Quality evaluation of monosomic and chromosome substitution lines of common wheat, Triticum aestivum, L.

by Charles William Green

A thesis submitted to the Graduate Faculty in partial fulfillment of the requirements for the degree of
MASTER OF SCIENCE in Agronomy
Montana State University

Abstract:

Three sets of substitution lines of the wheat variety Chinese Spring with chromosomes from the donor varieties Thatcher, Hope and Timstein were evaluated for quality to determine which chromosomes carried genes governing bread wheat quality. Chromosomes Hope 2A, 3A, 7B and 2D, Thatcher 4A, 2B and 2D and Timstein 1D, 2D and 6D all appeared to carry genes governing gluten strength. Milling characteristics appeared to be carried on chromosomes Hope 4A 3B, 3D and 5D, Thatcher 3B, 3D and 7D and Timstein 3B, 3D, 5D and 6D,. There was a direct relationship between the percent water absorption of the flour and the percent of damaged starch.

Starch gel electrophoresis of ten of the chromosome substitution lines and the Chinese'Spring and Thatcher parents was made. The electrophoretic patterns for the substitution lines were the same as for Chinese Spring except for Hope 2A, which showed a slightly different pattern. The Thatcher parent had a distinctively different pattern from Chinese Spring.

Several monosomic and disomic lines of Kharkof MC-22 and Kharkof MC-22 x Itana lines were also evaluated for quality. The most striking example of the monosomic effect on quality was shown by chromosome ID. Lines monosomic for 1D exhibited abnormal gluten characteristics. This indicates that chromosome 1D carries genes that govern baking quality which cannot operate effectively in the monosomic condition.

Starch gel electrophoresis showed the same electrophoretic patterns for the monosomic 1D and disomic 1D populations.

Each variety of wheat appears to have a distinctive electrophoretic pattern, but there does: not appear to be any association between electrophoretic pattern and quality.

1.95

QUALITY EVALUATION OF MONOSOMIC AND CHROMOSOME SUBSTITUTION LINES OF COMMON WHEAT, TRITICUM AESTIVUM, L.

by

CHARLES WILLIAM GREEN

A thesis submitted to the Graduate Faculty in partial
fulfillment of the requirements for the degree

of

MASTER OF SCIENCE

in

Agronomy

Approved:

E. R. Hehn
Head, Major Department

C. A. Watson
Chairman, Examining Committee

Graduate Dean

MONTANA STATE UNIVERSITY
Bozeman, Montana

March, 1966

ACKNOWLEDGEMENT

The author wishes to express sincere thanks to Dr. C. A. Watson for his advice and encouragement throughout the course of this study.

Special thanks to Dr. J. R. Welsh for his advice and for the genetic materials used in this study, and to Dr. F. H. McNeal for his general suggestions and amendments in manuscript preparation.

The author also wishes to thank Mrs. Maribeth Young for her assistance with the electrophoresis work.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF APPENDIX TABLES

LIST OF FIGURES

ABSTRACT

Three sets of substitution lines of the wheat variety Chinese Spring with chromosomes from the donor varieties Thatcher, Hope and Timstein were evaluated for quality to determine which chromosomes carried genes governing bread wheat quality. Chromosomes Hope 2A, 3A, 7B and 2D, Thatcher 4A, 2B and 2D and Timstein 1D, 2D and 6D all appeared to carry genes governing gluten strength. Milling characteristics appeared to be carried on chromosomes Hope 4A, 3B, 3D and 5D, Thatcher 3B, 3D and 7D and Timstein 3B, 3D, 5D and 6D. There was a direct relationship between the percent water absorption of the flour and the percent of damaged starch.

Starch gel electrophoresis of ten of the chromosome substitution lines and the Chinese Spring and Thatcher parents was made. The electrophoretic patterns for the substitution lines were the same as for Chinese Spring except for Hope 2A, which showed a slightly different pattern. The Thatcher parent had a distinctively different pattern from Chinese Spring.

Several monosomic and disomic lines of Kharkof MC-22 and Kharkof MC-22 x Itana lines were also evaluated for quality. The most striking example of the monosomic effect on quality was shown by chromosome 1D. Lines monosomic for 1D exhibited abnormal gluten characteristics. This indicates that chromosome 1D carries genes that govern baking quality which cannot operate effectively in the monosomic condition.

Starch gel electrophoresis showed the same electrophoretic patterns for the monosomic 1D and disomic 1D populations.

Each variety of wheat appears to have a distinctive electrophoretic pattern, but there does not appear to be any association between electrophoretic pattern and quality.

INTRODUCTION

Wheat varieties fall into several different classes, depending on morphological differences and potential market use. Hard red wheats are used primarily for bread production, while the chief use of white wheats is for pastry products. A good quality hard red wheat variety must have suitable milling properties, which include normal bolting, or sifting properties, and a high yield of flour. A bread flour of good quality has a high water absorption capacity, a medium to medium-long mixing requirement, satisfactory mixing tolerance, good loaf volume potentialities, and should yield a loaf having good internal crumb grain and texture with acceptable color.

The protein complex known as gluten is one of the most important components of bread wheat flour. The ability of a dough to expand and provide a large loaf is due to the unique properties of gluten. The variation in quality between different bread wheat flours of the world lies mainly in the quantity and quality of gluten they contain.

Breeding for bread wheat quality has been an objective in most wheat breeding programs for many years. If wheat breeders knew which chromosome or chromosomes carried the genes governing quality, their task would be simplified. With the development of monosomic (2n-1) and nullisomic (2n-2) lines in hexaploid wheat a new genetic tool became available for determining which chromosomes carry genes for a particular inherited character. For example, quality differences of the various monosomic lines should indicate which chromosomes carry the desired germ plasm. If a particular monosomic or nullisomic line differs from the normal, one can conclude that the missing chromosome carries a gene or genes which affect quality.

Monosomics and nullisomics can also be used by wheat breeders to transfer a particular chromosome pair from one wheat variety to another. With a complete set of these substitution lines, (21 lines each differing by one pair of chromosomes from a donor variety) the contribution of each donor variety chromosome to a particular character can be determined. By evaluating a given series of substitution lines for quality, one should be able to determine which donor variety chromosomes carry genes influencing quality by noting those lines that differ from the normal.

The objectives of this investigation were to locate the chromosome or chromosomes in bread wheat which carry genes that influence flour quality and to determine the biochemical basis for quality differences found in wheat. Quality evaluations of monosomic and chromosome substitution lines and a study of the protein from the flour of these wheats were made.

REVIEW OF LITERATURE

I. Wheat Proteins

Wheat flour consists of approximately 8-13% protein, 13-15% moisture, 65-70% starch, 0.8-1.5% fat, 1.5-2.0% sugar and 0.3-0.6% ash (12). The distinctive place of wheat flour in the economics of the world can be attributed chiefly to the unique properties of the proteins of wheat as compared to those of other cereal grains. For this reason, the wheat proteins have long been of great interest to cereal chemists and others associated with the cereal industries (1).

Protein is the name given to a class of organic compounds, each member of which consists of various amino acids linked together. An amino acid is an organic acid containing both amino (NH_2) and carboxylic (COOH) groups. There are 18 known amino acids in flour proteins, so one can see that the number of different combinations, that is, the number of different protein molecules that are possible is almost infinite (6). The molecular weights of flour proteins are known to vary from about 40,000 to 2 or 3 million (13). Wheat flour protein consists of approximately 50-55% carbon, 6.5-7.5% hydrogen, 15-19% nitrogen, 22-27% oxygen and 0-3.5% sulphur (12).

The earliest investigation of wheat proteins was the classic work of Osborne (21). His classification of wheat flour proteins on the basis of solubility characteristics has been the basis for much of the subsequent research in this area. He concluded that wheat proteins were comprised of five fractions: 1) a water soluble, heat-coagulable albumin; 2) a globulin, soluble in dilute salt solution; 3) an ill-defined proteose;

4) gliadin, soluble in 70% ethanol; and 5) glutenin, soluble in dilute acid and base. The latter two (gliadin and glutenin) make up the water insoluble gluten which is considered to be the protein complex responsible for the unique properties of wheat flour. Gluten is the viscid substance that gives adhesiveness to dough. This unique property of wheat flour makes possible the production of a "risen" loaf of bread.

Gliadin and glutenin, when hydrated, are quite different in physical properties (6). Glutenin is similar to gluten, although it is tougher and more rubbery and does not stretch as easily. On the other hand, gliadin is syrupy and flows readily. The properties of these two fractions are blended together in the whole gluten. The molecular weights of the proteins in these two fractions are known to be quite different; 40,000-50,000 for gliadin and 2-3 million for glutenin (13).

It has been well established by the work of many investigators that flour from different varieties of wheat yield gluten with varying physical properties, as does flour from the same wheat variety grown under various environmental conditions. Different types of equipment are available for measuring extensibility, mixing characteristics, plasticity, and elasticity of gluten. The problem has been to explain differences in terms of chemical or physical structure of the gluten proteins (1).

Over the years, numerous attempts have been made to fractionate gluten and obtain preparations of pure, individual protein components. A continuing effort has been made to fractionate gluten into its protein constituents in terms of electrophoretic behavior. Laws and France (17) studied the electrophoretic patterns of wheat gluten by moving boundary electrophoresis. They showed the presence of more than one component, together with evidence of component interaction which produced asymmetry in the patterns. Jones, et al. (15), also using moving boundary electrophoresis, observed at least four major components and one minor component in gluten. Their work also produced asymmetric patterns indicating component interaction.

In recent years gel electrophoresis (28) has been used in the study of flour proteins. This system was developed by chemists working with the proteins of blood plasma, and it has been adapted to the study of flour proteins. Since protein molecules are electrically charged, they will move through the pores of a gel at different rates depending on their relative electrical charge and molecular size. Starch and acrylamide are the gel media commonly employed for electrophoresis of flour proteins.

A typical starch gel electrophoresis pattern with wheat gluten shows from about eight to 32 fairly distinct bands, depending on the electrophoretic conditions employed and the wheat sample used. In addition, there is a heavy band at the bottom of the pattern. This heavy band is the starting point at which the protein solution was inserted into the gel. The protein in this band moves very little, if at all. Dimler (6) indicates that all of the protein of the gliadin moves into the gel, whereas none of the glutenin protein moves. Failure of the glutenin protein to move into the gel during starch gel electrophoresis is due to its heavy molecular weight (13). The glutenin molecules simply are too large to move through the extremely small pores of the starch gel.

Several investigators (8, 10, 14, 35) have used starch gel electrophoresis with varying degrees of success. Graham (10) found differences in the protein components of different wheat flours and she observed that the greatest differences occurred among the slow-moving protein components. Alton and Ewart (8) observed that the electrophoretic patterns of 8 different wheat varieties showed significant differences and concluded that, "in a single run, a 'fingerprint' could be obtained for most, if not all, of the flour proteins." Cluskey, et al. (4), Coulson and Sim (5) and others have also observed differences in electrophoretic composition of gluten from different varieties of wheat.

Recently, some investigators have been switching from starch gel to acrylamide gel (24). Acrylamide gel has the advantage of being transparent allowing it to be scanned with a densitometer, thus providing quantitative measurements.

Some investigators have tried to explain the differences between wheats in terms of their amino acid content. Pence, et al. (22) determined the amino acid content of the gluten from 17 wheat flours representing a complete range of types and varieties. The composition of the gluten was essentially uniform, despite the wide range in type and source of the glutens and the wide range in protein content and baking characteristics of the flours. Similar comparisons on a limited number of wheats are reported by Hepburn, et al. (11), who found no differences in the amino acid content of the proteins of two hard red spring and two hard red winter wheats. Simmonds (27), however, did observe small, but significant differences in the amino acid content of six Australian wheats.

The sulfur-containing amino acids, methionine, cysteine and cystine, have been of particular interest since they are believed to be involved in intra- and inter-molecular bonds which may determine physical properties of the gluten or dough (29, 32). The importance of the disulfide linkage to wheat gluten properties has been known for many years. Splitting of this linkage by adding a reducing agent to the dough will immediately destroy its elastic properties (6).

II. Bread Wheat Quality Inheritance

The proof that wheat quality characteristics are inherited is not lacking, but the determination of the number of genes involved is still a subject of considerable investigation. The early inheritance studies were conducted by making the appropriate crosses and then evaluating the segregating generations. Most of these studies suggested multiple gene inheritance, but the exact inheritance patterns were not determined.[1/]

The fact that wheat quality is strongly influenced by environment has made the determination of its inheritance difficult. This is compounded by the lack of accurate quality tests for evaluating small amounts of early generation material. If later generation material is used for complete milling and baking tests, the plant breeder is faced with the problem

---

[1/] Welsh, James R. A Monosomic Inheritance Study to Locate Genetic Factors for Protein Quality and Morphological Characters in Hard Red Winter Wheat. Doctor of Philosophy Thesis, Montana State College, 1963.

of propagating a large number of lines to insure the complete testing of all genotypes. These facts, combined with year-to-year variation due to environment, have presented serious problems in accurately determining bread wheat quality.

Recently Welsh and Hehn (34) and Mattern, et al. (19, 20) approached quality inheritance studies by use of monosomic and chromosome substitution lines, respectively. Welsh and Hehn (34) crossed monosomic lines of Kharkof MC-22, a relatively weak flour variety, with normal Itana, a strong flour quality variety. The monosomic Kharkof MC-22 lines were used as the females and the normal Itana lines as the pollen source. F_2 populations resulting from selfed monosomic and disomic F_1 plants were evaluated for quality by the use of the wheat meal fermentation time test and the farinograph test. It was found that the monosomic 1D lines exhibited extremely weak flour characteristics as determined by these two tests. Populations disomic for chromosome 1D reacted normally under both tests. This was considered evidence that chromosome 1D is extremely important in the determination of bread flour quality characteristics.

Mattern, et al. (19, 20) made a preliminary quality report on the effect of substituting Cheyenne chromosomes into the Chinese Spring background. These substitution lines were produced by the method outlined by Sears (26). Following the fourth backcross in seventeen of the lines, seed was increased for quality evaluation. The four remaining lines, 2A, 7A, 2B and 2D, had not yet reached the fourth backcross so they were not evaluated. Milling yield, flour particle size, protein content, flour ash, dough mixing characteristics, and baking properties were determined on the seventeen lines. Substitution line 5D was high in flour yield and line 6D was low in flour yield, indicating that chromosomes 5D and 6D carry genes that are important in determining milling yield. Chromosomes 4B, 7B, and 5D appeared to strengthen the dough mixing characteristics, whereas chromosome 1D appeared to weaken these characteristics as determined by the mixograph curves. Major factors influencing baking characteristics appeared to be located on chromosomes 4B, 7B and 1D. Chromosome 5B appeared to be important in determining flour particle size.

Kuspira and Unrau (16) studied the effect of substituting Thatcher chromosomes into a Chinese Spring background on several characteristics. Protein analysis of the grain from 19 Thatcher substitution lines suggested that five chromosomes, 5A, 5B, 7B, 3D and 4D, induced a significant increase in protein over Chinese Spring. It was proposed that at least five genes or sets of genes were responsible for protein increases in this set of substitution lines.

MATERIALS AND METHODS

Two types of plant materials, chromosome substitution lines and monosomic lines, were used for quality evaluation in this study.

I. Chromosome Substitution Lines

Three sets of substitution lines in the spring wheat variety Chinese Spring, with substituted chromosomes from donor varieties Hope, Thatcher and Timstein, were obtained in the fall of 1963 from Dr. John Kuspira, University of Alberta, Edmonton, Alberta, Canada. These substitution lines were produced from crosses of nullisomic (2n-2) Chinese Spring lines with the donor variety as suggested by Sears (26). The procedure can be described as follows:

1. Nullisomic Chinese Spring ♀ x donor variety ♂.
2. Backcross monosomic F_1 ♂ to nullisomic Chinese Spring ♀.
3. Repeat step 2 until the BC_5 generation is reached.
4. Self BC_5 monosomic plants and select disomic offspring.

Identification of monosomic, nullisomic and disomic plants was made by cytological observations.

Line 1A was missing in all three substitution series. Thatcher 1D and Timstein 7A substitution lines were also missing.

The substitution lines were grown in a randomized block design with four replications at Bozeman, Montana in 1964. The Thatcher parent and normal Chinese Spring parent were also included in the experiment. However, the Hope and Timstein parents were not included due to insufficient seed stocks of these two varieties.

During the summer of 1965, 200 grams of seed from each replicate of these lines were milled at the Western Wheat Quality Laboratory, Pullman, Washington. The milling system was a modification of the procedure developed at the Hard Red Wheat Quality Laboratory, Manhattan, Kansas (9). Brabender Quadrumat Sr. laboratory mill components, 8 inch Tyler testing sieves, and Strand sedimentation sieve shakers were employed. Breaking was accomplished with a Quadrumat Sr. laboratory break head mill with the sifter reel removed.

Middlings were reduced with a Quadrumat Sr. reduction head equipped with a vibratory feeder. The first three rolls of the reduction head were original equipment. A smooth roll was substituted in position 4 and adjusted as close to roll 3 as possible without touching. The mill and flow diagram are pictured in Figures 1 and 2, respectively.

All samples were tempered to 15% moisture for 18 hours with distilled water containing a wetting agent (0.1% Aerosol OT). Weights of tempered wheat varied from 198.5 g. to 204.6 g.

Break stock remaining on a 32 mesh Tyler sieve after 1 minute of sifting was weighed as bran. Middlings remaining on a 100 mesh Tyler sieve after 3 minutes of sifting were passed through the reduction head. Reduction stock remaining on a 100 mesh Tyler sieve after 3 minutes of sifting was weighed as shorts. Break and reduction flours passing through the 100 mesh Tyler sieves were combined as total flour. The flour was blended prior to analytical and farinograph tests. Flour yield calculations were based on weight of wheat milled.

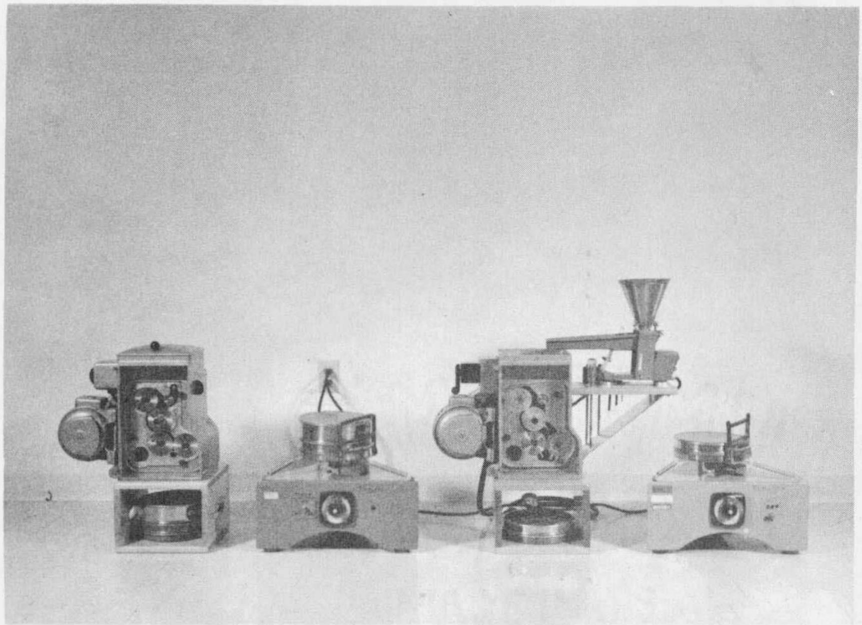


Figure 1. Brabender Quadrumat Sr. milling equipment as modified at Pullman, Washington.

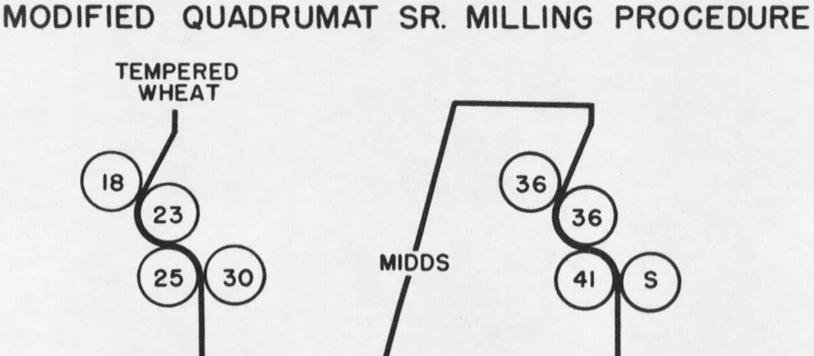


Figure 2. Flow diagram for Brabender Quadrumat Sr. milling system as modified at Pullman, Washington.

When sample weights, feed rates, roll settings and sifting times are all held constant, differences in milling performance are reflected by differences in total flour yield.

Starch damage was obtained by a method similar to that outlined by Donelson and Yamazaki (7). The reagents used were prepared as follows:

1. Buffer solution: Dissolve 3 ml. of glacial acetic acid in 4.1 g. of anhydrous sodium acetate and make up to 1 liter with water.
2. Sulfuric Acid, 3.58 N: Dilute 10 ml. of concentrated H_2SO_4 to 100 ml. with water.
3. Sodium tungstate solution, 12%: Dissolve 12.0 g. $Na_2WO_4 \cdot 2H_2O$ in water and dilute to 100 ml.
4. Alkali ferricyanide reagent, 0.1 N: Dissolve 33 g. pure, dry $K_3Fe(CN)_6$ and 44 g. anhydrous Na_2CO_3 in water and dilute to 1 liter. To standardize, add to 10 ml. of the solution 25 ml. acetic acid-salt solution (reagent 5) and 1 ml. soluble starch-KI solution (reagent 6) and titrate with 0.1 N thiosulfate. Exactly 10 ml. should be required to discharge the blue color completely.
5. Acetic acid-salt solution: Dissolve completely 70 g. KCl and 40 g. $ZnSO_4 \cdot 7H_2O$ in 750 ml. water, add slowly 200 ml. glacial acetic acid, and dilute to 1 liter.
6. Soluble starch-KI solution: Suspend 2 g. soluble starch in a small quantity of cold water and pour slowly into boiling water with constant stirring. Cool thoroughly, add 50 g. KI, dilute to 100 ml. and add 1 drop of saturated NaOH solution.

7. Thiosulfate solution, 0.1 N: Dissolve 24.82 g. $Na_2SO_3 \cdot 5H_2O$ and 3.8 g. of borax in water and dilute to 1 liter.

Starch damage was determined as follows: Place 2 g. of flour in a 50 ml. Erlenmeyer flask, add 0.2 g. Rhozyme 33 and 18.5 ml. of buffer solution (reagent 1) and mix thoroughly. Place immediately in a water bath set at 30° C. for 15 minutes. Remove from the water bath and add 0.8 ml. of 10% H_2SO_4 (reagent 2) and 0.8 ml. of sodium tungstate solution (reagent 3) and mix. Let stand 2 minutes and filter (No. 4 Whatman or equivalent), discarding the first 8-10 drops. Pipet 5 ml. of the extract into a 125 ml. Erlenmeyer flask, add 10 ml. of alkali ferricyanide solution (reagent 4), mix and immerse flask in boiling water for 20 minutes. Remove from boiling water, cool under running water and add 25 ml. of acetic acid-salt solution (reagent 5) and 1 ml. of starch-KI solution (reagent 6) and mix. Titrate with 0.1 N thiosulfate solution (reagent 7) and record the ml. of thiosulfate used to completely discharge the blue color. The milliliters of thiosulfate used were then converted to maltose values with the aid of the conversion table of Sandstedt (25) which is reproduced in Cereal Laboratory Methods (2). The maltose values were then converted to percent damaged starch by multiplying by the conversion factor 1.64 and dividing by 100.

The farinograph data (absorption, peak, stability and valorimeter) were obtained by the constant flour weight procedure (2) using a Brabender Farinograph equipped with a 50 g. mixing bowl. Protein content was obtained by the standard macro-Kjeldahl method.

The flour used for sedimentation was obtained by grinding approximately 50 g. of untempered wheat (approximately 10% moisture) with a Quadrumat Jr. mill with the sifter reel removed. The ground wheat was sifted over a 100 mesh Tyler sieve equipped with a bottom pan and shaken mechanically for 90 seconds. The flour was tested for sedimentation test by the standard method (2).

An analysis of variance and the least significant difference were determined on all data obtained.

Starch gel electrophoresis was run on the proteins of several of the substitution lines that differed in quality from the Chinese Spring check. The electrophoresis apparatus and procedure were similar to those described by Cluskey (3). The apparatus was composed of essentially three parts: a tray or trough which contains the gel medium, buffer chambers containing an electrode system and a constant voltage source (Figure 3). Dimensions of the tray and buffer chamber apparatus were 24 cm. by 19 cm. The gel was 15 cm^2 and 7 mm thick and came in direct contact with the buffer in each well.

Aluminum lactate-lactic acid containing 3 M urea was used as the buffer. It was prepared by dissolving 2.45 g. of aluminum lactate and 360 g. of urea in distilled water diluted to two liters. The pH was adjusted to 3.1 with lactic acid.

The protein was extracted from the flour in the following manner: Ten grams of flour was defatted by mixing with 20 ml. of n-butanol and filtering. The extraction was repeated three times. After the last filtration the residue was transferred to a beaker and allowed to air

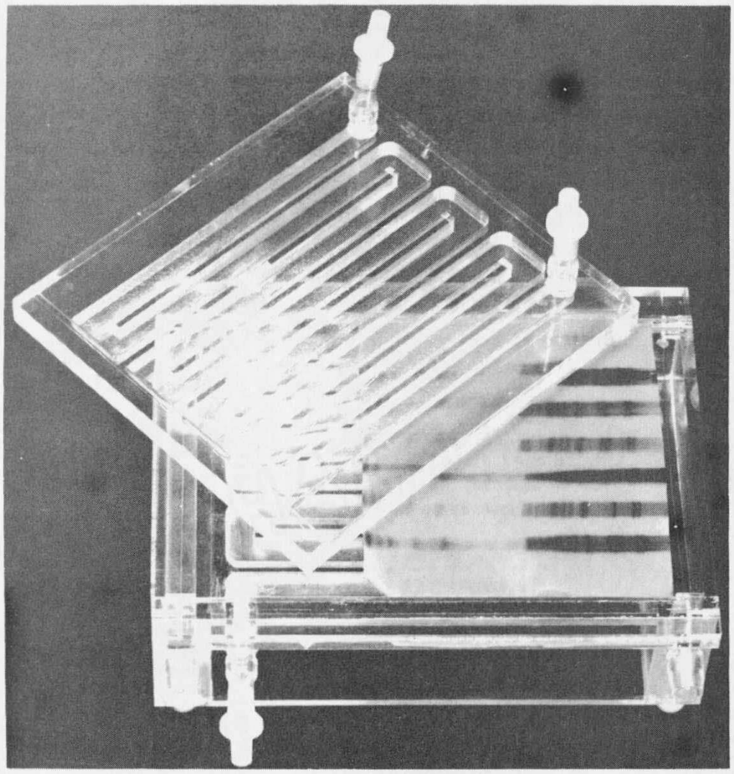


Figure 3. Starch gel electrophoresis apparatus

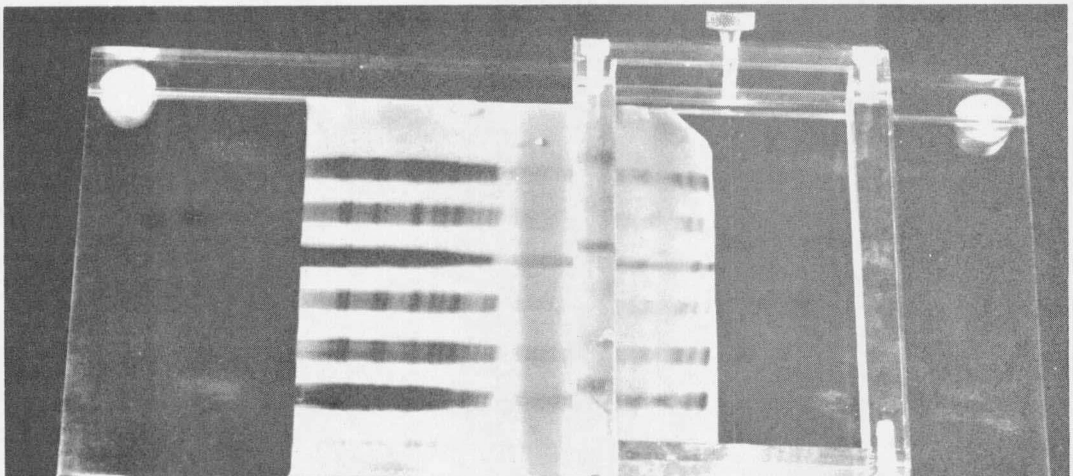


Figure 4. Apparatus used for slicing the starch gel

dry until all traces of alcohol were gone. The dried, defatted flour was mixed with 50 ml. of buffer for 12 minutes in a Sorval micro-homogenizer. Thirty-five ml. of 95% ethanol was added to the solution and the pH was adjusted to 6.5 with sodium hydroxide. The mixture was set in an ice bath until precipitation occurred. After the precipitate had formed, the solution was centrifuged for 30 minutes at 5,000 r.p.m. at 4° C. and the supernatant liquid decanted and dialyzed against water for 16 hours. After dialysis the solution was lypholyzed and this protein was used for electrophoresis.

The gel was prepared by mixing 52.0 g. of hydrolyzed starch and 400 ml. of buffer in a 1000 ml. Erlenmeyer flask. This mixture was heated over an open flame with constant stirring until it started to boil. Heat was quickly removed and the mixture was allowed to set for a few minutes until most of the foam had disappeared. The solution was then poured into a gel tray, covered with a glass plate, and allowed to gel.

For electrophoresis, one mg. of lypholyzed protein was dissolved in 4 drops of buffer containing 30% ethanol. A piece of filter paper 3 mm. by 6 mm. was soaked in this solution and placed in a small slit in the gel about 2 cm. from the cathode end. An indicator (Saffrain 0) was placed in the gel parallel to the protein sample.

The power supply was turned on and run at 110 mA until the indicator reached the anode end of the gel (approximately 3 hours). The gel was removed and sliced horizontally with a thin wire (Figure 4) and each half was placed in a 2% Nigrosin water-soluble dye for 10 minutes. The excess dye was removed by repeated washings with water.

II. Monosomic Lines

Several monosomic and disomic lines of Kharkof MC-22 and Kharkof MC-22 x Itana lines were analyzed for quality. The Kharkof MC-22 lines have the following history. Cytologically identified monosomic and disomic plants were grown in the field in 1962. The progeny from this material were grown in three replications in the field in 1964 and the harvested seed was used for study. Therefore, the monosomic samples would represent the second selfed generation following identification as monosomics. Theoretical calculations, based on work reported by Sears (26), can be used to predict that this material is 56% monosomic and 44% disomic, if one assumes the progeny will be 75% monosomic and 25% disomic from a selfed monosomic. The disomic lines represent normal plants (2n = 42) that have been recovered from selfed monosomics. Wheat protein, sedimentation value and farinograph data were obtained on all samples. Wheat protein was determined by the Udy ion-binding method (33). An analysis of variance was run on the data and the least significant difference was determined.

The Kharkof MC-22 x Itana lines represent the F_3 populations from monosomic or disomic F_1's of a Kharkof MC-22 x Itana cross. The monosomic and disomic F_1's were identified in the greenhouse in 1961. The F_2's were grown in 1962 and the F_3's were grown at several locations in Montana in 1964. Calculations can be made to show that theoretically the lines should be 42% monosomic and 48% disomic.

A composite of 100 g. from Havre, 125 g. from Moccasin, 150 g. from Sidney and 800 g. from Bozeman was made for quality evaluation. Starch damage, kernel weight, test weight, flour yield, flour ash, flour protein, sedimentation value, farinograph data and the percent by weight of wheat remaining on a 6½/64" barley screen after 1 minute of sifting were obtained on each composite.

The wheat was milled on a Buhler Laboratory Experimental Mill and the milling yield was determined. Flour ash was determined by ashing 5.0 g. of flour overnight at 575° C. Flour protein was obtained by the Udy ion-binding method (33).

Seven samples consisting of Itana, Cheyenne, Chinese Spring, Kharkof MC-22 disomic, Kharkof MC-22 normal, Kharkof MC-22 monosomic 1D and Kharkof MC-22 x Itana bulked F_2's were compared for different quality characteristics. The Kharkof MC-22 disomic represents a disomic line that was recovered from a known monosomic line whereas the Kharkof MC-22 normal represents the original Kharkof MC-22 line that had not been changed to the monosomic condition. The Kharkof MC-22 disomic and Kharkof MC-22 normal should have the same genetic makeup. These samples were milled at the Hard Winter Wheat Quality Laboratory, Kansas State University, Manhattan, Kansas, using their micro-milling system (9) and the flour yield was determined. Protein was determined on the flour and bran fractions by the macro-Kjeldahl method. Samples of each of the seven flours were sent to the Western Utilization Research and Development Division, Albany, California for sulfhydryl determinations. The procedure used was that outlined by Sokol, _et al_. (30).

Amino acid analyses were made on the normal Chinese Spring, Kharkof Mc-22 normal and Kharkof MC-22 monosomic 1D lines using a Technicon automatic amino acid analyzer. Hydrolysis was accomplished by mixing 50 mg. of flour in 100 ml. of constant boiling hydrochloric acid (approximately 6 M) and heating for 24 hours at 100° C. The HCl was then lyphilized off and the remaining material was dissolved twice in water followed by lypholizing. The final hydrolyzed material was then dissolved in 0.5 ml. of H_2O and 0.15 ml. of this solution was placed on the analyzer column for analysis. The percent by weight of each amino acid of the total recovered was determined.

Starch gel electrophoresis was run on the proteins of the seven samples milled at Kansas State University.

RESULTS AND DISCUSSION

I. Chromosome Substitution Lines

Averages and individual replication data on percent protein, milling yield, sedimentation values, starch damage and farinograph values for absorption, peak, stability and valorimeter are given in the Appendix, Tables I-VIII, respectively.

The only line significantly higher in protein than Chinese Spring was Timstein 3B (Table I). This indicates that Chromosome 3B in Timstein carries a gene that is responsible for increasing protein within the endosperm. None of the Thatcher substitution lines were significantly higher in protein than Chinese Spring even though the Thatcher parent was considerably higher, 13.6% vs. 16.0%. This indicates that (1) more than one Thatcher chromosome affects percent protein and that protein content probably has a complex inheritance pattern, or (2) that the genes involved in this trait are carried on one or both of the homoeologous chromosomes (1A and 1D) which were not tested.

Kuspira and Unrau (16) observed five Thatcher substitution lines significantly higher in protein than Chinese Spring and concluded that at least five genes or groups of genes affected this character. The inconsistency of the data presented by Kuspira and Unrau and the data presented herein may be due to insufficient testing and more data will be required to solve the problem.

The data in Table II show the milling yield of the chromosome substitution lines. Chromosome 3B and 3D of each variety appear to carry genetic factors which affect milling yield. Chromosome 3B increased milling

Table I. Protein percentages of chromosome substitution lines. The values are averages of four replications.

Line	Substitution Set Hope	 Thatcher	 Timstein
1B	13.9	13.8	13.2
1D	13.5	----	13.5
2A	14.6	14.3	13.2
2B	13.7	14.0	14.4
2D	14.2	14.7	13.6
3A	14.7	13.6	13.6
3B	13.3	14.2	15.1*
3D	13.8	14.3	13.9
4A	14.3	14.0	13.7
4B	14.2	14.1	13.2
4D	14.2	14.4	14.2
5A	14.1	14.3	13.5
5B	13.8	13.8	13.9
5D	14.5	14.2	14.6
6A	14.5	13.6	13.6
6B	13.6	14.0	14.1
6D	14.2	13.8	14.3
7A	13.8	14.5	----
7B	14.5	14.1	13.8
7D	14.6	14.5	14.8

Thatcher Parent	16.0*
Chinese Spring (Check)	13.6
L.S.D. .01	1.3

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

Table II. Milling yield of chromosome substitution lines. The values given are percent flour yield and are the averages of four replications.

Line	Substitution Set Hope	 Thatcher	 Timstein
1B	55.5	57.0	56.3
1D	54.6	----	57.1
2A	56.4	55.1	56.1
2B	56.8	55.7	56.0
2D	55.8	56.6	53.7
3A	56.1	56.4	56.5
3B	58.3*	53.0*	59.6*
3D	57.4*	58.0*	57.9*
4A	57.7*	55.9	56.9
4B	53.9	54.2	55.5
4D	55.1	57.1	56.1
5A	55.1	53.6	56.3
5B	54.6	56.0	55.8
5D	63.4*	55.8	59.9*
6A	54.4	55.6	56.0
6B	56.1	54.7	55.8
6D	54.4	55.5	52.9*
7A	56.0	57.6*	----
7B	53.9	55.8	55.8
7D	54.6	52.8*	56.3

Thatcher Parent	62.3*
Chinese Spring (Check)	55.2
L.S.D. .01	2.0

---

* Indicates that the value is significantly different from Chinese Spring at the .01 probability level.

yield in the Hope and Timstein set, but decreased milling yield in the Thatcher set. This indicates that Thatcher carries a different allele than the other two varieties, possibly a recessive gene. Chromosomes 3B and 3D are homoeologous chromosomes and according to theory each might be expected to carry a gene or genes that govern a given inherited character. Chromosome 5D in Hope and Timstein also appeared to carry genetic factors influencing milling yield. This chromosome is common to the one in Cheyenne which was shown to carry genetic factors affecting milling yield by Mattern, et al. (19, 20). Other chromosomes carrying factors influencing milling yield were Hope 4A, Thatcher 7A and 7D, and Timstein 6D.

The sedimentation test gives a measure of quantity and quality of the gluten. This test is based on the theory that gluten protein absorbs water and swells when treated with lactic acid under certain conditions and that a gluten with good quality absorbs more water, and thus swells more, than a poor quality gluten.

The data in Table III show the sedimentation values for the chromosome substitution lines. Chromosomes 2A, 2D, 3A, 7B and 7D in Hope appear to carry genetic factors which increased sedimentation. The Hope 2A line had an exceptionally high sedimentation value of 52.9 as compared to 34.9 for Chinese Spring. Chromosomes 4A and 2D in Thatcher appeared to carry genetic factors affecting sedimentation; 4A caused a decrease and 2D caused an increase in sedimentation values. In the Timstein substitution set, genetic factors causing increased sedimentation were carried on chromosomes 1B, 2B, 3B and 2D while factors causing decreased sedimentation

Table III. Sedimentation values of chromosome substitution lines. The values given are in cubic centimeters and are averages of four replications.

Line	Substitution Set		
	Hope	Thatcher	Timstein
1B	39.5	37.7	40.8*
1D	34.8	----	20.0*
2A	52.9*	36.7	32.8
2B	32.1	39.2	40.4*
2D	45.4*	49.2*	46.9*
3A	47.0*	34.1	32.1
3B	35.3	37.9	40.0*
3D	33.4	37.6	34.0
4A	31.3	28.7*	37.2
4B	36.6	33.8	32.0
4D	35.6	35.2	36.7
5A	34.1	32.4	35.4
5B	34.6	34.9	33.8
5D	39.4	35.5	36.6
6A	35.2	31.0	29.2*
6B	32.9	36.4	34.6
6D	31.5	35.1	31.6
7A	35.2	36.9	----
7B	43.5*	34.8	33.2
7D	39.8*	34.6	35.6
		Thatcher Parent	59.5*
		Chinese Spring (Check)	34.9
		L.S.D. .01	4.9

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

were on chromosomes 1D and 6A. Substitution line 1D was exceptionally low in sedimentation (20.0) indicating that this chromosome carries a gene or genes that induce the formation of low quality gluten within the endosperm. The only chromosome affecting sedimentation that was common to all three varieties was 2D which increased sedimentation.

Starch damage is a measure of the percent starch granules that are damaged during milling and is indicative of kernel hardness. Therefore, those lines which have more starch damage than Chinese Spring may have harder endosperms. Table IV gives the starch damage of the chromosome substitution lines. Chromosomes 2B and 5D in Hope, 2B, 4A, 5A and 7A in Thatcher, and 3B, 3D, 5D and 7D in Timstein increased endosperm hardness when substituted into Chinese Spring as indicated by the percent damaged starch.

The farinograph is a physical dough-testing instrument. It is essentially a recording dough mixer that measures the plasticity and mobility of the dough when subjected to a prolonged, relatively gentle, mixing action at a constant temperature. Four measurements, absorption, peak, stability and valorimeter can be obtained from the farinogram. A representative farinogram for each substitution line is given in Figures 5-7.

The data in Table V show the absorption of the substitution lines. Substitution lines Timstein 3B and 5D were exceptionally high in absorption with values of 68.0% and 67.1% as compared to 61.1% for Chinese Spring. This indicates that these chromosomes carry factors that are important for increasing absorption when substituted into Chinese Spring. Other

Table IV. Starch damage of chromosome substitution lines. The values given are percent damaged starch and are averages of four replications.

	Substitution Set		
Line	Hope	Thatcher	Timstein
1B	5.64	5.96	6.10
1D	5.86	----	6.28
2A	5.95	6.20	5.51
2B	6.47*	7.06*	6.09
2D	5.94	6.25	5.53
3A	6.18	5.94	6.38
3B	5.98	5.29	9.21*
3D	6.10	5.73	6.49*
4A	6.27	6.61*	6.11
4B	5.89	6.01	5.71
4D	5.43	6.06	5.29
5A	5.76	6.53*	6.29
5B	5.74	6.09	6.26
5D	8.30*	5.90	9.06*
6A	5.61	5.88	6.05
6B	5.71	6.09	6.02
6D	6.01	5.99	5.97
7A	6.09	7.60*	----
7B	5.77	6.00	5.80
7D	5.58	6.18	7.65*

Thatcher Parent	7.41*
Chinese Spring (Check)	5.84
L.S.D. .01	0.59

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

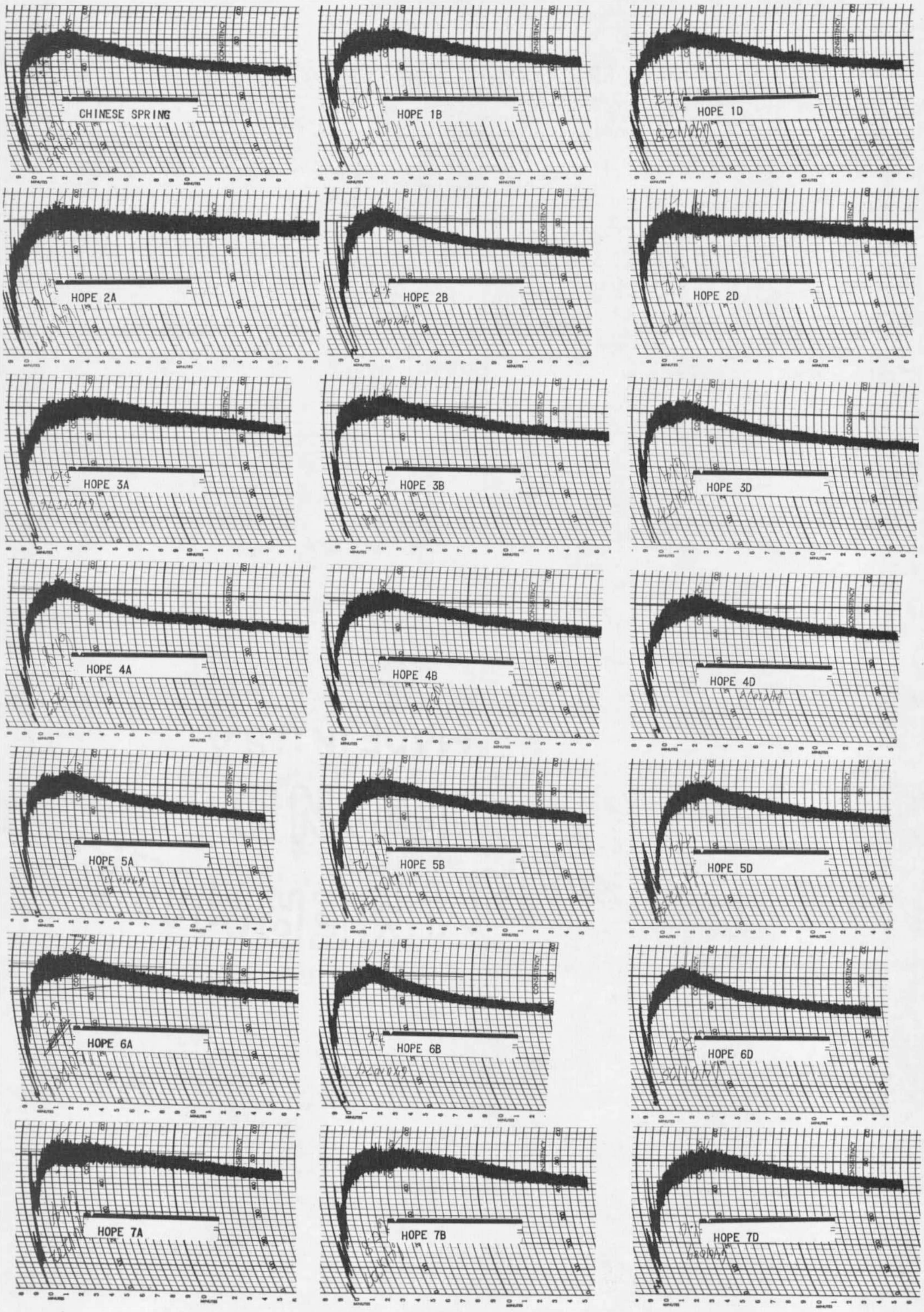


Figure 5. Representative farinograms of the Hope chromosome substitution set.

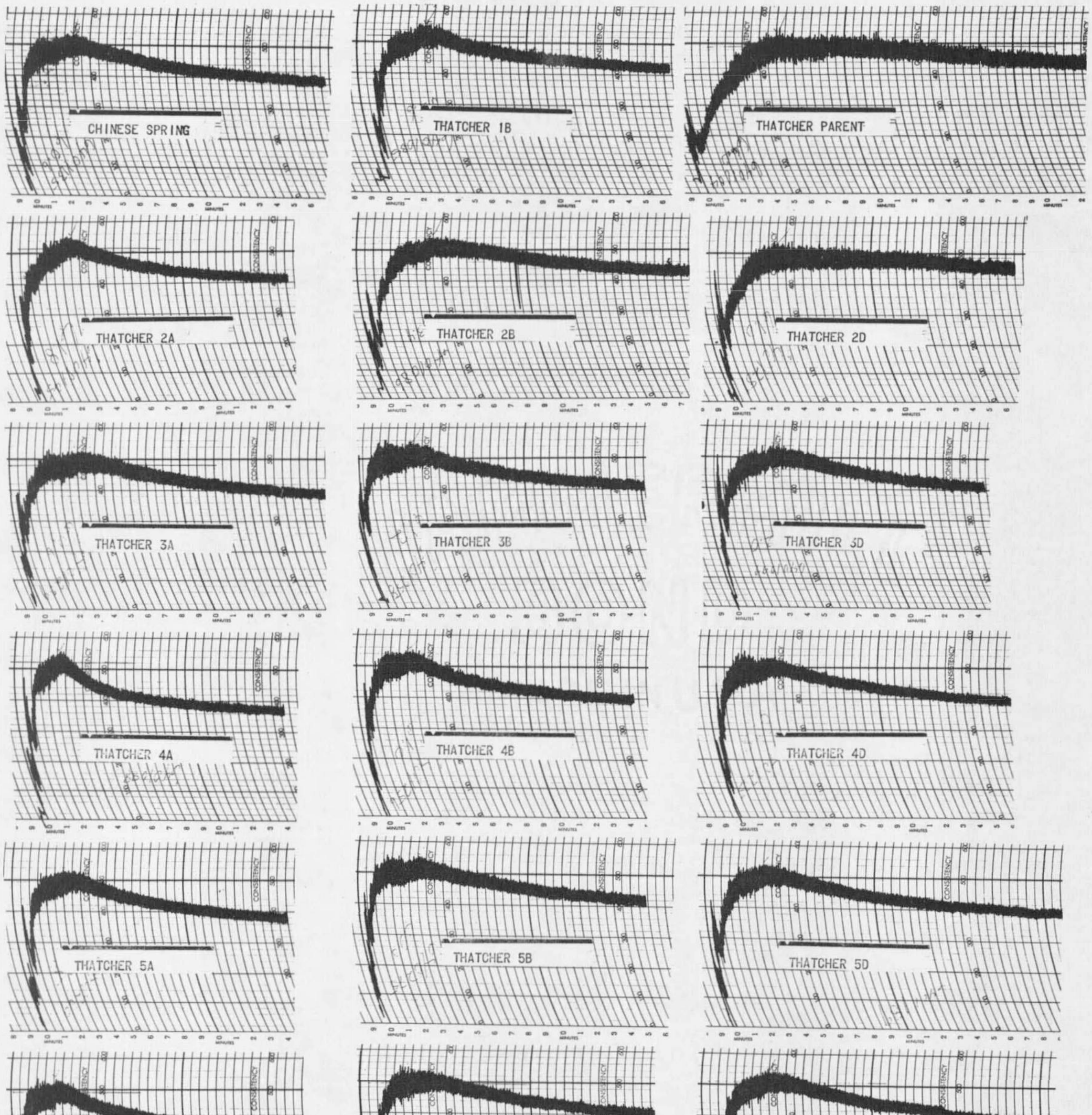


Figure 6. Representative farinograms of the Thatcher chromosome substitution set.

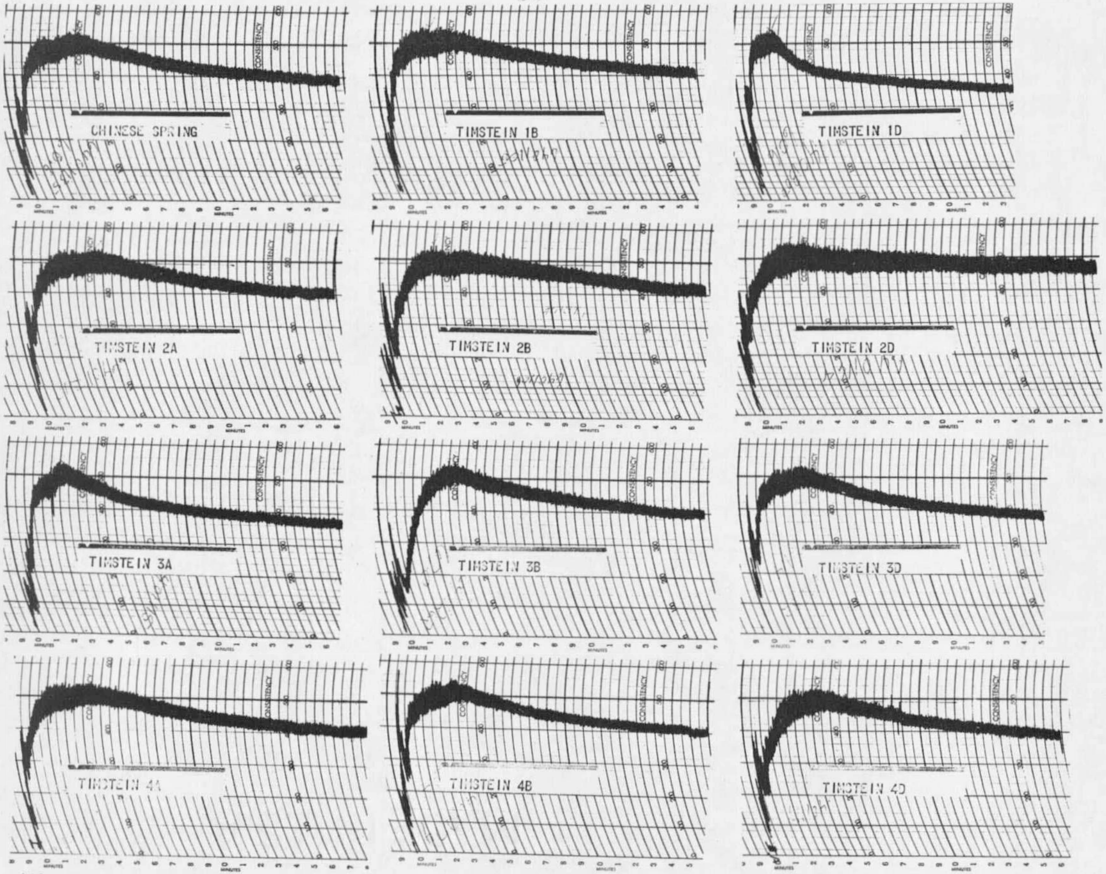


Figure 7. Representative farinograms of the Timstein chromosome substitution set.

Table V. Water absorption of chromosome substitution lines. The values are given in percent and are the averages of four replications.

Line	Substitution Set Hope	 Thatcher	 Timstein
1B	61.2	61.5	61.0
1D	61.7	----	60.4
2A	62.6*	62.0	60.4
2B	62.4	62.4	61.3
2D	61.3	60.6	60.4
3A	62.2	60.5	61.4
3B	59.5*	61.9	68.0*
3D	61.6	61.2	61.7
4A	62.6*	63.5*	61.4
4B	61.2	61.4	60.3
4D	60.4	60.5	59.2*
5A	61.8	63.0*	61.6
5B	60.9	59.9	61.0
5D	64.7*	61.5	67.1*
6A	61.6	60.7	60.5
6B	59.6	61.4	61.0
6D	62.4	61.3	61.7
7A	61.9	64.1*	----
7B	60.7	60.9	59.7
7D	61.2	63.6*	65.0*

Thatcher Parent	64.9*
Chinese Spring (Check)	61.1
L.S.D. .01	1.4

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

chromosomes that appeared to carry factors governing absorption are: Hope 2A, 3B, 4A, and 5D; Thatcher 4A, 5A, 7A, and 7D; and Timstein 4D and 7D. Hope 3B and Timstein 4D were exceptionally low in water absorption.

There was a highly significant r value of 0.88 between starch damage and water absorption. This might be expected, since broken or damaged starch granules provide more surface area for the water to be absorbed. However, in some cases those lines which had high water absorption did not have a greater amount of damaged starch. Hope and Thatcher 2B and Timstein 3D were significantly higher in starch damage but they were not significantly higher in water absorption. Hope 2A and 4A, Thatcher 7D and Timstein 6D were high in water absorption but not in starch damage. Those which were high in both starch damage and water absorption were Hope 5D, Thatcher 4A, 5A and 7A, and Timstein 3B, 5D and 7D. The high starch damage and water absorption of Timstein 3B may be due to its high protein content. However, the high starch damage and water absorption of the other substitution lines cannot be attributed to high protein content since there was no significant difference in protein content in the other substitution lines.

The farinograph peak is the time required for maximum dough development, or consistency. Table VI presents the peak time for the chromosome substitution lines. There was little difference in peak time between the substitution lines. Substitution lines Timstein 1D and 2D and Thatcher 4A had significantly lower peak times and substitution line Hope 3A had a significantly higher peak time than Chinese Spring. None of the Thatcher substitution lines tested approached the Thatcher parent in peak time,

Table VI. Peak time of chromosome substitution lines. The values are given in minutes and are averages of four replications.

Line	Substitution Set Hope	 Thatcher	 Timstein
1B	3.9	4.0	3.9
1D	3.3	---	2.0*
2A	4.1	3.5	3.9
2B	2.9	4.5	3.4
2D	3.0	4.2	2.7*
3A	4.8*	3.7	3.4
3B	4.0	3.6	4.2
3D	3.4	4.2	3.4
4A	3.1	2.6*	3.4
4B	4.4	3.2	3.5
4D	4.0	3.4	3.6
5A	3.4	3.1	3.6
5B	3.9	3.7	3.4
5D	4.3	3.6	3.9
6A	3.8	3.1	3.0
6B	3.4	3.6	3.5
6D	3.5	3.6	2.9
7A	3.5	3.9	---
7B	4.1	3.6	3.1
7D	4.0	3.6	3.9
		Thatcher Parent	7.1*
		Chinese Spring (Check)	3.7
		L.S.D. .01	1.0

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

indicating that this character is either complexly inherited with several chromosomes effective, or that genes governing peak time in Thatcher are located on one of the chromosomes (1A or 1D) not tested.

Stability gives an indication of the tolerance of flour to mixing and is defined as the difference in time between the point where the top of the curve first intercepts the 500 B.U. line, and the point where the top of the curve leaves the 500 B.U. line on the farinogram. Table VII presents stability values for the chromosome substitution lines. Homoeologous chromosomes 2A and 2D in Hope, and 2B and 2D in both Thatcher and Timstein have an increasing effect on stability when substituted into Chinese Spring. This indicates that these chromosomes carry factors that are important in causing increased mixing tolerance of the flour. Other chromosomes carrying genes that induce increased stability are Hope 3A and 7B and Timstein 1B. The Hope 2A substitution line had exceptionally good mixing tolerance with a stability of 16.0 minutes as compared to 4.0 minutes for Chinese Spring. The data also indicate that Thatcher 4A and Timstein 1D carry factors which induce reduced mixing tolerance of the flour.

The valorimeter value is an empirical, single-figure quality score and is based on peak time and stability. This value is derived from the farinogram by means of a special template supplied by the manufacturer of farinograph equipment. The valorimeter value is probably a better indication of bread baking quality than any of the other tests used in this study.

Table VII. Farinogram stability of chromosome substitution lines. The values given are in minutes and are the averages of four replications.

Line	Substitution Set		
	Hope	Thatcher	Timstein
1B	5.5	3.8	5.8*
1D	4.0	---	1.6*
2A	16.0*	3.3	4.0
2B	3.2	6.6*	7.1*
2D	9.5*	12.1*	9.6*
3A	10.0*	4.1	2.8
3B	4.6	4.1	3.0
3D	3.1	4.2	3.5
4A	2.6	1.5*	4.7
4B	5.2	3.0	3.7
4D	4.4	3.4	4.4
5A	4.5	3.1	4.1
5B	4.7	5.2	3.6
5D	3.5	4.1	3.3
6A	5.0	2.9	3.0
6B	3.6	4.2	3.7
6D	2.5	4.4	2.4
7A	5.2	4.0	---
7B	7.3*	4.2	4.0
7D	5.0	3.4	3.2

Thatcher Parent	12.4*
Chinese Spring (Check)	4.0
L.S.D. .01	1.7

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

Valorimeter values for the substitution lines are given in Table VIII. Chromosomes 2A, 2D, 3A and 7B in Hope, 2B and 2D in Thatcher and 2D in Timstein appear to carry genetic factors that induce increased flour quality when substituted into Chinese Spring. Chromosomes 4A in Thatcher and 1D, 6A and 6D in Timstein appear to carry factors that induce decreased flour quality when substituted into Chinese Spring. Chromosome 1D is common to the one in Kharkof MC-22 that has been identified with quality factors by Welsh and Hehn (34).

Table IX presents a summary of the chromosome substitution lines that significantly differ from Chinese Spring in some quality characteristic, together with the quality characteristic in which they differ.

Using Chinese Spring as a check, substitution line Hope 2A had very strong gluten as indicated by sedimentation, stability and valorimeter values. It also had high water absorption. Hope 3A had relatively strong gluten and increased peak time. Hope 4A had high milling yield and absorption. Hope 3B had a high milling yield, but low absorption. Hope 7B and 2D had relatively strong glutens. Hope 3D had a high milling yield. Hope 5D had very high milling yield, starch damage and water absorption. Hope 7D had high sedimentation.

In the Thatcher substitution set, Thatcher 4A had weak gluten, low peak time, but high starch damage and absorption. Thatcher 5A had high starch damage and absorption. Thatcher 7A had high milling yield, starch damage and absorption. Thatcher 2B had high starch damage. Thatcher 3B had low milling yield. Thatcher 2D had very strong gluten. Thatcher 3D

Table VIII. Valorimeter values of chromosome substitution lines. The numbers given are the averages of four replications.

	Substitution Set		
Line	Hope	Thatcher	Timstein
1B	52.0	52.2	53.0
1D	49.0	----	35.7*
2A	64.5*	48.0	50.5
2B	44.7	56.7*	53.2
2D	57.7*	63.5*	60.0*
3A	62.2*	49.2	46.2
3B	51.5	49.0	51.5
3D	47.0	53.0	46.2
4A	45.2	40.0*	49.7
4B	51.5	45.7	47.7
4D	51.5	47.7	49.7
5A	48.0	45.7	49.2
5B	51.5	53.0	49.0
5D	55.0	50.0	50.2
6A	51.2	45.2	44.0*
6B	48.5	50.2	48.0
6D	46.2	49.2	42.7*
7A	51.0	49.5	----
7B	57.0*	49.0	45.5
7D	54.0	49.7	49.2

Thatcher Parent	69.7*
Chinese Spring (Check)	50.2
L.S.D. .01	5.4

* Indicates the value is significantly different from Chinese Spring at the .01 probability level.

Table IX. Chromosome substitution lines that were significantly different at the .01 level from the Chinese Spring check. The values are averages of four replications.

		Protein %	Milling %	Sedimentation, cc.	Starch Damage %	Absorption %	Peak min.	Stability, min.	Valorimeter
Hope	2A			52.9		62.6		16.0	64.5
	3A			47.0			4.8	10.0	62.2
	4A		57.7			62.6			
	2B				6.47				
	3B		58.3			59.5			
	7B			43.5				7.2	57.0
	2D			45.4				9.5	57.7
	3D		57.4						
	5D		63.4		8.30	64.7			
	7D			39.8					
Thatcher	4A			28.7	6.61	63.5	2.6	1.5	40.0
	5A				6.53	63.0			
	7A		57.6		7.60	64.1			
	2B				7.06			6.6	56.7
	3B		53.0						
	2D			49.2				12.1	63.5
	3D		58.0						
	7D		52.8			63.6			
Timstein	6A			29.2					44.0
	1B			40.8				5.7	
	2B			40.4				7.1	
	3B	15.1	59.6	40.0	9.21	68.0			
	1D			20.0			2.0	1.6	35.7
	2D			46.9			2.7	9.6	60.0
	3D		57.9		6.49				
	4D					59.2			
	5D		59.9		9.06	67.1			
	6D		52.9						42.7
	7D				7.65	65.0			
Thatcher Parent		16.0	62.3	59.5	7.41	64.9	7.1	12.4	69.7
Chinese Spring (Check)		13.7	55.2	34.9	5.84	61.1	3.7	4.0	50.2
L.S.D. .01		1.3	2.0	4.9	0.59	1.4	1.0	1.7	5.4

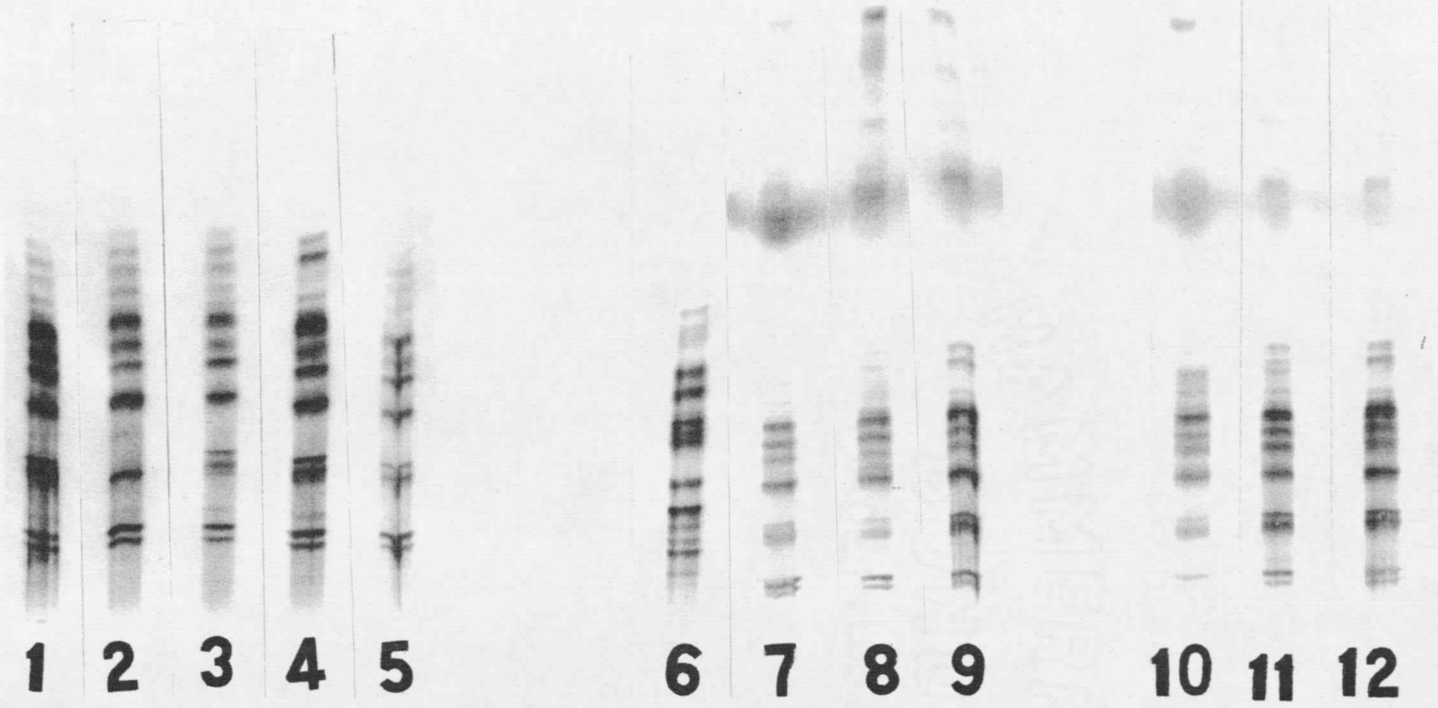
had higher milling yield. Thatcher 7D had low milling yield and high absorption. The Thatcher parent was very high in all of the quality characteristics tested.

In the Timstein substitution set, Timstein 6A had low sedimentation and valorimeter value. Timstein 1B and 2B were high in sedimentation and stability. Timstein 3B had high protein, milling yield, sedimentation, starch damage and absorption. Timstein 1D had very low gluten strength and low peak time. Timstein 2D had strong gluten and a low peak time. Timstein 3D had high milling yield and starch damage. Timstein 4D had low absorption. Timstein 5D had high milling yield, starch damage and absorption. Timstein 6D had low milling yield and valorimeter value. Timstein 7D had high starch damage and water absorption.

It is evident from the data presented that there are several chromosomes within a wheat variety that carry quality factors. It is also apparent that homologous chromosomes in wheat do not necessarily carry the same quality factors since the effect of a particular chromosome of one variety does not necessarily cause the same effect as its homolog in another variety, when each is substituted into a Chinese Spring background.

Starch gel electrophoresis patterns of ten of the chromosome substitution lines and the Chinese Spring and Thatcher parents are presented in Figure 8.

Hope 2A, which had a strong gluten, has a slightly different electrophoretic pattern from Chinese Spring, with the difference appearing in the area of the third and fourth band from the bottom. None of the other Hope



1. Chinese Spring
2. Hope 2A
3. Hope 3A
4. Hope 2D
5. Hope 5D
6. Thatcher Parent
7. Thatcher 4A
8. Thatcher 2B
9. Thatcher 2D
10. Timstein 6A
11. Timstein 1D
12. Timstein 2D

Figure 8. Electrophoretic patterns of ten chromosome substitution lines and the Chinese Spring and Thatcher parents.

chromosome substitution lines tested (3A, 2D and 5D) appeared to be different from Chinese Spring.

The Thatcher parent has a distinctively different electrophoretic pattern than Chinese Spring, however, all three of the Thatcher substitution lines tested (4A, 2B and 2D) appear to have the same pattern as Chinese Spring. This indicates that recovery of the Chinese Spring electrophoretic characteristics in these substitution lines was very good and that none of the chromosomes tested (4A, 2B and 2D) alter the electrophoretic behavior when substituted into Chinese Spring.

The three Timstein substitution lines tested (6A, 1D and 2D) all appeared to have the same electrophoretic pattern as Chinese Spring.

With the exception of Hope 2A, none of the chromosome substitution lines tested showed qualitative differences in electrophoretic components, even though a wide range in quality characteristics was observed between the lines. However, there may be some quantitative differences in the electrophoretic components between some of the substitution lines. This is indicated by the differences in the relative stain concentration of the bands between some of the lines. No attempt was made to obtain quantitative measurements in this study and it is proposed that this be done in the future. It is also proposed that the flour protein be separated into several fractions by some other method (possibly column chromatography) and each of these fractions be further separated by electrophoresis. This may lead to the detection of minute differences.

II. Monosomic Lines

Wheat protein, sedimentation, and farinograph data obtained from the Kharkof MC-22 monosomic and disomic lines are given in the Appendix Table IX. A summary of this data is presented in Table X and a representative farinogram for each line is presented in Figure 9.

The monosomic 1D lines have extremely poor gluten quality as indicated by peak, stability, valorimeter and sedimentation data. However, the protein content was not reduced. This indicates that the poor quality of monosomic 1D, as compared to its disomic, is not due to a lack in total protein, but rather to differences in the quality of the protein. This can be considered evidence that chromosome 1D is important in the determination of protein quality and that the gene or genes on this chromosome affecting protein quality cannot operate effectively in the 3n-2 condition of the endosperm. These results compare favorably with those reported by Welsh and Hehn (34). Chromosome 1D is common to the chromosome in Timstein shown to carry genetic factors inducing low quality gluten when substituted into Chinese Spring in the previous section of this thesis.

Monosomic line 5D was significantly higher in water absorption, indicating that chromosome 5D carries genetic factors influencing water absorption. This chromosome is common to the one in Hope and Timstein shown to carry genetic factors governing absorption in the previous section of this thesis.

The data in Table XI show the results obtained from the Kharkof MC-22 x Itana wheat lines. The farinogram for each line is pictured in Figure 10. Interpretation of these data is difficult since there were no

Table X. Mean values and statistical data for quality characteristics of several monosomic and disomic lines of Kharkof MC-22. Averages are of three replications.

Line	Protein (%)	Farinograph Data Abs. (%)	Peak (min.)	Stab. (min.)	Val.	Sed. Value (cc)
Grand Mean	17.8	62.4	14.4	18.2	87.0	66.9
L.S.D. (.01)	0.90	1.78	4.98	2.49	8.44	5.44
1-A (M)	17.9	61.8	15.5	20.2*	90.7	70.5
2-A (M)	17.9	62.5	12.8	16.7	84.0	69.8
2-A (D)	18.2	62.2	16.2	21.0	91.0	70.2
3-A (M)	18.6	63.7	17.7	23.7*	94.7	69.7
3-A (D)	17.6	62.5	16.0	19.7	92.0	69.5
5-A (M)	18.3	62.7	17.5	20.3	92.3	70.2
5-A (D)	17.5	62.4	16.5	20.3	91.7	70.3
6-A (M)	17.3	62.3	14.7	17.8	89.3	66.7
7-A (M)	17.8	62.6	12.2	17.5	89.0	65.2
1-B (M)	18.4	62.7	9.5	11.3*	76.0*	65.5
2-B (M)	18.2	62.5	15.2	18.0	89.0	70.0
2-B (D)	17.3	62.5	16.3	16.8	91.0	70.3
5-B (M)	17.9	63.3	17.5	15.5*	92.7	70.7
6-B (M)	17.9	61.9	14.0	19.3	88.3	65.2
7-B (M)	17.5	61.7	17.3	25.8*	94.3	68.7
1-D (M)	18.1	61.6	4.7*	4.2*	54.0*	40.8*
1-D (M)	18.2	61.7	4.5*	4.2*	53.3*	45.5*
1-D (D)	17.5	62.3	15.3	21.2*	91.0	70.3
3-D (M)	17.4	61.7	14.7	16.8	88.7	69.5
3-D (D)	17.3	61.7	12.8	17.5	84.3	67.3
4-D (M)	17.4	62.6	17.3	21.2*	93.7	69.0
4-D (D)	17.2	62.2	15.3	22.7*	91.0	68.3
5-D (M)	18.5	64.7*	12.8	22.2*	85.7	57.7*
5-D (D)	17.4	62.2	16.7	19.0	92.3	69.8
6-D (M)	18.3	62.2	18.2	23.3*	94.7	70.8
6-D (D)	18.2	62.8	12.8	18.3	85.0	67.0
K MC-22	17.1	62.0	14.3	18.2	88.3	67.5

* Indicates the value is significantly different from the grand mean at the .01 level.

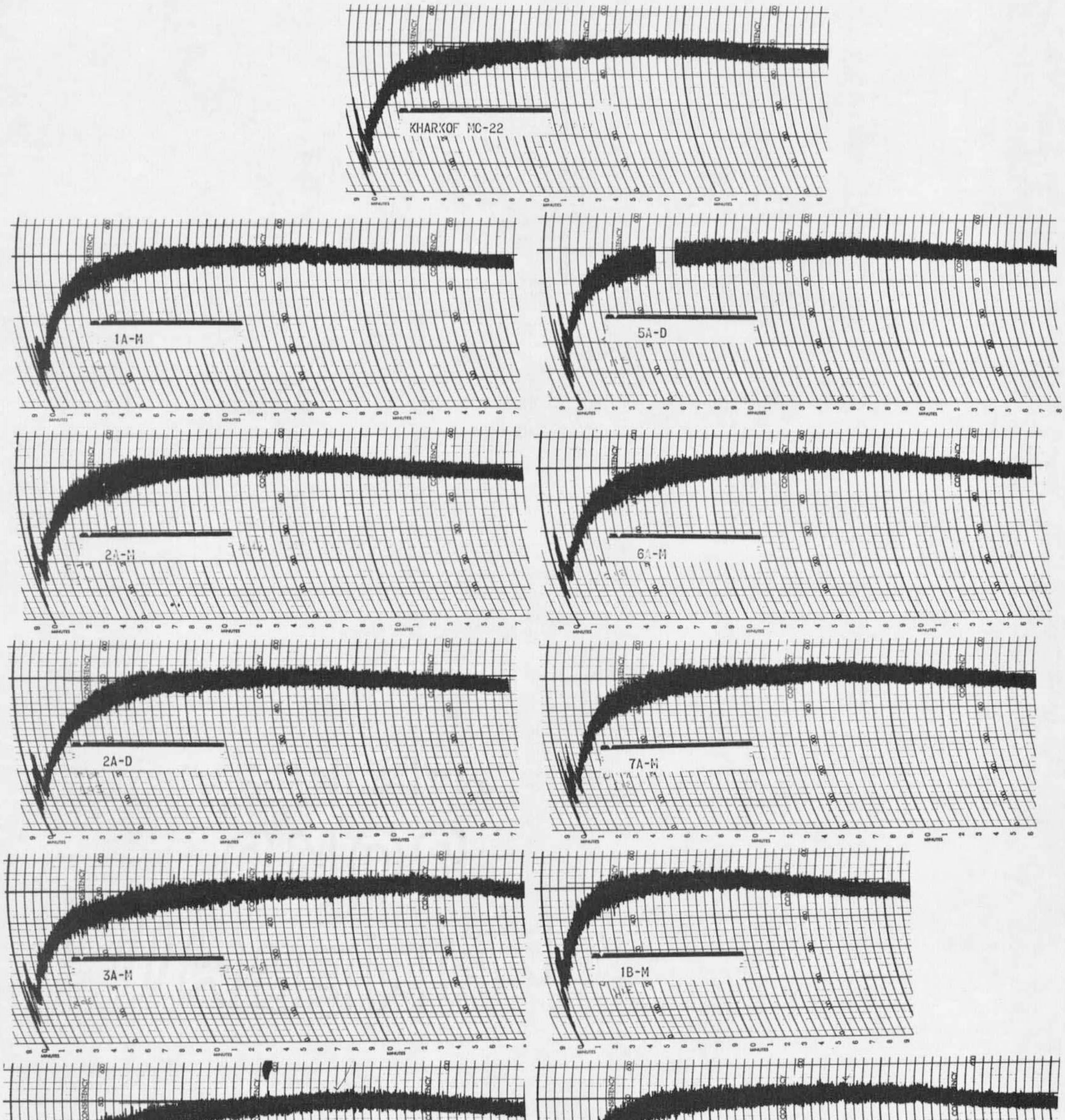


Figure 9. Farinograms for several Kharkof MC-22 monosomic and disomic wheat lines.

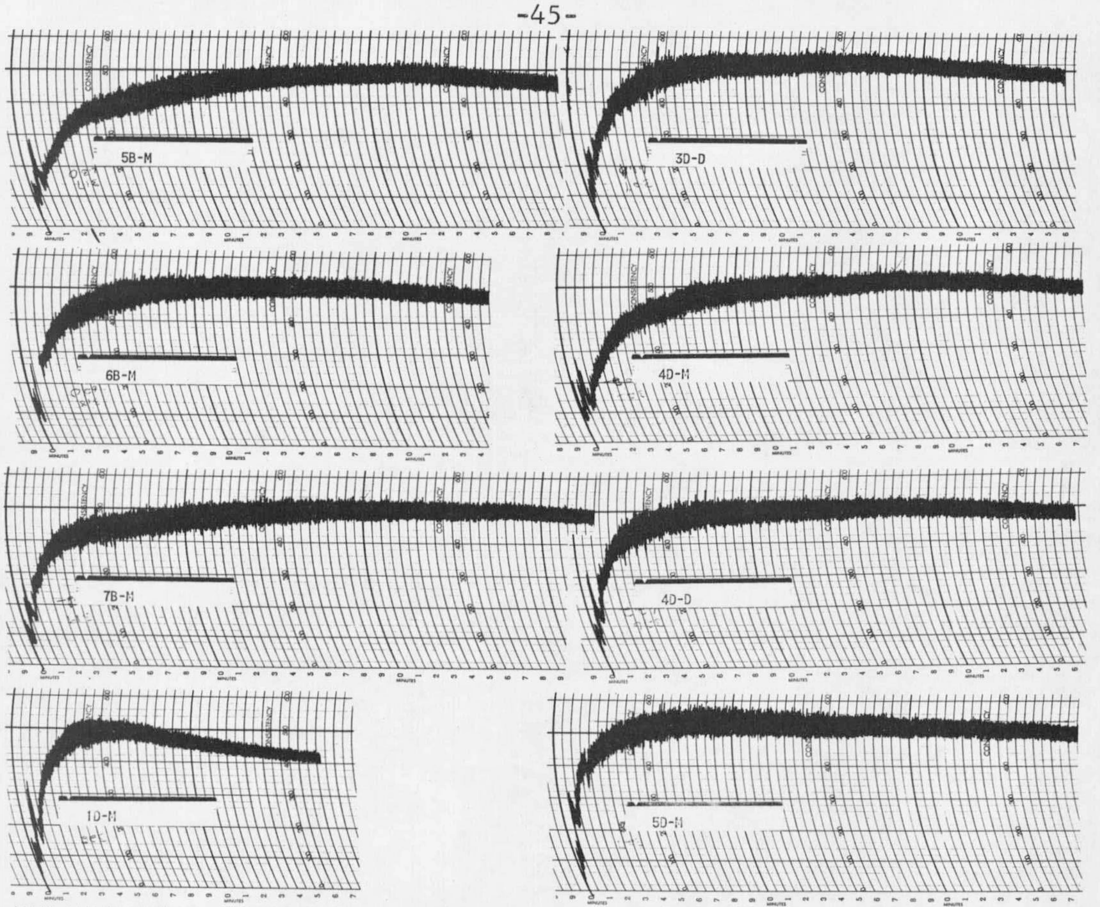


Figure 9. (Continued)

Table XI. Quality data for several Kharkof MC-22 x Itana monosomic and disomic wheat lines. Material is the F_3 populations from monosomic or disomic identified plants.

Variety	Starch Damage (%)	% on 6½/64" Screen	Kernel Weight (mg.)	Test Weight (lbs/bu)	Flour		Farinograph Data				Flour Prot. (%)	Sed. Val. (cc)
					Yield (%)	Ash (%)	Abs. (%)	Peak (min.)	Stab. (min.)	Val.		
K MC-22 x It.	7.13	18.0	28.3	61.2	70.8	0.42	60.2	6.5	10.0	67	13.1	68.0
1-A x It.(M)	4.97	14.9	27.3	60.5	64.5	0.41	57.0	7.0	10.0	69	12.7	70.0
2-A x It.(M)	6.20	18.7	25.7	60.4	66.5	0.40	60.0	7.5	15.0	73	13.3	71.0
2-A x It.(D)	5.46	15.8	25.5	60.6	68.8	0.38	59.0	6.0	12.0	67	12.7	69.0
3-A x It.(M)	5.46	21.4	26.5	60.3	68.0	0.37	58.3	6.5	13.0	69	12.8	71.5
3-A x It.(D)	6.20	18.9	26.6	61.3	69.5	0.37	60.5	7.0	10.0	70	13.0	69.0
4-A x It.(M)	5.95	16.8	25.4	61.2	65.9	0.37	59.0	5.5	12.5	67	12.6	68.0
4-A x It.(D)	6.40	21.1	26.9	60.9	69.7	0.36	59.2	6.5	12.0	69	12.3	71.0
5-A x It.(M)	6.89	9.6	23.9	60.8	69.4	0.37	60.0	7.0	13.5	71	12.7	72.0
7-A x It.(M)	6.89	21.5	26.8	61.1	71.2	0.37	60.2	6.0	7.5	67	12.9	67.5
7-A x It.(D)	5.46	25.7	27.6	61.5	66.7	0.35	58.8	6.0	8.5	66	12.6	71.0
1-B x It.(M)	5.71	20.8	26.2	60.8	66.2	0.35	59.0	7.0	7.5	68	13.4	69.0
1-B x It.(D)	6.64	18.2	26.1	61.2	69.5	0.35	60.8	6.0	11.0	65	12.9	70.0
2-B x It.(M)	5.95	23.4	24.9	60.2	69.2	0.36	60.4	6.0	9.0	67	13.5	71.0
2-B x It.(D)	6.64	19.4	26.5	61.0	69.9	0.33	59.5	6.5	12.0	69	12.5	70.0
3-B x It.(D)	5.71	20.8	26.4	61.5	67.4	0.34	58.0	7.0	13.0	70	12.3	68.5
4-B x It.(M)	6.20	21.8	27.0	61.5	72.0	0.38	59.4	7.0	10.5	69	12.9	70.0
5-B x It.(M)	6.64	18.7	26.1	60.6	71.3	0.38	58.7	6.5	11.0	68	12.9	69.0
5-B x It.(D)	5.46	21.0	26.9	61.3	67.1	0.36	58.0	5.5	11.0	66	12.2	69.0
6-B x It.(D)	5.46	25.5	27.2	62.0	67.8	0.34	57.4	6.0	12.0	68	12.3	68.0
7-B x It.(M)	5.22	27.0	28.1	62.2	63.1	0.35	58.0	6.5	12.5	69	11.8	67.0
1-D x It.(M)	5.22	20.9	27.9	60.8	68.0	0.35	58.5	5.5	6.0	62	12.6	60.0
1-D x It.(D)	5.71	25.7	28.5	62.1	68.9	0.34	57.4	5.5	8.0	64	12.0	65.0

Table XI. (Continued)

Variety	Starch Damage (%)	% on 6½/64" Screen	Kernel Weight (mg.)	Test Weight (lbs/bu)	Flour Yield (%)	Flour Ash (%)	Farinograph Data Abs. (%)	Farinograph Data Peak (min.)	Farinograph Data Stab. (min.)	Farinograph Data Val.	Flour Prot. (%)	Sed. Val. (cc)
2-D x It.(M)	5.95	25.5	27.3	61.6	69.0	0.35	59.5	6.5	11.0	69	12.7	70.0
3-D x It.(D)	6.89	24.0	27.2	61.7	69.6	0.34	60.8	7.5	12.0	72	12.7	69.5
4-D x It.(M)	6.20	16.8	25.6	61.7	67.4	0.34	60.0	8.5	18.0	78	12.8	71.0
4-D x It.(D)	5.95	20.2	25.3	61.8	68.6	0.35	59.0	8.5	21.0	80	12.8	70.0
5-D x It.(M)	5.95	22.4	27.3	61.8	67.4	0.34	60.3	7.6	12.5	71	12.0	68.0
5-D x It.(D)	7.92	20.4	26.7	61.2	69.4	0.39	63.2	8.5	17.0	76	13.7	71.0
6-D x It.(M)	7.13	7.5	24.5	61.1	67.2	0.37	61.2	7.5	18.0	74	12.6	69.0
6-D x It.(D)	6.64	21.4	26.6	61.4	66.1	0.37	58.0	6.0	10.0	67	12.5	67.0
K MC-22	5.46	23.0	26.6	59.6	64.6	0.38	59.5	5.5	9.0	64	12.8	71.0
Itana	7.13	14.2	26.1	63.2	70.5	0.34	61.3	9.0	18.5	79	12.5	72.5
Grand Mean (n=33)		20.0	26.5	61.2	68.2	0.36	59.4	6.7	12.0	69	12.7	69.2
Monosomic Mean (n=11)		19.0	26.1	60.9	68.0	0.36	59.6	6.7	11.8	69	12.9	68.6
Disomic Mean (n=11)		20.7	26.7	61.3	68.6	0.36	59.4	6.5	12.0	69	12.6	69.3

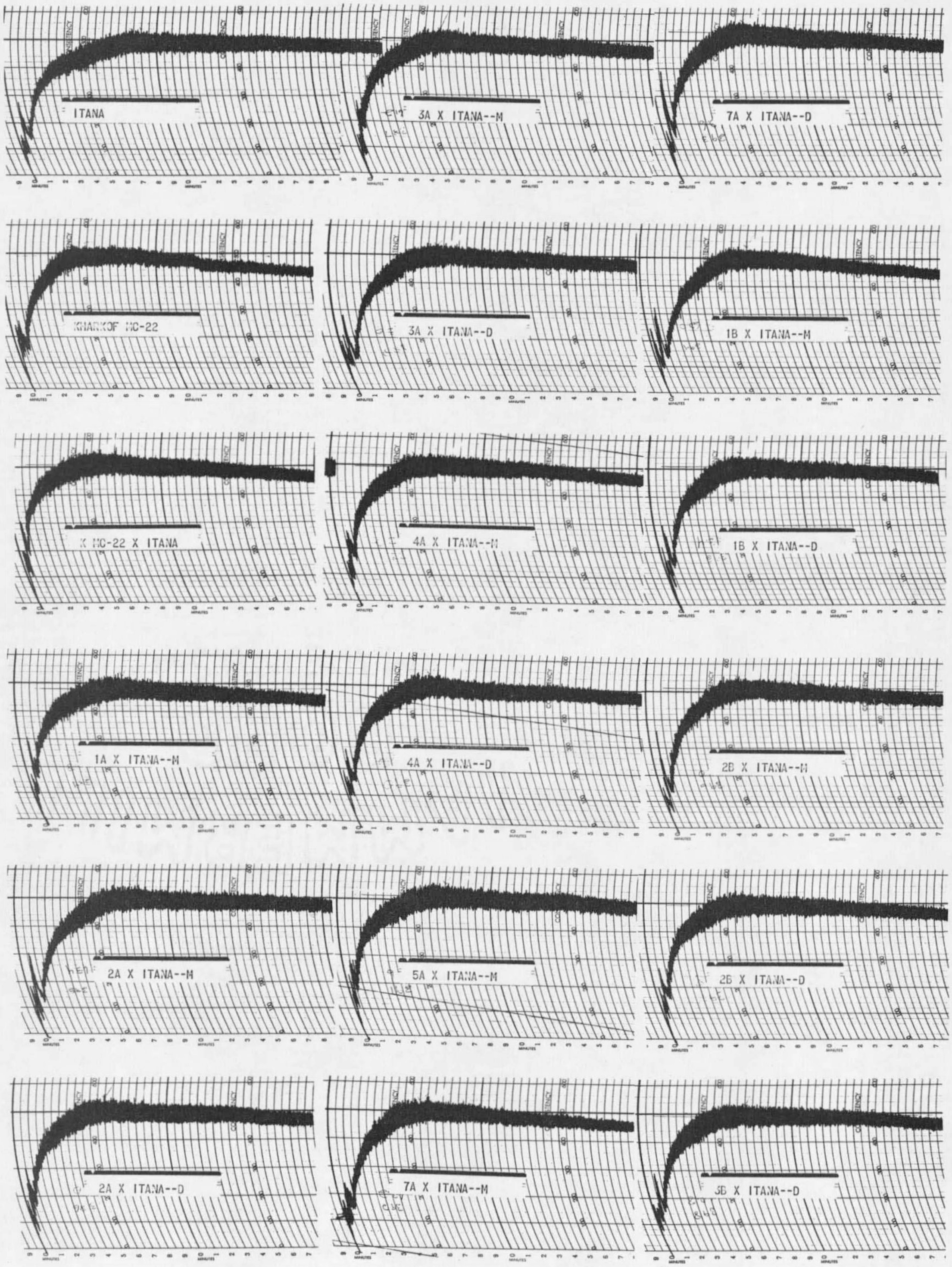


Figure 10. Farinograms for several Kharkof MC-22 x Itana monosomic and disomic wheat lines.

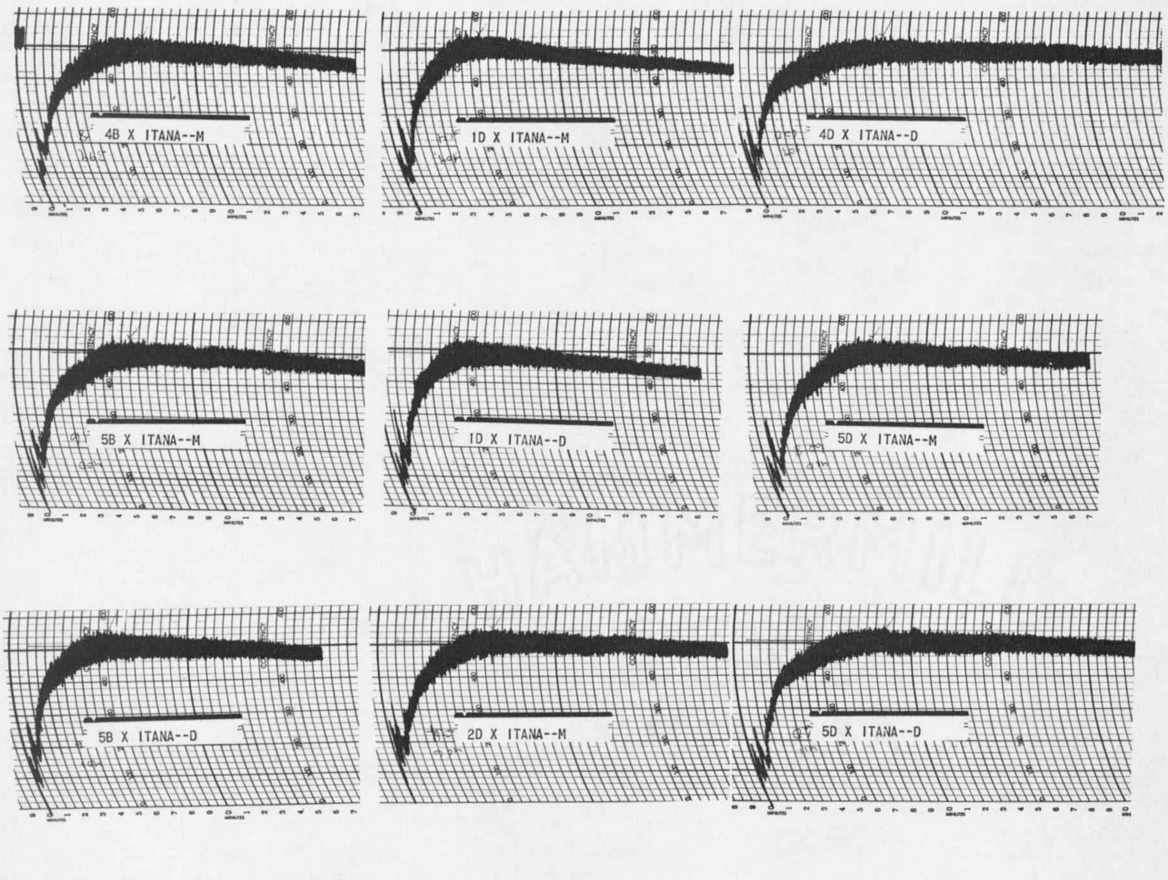


Figure 10. (Continued)

replications, no statistical analyses were made and there were large variations in the quality characteristics of the different segregating populations. Theoretical calculations in the Materials and Methods section show this material to be 42% monosomic as compared to 56% monosomic for the Kharkof MC-22 material, and this could account in part for the lesser effect of chromosome 1D.

The data in Table XII show the milling results obtained from the seven samples milled at Kansas State University. The Kharkof MC-22 monosomic 1D line gave a lower milling yield than the normal and disomic Kharkof MC-22. This may indicate that chromosome 1D carries genetic factors affecting milling yield as well as factors governing gluten quality. This was only one sample and was not replicated, so verification of the data must await further testing.

Table XIII gives the protein in the bran and flour fractions of these seven samples as determined by the macro-Kjeldahl method. The monosomic 1D line was higher in protein in both fractions as compared to its disomic. The monosomic 1D line of the material used in Table X was also as high, or higher, in protein than its disomic as determined by the Udy ion-binding method. This is of interest since the macro-Kjeldahl method measures protein in terms of total nitrogen and the Udy ion-binding method measures protein in terms of ion-binding properties, yet both indicate the monosomic 1D line to be as high or higher in protein than its disomic.

The sulfhydryl content of the seven samples is given in Table XIV. There does not appear to be any association between sulfhydryl content and quality of the flour.

Table XII. Micro milling results obtained from seven wheat varieties milled at Kansas State University.

Pedigree	Bran (%)	Shorts (%)	Red Dog (%)	Flour (%)
Itana	24.0	2.0	1.2	72.8
Cheyenne	23.8	1.6	1.0	73.5
Chinese Spring	33.1	1.5	1.4	63.9
Kharkof MC-22 Disomic	28.3	2.5	1.9	67.3
Kharkof MC-22 Normal	29.8	2.8	1.9	65.5
Kharkof MC-22 Monosomic 1D	33.2	2.5	4.9	59.4
Kharkof MC-22 x Itana Bulked F_2	27.8	2.0	4.6	65.4

Table XIII. Percent protein in the bran and flour fractions of seven wheat varieties. Protein determined by the macro-Kjeldahl method.

Pedigree	Bran Protein (%)	Flour Protein (%)
Itana	16.8	12.0
Cheyenne	15.5	12.7
Chinese Spring	19.0	15.2
Kharkof MC-22 Disomic 1D	16.9	13.0
Kharkof MC-22 Normal	15.6	12.6
Kharkof MC-22 Monosomic 1D	18.0	14.8
Kharkof MC-22 x Itana Bulked F_2	14.8	11.5

Table XIV. Sulfhydryl content in the flour of seven wheat varieties.

Pedigree	-SH Content, Dry Basis μ eq. per g.	Standard Deviation (from 3 titrations) μ eq. per g.
Itana	1.28	±.01
Cheyenne	0.94	.02
Chinese Spring	1.44	.10
Kharkof MC-22 Disomic	1.13	.07
Kharkof MC-22 Normal	0.81	.01
Kharkof MC-22 Monosomic 1D	0.93	.01
Kharkof MC-22 x Itana Bulked F_2	0.83	.12

Table XV. Amino acid analysis of three wheat variety flours. Values given are the percent by weight of each amino acid of the total amino acids recovered.

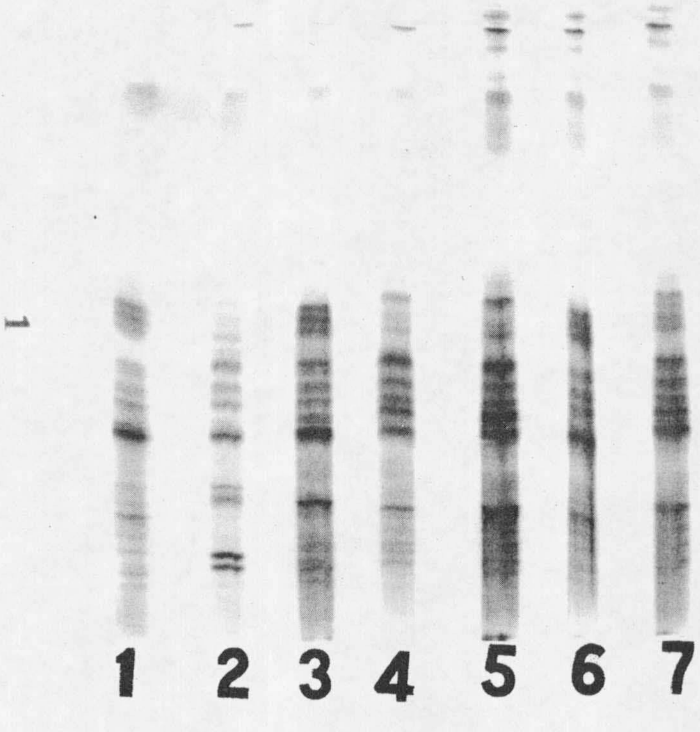
Amino Acid	Chinese Spring	Kharkof MC-22 Normal	Kharkof MC-22 Monosomic 1D
Aspartic acid	5.72	4.47	4.44
Threonine	3.72	2.46	2.36
Serine	6.50	6.12	4.64
Glutamic acid	24.25	34.93	42.98
Proline	10.90	13.20	7.97
Glycine	3.99	2.99	3.67
Alanine	3.60	2.22	3.24
Valine	4.10	3.07	2.35
Cystine	3.67	3.56	3.24
Methionine	0.65	0.41	1.64
Iso-leucine	3.43	2.98	1.78
Leucine	6.95	6.86	5.61
Threonine	3.45	2.88	3.17
Phenylalanine	5.32	4.52	4.28
Lysine	2.10	1.83	1.83
Hestidine	2.17	1.91	1.64
Arginine	3.55	3.43	2.96

The amino acid analysis of Chinese Spring, Kharkof MC-22 normal and Kharkof MC-22 monosomic 1D is reported in Table XV. This preliminary data indicates that there may be differences between the lines in relative amounts of some of the amino acids. Kharkof monosomic 1D showed a low content of serine, proline, valine and leucine compared to Chinese Spring and Kharkof MC-22. Chinese Spring was higher in aspartic acid, threonine, alanine, and valine and low in glutamic acid. Kharkof MC-22 showed a high content of proline and a low content of alanine.

If these differences are real, then wheat breeders may be able to alter the amino-acid content of wheat, and may be able to produce wheat that has a better balance of amino acids from the nutritional standpoint. Again, it should be mentioned that these data are on only one sample and verification of these results will have to be made at a later date on more samples.

Starch gel electrophoresis patterns of the seven samples milled at Kansas State University are presented in Figure 11.

The Itana, Chinese Spring, Cheyenne and Kharkof MC-22 lines all appear to have different patterns, especially among the slower moving components, with Chinese Spring showing a distinctively different pattern. The Chinese Spring used in this group has the same electrophoretic pattern as the Chinese Spring used in the chromosome substitution line material. This is of interest since these two samples were grown in different years, yet both have the same electrophoretic pattern. This may indicate that the year-to-year variation in environment has little effect upon the electrophoretic components of a wheat variety. However, this conclusion is



1 Itana
2 Chinese Spring
3 Cheyenne
4 Kharkof MC-22 disomic
5 Kharkof MC-22 normal
6 Kharkof MC-22 monosomic
7 Kharkof MC-22 x Itana, Bulked F_2

Figure 11. Electrophoretic patterns for seven wheat flour samples.

based on only one variety grown in two different years, and more testing will be needed to confirm this conclusion.

The Kharkof MC-22 disomic, Kharkof MC-22 normal and Kharkof MC-22 monosomic lines all appear to have the same electrophoretic patterns. This is to be expected, since the Kharkof MC-22 disomic and Kharkof MC-22 normal lines should be genetically the same. The Kharkof MC-22 monosomic material is theoretically 25% disomic so one would not expect a qualitative difference in this material from the disomic or normal material. However, there might be a quantitative difference which was not determined in this study.

It is proposed that material that is 100% monosomic be used for comparing the monosomic and disomic lines. This could be accomplished by cutting the wheat kernel in half, using the protein in the brush end half for electrophoresis, and growing a new plant from the germ end half. By cytological observation of the pollen mother cells from the new plant, one could determine if the seed was monosomic or disomic.

Although different varieties appear to show different electrophoretic patterns, there appears to be no association between the electrophoretic patterns and quality.

APPENDIX

Appendix Table I. Percent flour protein by replication, corrected to 14% moisture. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	15.0	14.5	14.7	14.1	14.57
	3A	15.6	14.6	14.2	14.5	14.72
	4A	14.6	13.1	14.7	14.9	14.32
	5A	12.8	14.6	14.3	14.8	14.12
	6A	13.9	15.1	14.2	14.7	14.47
	7A	13.0	13.3	14.9	14.1	13.82
	1B	13.9	13.9	13.8	13.9	13.87
	2B	13.8	13.5	13.8	13.6	13.67
	3B	13.7	12.8	13.9	12.9	13.32
	4B	13.4	13.4	15.0	15.0	14.20
	5B	14.2	14.0	13.5	13.5	13.80
	6B	14.0	13.4	13.2	13.6	13.55
	7B	14.4	14.4	14.9	14.4	14.52
	1D	13.5	13.6	14.3	12.5	13.47
	2D	14.5	13.9	13.9	14.5	14.20
	3D	14.1	13.7	13.6	13.8	13.80
	4D	14.8	14.2	14.3	13.7	14.25
	5D	14.6	13.7	15.0	14.6	14.47
	6D	14.4	14.1	15.1	14.2	14.20
	7D	14.9	14.0	15.1	14.5	14.62
Thatcher	2A	14.8	13.7	15.2	13.5	14.30
	3A	13.9	12.9	13.4	14.0	13.55
	4A	14.1	13.9	14.2	13.8	14.00
	5A	14.0	14.3	13.8	15.2	14.32
	6A	13.1	12.9	14.3	14.2	13.62
	7A	14.5	14.3	14.2	14.9	14.47
	1B	14.5	13.1	13.2	14.3	13.77
	2B	14.4	13.8	13.8	14.1	14.02
	3B	14.2	13.8	14.5	14.4	14.22
	4B	13.3	13.5	14.8	14.8	14.10
	5B	13.3	13.3	14.5	14.2	13.82
	6B	13.6	14.2	14.6	13.6	14.00
	7B	13.4	13.9	14.9	14.1	14.07
	2D	14.4	14.6	14.6	15.1	14.67
	3D	14.5	14.4	14.4	13.8	14.27
	4D	13.8	14.3	14.9	14.5	14.37
	5D	15.0	14.1	14.3	13.6	14.25
	6D	15.0	13.4	13.2	13.4	13.75
	7D	14.6	13.9	13.9	15.5	14.47
Thatcher Parent		16.6	16.0	15.4	15.9	15.97

Appendix Table I. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	13.4	12.3	13.1	14.0	13.20
	3A	13.2	12.9	13.6	14.8	13.62
	4A	13.1	14.0	13.7	14.0	13.70
	5A	13.3	13.7	13.7	13.2	13.47
	6A	13.1	13.6	13.7	13.9	13.57
	1B	13.3	13.3	13.1	12.9	13.15
	2B	14.3	14.3	14.1	14.9	14.40
	3B	14.2	15.2	15.4	15.5	15.07
	4B	12.4	13.1	13.5	13.8	13.20
	5B	13.2	14.2	14.1	14.1	13.90
	6B	13.5	14.4	14.7	13.8	14.10
	7B	12.8	13.9	14.5	14.0	13.80
	1D	13.9	13.5	13.4	13.1	13.47
	2D	13.1	13.9	15.5	14.5	13.60
	3D	14.0	14.0	13.7	13.8	13.87
	4D	14.6	14.7	14.1	13.6	14.25
	5D	14.7	14.3	14.1	15.2	14.57
	6D	13.8	14.0	14.9	14.6	14.32
	7D	14.9	14.8	14.6	14.8	14.77
Chinese Spring		12.7	12.6	14.8	14.5	13.65

Appendix Table II. Percent flour yield by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	55.22	57.70	56.29	56.36	56.39
	3A	53.47	56.58	57.50	56.73	56.07
	4A	57.00	57.51	59.55	56.68	57.68
	5A	55.87	55.92	54.88	53.74	55.10
	6A	55.17	54.81	56.23	51.51	54.43
	7A	58.15	57.57	53.00	55.11	55.96
	1B	55.87	56.01	54.54	55.47	55.47
	2B	55.87	56.49	57.74	57.12	56.81
	3B	59.05	58.37	58.15	57.62	58.30
	4B	56.37	56.06	52.31	50.79	53.88
	5B	55.17	53.33	54.11	55.80	54.60
	6B	57.98	56.03	55.82	54.58	56.10
	7B	55.80	53.74	53.04	52.86	53.86
	1D	55.39	54.13	53.59	55.32	54.61
	2D	57.33	57.07	55.11	53.64	55.79
	3D	55.78	57.49	59.24	57.22	57.43
	4D	54.91	53.96	54.75	56.72	55.09
	5D	64.20	63.60	62.95	62.92	63.42
	6D	55.76	54.19	52.42	55.13	54.37
	7D	54.38	56.12	53.88	53.96	54.58
Thatcher	2A	54.00	55.46	53.57	57.36	55.10
	3A	56.45	58.18	56.05	55.09	56.44
	4A	56.37	57.50	54.24	55.34	55.86
	5A	55.04	53.96	53.15	52.38	53.63
	6A	57.90	56.25	54.70	53.75	55.65
	7A	57.98	57.12	57.86	57.57	57.63
	1B	57.92	56.01	58.42	55.49	56.96
	2B	56.00	55.11	56.01	55.85	55.74
	3B	55.35	54.18	50.52	52.02	53.02
	4B	56.39	54.16	53.15	53.00	54.17
	5B	57.78	55.76	54.05	56.30	55.97
	6B	56.79	52.94	54.13	54.78	54.66
	7B	56.28	56.05	55.57	55.14	55.76
	2D	55.46	58.67	56.25	56.14	56.63
	3D	57.07	57.78	58.70	58.27	57.96
	4D	56.57	56.57	58.07	57.20	57.10
	5D	53.45	56.96	55.29	57.39	55.77
	6D	54.96	55.31	56.15	55.45	55.47
	7D	52.49	53.52	54.60	50.59	52.80
Thatcher Parent		61.86	60.80	64.03	62.65	62.34

Appendix Table II. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	56.98	56.53	54.63	56.30	56.11
	3A	58.79	57.02	56.14	54.17	56.53
	4A	55.00	57.85	57.59	57.14	56.90
	5A	56.28	56.57	55.58	56.82	56.31
	6A	55.57	55.75	56.32	56.30	55.99
	1B	58.63	55.29	55.30	56.10	56.33
	2B	55.70	55.72	57.20	55.27	55.97
	3B	60.75	59.15	60.29	58.04	59.55
	4B	56.37	56.50	54.42	54.62	55.48
	5B	55.58	55.28	56.31	56.16	55.83
	6B	56.25	54.68	55.51	56.82	55.82
	7B	56.68	57.48	54.11	54.97	55.81
	1D	57.01	57.04	56.76	57.54	57.09
	2D	57.52	53.38	50.20	53.50	53.65
	3D	57.21	59.10	57.03	58.14	57.87
	4D	56.40	55.25	56.82	55.86	56.08
	5D	57.69	62.09	60.20	59.49	59.86
	6D	53.69	53.54	51.18	53.40	52.95
	7D	55.66	56.69	55.89	56.87	56.28
Chinese Spring		55.66	55.86	54.18	54.99	55.17

Appendix Table III. Sedimentation values in cc. by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	56.0	49.5	53.0	53.0	52.87
	3A	50.0	48.0	43.0	47.0	47.00
	4A	32.0	30.0	30.0	33.0	31.25
	5A	34.0	33.0	33.5	36.0	34.12
	6A	30.0	43.0	32.0	36.0	35.25
	7A	31.0	34.0	36.0	40.0	35.25
	1B	42.0	40.0	37.0	39.0	39.50
	2B	35.0	30.0	31.5	32.0	32.12
	3B	37.0	35.0	33.0	36.0	35.25
	4B	35.0	36.0	35.0	40.5	36.62
	5B	36.0	34.0	34.5	34.0	34.62
	6B	30.0	33.0	34.0	34.5	32.87
	7B	45.0	47.0	42.0	40.0	43.50
	1D	36.0	34.0	35.0	34.0	34.75
	2D	50.0	42.5	41.0	48.0	45.37
	3D	35.0	33.0	32.0	33.5	33.37
	4D	40.0	35.0	33.0	34.5	35.62
	5D	35.0	35.0	45.0	42.5	39.37
	6D	30.0	32.0	32.0	32.0	31.50
	7D	39.0	40.0	40.0	40.0	39.75
Thatcher	2A	36.0	35.0	37.0	39.0	36.75
	3A	32.0	33.0	35.0	36.5	34.12
	4A	27.0	30.5	28.0	29.5	28.75
	5A	31.0	31.0	33.5	34.0	32.37
	6A	29.0	29.0	32.0	34.0	31.00
	7A	34.0	36.0	36.5	41.0	36.87
	1B	38.0	34.5	36.5	42.0	37.75
	2B	42.0	38.0	37.0	40.0	39.25
	3B	35.0	37.5	39.0	40.0	37.87
	4B	31.0	34.0	35.0	35.0	33.75
	5B	32.0	37.0	35.5	35.0	34.87
	6B	34.0	33.0	40.0	35.5	36.37
	7B	34.0	38.0	33.0	34.0	34.75
	2D	51.0	47.0	44.0	55.0	49.25
	3D	40.0	35.5	37.0	38.0	37.62
	4D	35.0	36.0	33.0	37.0	35.25
	5D	36.0	37.0	34.0	35.0	35.50
	6D	40.0	34.5	32.0	34.0	35.12
	7D	37.0	33.0	33.0	35.5	34.62
Thatcher Parent		62.0	58.0	58.0	60.0	59.50

Appendix Table III. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	34.0	28.0	33.0	36.0	32.75
	3A	30.0	32.5	32.0	34.0	32.12
	4A	37.5	38.5	35.0	38.0	37.25
	5A	35.5	37.0	35.0	34.0	35.37
	6A	29.0	28.5	29.0	30.5	29.25
	1B	42.0	41.0	40.0	40.0	40.75
	2B	46.5	35.0	37.0	43.0	40.37
	3B	43.0	38.0	36.0	43.0	40.00
	4B	30.0	31.0	32.0	35.0	32.00
	5B	34.0	34.0	34.0	33.0	33.75
	6B	33.0	36.0	34.0	35.5	34.62
	7B	33.0	33.5	33.0	33.5	33.25
	1D	20.0	21.0	20.0	19.0	20.00
	2D	40.5	48.0	48.0	51.0	46.87
	3D	34.0	35.0	30.0	37.0	34.00
	4D	37.0	38.0	35.0	37.0	36.75
	5D	35.0	36.0	37.5	38.0	36.62
	6D	30.0	30.5	34.0	32.0	31.62
	7D	37.0	36.0	34.5	35.0	35.62
Chinese Spring		36.0	33.0	33.0	37.5	34.87

Appendix Table IV. Percent damaged starch by replication. Maltose value x 1.64 ÷ 100. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	5.96	5.79	5.79	6.26	5.95
	3A	6.01	6.23	6.07	6.43	6.18
	4A	6.18	6.55	6.23	6.12	6.27
	5A	5.79	5.85	5.64	5.79	5.76
	6A	5.74	5.96	5.48	5.28	5.61
	7A	6.30	6.23	6.12	5.74	6.09
	1B	5.79	6.01	5.38	5.38	5.64
	2B	6.13	6.43	6.66	6.66	6.47
	3B	6.08	5.74	6.43	5.69	5.98
	4B	5.85	6.60	5.38	5.74	5.89
	5B	5.74	5.58	5.74	5.90	5.74
	6B	5.84	6.01	5.85	5.17	5.71
	7B	5.79	6.01	5.64	5.64	5.77
	1D	5.74	6.55	5.00	6.17	5.86
	2D	6.01	6.01	5.85	5.90	5.94
	3D	5.64	6.88	6.31	5.59	6.10
	4D	5.43	5.74	5.43	5.12	5.43
	5D	8.38	8.62	7.95	8.28	8.30
	6D	6.28	6.23	5.79	5.74	6.01
	7D	5.43	5.33	5.54	6.02	5.58
Thatcher	2A	6.55	6.83	5.74	5.69	6.20
	3A	6.41	6.33	5.43	5.59	5.94
	4A	6.78	6.98	6.26	6.43	6.61
	5A	6.38	6.98	5.97	6.81	6.53
	6A	6.08	6.50	5.38	5.59	5.88
	7A	8.38	7.50	6.76	7.79	7.60
	1B	5.96	6.50	5.64	5.74	5.96
	2B	7.15	6.83	6.97	7.30	7.06
	3B	5.74	5.04	5.23	5.17	5.29
	4B	6.08	6.60	5.69	5.69	6.01
	5B	6.38	5.69	6.17	6.12	6.09
	6B	6.08	6.65	5.64	6.02	6.09
	7B	6.01	6.55	5.90	5.54	6.00
	2D	6.38	6.08	6.43	6.12	6.25
	3D	5.90	5.69	5.90	5.43	5.73
	4D	6.88	5.89	5.74	5.74	6.06
	5D	5.96	6.23	5.54	5.90	5.90
	6D	5.90	6.65	5.59	5.85	5.99
	7D	6.55	6.08	6.02	6.07	6.18
Thatcher Parent		6.43	8.22	7.69	7.30	7.41

Appendix Table IV. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	5.69	5.69	5.28	5.38	5.51
	3A	6.43	6.59	6.38	6.12	6.38
	4A	6.18	5.85	6.17	6.26	6.11
	5A	6.28	6.86	6.02	6.02	6.29
	6A	6.23	5.90	6.43	5.64	6.05
	1B	6.13	6.22	6.17	5.90	6.10
	2B	6.60	5.54	6.22	6.02	6.09
	3B	9.49	9.09	9.48	8.81	9.21
	4B	6.28	5.97	5.64	5.00	5.71
	5B	6.65	6.43	6.07	5.90	6.26
	6B	6.33	6.02	6.07	6.38	6.02
	7B	6.23	6.12	5.48	5.38	5.80
	1D	6.18	6.76	5.90	6.31	6.28
	2D	5.85	5.17	5.64	5.48	5.53
	3D	6.88	6.76	6.22	6.12	6.49
	4D	5.43	5.43	5.28	5.05	5.29
	5D	9.18	9.02	8.95	9.09	9.06
	6D	6.08	6.26	5.48	6.07	5.97
	7D	7.77	7.69	7.63	7.51	7.65
Chinese Spring		6.01	5.85	5.69	5.84	5.84

Appendix Table V. Percent water absorption by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	63.4	62.0	62.8	62.2	62.60
	3A	63.0	61.4	61.6	63.0	62.25
	4A	62.0	62.8	63.2	62.4	62.60
	5A	60.8	62.2	61.8	62.6	61.85
	6A	60.4	63.2	61.4	61.6	61.65
	7A	60.6	61.8	63.6	61.8	61.95
	1B	62.2	61.4	60.2	60.8	61.15
	2B	62.4	61.4	63.2	62.8	62.45
	3B	59.4	60.2	59.4	59.0	59.50
	4B	60.4	60.0	62.0	62.4	61.20
	5B	61.0	61.2	61.2	60.2	60.90
	6B	59.4	60.4	59.4	59.4	59.65
	7B	60.6	60.2	60.8	61.2	60.70
	1D	61.8	61.2	62.6	61.4	61.75
	2D	62.0	61.4	60.6	61.2	61.30
	3D	62.2	61.6	61.2	61.4	61.60
	4D	60.6	61.4	60.2	59.4	60.40
	5D	64.6	64.8	65.0	64.4	64.70
	6D	62.6	62.0	62.8	62.2	62.40
	7D	61.0	61.0	61.0	62.0	61.25
Thatcher	2A	62.4	61.2	62.4	62.0	62.00
	3A	60.6	59.8	59.8	61.8	60.50
	4A	63.8	63.0	63.4	64.0	63.55
	5A	63.0	63.8	62.8	62.6	63.05
	6A	60.2	60.0	60.4	62.2	60.70
	7A	63.4	64.8	63.4	64.8	64.10
	1B	63.4	60.8	60.6	61.2	61.50
	2B	63.4	62.4	61.6	62.4	62.45
	3B	63.2	62.2	61.2	61.2	61.95
	4B	61.4	61.0	62.4	61.0	61.45
	5B	58.8	59.2	61.4	60.4	59.95
	6B	61.6	61.6	61.4	61.2	61.45
	7B	61.0	59.8	62.2	60.8	60.95
	2D	60.8	61.4	60.0	60.4	60.65
	3D	62.0	61.2	61.2	60.4	61.20
	4D	60.0	59.8	61.6	60.8	60.55
	5D	62.0	61.6	61.6	61.0	61.55
	6D	62.4	60.8	61.0	61.0	61.30
	7D	64.0	63.0	63.0	64.4	63.60
Thatcher Parent		65.6	65.8	64.6	63.6	64.90

Appendix Table V. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	60.0	60.4	60.2	61.2	60.45
	3A	61.0	59.8	60.6	64.2	61.40
	4A	61.0	60.8	61.8	62.2	61.45
	5A	61.2	61.6	61.6	62.0	61.60
	6A	60.0	60.6	60.6	61.0	60.55
	1B	61.0	61.8	61.0	60.2	61.00
	2B	60.6	61.0	61.0	62.8	61.35
	3B	66.8	69.6	68.4	67.4	68.05
	4B	59.8	61.0	60.0	60.4	60.30
	5B	60.8	60.4	62.0	61.0	61.05
	6B	60.6	60.4	62.4	60.6	61.00
	7B	58.2	60.4	61.2	59.2	59.75
	1D	60.2	60.4	60.6	60.6	60.45
	2D	59.0	59.4	62.2	61.2	60.45
	3D	61.4	62.6	61.4	61.4	61.70
	4D	58.8	59.2	59.2	59.6	59.20
	5D	66.6	67.4	66.8	67.8	67.12
	6D	60.6	61.8	62.6	61.8	61.70
	7D	64.8	64.8	65.8	64.8	65.05
Chinese Spring		60.2	60.6	62.2	61.2	61.05

Appendix Table VI. Farinograph peak in minutes by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	3.0	5.0	4.0	4.5	4.12
	3A	5.0	6.5	4.5	3.0	4.75
	4A	3.0	3.5	3.0	3.0	3.12
	5A	3.5	3.0	4.0	3.0	3.37
	6A	3.5	4.5	3.0	4.0	3.75
	7A	4.5	3.0	4.0	2.5	3.50
	1B	4.0	3.5	4.0	4.0	3.87
	2B	3.0	3.5	3.0	2.0	2.87
	3B	4.0	4.0	4.0	4.0	4.00
	4B	4.5	4.5	4.0	4.5	4.37
	5B	4.0	3.5	4.0	4.0	3.87
	6B	3.5	3.0	3.0	4.0	3.37
	7B	4.5	3.5	4.5	4.0	4.12
	1D	3.0	3.5	3.0	3.5	3.25
	2D	3.0	3.0	3.5	2.5	3.00
	3D	3.0	3.0	4.0	3.5	3.37
	4D	4.0	4.0	4.0	4.0	4.00
	5D	5.0	4.0	4.5	5.0	4.62
	6D	4.0	3.5	3.5	3.0	3.50
	7D	4.5	4.0	4.5	3.0	4.00
Thatcher	2A	3.0	4.0	3.5	3.5	3.50
	3A	3.5	4.0	4.5	3.0	3.75
	4A	2.5	2.5	2.5	3.0	2.62
	5A	3.0	2.5	4.0	3.0	3.12
	6A	3.0	2.5	4.0	3.0	3.12
	7A	4.5	4.0	4.0	3.0	3.87
	1B	4.0	4.0	4.0	4.0	4.00
	2B	4.5	5.0	4.0	4.5	4.50
	3B	3.5	2.5	5.0	3.5	3.62
	4B	3.0	3.5	3.5	3.0	3.25
	5B	4.5	3.0	4.0	3.5	3.75
	6B	3.5	3.5	4.5	3.0	3.62
	7B	3.5	4.0	3.5	3.5	3.62
	2D	4.5	4.0	4.0	4.5	4.25
	3D	4.0	4.0	4.5	4.5	4.25
	4D	3.0	4.0	3.0	3.5	3.37
	5D	4.5	3.0	3.5	3.5	3.62
	6D	4.0	3.5	3.5	3.5	3.62
	7D	4.0	3.0	3.5	4.0	3.62
Thatcher Parent		6.0	8.0	6.5	8.0	7.12

Appendix Table VI. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	4.0	4.0	4.5	3.0	3.87
	3A	3.0	4.0	3.5	3.0	3.37
	4A	4.0	3.0	3.5	3.0	3.37
	5A	3.5	3.0	4.0	4.0	3.62
	6A	2.0	3.0	3.0	4.0	3.00
	1B	3.0	4.0	4.5	4.0	3.87
	2B	3.5	3.0	4.0	3.0	3.37
	3B	5.0	3.5	4.5	4.0	4.25
	4B	3.5	3.5	3.0	4.0	3.50
	5B	3.5	4.0	4.0	3.5	3.75
	6B	3.5	4.0	3.5	3.0	3.50
	7B	3.0	3.5	2.5	3.5	3.12
	1D	2.0	2.0	2.0	2.0	2.00
	2D	3.0	2.5	2.5	3.0	2.75
	3D	3.0	3.5	3.5	3.5	3.37
	4D	4.0	4.0	3.0	3.5	3.62
	5D	4.0	3.5	4.0	4.0	3.87
	6D	3.0	3.0	3.0	2.5	2.87
	7D	3.5	4.0	4.0	4.0	3.87
Chinese Spring		4.0	4.0	3.0	4.0	3.75

Appendix Table VII. Farinograph stability in minutes by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	15.0	16.0	17.0	16.0	16.00
	3A	7.0	12.0	12.0	9.0	10.00
	4A	2.5	2.5	3.0	2.5	2.62
	5A	4.0	5.0	4.5	4.5	4.50
	6A	3.0	8.0	4.0	5.0	5.00
	7A	4.5	5.0	5.0	6.5	5.25
	1B	4.0	5.5	7.5	5.0	5.50
	2B	3.0	3.0	3.0	4.0	3.25
	3B	3.5	5.0	4.0	6.0	4.62
	4B	4.5	4.5	5.5	6.5	5.25
	5B	4.0	4.5	5.5	5.0	4.75
	6B	3.5	3.0	3.5	4.5	3.62
	7B	6.0	9.0	7.0	7.0	7.25
	1D	3.0	4.0	4.0	5.0	4.00
	2D	9.0	8.0	12.0	9.0	9.50
	3D	2.5	3.0	3.0	4.0	3.12
	4D	4.5	4.0	5.0	4.0	4.37
	5D	3.5	3.5	4.0	3.0	3.50
	6D	2.5	2.5	2.5	2.5	2.50
	7D	4.5	4.0	5.5	6.0	5.00
Thatcher	2A	3.0	4.0	3.0	3.0	3.25
	3A	3.5	4.0	5.0	4.0	4.12
	4A	1.5	1.5	1.0	2.0	1.50
	5A	3.0	2.5	3.5	3.5	3.12
	6A	3.0	3.0	2.5	3.0	2.87
	7A	4.0	4.0	4.0	4.0	4.00
	1B	3.5	3.5	3.0	5.0	3.75
	2B	7.0	6.0	7.0	6.5	6.62
	3B	3.0	3.5	5.0	5.0	4.12
	4B	3.5	2.0	3.0	3.5	3.00
	5B	5.5	6.0	4.5	5.0	5.25
	6B	3.5	4.0	5.5	4.0	4.25
	7B	5.0	4.0	3.5	4.5	4.25
	2D	14.0	10.0	13.0	11.5	12.12
	3D	4.0	4.0	3.5	5.5	4.25
	4D	3.0	4.0	2.5	4.0	3.37
	5D	4.0	3.5	4.0	5.0	4.12
	6D	4.0	4.0	5.5	4.0	4.37
	7D	3.5	3.0	4.0	3.0	3.37
Thatcher Parent		11.5	13.0	12.0	13.0	12.37

Appendix Table VII. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	4.0	4.0	5.0	3.0	4.00
	3A	2.0	3.0	3.5	2.5	2.75
	4A	4.5	5.5	5.5	3.5	4.75
	5A	4.0	4.0	4.5	4.0	4.12
	6A	3.0	3.5	3.5	2.0	3.00
	1B	5.0	7.0	5.0	6.0	5.75
	2B	7.5	4.0	8.0	9.0	7.12
	3B	3.5	3.0	2.5	3.0	3.00
	4B	2.0	3.5	5.5	4.0	3.75
	5B	3.0	3.0	4.5	4.0	3.62
	6B	3.5	4.0	3.5	4.0	3.75
	7B	4.5	4.0	3.5	4.0	4.00
	1D	1.5	1.5	2.0	1.5	1.62
	2D	8.0	11.0	8.5	11.0	9.62
	3D	3.5	3.0	4.5	3.0	3.50
	4D	4.5	5.0	4.0	4.0	4.37
	5D	3.0	3.5	3.5	3.0	3.25
	6D	2.5	2.5	2.5	2.0	2.37
	7D	3.0	4.0	3.0	3.0	3.25
Chinese Spring		5.0	3.0	2.5	5.5	4.00

Appendix Table VIII. Farinograph valorimeter values by replication. Chromosome substitution lines.

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Hope	2A	62	66	64	66	64.5
	3A	60	67	64	58	62.2
	4A	44	48	44	45	45.2
	5A	48	45	53	46	48.0
	6A	45	61	47	52	51.2
	7A	53	47	52	52	51.0
	1B	47	50	57	54	52.0
	2B	45	48	44	42	44.7
	3B	50	52	50	54	51.5
	4B	53	44	53	56	51.5
	5B	50	50	53	53	51.5
	6B	46	44	52	52	48.5
	7B	55	57	57	59	57.0
	1D	46	50	48	52	49.0
	2D	58	56	60	57	57.7
	3D	44	44	50	50	47.0
	4D	52	50	52	52	51.5
	5D	58	52	54	56	55.0
	6D	49	47	46	43	46.2
	7D	56	52	55	53	54.0
Thatcher	2A	44	52	48	48	48.0
	3A	47	51	53	46	49.2
	4A	40	40	38	42	40.0
	5A	45	41	51	46	45.7
	6A	45	42	50	44	45.2
	7A	53	48	51	46	49.5
	1B	52	52	51	54	52.2
	2B	58	57	56	56	56.7
	3B	48	43	55	50	49.0
	4B	46	47	44	46	45.7
	5B	54	54	52	52	53.0
	6B	48	48	56	49	50.2
	7B	50	53	43	50	49.0
	2D	66	62	63	63	63.5
	3D	52	52	53	55	53.0
	4D	46	52	45	48	47.7
	5D	54	46	50	50	50.0
	6D	50	49	50	48	49.2
	7D	52	46	50	51	49.7
Thatcher Parent		67	72	68	72	69.7

Appendix Table VIII. (Continued)

Line		Rep I	Rep II	Rep III	Rep IV	Avg.
Timstein	2A	52	50	54	46	50.5
	3A	44	50	48	43	46.2
	4A	52	49	51	47	49.7
	5A	48	47	52	50	49.2
	6A	41	46	45	44	44.0
	1B	49	54	54	55	53.0
	2B	54	46	57	56	53.2
	3B	55	48	53	50	51.5
	4B	46	45	48	52	47.7
	5B	47	50	50	49	49.0
	6B	48	52	47	45	48.0
	7B	47	45	42	48	45.5
	1D	35	34	38	36	35.7
	2D	58	62	60	60	60.0
	3D	46	45	46	48	46.2
	4D	52	52	47	48	49.7
	5D	50	48	52	51	50.2
	6D	44	43	44	40	42.7
	7D	46	51	50	50	49.2
Chinese Spring		53	51	44	53	50.2

Appendix Table IX. Quality characteristics for three replications of 17 monosomic and 9 disomic lines of Kharkof MC-22 wheat.

Chromosome		Farinograph Prot.	Abs.	Peak	Stab.	Val.	Sed.
		(%)	(%)	(min.)	(min.)		(cc)
1-A monosomic		17.4	61.5	15.5	19.0	91	70.0
		18.3	62.0	15.5	20.5	90	70.5
		18.1	61.8	15.5	21.0	91	71.0
	$\bar{X}$	17.9	61.8	15.5	20.2	90.7	70.5
2-A monosomic		17.5	61.4	7.5	15.0	72	69.0
		18.3	63.6	16.0	18.0	91	70.0
		18.0	62.5	15.0	17.0	89	70.5
	$\bar{X}$	17.9	62.5	12.8	16.7	84.0	69.8
disomic		18.2	61.2	12.5	23.0	89	70.0
		18.2	63.4	19.0	20.0	92	70.0
		18.3	62.0	17.0	20.0	92	70.5
	$\bar{X}$	18.2	62.2	16.2	21.0	91.0	70.2
3-A monosomic		18.7	63.5	16.5	24.5	95	69.0
		18.6	64.0	16.5	22.5	93	70.0
		18.5	63.5	20.0	24.0	96	70.0
	$\bar{X}$	18.6	63.7	17.7	23.7	94.7	69.7
disomic		18.3	64.0	18.0	18.0	95	69.5
		16.4	62.0	15.5	20.0	91	70.0
		18.0	61.6	14.5	21.0	90	69.0
	$\bar{X}$	17.6	62.5	16.0	19.7	92.0	69.5
5-A monosomic		18.5	62.7	20.5	21.0	96	70.5
		18.1	63.0	16.5	19.0	91	70.0
		18.2	62.5	15.5	21.0	90	70.0
	$\bar{X}$	18.3	62.7	17.5	20.3	92.3	70.2
disomic		18.0	62.6	16.0	22.0	91	69.0
		17.3	61.7	16.0	22.0	91	71.0
		17.2	63.0	17.5	17.0	93	71.0
	$\bar{X}$	17.5	62.4	16.5	20.3	91.7	70.3

Appendix Table IX. (Continued)

		Farinograph					
Chromosome		Prot.	Abs.	Peak	Stab.	Val.	Sed.
		(%)	(%)	(min.)	(min.)		(cc)
6-A monosomic		17.5	62.3	15.5	19.0	91	70.0
		17.1	62.0	14.0	16.5	88	62.0
		17.2	62.6	14.5	18.0	89	68.0
	$\bar{X}$	17.3	62.3	14.7	17.8	89.3	66.7
7-A monosomic		18.0	63.4	16.5	20.0	92	69.0
		17.3	61.5	14.0	19.5	88	66.5
		18.0	62.8	6.0	13.0	87	60.0
	$\bar{X}$	17.8	62.6	12.2	17.5	89.0	65.2
1-B monosomic		19.1	64.6	9.0	13.0	75	66.0
		17.6	61.3	10.0	11.0	78	65.5
		18.5	62.3	9.5	10.0	75	65.0
	$\bar{X}$	18.4	62.7	9.5	11.3	76.0	65.5
2-B monosomic		18.3	63.0	18.0	20.0	94	70.0
		18.3	62.5	13.5	17.0	86	67.0
		18.1	62.0	14.0	17.0	87	73.0
	$\bar{X}$	18.2	62.5	15.2	18.0	89.0	70.0
disomic		17.5	63.3	17.0	16.5	92	71.0
		17.1	62.3	16.5	16.0	91	70.0
		17.4	62.0	15.5	18.0	90	70.0
	$\bar{X}$	17.3	62.5	16.3	16.8	91.0	70.3
5-B monosomic		18.1	63.0	18.0	17.0	94	71.0
		17.8	62.8	17.0	15.5	91	71.0
		17.9	64.0	17.5	14.0	93	70.0
	$\bar{X}$	17.9	63.3	17.5	15.5	92.7	70.7
6-B monosomic		18.6	62.7	15.5	20.0	91	69.0
		17.4	61.5	13.5	20.5	88	63.0
		17.6	61.4	13.0	17.5	86	63.5
	$\bar{X}$	17.9	61.9	14.0	19.3	88.3	65.2

Appendix Table IX. (Continued)

Chromosome		Farinograph					
		Prot.	Abs.	Peak	Stab.	Val.	Sed.
		(%)	(%)	(min.)	(min.)		(cc)
7-B monosomic		17.8	63.2	20.0	23.0	96	70.0
		17.3	60.7	16.0	27.5	93	67.0
		17.3	61.2	16.0	27.0	94	69.0
	$\bar{X}$	17.5	61.7	17.3	25.8	94.3	68.7
1-D monosomic		17.9	61.0	5.0	6.5	58	49.0
		18.0	61.0	4.5	3.0	52	35.0
		18.3	62.8	4.5	3.0	52	38.5
	$\bar{X}$	18.1	61.6	4.7	4.2	54	40.8
monosomic		18.1	61.0	4.0	5.0	52	47.5
		18.4	62.8	4.5	3.5	53	45.0
		18.1	61.2	5.0	4.0	55	44.0
	$\bar{X}$	18.2	61.7	4.5	4.2	53.3	45.5
disomic		17.7	62.4	15.5	22.0	91	71.0
		17.1	61.6	15.5	22.0	92	71.0
		17.8	63.0	15.0	19.5	90	69.0
	$\bar{X}$	17.5	62.3	15.3	21.2	91.0	70.3
3-D monosomic		17.3	62.4	16.5	15.5	92	69.0
		17.2	61.2	13.5	19.0	87	69.0
		17.6	61.6	14.0	16.0	87	70.5
	$\bar{X}$	17.4	61.7	14.7	16.8	88.7	69.5
disomic		17.7	63.0	15.5	19.5	91	70.0
		16.8	61.2	15.0	19.0	90	66.5
		17.5	60.8	8.0	14.0	72	65.5
	$\bar{X}$	17.3	61.7	12.8	17.5	84.3	67.3
4-D monosomic		17.4	62.7	19.0	19.5	95	68.5
		17.4	62.0	16.5	23.0	93	67.0
		17.3	63.0	16.5	21.0	93	71.5
	$\bar{X}$	17.4	62.6	17.3	21.2	93.7	69.0

Appendix Table IX. (Continued)

Chromosome		Farinograph					Sed.
		Prot.	Abs.	Peak	Stab.	Val.	
		(%)	(%)	(min.)	(min.)		(cc)
4-D disomic		17.4	62.7	16.0	23.0	92	69.0
		16.4	61.3	14.5	24.0	90	64.0
		17.7	62.6	15.5	21.0	91	72.0
	$\bar{X}$	17.2	62.2	15.3	22.7	91.0	68.3
5-D monosomic		19.1	65.7	8.5	20.5	76	54.0
		18.0	64.0	15.0	26.0	91	59.0
		18.3	64.3	15.0	20.0	90	60.0
	$\bar{X}$	18.5	64.7	12.8	22.2	85.7	57.7
disomic		17.3	63.0	19.0	21.0	95	71.0
		17.2	61.6	16.0	19.0	91	68.0
		17.8	62.0	15.0	17.0	91	70.5
	$\bar{X}$	17.4	62.2	16.7	19.0	92.3	69.8
6-D monosomic		18.4	62.6	21.0	23.5	97	72.0
		18.4	62.7	18.0	22.0	95	70.5
		18.1	61.4	15.5	24.5	92	70.0
	$\bar{X}$	18.3	62.2	18.2	23.3	94.7	70.8
disomic		17.5	62.5	14.0	17.0	87	64.0
		18.9	62.8	12.5	15.5	84	70.0
		17.8	62.5	12.0	16.5	84	67.0
	$\bar{X}$	18.2	62.8	12.8	18.3	85.0	67.0
K MC-22		17.4	62.0	16.5	18.5	92	70.5
		16.7	62.5	13.0	18.0	86	67.0
		17.3	61.4	13.5	18.0	87	66.0
	$\bar{X}$	17.1	62.0	14.3	18.2	88.3	67.5

LITERATURE CITED

1. Abbott, D. C. What do we know about wheat proteins. Cereal Sci. Today. 4:9. 1959.

2. American Association of Cereal Chemists. Cereal laboratory methods (7th ed.). The Association: St. Paul, Minn. 1962.

3. Cluskey, James E. Note on a simplified gel electrophoresis apparatus used in wheat gluten protein research. Cereal Chem. 6:41. 1964.

4. Cluskey, J. E., Taylor, W. W., Charley, Helen, and Senti, F. R. Electrophoretic composition and intrinsic viscosity of glutens from different varieties of wheat. Cereal Chem. 38:4. 1961.

5. Coulson, C. B. and Sim, A. K. Wheat proteins: I. Fractionation and varietal variation of endosperm proteins of T. vulgare. J. Sci. Food Agric. 16:8. 1965.

6. Dimler, R. J. Gluten - the key to wheat utility. Baker Digest 37:1 1963.

7. Donelson, J. R. and Yamazaki, W. T. Note on a rapid method for the estimation of damaged starch in soft wheat flours. Cereal Chem. 39:6. 1962.

8. Elton, G. A. H. and Ewart, J. A. D. Starch gel electrophoresis of cereal proteins. J. Sci. Food Agric. 13:1. 1962.

9. Finney, K. F., Rubenthaler, G. L., Bolte, L. C., Hoseney, R. C., Shogren, M. D., Barnhort, C. M. and Shellenberger, J. A. Quality characteristics of hard winter wheat varieties grown in the southern, central and northern Great Plains of the United States, 1962 crop. U. S. Dept. Agr. Mimeographed Publ. No. CR-10-64.

10. Graham, J. S. D. Starch-gel electrophoresis of wheat flour proteins. Aust. Jour. of Biol. Sci. 16:2. 1963.

11. Hepburn, F. N., Lewis, E. W. Jr., and Elvehjem, C. A. The amino acid content of wheat, flour and bread. Cereal Chem. 34:5. 1957.

12. Jones, D. W. and Amos, A. J. Modern cereal chemistry. Northern Publishing Co. Ltd., Liverpool, England. 1957.

13. Jones, R. W., Babcock, G. E., Taylor, N. W. and Senti, F. R. Molecular weights of wheat gluten fractions. Arch. of Biochem. and Biophy. 94:3. 1961.

14. Jones, R. W. and Dimler, R. J. Electrophoretic composition of glutens from air-classified flours. Cereal Chem. 39:4. 1962.

15. Jones, R. W., Taylor, N. W., and Senti, F. R. Electrophoresis and fractionation of wheat gluten. Arch. of Biochem. and Biophys. 84:2. 1959.

16. Kuspira, John and Unrau, John. Genetic analysis of certain characters in common wheat using whole chromosome substitution lines. Can. J. Plant Sci. 37:3. 1957.

17. Laws, W. D. and France, W. G. A comparative study of some protein fractions of wheat flour. Cereal Chem. 25:4. 1963.

18. Lee, J. W. Zone electrophoresis of wheat gluten of polyacrylamide gel. Biochem. and Biophys. Acta. 69:1. 1963.

19. Mattern, Paul J., Morris, Rosalind, Schmidt, J. W. and Johnson, V. A. Preliminary report on the use of chromosome substitution lines for inheritance studies of milling and dough handling properties of Cheyenne wheat. Bulletin - Association of Operative Millers. December, 1963.

20. Mattern, Paul J., Morris, Rosalind, Schmidt, J. W. and Johnson, V. A. Chromosome substitution lines for studying the inheritance of quality factors of Cheyenne wheat. Proceedings - Tenth Hard Red Winter Wheat Workers Conference, Colorado State University, February 1965.

21. Osborne, T. B. The proteins of the wheat kernel. Published by Carnegie Inst. of Washington D. C. Publ. No. 84. 1907.

22. Pence, J. W., Mecham, D. K., Elder, Angeline H., Lewis, J. C., Snett, Neva S., and Olcott, H. S. Characterization of wheat gluten. II. Amino acid composition. Cereal Chem. 27:4. 1950.

23. Pence, J. W. and Nimmo, C. C. New knowledge of wheat proteins. Bakers Digest. 38:1. 1964.

24. Raymond, Samuel and Wang, Yi-Ju. Preparation and properties of acrylamide gel for use in electrophoresis. Analy. Biochem. 1:3. 1960.

25. Sandstedt, R. M. The adaptation of the ferrocyanide maltose method to high diastatic flour. Cereal Chem. 14:4. 1937.

26. Sears, E. R. Nullisomic analysis in common wheat. American Naturalist 87:835. 1953.

27. Simmonds, D. H. Variations in the amino acid composition of Australian wheats and flours. Cereal Chem. 39:6. 1962.

28. Smithies, O. Zone electrophoresis in starch gels: Group variation in the serum proteins of normal human adults. Biochem. Jour. 61:4. 1955.

29. Sokol, H. A. and Mecham, D. K. Sulfhydryl group in flour. Bakers Digest, 34:6, 1960.

30. Sokol, H. A., Mecham, D. K. and Pence, J. W. Further studies on the determination of sulfhydryl groups in wheat flours. Cereal Chem. 36:2. 1959.

31. Stone, C. D. and Hamdy, M. K. Protein complex of dough. Bakers Digest 38:4, 1964.

32. Sullivan, Betty, Proteins in flour. Jour. Agr. Food Chem. 2:24. 1954.

33. Udy, D. C, Estimation of protein in wheat and flour by ion-binding. Cereal Chem. 33:3. 1956.

34. Welsh, J. R. and Hehn, E. R. The effect of chromosome 1D on hexaploid wheat flour quality. Crop Science 4:3. 1964.

35. Woychik, J. H., Boundy, J. A. and Dimler, R. J. Starch gel electrophoresis of wheat gluten proteins with concentrated urea. Arch. Biochem. and Biophy. 94:3. 1961.

[redacted]