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ANEUPLOID ANALYSIS FOR PROTEIN CONTENT IN A WHEAT–RYE RECOMBINANT

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ABSTRACT

Monosomic series of wheat variety Chinese Spring has been utilised for locating genes on specific chromosomes controlling protein content in Selection 111, a recombinant of wheat and rye, which possesses 1000-grain weight of 61.1 g. This analysis has revealed that major genes of protein are on chromosome 1A of Selection 111.

Key words: Monosomics, Chinese Spring, wheat-rye recombinant, gene location, protein content.

A complete range of aneuploid lines, nullisomics, monosomics, trisomics and tetrasomics in *Triticum aestivum* var. Chinese Spring was made available for analysis by Sears [1]. Since then these aneuploid lines have been used for understanding the evolution of tetraploid and hexaploid wheats [2] for locating genes on specific chromosomes governing quantitative and qualitative characters [3–7] and for transferring desirable traits from alien species to breadwheat [8, 9]. In the present study, monosomic lines of var. Chinese Spring have been used to determine specific chromosome(s) controlling high protein content in a wheat–rye recombinant, selection 111, which possesses extremely high 1000-grain weight (61–75 g) and protein content (15–16%). Monosomic F_2 data were analysed for locating the gene(s) for high protein content on specific chromosomes of Selection 111.

MATERIALS AND METHODS

Deficiency for gene Ph of *Triticum aestivum* has been successfully utilized in transferring desirable traits from *Secale cereale* to breadwheat through induced homoeologus recombination. A lot of variability has been generated for characters like rust resistance, spike length, spikelet number, plant height, grain yield, grain weight, grain protein content etc. These wheat–rye homoeologous recombinants have been designated as selections. Selection 111 is one of them which possesses unique features of high 1000-grain weight (61–75 g) and high protein content (15–16%). This selection was chosen for locating gene(s) for high protein content on specific chromosomes. For this purpose monosomic plants (2n=41) in all the 21 monosomic lines of wheat var. Chinese Spring were identified cytologically and were crossed with Selection 111. The monosomic F_1 hybrids were identified in all the 21 lines. Seeds obtained from these identified F_1 monosomic plants and the disomic F_1 (control cross of Chinese Spring × Selection 111) plants were space planted in the field to raise F_2 populations.

Seeds were harvested from all F_2 plants and data recorded on grain number and grain weight from each plant (Table 1). From these data, 1000-grain weight was calculated. Seeds thus obtained were analysed for absolute protein content.

Seeds obtained from the monosomic, disomic F_2 plants, and parents were ground in Udy Cyclotec Mill. A measured quantity of whole grain meal was taken from all the plants and used for protein estimation (%N × 5.7) by the Macrokjeldahl method on the Tecator Kjeltec System II [10].

Table 1. Protein analysis in F_2 populations of monosomic plants (F_1 monosomics of var. Chinese Spring and Sel. 111) for locating genes on specific chromosomes

Variety & F_2	No. of plants	1000-grain weight (g)	Protein (%)	Total protein in 1000 grains (g)	t value
Chinese Spring	5	26.0	13.3	3.5 ± 0.11	
Sel. 111	4	61.1	16.0	9.8 ± 0.14	
F_2					
Chinese Spring × Sel. 111	39	35.6	13.2	4.7 ± 0.13	
Mono IA × Sel. 111	16	40.3	16.1	6.5 ± 0.20	7.5**
Mono IB × Sel. 111	29	33.4	15.6	5.2 ± 0.19	1.9
Mono ID × Sel. 111	34	32.5	16.1	5.2 ± 0.19	1.8
Mono 2A × Sel. 111	14	31.3	13.7	4.3 ± 0.15	2.0
Mono 2B × Sel. 111	16	29.7	14.9	4.4 ± 0.11	1.76
Mono 2D × Sel. 111	17	31.8	14.0	4.5 ± 0.19	0.86
Mono 3A × Sel. 111	21	28.7	15.7	4.5 ± 0.15	1.00
Mono 3B × Sel. 111	29	34.6	14.7	5.1 ± 0.17	2.00
Mono 3D × Sel. 111	20	31.4	14.7	4.6 ± 0.19	0.50
Mono 4A × Sel. 111	20	31.8	15.8	5.0 ± 0.13	1.66
Mono 4B × Sel. 111	13	29.7	14.3	4.2 ± 0.21	2.08
Mono 4D × Sel. 111	15	33.2	15.1	5.0 ± 0.12	1.66
Mono 5A × Sel. 111	24	32.6	15.1	4.9 ± 0.13	1.11
Mono 5B × Sel. 111	16	30.2	15.2	4.6 ± 0.15	0.50
Mono 5D × Sel. 111	17	31.7	15.0	4.8 ± 0.16	2.00
Mono 6A × Sel. 111	44	32.3	13.8	4.5 ± 0.13	1.11
Mono 6B × Sel. 111	16	30.3	14.8	4.5 ± 0.12	1.11
Mono 6D × Sel. 111	20	30.0	15.3	4.6 ± 0.14	0.50
Mono 7A × Sel. 111	14	33.5	14.6	4.9 ± 0.14	1.00
Mono 7B × Sel. 111	23	30.4	14.0	4.3 ± 0.12	0.18
Mono 7D × Sel. 111	24	29.8	14.4	4.3 ± 0.13	2.17

**Significant at 1% level.

RESULTS

Data on grain protein are presented in Table 1. Variety Chinese Spring contains 13.3% grain protein, whereas the donor parent Sel. 111 has 16.0% protein. The disomic F_2 showed mean protein content of 13.2%. The protein content means of the F_2 of monosomics and disomics are compared on per cent protein basis and it is observed that

most of the monosomic F_2 have higher protein content than the disomic F_2. Comparison on the basis of protein content is probably not correct, as the lines with high protein content have lower grain weight. This indicates that the high protein content is not a result of increase in the absolute protein content but because of reduction in grain weight. Therefore, it would be more appropriate to compare the total protein contained in a unit grain number (in the present study 1000 grains).

The total amount of protein in 1000 grains of all the monosomic, disomic F_2 and parents was calculated by the following formula:

$$\text{Quantity of protein in 1000 grains(g)} = \frac{\text{\% protein} \times \text{1000-grain weight}}{100}$$

The values thus obtained are recorded under column "total of protein in 1000 grains" (Table 1). When these values are compared, it is observed that only one line, 1A, exhibited higher amount of absolute protein over disomic F_2.

DISCUSSION

Genes affecting total protein content of wheat (*T. aestivum* L.) kernels or flour have been associated with each of the 21 chromosomes in different varieties [11, 12]. There are also reports suggesting involvement of a few chromosomes for protein synthesis in wheat [13–18].

In the present study, major gene(s) for high protein synthesis, beside others with minor effects, have been located on chromosome 1A in Sel. 111, which alone is responsible for increase in protein productivity per grain to the tune of 37.94%.

The present study supports some previous investigations on mapping of genes regulating protein synthesis in some wheat cultivars. Utilizing aneuploid analysis, Brown et al. [16] and Zehatschek et al. [18] have shown that chromosomes 1A, 1B and 1D carry genes for protein synthesis in the wheat varieties studied by them. Lawrence and Shepherd [17] have reported the involvement of chromosomes 1A and 6A controlling this character.

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