57	-.45	-.49	.19
Atlas 66 X LA7627558	-.71*	-.54	-.68	-.27	-	-	-	-

*, ** Significant at P = 0.05 and 0.01, respectively.

CHAPTER V

SUMMARY

This study consisted of three separate experiments which are referred to as experiments 1, 2, and 3.

In experiment 1, a replicated nursery consisting of 10 putative mutant lines and five checks (one parent line and four wheat cultivars) was conducted at the North Central Agronomy Research Station, Lahoma, Oklahoma, to determine the line or lines that have high grain protein as well as high protein yield. The experiment was carried out during the 1978-79 growing season. It contained six replications. The plots were 3 meters long and 0.30 meters wide. The characters investigated were grain protein and protein yield. Analyses of variance indicated that there were significant differences due to varieties and lines for grain protein and protein yield. Grain protein and protein yield were significant at the 0.01 level of probability. The least significant differences was used for the comparison of the averages. Four lines (LA7626305, LA7627378, LA7627390, and LA7627610) revealed a significantly higher grain protein and higher protein yield than their mother line (5*KAW//DS28A/PNC). These results indicated that mutations for grain protein were produced in these lines. The other

lines, however, also were either higher in grain protein or higher in protein yield than the mother line. These results provided additional evidence for the usefulness of the induction of genetic variability for grain protein in wheat.

In experiment 2, the parental, F_1, and F_2 populations were derived from backcrossing five mutant lines to their mother line. The planting arrangement was a completely randomized design, and the experimental units were individual plants. Tests were conducted at the Agronommy Research Station, Stillwater, Oklahoma, and at the North Central Agronomy Research Station, Lahoma, Oklahoma, during the 1980-1981 crop season.

Protein content, grain yield, tiller number, and height were the characters investigated. Broad-sense heritability estimates were calculated for all crosses. The estimates ranged from .00 to .70. Mutant lines LA7626993, LA7627610, and LA7627558 showed medium to high heritability estimates in their corrsponding crosses, indicating the promising values of these mutants as a genetic source for high protein. Positive as well as negative associations between grain protein and grain yield, tiller number, and height were found by calculating the simple phenotypic correlations. Generally, most of the negative correlations were not statistically significant. Mutant line LA7626993, which showed the highest heritability estimates, positive correlations between grain protein and tiller number at both locations, and positive correlation between grain protein

and grain yield at one location when backcrossed to the mother line, seemed to be the most promising mutant line.

In general, the results confirmed the presence of genetic variability for protein induced by mutation in these mutant lines.

In experiment 3, the parental, F_1, F_2, BC_1, and BC_2 populations under study were derived from three wheat cultivar (Atlas 66, Plainsman V, Vona) and one mutant line (LA7627558). These materials were evaluated in a space-planted, completely randomized design during the crop season in 1981 at the Agronomy Research Station, Stillwater, Oklahoma and at the North Central Agronomy Research Station, Lahoma, Oklahoma.

Tiller number, kernels/spike, kernel weight, grain yield, and grain protein were the characters studied. Heritability for protein was estimated in broad-sense as well as narrow-sense. Heritability estimates ranged from .28 to 1.00, indicating the effectiveness of selection and considerable progress toward improving protein content in these materials. Estimates of additive and nonadditive gene action indicated that additive gene action was more pronounced for grain protein. Narrow-sense heritability estimates were in general higher than broad-sense estimates. This was attributed to the sampling error, differential responses of the F_2 and backcrosses to the environment, or both. The differences between broad-sense and narrow-sense

heritability estimates in the same population were attributed to the unequal environmental influences in the generations used in calculating each of the heritability estiamtes. Simple phenotypic correlations between protein and yield, and yield-related characters were calculated for all crosses. Negative associations as well as positive associations between grain protein and yield, grain protein and tiller number, and grain protein and kernels/spike were observed. Negative correlations between grain protein and kernel weight were also found. Since most of the negative correlations were not statistically significant and were low in magnitudes, simultaneous selection for high protein and high yield should be possible.

VITA

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