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CHROMOSOMAL ASSOCIATION WITH GLIADIN PROTEINS IN THE WHEAT VARIETY 'CHEYENNE'[1]

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ABSTRACT

Gliadin protein patterns from 'Cheyenne' chromosome substitution lines in 'Chinese Spring' were examined for possible association with desirable dough-handling and bread-baking properties. In a previous report, chromosomes 4B, 7B, and 5D have been associated with desirable dough-handling properties. However, in the present study, gliadin protein patterns of chromosomes 4B, 7B and 5D were not similar. Likewise, chromosomes 1B, 4B, and 7B which were previously noted for their association with desirable loaf characteristics did not share distinctive protein patterns. Marked differences among gliadin patterns for Cheyenne chromosomes both between and within the three genomes of wheat were apparent. Their meaning in terms of flour quality factors is unclear.

Additional index words: *Triticum*, wheat, substitution lines.

THE HARD red winter wheat variety, *Triticum aestivum* L. em. Thell (aestivum group) 'Cheyenne', has long been recognized as a desirable strong gluten wheat with satisfactory milling properties. Heyne and Finney (2) found by crossing Cheyenne and 'Chiefkan' (a poor flour quality type) that the dough-handling and loaf volume properties of Cheyenne were controlled by partial dominance. These findings suggested that individual chromosome substitutions might be useful in determining those chromosomes contributing major genes for Cheyenne's desirable milling, dough-handling and baking properties. Cheyenne chromosome substitution lines were developed in the variety, 'Chinese Spring,' at the University of Nebraska, and dough-handling and baking properties have been reported (5). Cheyenne chromosomes 4B, 7B, and 5D contributed genes for strong dough-mixing characteristics, while genes on chromosomes 1B, 4B, and 7B contributed to loaf volume. Lesser effects on loaf volume were noted from chromosomes 4D, 5D, and 7D. Since there is an association between the amount and nature of flour proteins and bread quality (6,7) the gluten proteins were extracted for electrophoretic examination.

Materials And Methods

A detailed description of the development of the Cheyenne substitution lines was given by Morris et al. (5) along with pertinent chemical analyses of the flour (4). For their studies and the present study tests were made after four backcrosses to Chinese Spring for all substitution lines except chromosomes 2A[3] (no backcross), 2D (one backcross), and 2B[3] and 7A (two backcrosses). There is some doubt about the identity of the substituted chromosomes in the lines for 2A, 1D, and 4D. Therefore, these lines are being redeveloped.

Starch was washed from the gluten proteins of a flour dough from each line with a 0.1% NaCl solution. The gluten proteins were taken up in 0.1% acetic acid and centrifuged at 20,000 *g* to remove remaining starch before lyophilization. Lyophilized proteins were taken up (4% final concentration) in 0.1% acetic acid for electrophoresis. Starch gel electrophoresis similar to the system of Woychik et al. (8) was used. Aluminum lactate buffer used (3) was modified as follows: 1.55 g aluminum lactate plus 2.80 g glycine were adjusted to pH 3.2 with lactic acid and water added to give 1 liter volume. Electrophoretic runs were completed in about 5½ hr. Gels were stained in 0.5% aqueous nigrosin (water-soluble) solution. The gliadin components of gluten moved in the gels while glutenin remained at the origin.

Seven electrophoresis samples were run simultaneously. Each set of seven consisted of a Cheyenne standard plus two chromosome numbers from each of the A, B, and D genomes (e.g., 1A, 1B, 1D, etc.). Cheyenne and Chinese Spring were compared within the same run also. Only those electrophoretic sets in which the bands of Cheyenne traveled the same distance were used. At least three runs of each set were made to demonstrate repeatibility. By this procedure the mobilities of all proteins illustrated are considered relative to Cheyenne and are, therefore, relative to each other.

Results And Discussion

Electrophoretic patterns for the parents and each substitution line are illustrated in Fig. 1. The Chinese Spring and Cheyenne patterns are distinctive. The patterns for the substitution lines are presented by homoeologous groups.

Note in Fig. 1 and 2 that the origins of all patterns are aligned. Primarily qualitative protein differences are to be considered from the results. However, some semiquantitative differences appear quite obvious.

1A, 1B, 1D — Chinese Spring and 1D are nearly identical except that the former has two slow-moving, dark bands and the latter only one. Similarly, 1B and 1D differ mainly in the slower moving bands.

2A, 2B, 2D — While all patterns within group 2 are distinctive from each other, 2A (no backcross) remains similar to Cheyenne but carries the faint leading band characteristic of Chinese Spring. The 2B pattern is essentially identical to that of Chinese Spring. Similarities in major bands are noted between 2D and Cheyenne.

3A, 3B, 3D — The similar group 3 patterns resemble Chinese Spring with 3A and 3D being nearly identical.

4A, 4B, 4D — The 4A and 4B patterns vary only in minor bands. Four faint, slow bands, more than in either parent, appeared in 4D, and also in 7A. Chinese

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[3] In this paper 2A = XIII and 2B = II since the photographs were taken before Chapman and Riley (1) reported that chromosome XIII belongs to the B genome (2B) and II to the A genome (2A).

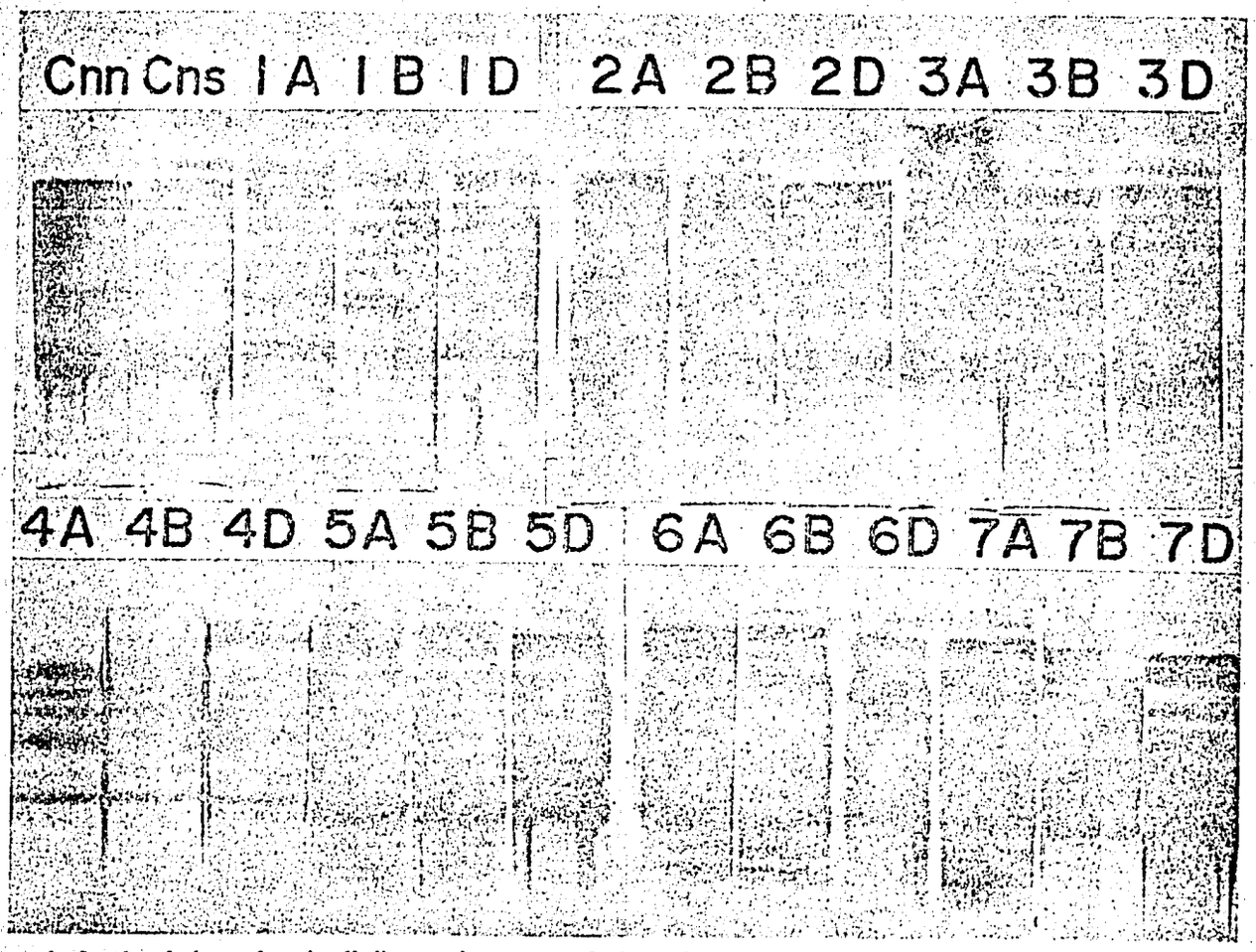

Figure 1. Starch gel electrophoretic gliadin protein patterns of Cheyenne (Cnn), Chinese Spring (Cns), and each chromosome substitution line for the 7 homoeologous groups involving the A, B, and D genomes of wheat. Origins of the patterns are opposite the labelled end.

Spring has only three such bands as do 5A, 5B, 6A, and 6B.

5A, 5B, 5D – Patterns of all three resemble Chinese Spring. The three faint, slow bands common to Chinese Spring, 5A, and 5B are absent in 5D. Mobilities of the three leading 5A, 5B, and 5D bands differ slightly from those of the Chinese Spring leading bands.

6A, 6B, 6D – The major bands in 6A compare well with the Cheyenne pattern. The patterns of Chinese Spring and 6B are very similar and resemble 6D except for the absence of the faint, slow bands in 6D.

7A, 7B, 7D – The major bands of 7A have nearly identical mobilities to those of 6D. The major bands of the 7B pattern are similar to those of Chinese Spring, 6D, and 7A; however, the general mobility of some bands differs. By contrast, the 7D pattern is essentially identical to that of Cheyenne.

The substitution lines most closely resembling Cheyenne are 2D (only one backcross) and 7D. The heavy protein bands in 6A patterns are similar to those of Cheyenne. Patterns most similar to that of Chinese Spring are noted in 1D, 3A, 3B, 3D, 5A, 5B, 6B, 6D, and 7A (minor band differences exist in all cases). The remaining substitution line patterns are most distinctively different from those of either parent.

There appears to be no definite gliadin protein pattern associated with genes of chromosomes 4B, 7B

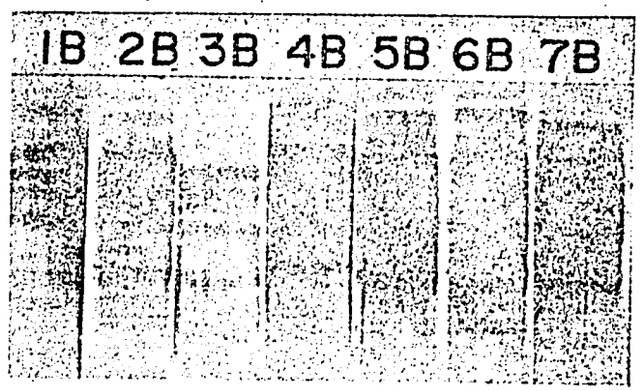

Figure 2. Rearranged gliadin protein electrophoretic patterns of Cheyenne substitution lines from Fig. 1 illustrate chromosomal-associated variability within the B genome.

and 5D which contribute to strong dough-handling properties. Neither is there a gliadin protein pattern common to chromosomes 1B, 4B, and 7B which influence high loaf volume and other desirable loaf characteristics (5). The relationships between gliadin protein constituents and bread and dough quality factors is likely much too complex to be made apparent by simple electrophoretic patterns. Probably the

interaction of proteins with other flour constituents is involved.

The electrophoretic patterns of the B genome in Fig. 1 are given in Fig. 2. It is encouraging to note that individual chromosomes can be associated with distinctly different gliadin protein patterns within a genome.

The potential utility of the type of data present awaits a more complete characterization of other chromosome- and gene-associated protein differences, plus a clearer understanding of how proteins are specifically involved in flour quality.

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