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CHROMOSOMAL LOCATIONS OF GENES FOR HIGH PROTEIN IN THE WHEAT CULTIVAR ATLAS 66[1]

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SUMMARY

The monosomic method and the chromosome-substitution method were used to determine the chromosomes involved in the high-protein characteristic of the wheat cultivar 'Atlas 66'. The monosomic studies indicated that chromosomes 5A, 5B, and 5D contributed to high protein, and 5D might be responsible for the association between high protein and leaf-rust resistance. Comparisons between the Atlas 66 group-5 chromosomes substituted in 'Chinese Spring' background and the parental cultivars indicated that 5D was involved in high protein, but the contributions of 5A and 5B were not clear.

The soft winter wheat cultivar 'Atlas 66' is a valuable source of high-protein germplasm in breeding programs because the trait is highly heritable and appears to depend on a relatively low number of genes (see JOHNSON *et al.*, 1968, for review of papers). The concept of few genes was based in part on a close association between leaf-rust resistance and high protein in lines derived from crosses between Atlas 66, which is resistant to leaf rust, and a susceptible, low-protein cultivar 'Wichita'.

The assignment of the genes for high protein to specific chromosomes would provide information for the efficient use of this trait in breeding programs. Therefore, we have used the cytogenetic methods of monosomic analysis and chromosome substitution to determine the gene-chromosome associations.

MONOSOMIC STUDIES

Crosses were made between the set of Wichita monosomics, developed at Kansas State University and the University of Nebraska, and some high-protein lines derived from crosses between Atlas 66 and Wichita. F_1 progenies were grown in a greenhouse, and monosomic or disomic plants were identified by meiotic observations. Each F_2 progeny was planted in a four-row plot at Lincoln, Nebraska, in the fall of

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1963. For each chromosome, there were usually 21 progenies in three sets of seven progenies each. Most progenies came from F_1 monosomic plants, but 97 came from F_1 disomics. Plots of the Atlas 66-Wichita high-protein parent were interspersed through the planting, and three plots of a low-protein cultivar "Comanche" were included.

Notes were taken on one set for adult-plant reactions to natural occurrences of leaf rust *(Puccinia recondita)*. Seeds of each progeny were harvested in the summer of 1964 and bulked before grain weights were recorded. Grain samples were analyzed for nitrogen by AACC Method 46-11 (1962), and protein values were obtained by the conversion factor of percent N x 5.7.

The protein content and yield of kernels produced on F_2 plants are presented in Table 1, along with the high-protein parent and Comanche, which is slightly higher than Wichita in protein content. The progenies for chromosomes 2B, 3A, 3B, 4B, and 7D were not included, because univalent shift had occurred in the Wichita monosomic lines.

Table 1. Protein content and yield of grain produced on F_2 plants from crosses of Wichita monosomics and Atlas 66-Wichita high-protein lines. Field-grown at Lincoln, Nebraska, 1963-64.

Material	No. progenies	Mean protein (%)[1]	Mean yield g/4-row plot
Atlas 66 x Wichita	22	16.90	334
Comanche	3	13.80	309
F_2 progenies from F_1 disomics	97	15.10	329
F_2 progenies from F_1 monosomics for chromosome			
1A	15	15.25	381
1B	14	15.25	317
1D	12	14.85	352
2A	6	15.25	280
2D	14	14.90	340
3D	9	14.95	321
4A	12	15.20	315
4D	13	15.25	304
5A	15	15.70	303
5B	15	15.70	328
5D	11	15.40	324
6A	12	14.65	355
6B	13	15.25	332
6D	12	15.20	323
7A	15	15.15	342
7B	16	14.95	318

[1]14% moisture

The disomic progenies averaged 15.10% protein, and the monosomic progenies for all chromosomes except group 5 ranged from 14.65 to 15.25% protein. Monosomic progenies for 5A, 5B, and 5D had higher protein values than any of the other monosomic progenies or the disomic progenies. They were lower than the Atlas 66-Wichita parent, but some individual progenies overlapped some of the parental plots in protein content. These results indicated that the Atlas 66 group-5 chromosomes had contributed genes for high protein. The involvement of chromosome 5D was strengthened by the observations on leaf-rust reaction. Three out of five F_2 progenies from F_1 monosomic 5D plants had all or most of the plants in the resistant category, whereas most of the other progenies from F_1 monosomics or disomics segregated for a different frequency of resistant and susceptible plants. The Atlas 66-Wichita parental line gave a 5MR reaction in most plots. In view of the close association between high protein and leaf-rust resistance in derivatives of Atlas 66, 5D may be the chromosome carrying this linkage.

The monosomic method is not entirely satisfactory for determining the chromosomes involved in a trait such as protein content. Each monosomic progeny is expected to contain a mixture of monosomic and disomic plants. The disomic contribution could lessen the effect of a specific chromosome when grain from all plants of a progeny is bulked. Furthermore, the protein tests were made on the F_3 seeds, in which the proportion of disomics would be increased over that of the F_2 generation. For these reasons, we decided to use the chromosome-substitution approach.

CHROMOSOME SUBSTITUTIONS

Based on the results of the monosomic study, we selected chromosomes 5A, 5B, and 5D of Atlas 66 to make single substitutions in the genetic background of 'Chinese Spring'. Initial crosses were made in 1967 between Chinese Spring monosomics, originally obtained from Dr. E. R. Sears, and Atlas 66. Backcrosses were made between monosomic progeny and Chinese Spring monotelosomic or monoisosomic stocks, also obtained from Dr. Sears. After two backcrosses, disomic plants were obtained by selfing monosomic plants. In February, 1972, seeds from the parental cultivars and from the disomic plants of each chromosome substitution were sown in a greenhouse soil bed. Each substitution line included two rows, 40 seeds per row. After harvest, grain weights were recorded, and grain protein was determined as in the monosomic study, but using AACC Method 46-12 (1962).

Grain proteins and yields for the chromosome-substitution lines and the parental lines are given in Table 2. The planting included

Table 2. Grain protein content and yield of Atlas 66 chromosome-group-5 disomic substitutions in Chinese Spring (CS) after two backcrosses, and the parental lines. Greenhouse-grown at Lincoln, Nebraska, 1972. Substitutions with values on the same line were derived from sister disomic plants.

Material	Grain protein[1] %	Grain yield, grams per 40 plants
Atlas 66	20.05	199
Chinese Spring	13.55, 16.10	183, 254
CS^3 x Atlas 66 5A	16.00	144
CS^3 x Atlas 66 5B	14.85, 15.50 15.15, 15.20, 14.80	210, 203 185, 195, 213
CS^3 x Atlas 66 5D	17.00, 16.45 17.45, 16.40, 17.35, 18.20	208, 194 128, 205, 143, 98

[1]14% moisture

one two-row plot of Atlas 66 and two plots of Chinese Spring. It is not known why the two Chinese Spring plots differed in protein content by approximately 2½%. One plot was at one end of the soil bed and the other plot in the middle of the bed, with approximately 6 meters between the two plots. There was apparently some

differentiating environmental effect. Only one disomic line was available for 5A, but for both 5B and 5D there were several lines, with two lineages represented for each chromosome. Grain yields for 5A and for three lines of 5D were considerably lower than the rest, and this may have increased protein values. In view of the variation in protein content of Chinese Spring, it is hard to decide whether 5A and 5B can influence high protein. However, it is evident that 5D makes a contribution.

Six backcrosses have now been made to Chinese Spring for the group-5 chromosomes. The next step will be to obtain the disomic lines and get enough seed increase so that replications can be used to determine their effects on protein content.

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