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ANEUPLOID ANALYSIS OF A RECOMBINANT OF WHEAT AND RYE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS

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ABSTRACT

Monosomic analysis conducted on a wheat–rye recombinant (Sel-26) to assign major genes for yield and yield attributing characters to its specific chromosomes by employing Chinese Spring monosomic series revealed that chromosomes 3A, 3D and 4A of Sel-26 carry genes which enhance yield while 6B harbours genes which decrease the yield. Chromosomes 5A, 5B and 6B of Sel-26 have major recessive genes for low seed weight along with minor genes in 4B, 4D, 5D and 7D. It was indicated that grains per spike increased due to genes on chromosome 6B and reduced by those on chromosome 5B. Two chromosomes, 4A and 4B, carry genes for higher tiller number in Sel-26.

Keywords: Monosomic series, wheat–rye recombinant, yield attributes, gene location.

Conventional genetic analyses of a quantitative character estimates the combined effects of segregating loci and can rarely identify the effects of any particular gene or a group of linked or unlinked genes. It is important to distinguish control by a few genes with major effect from that of many genes with minor effect as it has important bearing on selection strategy.

The most powerful way of identifying the number of genetic factors segregating in wheat is to use aneuploid techniques. It allows the variation to be partitioned into the effects of individual chromosomes and then into the effects of individual arms or regions of these chromosomes. This method estimates the number and locations of factors and, also the relative size of effects [1–7].

The major criticism against the use of monosomic analyses to define quantitative characters is that the effect of chromosome dosage can be as large or even larger than the

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allelic differences under investigation [8]. At the same time, nonavailability of appropriate genetic stocks, time and labour put a serious constraint on the use of other aneuploid analyses. Therefore, the monosomic analyses is still being preferred [9–11] due to its operational convenience. In the present study also, monosomic analyses was employed to locate genes in specific chromosomes of a wheat–rye recombinant, designated Selection-26 (Sel-26), which was earlier induced by chromosome 5B manipulations [12]. For analysis, monosomic lines of the wheat variety Chinese Spring were used, about which a lot of data are already available from nullisomic, monosomic and telocentric analyses. This provided an added advantage in explaining the results of the present study.

MATERIALS AND METHODS

The material used in the present study was a complete set of 21 monosomic lines of Chinese Spring (CS) and a homoeologous recombinant of wheat (*Triticum aestivum* L.) and rye (*Secale cereale* L.) designated as Selection-26 (Sel-26).

To carry out F_2 monosomic analysis, cytologically identified monosomic plants of all the 21 CS monosomic lines were crossed to Sel-26 (used as male parent). The F_2 seeds were collected from mono-F_1 plants of all the 21 mono-F_1 lines and sown in replicated trial in randomised block design. Observations were recorded on yield/plant, 100-grain weight, grains/ear, fertility level, and tillers/plant.

The F_2 data were subjected to analysis of variance (ANOVA) according to Cochran and Cox [13]. The observations on 100-seed weight and number of grains per ear were also subjected to a χ^2 test, after distributing these characters to appropriate classes.

The statistical significance of means for different characters as compared with the control was assessed by t test.

RESULTS AND DISCUSSION

Analysis of variance for different characters shows that F_2 populations derived from mono-F_1 and disomic-F_1 differed significantly for all the characters studied (Table 1). Therefore, different characters means of the F_2 populations derived from monosomic F_1 plants were tested for their difference from normal F_2 (check) mean by t test (Table 2).

YIELD PER PLANT

The mean single-plant yield of Sel-26 was 23.58 g and that of CS 11.64 g (Table 2). Normal F_2 plants yielded almost equal to the mean yield of CS, showing dominance for lower yield. Three F_1 monosomic-derived F_2 lines for chromosomes 3A, 3D and 4A gave significantly higher grain yield than normal F_2, suggesting that these chromosomes of Sel-26 carry genes

for higher yield. The monosomic F_1-derived line 6B yielded significantly lower than the control cross. Therefore, it could be concluded that yield suppressing genes reside in chromosome 6B of Sel-26.

Table 1. ANOVA (MSS) for different yield attributing characters in the wheat–rye recombinant Sel-26

Source	d.f.	Yield per plant	100-seed weight	Grains per year	Tillers per plant	Fertility level
Replications	2	11.76*	0.07*	1.50	7.38	0.009
Treatments	22	23.76*	0.19*	23.71**	22.89**	0.039**
Error	44	2.71	0.01	3.99	4.18	0.10
Total	68	9.77	0.07	11.27	10.33	0.019

*,**Significant at 5% and 1% levels, respectively.

The positive effect of chromosome 3A on yield was also reported earlier [2, 4]. Yoshida and Kawaguchi [14] reported that 3A and 3AL of CS caused slight increase in yield, therefore, the favourable effect of 3A in Sel-26 could be due to absence of this chromosome from CS in the present material.

The negative effect of 6B on yield recorded in the present study was also reported by Watanabe et al. [15]. Contrary to the present findings, positive effect of 6B as was also reported by [3, 9]. Effect of 3D on yield has not been reported so far.

1000-GRAIN WEIGHT

Sel-26 produces bold seeds, with average 1000-grain weight 37.0 g, which is about 50% higher than the average 25.4 g 1000-grain weight of CS (Table 2). The mean 1000-grain weight of normal F_2 (check) was 33.1 g, showing dominance of higher seed weight.

The mean 1000-grain weights of the monosomic lines for chromosomes 4D, 5A, 5B, 5D, 6B and 7D in F_2 were significantly lower than in the normal F_2 plants, the lowest being in line 6B (Table 2). For the mean yield also the F_2 line derived from 6B had shown lowest yield of 9.73 g per plant (Table 2).

The individual plants were classified in two classes on the basis of grain weight: lighter < 30 g and heavier with > 30 g, 1000- grain weight to test the frequencies of goodness of fit. Normal F_2 plants gave apparent 1:3 (light: heavy seed) segregation ratio. The F_2 lines 1D, 4B, 4D, 5A, 5B, 5D, 6B and 7D deviated from 1:3 ratio. All these lines, except 1D, had more of light seeded plants (Table 3).

The monogenic 1:3 (light:heavy seed) ratio obtained in normal F_2 population does not agree with the 8 critical lines obtained. 5A, 5B and 6B show presence of major recessive genes for low seed weight as exhibited by very high χ^2 value (Table 3). Therefore, the apparent 1:3 ratio could be a change to trigenic 10:54 ratio, with major genes on these chromosomes and

modifiers for low seed weight on 4B, 4D, 5D and 7D. Yoshida and Kawaguchi [14] reported that CS mono-1D, 2D and 3A produce slightly heavier seeds and mono-3D and 5D produce lighter seeds. Therefore, heavier seeds in 1D and lighter seeds in 5D in the present study could be due to the effect of monosomic condition of these chromosomes. Reduction in seed weight due to 4B and 4D, as observed in the present study, was reported by Goud and Sridevi [9].

The genes for high seed weight seem to be distributed on all other chromosomes of Sel-26, except the 8 chromosomes mentioned above.

GRAINS PER EAR AND FERTILITY LEVEL

Sel-26 contains more grains (average 44.4) per spike than CS (33.5) (Table 2). The control F_2 shows dominance for higher seed number, the average number of grains per spike being 40.9.

The monosomic derived F_2 lines 4B, 5A, 6A, 6B and 7B deviated significantly from the disomic F_2 mean. The lines 4B and 6A produced fewer and 5A, 6B and 7B produced more grains per spike.

The homogeneity test applied to two classes of higher (> 40) and lower number of seeds per spike (< 40) showed that 4B and 6B deviated from normal F_2 segregation ratio, while 3A, 4D, 5A, 5B and 7A had a poor fit to the normal F_2 ratio (Table 4). The lines 5A,

Table 2. Mean values of yield characters in F_2 populations derived from monosomic F_1s (mono CS x Sel-26), parents and control cross

Monosomic and parent variety	Yield per plant (g)	1000-seed weight (g)	No. of grains per ear	Tillers per plant	Fertility level (seeds/ spikelet)
1A	13.2	33.3	40.4	16.6	1.74
1B	12.4	32.3	40.2	16.0	1.67
1D	12.6	33.7	41.5	16.2	1.82
2A	13.5	34.2	40.8	16.7	1.74
2B	12.7	34.2	42.6	19.0	1.72
3A	16.1**	33.5	41.6	19.1	1.74
3B	12.21	34.1	41.8	15.9	1.89
3D	16.5**	32.3	40.9	18.1	1.75
4A	15.5**	32.6	38.5	25.5	1.61*
4B	14.5	32.2	36.2**	21.8*	1.61*
4D	12.4	31.2*	39.0	17.2	1.65
5A	11.9	27.9**	44.1**	18.1	1.91
5B	11.0	29.8*	42.7	17.6	1.79
5D	10.7	31.0*	40.5	14.7	1.69
6A	10.9	32.3	37.6**	15.9	1.75
6B	9.7*	26.5**	47.7**	13.9	1.97*
6D	11.8	31.6	41.8	15.4	1.71
7A	12.7	31.5	38.2	18.6	1.65
7B	11.2	32.0	44.4*	16.5	1.89
7D	14.0	30.7*	41.4	16.9	1.86
F_2	12.4	33.1	40.9	16.9	1.78
CS	11.6	25.4	33.5	15.2	1.56
Sel-26	23.6	37.0	44.4	23.8	1.91
CD 5%	2.6	1.9	3.2	3.3	0.158
CS 1%	3.5	2.5	4.2	4.3	0.207

*,** Significant deviation of the line from normal F_2 mean at 5% and 1% levels, respectively.

Note. Mono-2D derived F2 population not available because of very small number of F2 seeds. The line could not be multiplied.

F_2—Control cross (disome x disome).

5B and 6B developed more higher seeded spikes while the remaining lines had more spikes with fewer seeds.

Chromosomes 6B and 4B seem to affect grain number: 6B increases and 4B reduces the grain number. Other chromosomes, viz. 5A and 5B influenced this character in the positive direction, while 3A, 7A and 7B had detrimental effect (Table 2) on grain formation.

Positive effect of 6B in increasing grain number per ear was reported by Law [1]. The negative effect of chromosome 4B was recorded by Miazga and Chrzastek [16], and Goud and Sridevi [9] reported involvement of many other chromosomes in addition to 4B.

TILLERS PER PLANT

Sel-26 forms more tillers plant (23.8) than CS (15.2) (Table 2).

The mean tiller number of the control disomic F_2 (16.9) was comparable with the parent CS, showing dominance of low tiller number. Two lines, 4A and 4B, developed significantly higher number of tillers. The former line showed transgressive segregation as compared with the higher tiller parent Sel-26 (Table 2).

Table 3. F_2 segregation of plants derived from F_1 monosomic and disomic hybrids between monosomic Chinese Spring and Sel-26 for 1000-seed weight

Monosomic and parent variety	100-seed weight		Total F_2 plants	χ^2 value (1:3)	P value
	light <30.0g	heavy >30.0g			
1A	36	149	185	3.0288	0.10–0.05
1B	32	140	172	3.7519	0.10–0.05
1D*	21	150	171	14.7544	0.05
2A	20	93	113	3.2124	0.10–0.05
2B	11	37	48	0.1111	0.80–0.70
3A	13	56	69	1.3961	0.30–0.20
3B	7	41	48	2.7777	0.10–0.05
3D	30	84	114	0.1053	0.80–0.70
4A	19	54	73	0.0411	0.90–0.80
4B*	65	123	188	9.1915	0.01–0.001
4D*	83	156	239	12.0628	0.05
5A*	159	93	252	195.0476	0.05
5B*	114	144	258	50.6512	0.05
5D*	85	164	249	11.0857	0.05
6A	16	63	79	0.9494	0.50–0.30
6B*	210	80	290	347.7011	0.05
6D	36	95	131	0.4300	0.70–0.50
7A	49	122	171	1.2183	0.30–0.20
7B	64	158	222	1.7357	0.20–0.10
7D*	66	107	173	15.9557	0.05
F_2	47	142	189	0.0018	0.98–0.95
CS	76	3	79	—	—
Sel-26	13	166	179	—	—

F_2–Normal disomic control cross. *Critical line.

Mono-2D derived F_2 population not available because of very small number of F_2 seeds. The line could not be multiplied.

The two chromosomes, 4A and 4B, are thus expected to carry genes for higher tiller number in Sel-26 as no other lines contributed to the higher tillering in this recombinant.

Studies of Law [1] and Sasaki et al. [3] reported negative effect of chromosomes 7B and 6D, respectively on tillering. Watanabe et al. [15] also observed negative effect of chromosomes 2A, 3B, 4B and 6B on tiller formation while Miazga and Chrzastek [16] recorded higher tiller number due to chromosomes 1D, 2D, 7B and 7D. Goud and Sridevi [9] reported negative effect of chromosomes 3B, 7B and 5D and positive effect of 1B, 2A, 6A, 7A and 2B on this character.

None of the above cited studies suggest involvement of chromosomes 4A and 4B in increasing tiller number, as has been observed in the present study. However, majority of reports have indicated distribution of genes for tillering in many chromosomes.

Table 4. Segregation of F_2 plants, derived from F_1 monosomic and disomic hybrids between monosomic Chinese Spring and Sel-26 for grains per spike

Monosome and parent variety	Grains per spike		Total F_2 plants	χ^2 value (98:128)	P value
	low (< 40)	high (> 40)			
1A	68	83	151	0.1715	0.70–0.50
1B	84	108	192	0.0117	0.95–0.90
1D	71	94	165	0.0074	0.95–0.90
2A	81	86	167	1.7966	0.20–0.10
2B	20	28	48	0.0562	0.50–0.30
3A*	27	19	46	4.4033	0.05–0.02
3B	20	31	51	0.3571	0.70–0.50
3D	47	60	107	0.0138	0.95–0.90
4A	39	35	74	2.6284	0.20–0.10
4B*	74	51	125	12.7567	0.05
4D*	121	114	235	6.3191	0.02–0.01
5A*	76	148	224	8.1179	0.01–0.001
5B*	75	138	213	5.7629	0.02–0.01
5D	110	122	232	1.5502	0.30–0.20
6A	43	59	102	0.0604	0.90–0.80
6B*	53	177	230	38.6659	0.05
6D	68	100	168	0.5700	0.50–0.30
7A*	95	83	178	7.2592	0.01–0.001
7B	97	151	248	1.8239	0.20–0.10
7D	69	100	169	0.4420	0.70–0.50
F_2	98	128	228	—	—
CS	62	11	73	—	—
Sel-26	15	70	85	—	—

F_2—Normal disomic. *Critical line.

Mono-2D derived F_2 population not available because of very small number of F_2 seeds. This line could not be multiplied.

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