

GENE TRANSFER FROM RYE TO WHEAT AND THEIR LOCATION

DALMIR SINGH

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110012

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ABSTRACT

The wheat-rye recombinant, Selection 229, reported earlier is characterized by hairy peduncles, brown spikes, and red grain colour. It is cytologically and morphologically stable. Phenotypically the plants resemble *aestivum* varieties, show good spike fertility and produce well-filled grains. F₂ segregation suggests that these traits are governed by three independent dominant genes. Monosomic analysis revealed that in S-229, the genes controlling hairy peduncle, brown spike and red grain are located on chromosomes 5A, 1B and 3B, respectively.

Key words: *Triticum aestivum*, *Secale cereale*, 5B deficiency, homoeologous recombination, hairy peduncle, brown spike, red grain, monosomic analysis.

A wheat-rye recombinant, Selection 229 (S-229), was reported [1] to carry genes for hairy peduncle, brown spike, and red grain. These traits were transferred from rye to wheat presumably through homoeologous recombination in the absence of chromosome 5B of *T. aestivum*. The presence of *Ph 1* gene on long arm of chromosome 5B prevents pairing between homoeologous chromosomes [2, 3] of wheat and alien chromosomes. Cytological analysis of S-229 showed regular 21 II at meiotic metaphase I. Regular chromosome pairing was also observed in the F₁ hybrids of S-229 and other varieties of *T. aestivum*. This paper reports location of the genes controlling these traits on specific chromosomes of S-229, using monosomic lines of variety Chinese Spring having smooth peduncle, white spike, and red grain.

MATERIALS AND METHODS

A cross between monosomic 5B of hexaploid wheat variety Pb. C591 and Russian rye (2n=14) yielded 3 plants, all with 28 chromosomes. One of the hybrid plants showed very high chromosome pairing. Thirty seven spikes of this plant were backcrossed to different varieties of *T. aestivum*. The plants obtained from these backcrosses were selfed and selection

for several generations lead to the isolation of a number of wheat-rye recombinants, and S-229 is one of them. The third parent of S-229 was a derivative of cv. Bounty from USDA having white spikes and seeds.

S-229 was crossed with all the 21 identified monosomic plants of Chinese Spring using as male parent. The monosomic and disomic hybrid plants were cytologically identified in F₁, and data recorded on them for hairy peduncle, spike and grain colour. Seeds were harvested separately from all the cytologically identified monosomic and disomic hybrid plants, and sown in the field to observe F₂ segregation for hairy peduncle, spike and grain colour. The data were recorded at maturity on all F₂ plants for these traits and analysed for goodness of fit to the expected ratios using χ^2 test.

RESULTS AND DISCUSSION

F₁ HYBRIDS

All the F₁ hybrids had hairy peduncle, brown spikes and red grains. The presence of these traits in the F₁ plants indicates that S-229 had no selective disadvantage in male transmission due to the presence of rye genes.

F₂ POPULATIONS

Hairy peduncle. The disomic cross of Chinese Spring and S-229 produced 338 plants in the F₂: 245 with hairy and 93 with smooth peduncle, representing the ratio of 3 : 1 (Table 1). The monogenic segregation ratio suggests a single dominant gene responsible for hairy peduncle. All the F₂ populations of monosomic hybrids also segregated for the expected monogenic ratio 3 : 1 (Table 1) except the progeny of monosomic 5A. The F₂ population of monosomic 5A had 125 plants with hairy peduncle and 4 plants with smooth peduncle. This deviated significantly from the expected monogenic ratio of 3 : 1, suggesting that the gene controlling hairy peduncle is located on chromosome 5A of S-229. Using rye-wheat chromosome addition lines, it has been shown that the *Hp* (hairy peduncle) gene is located on the long arm of chromosome 5R [4].

Spike colour. The F₂ populations of the monosomic and disomic hybrid plants also segregated for spike colour in the ratio of 3 brown : 1 white, except the F₂ population of monosomic line 1B (Table 2). This F₂ progeny had 121 plants with brown and 5 with white spikes (these 5 plants could be nullisomics). These results suggest that the gene controlling spike colour in S-229 is located on chromosome 1B. This chromosome was earlier reported to be carrying the gene controlling spike colour [5, 6].

Table 1. F₂ segregation of the monosomic and disomic F₁ hybrids of the crosses between S-229 and monosomics of var. Chinese Spring for hairy peduncle

Parent/ cross	Hairy peduncle	Smooth peduncle	χ^2 (3:1)	P
Chinese Spring (C.S.) S-229	S-229 100	100 —	— —	— —
C.S. Disome x S-299	245	93	1.14	0.30–0.20
1A x S-229	255	94	0.69	0.50–0.30
1B x S-229	91	35	0.51	0.50–0.30
1D x S-229	68	28	0.88	0.50–0.30
2A x S-229	80	33	1.06	0.50–0.30
2B x S-229	95	37	0.64	0.50–0.30
2D x S-229	88	26	0.29	0.70–0.50
3A x S-229	113	34	0.27	0.70–0.50
3B x S-229	115	45	0.83	0.50–0.30
3D x S-229	85	30	0.10	0.80–0.70
4A x S-229	82	34	1.14	0.30–0.20
4B x S-229	230	83	0.38	0.70–0.50
4D x S-229	141	55	0.97	0.50–0.30
*5A x S-229	125	4	32.99	< 0.10
5B x S-229	60	25	0.88	0.50–0.30
5D x S-229	52	22	0.88	0.50–0.30
6A x S-229	112	44	0.85	0.50–0.30
6B x S-229	126	38	0.29	0.70–0.50
6D x S-229	76	30	0.61	0.50–0.30
7A x S-229	74	20	0.69	0.50–0.30
7B x S-229	91	36	0.75	0.50–0.30
7D x S-229	83	35	1.36	0.30–0.20

*Monosomic line involved in controlling hairy peduncle.

Table 2. F₂ segregation of the monosomic and disomic F₁ hybrids of the crosses between S-229 and monosomics of var. Chinese Spring for spike colour

Parent/ cross	Brown spike	White spike	χ^2 (3:1)	P
Chinese Spring (C.S.) -229	— 100	100 —	— —	— —
C.S. Disome x S-299	246	92	0.88	0.50–0.30
1A x S-229	254	93	0.91	0.50–0.30
*1B x S-229	121	5	29.72	<0.01
1D x S-229	69	27	0.50	0.50–0.30
2A x S-229	81	32	0.66	0.50–0.30
2B x S-229	95	37	0.64	0.50–0.30
2D x S-229	81	33	0.94	0.50–0.30
3A x S-229	108	39	0.18	0.70–0.50
3B x S-229	114	46	1.20	0.30–0.20
3D x S-229	83	31	0.10	0.80–0.70
4A x S-229	82	34	1.14	0.30–0.20
4B x S-229	230	83	0.38	0.70–0.50
4D x S-229	142	54	0.68	0.50–0.30
5A x S-229	103	36	1.61	0.30–0.20
5B x S-229	61	24	0.47	0.50–0.30
5D x S-229	52	22	0.88	0.50–0.30
6A x S-229	113	43	0.54	0.50–0.30
6B x S-229	127	37	0.52	0.50–0.30
6D x S-229	77	29	0.31	0.70–0.50
7A x S-229	74	20	0.68	0.50–0.30
7B x S-229	92	35	0.44	0.70–0.50
7D x S-229	84	34	0.91	0.50–0.30

*Monosomic line involved in controlling spike colour

Grain colour. The F₂ populations of the cross S-229 x Chinese Spring involving 19 monosomic hybrids segregated for grain colour in the ratio of 15 : 1 (Table 3), suggesting the involvement of two dominant genes for red grain colour in this cross. Variety Chinese Spring is known to carry only one dominant gene for grain colour on chromosome 3D [7].

Therefore, it is reasonable to assume that the other gene was contributed by S-229. The F₂ of the monosomic F₁ hybrid of chromosome 3D segregated in the monogenic ratio of 3 red : 1 white while, the F₂ of the monosomic F₁ hybrid of chromosome 3B produced mostly red (147 red : 3 white) indicating that red grain colour in these two cultures (Chinese Spring and S-229) is controlled by two independent dominant genes. Since chromosome 3D is already known to carry the gene for red grain in Chinese Spring [7], chromosome 3B can be assumed to carry the gene for red grain colour in S-229. It is, therefore, likely that a segment of rye chromosome carrying the gene for red grain colour was transferred to chromosome 3B of cv. Pb. 6591 used in the initial intergeneric cross [1].

Location of the genes controlling hairy peduncle, brown spike, and red grain colour on three different chromosomes, which got transferred through homoeologous recombination from rye to wheat in the absence of chromosome 5B of *T. aestivum*, indicates that desirable traits can also be transferred from *Secale cereale* to cultivated wheats through homoeologous recombination. This approach is presently being utilized to transfer genes for rust resistance from *Secale* to cultivated wheat.

Table 3. F₂ segregation of the monosomic and disomic F₁ hybrids of the crosses between S-229 and monosomics of var. Chinese Spring for grain colour

Parent/cross	Red grain	White grain	χ^2	P
Chinese Spring (C.S.)	100	—	—	—
S-229	100	—	—	—
C.S. disome x S-299	314	25	0.41 (15:1)	0.70-0.50
1A x S-229	326	23	0.06 "	0.80-0.70
1B x S-229	116	10	0.61 "	0.50-0.30
1D x S-229	87	9	1.60 "	0.20-0.10
2A x S-229	104	9	0.56 "	0.50-0.30
2B x S-229	121	11	0.97 "	0.50-0.30
2D x S-229	105	9	0.52 "	0.50-0.30
3A x S-229	139	8	0.16 "	0.70-0.50
3B x S-229	147	3	5.25 "	>0.01
3D x S-229	89	25	0.57 (3:1)	0.50-0.30
4A x S-229	107	9	0.45 (15:1)	0.70-0.50
4B x S-229	290	23	0.64 "	0.50-0.30
4D x S-229	151	15	2.14 "	0.02-0.01
5A x S-229	118	11	1.14 (15:1)	0.30-0.20
5B x S-229	81	4	0.34 "	0.70-0.50
5D x S-229	68	6	0.43 "	0.75-0.50
6A x S-229	144	12	0.55 "	0.50-0.30
6B x S-229	150	14	1.46 "	0.30-0.20
6D x S-229	97	9	0.91 "	0.50-0.30
7A x S-229	86	8	0.82 "	0.50-0.30
7B x S-229	116	11	1.26 "	0.30-0.20
7D x S-229	108	10	0.91 "	0.50-0.30

*Monosomic line involved in controlling grain colour.

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