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Short Communication

Rye chromosome composition and seed characters in hexaploid triticale (X *Triticosecale* WITTMACK)

D. Saranya* and V. R. K. Reddy[1]

PG and Research Department of Botany, Government Arts College, Ooty, The Nilgiris 643 002, Tamilnadu; [1]Genetics Laboratory, Department of Botany, Bharathiar University, Coimbatore 641 046, Tamilnadu

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Abstract

The individual characteristic features of chromosomes in Petkus rye (diploid) and 82 hexaploid triticale accessions were assessed to identify the replaced rye chromosome pair(s) in triticale and its effect on kernel characters. Giemsa-C-banding technique was used for the study. Results revealed that 24 hexaploid triticales showed full complement of rye chromosome, 34 had replacement of one pair and 24 had replacement of two pairs of rye chromosomes. Triticale strains with 2R/2D and 4R/4D substitutions had higher and medium seed set, respectively. Seed set was considerably high when both with 2R/2D and 4R/4D substitution occured together.

Key words: Triticale, -Giemsa C-banding, chromosome substitution, rye

Derivative between wheat and rye dates back to 1875, but until recently efforts were taken continuously to develop high yielding triticales as a field crop (Schinkel, 2002; Thiemt and Oettler, 2008). During crossing between wheat and triticale or wheat and rye, useful characters from rye genome were transferred to wheat either in the form of substitutions, additions or translocations (Chang and de Jong, 2005; Hesler et al. 2007). The objective of the study was to identify by individual characteristics features of Petkus rye chromosomes and the chromosome constitution of different hexaploid triticale strains using Giemsa C-banding technique to identify the replaced rye chromosome pair(s) or in triticale and to study the relation of rye chromosomal substitutions with kernel characters such as seed shriveling and seed setting in different hexaploid triticales.

The seed material consisted of one variety of diploid rye (*Secale cereale* L. 2n=14) var. Petkus rye and eighty two varieties of hexaploid triticale (-X *Triticosecale* Wittmack) in which 74 were spring triticales and 8 winter triticales. Individual R-genome chromosomes in rye and possible R/D substitutions in different hexaploid triticales were studied using Giemsa banding technique with some modification (Gill and Kimber, 1974) and (Weimarck, 1974). The seed characters were recorded based on the classifications of Bennett (1977) and Gill et al. (1981). The seed traits included average seed set [classified as low (below 50%), medium (50-60%) and high (65% and above)], 100-grain weight, volume of water displaced by 100 grains, kernel shriveling (classified as very low, low, medium and high based on visual observation) and test weight.

On the basis of R/D substitution, it was clear that out of 82 hexaploid triticale genotypes, 24 possessed full complement of rye chromosomes (7 pairs as revealed by 14 banded chromosomes), 34 had one pair of replaced rye chromosomes (12 banded chromosomes) and 24 had two pairs of replaced rye chromosomes (10 banded chromosomes). In triticales, where one pair is replaced, 2R was replaced in 16 triticale genotypes, 3R in 4 genotypes, 4R/7R in 11 triticale genotypes, and 5R in 3 triticale varieties. In the 24 triticales, where two pairs of R genome chromosomes were replaced, 2R and 4R/7R were

*Corresponding author's e-mail: sharanyaasenthil121@gmail.com
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Table 1. The data on chromosome composition and seed characters in different hexaploid triticale accessions

S.No.	Triticale/ accessions	Average seed set (%)	100-grain weight (g)	Volume(ml) of water displaced by 100 grains	Grain shriveling	Test weight (kg/hl)
1	DT 46	57.6	2.48	2.81	Medium	61
2	TL 238	58.5	2.68	2.92	Medium	64
3	TL 257	54.3	2.53	2.71	High	52
4	TL 319	59.5	2.70	3.01	Medium	63
5	Armadillo	59.8	2.54	2.83	Medium	62
6	Karl	57.5	2.92	2.86	Medium	64
7	DT 78	58.5	2.94	2.88	Medium	55
8	6T 204	58.6	2.517	2.83	Medium	63
9	6T 208	53.5	2.69	2.83	High	56
10	6T 209	57.6	2.47	2.80	Medium	62
11	Dua	62.3	2.48	3.05	Medium	58
12	Towan	62.5	2.49	3.04	Medium	59
13	Rufus	53.7	2.63	2.76	Medium	58
14	Tobruk	55.8	2.82	2.82	Medium	63
15	Yukuri	63.4	2.77	2.84	Medium	56
16	Pika	53.6	2.37	2.68	High	55
17	Banjo	57.6	2.49	2.80	Medium	60
18	Rhino	52.2	2.49	2.54	Medium	52
19	Beagle	53.4	2.62	2.63	Medium	53
20	Alamos	54.8	2.57	2.69	Medium	59
21	Eronga	57.8	2.52	2.82	Medium	61
22	Borhane	52.6	2.71	2.79	Medium	59
23	Juanillo	52.5	2.60	2.65	Medium	51
24	Marvel	54.5	2.52	2.71	High	53
25	Armadillo"S"	76.4	2.91	3.01	Medium	53
26	Fahad "S"	75.4	2.67	2.77	High	52
27	Bronco "S"	78.4	2.89	2.98	High	56
28	Passi	81.3	2.46	2.69	High	53
29	OAC Triwell*	75.6	2.68	2.78	High	53
30	OAC Wintir*	71.2	2.51	2.78	High	53
31	OAC Decade	81.5	2.49	3.01	High	55
32	Kramer	76.5	2.91	3.01	Medium	53
33	Tahara	76.2	2.89	3.00	Medium	52
34	Tickit	86.8	2.71	3.22	Medium	56
35	Treat	76.4	2.90	3.07	Medium	55
36	Rosner	74.5	2.69	2.76	High	56
37	Jaywick	68.2	2.41	2.76	High	54
38	Speedee	81.2	2.81	3.01	Medium	57
39	TCL 38*	69.4	2.34	2.63	High	54
40	TCL 39*	75.6	2.68	2.78	High	53
41	UH 116	49.4	2.68	2.56	High	50
42	Lasko	48.5	2.70	2.61	High	51
43	Pollmer	47.4	2.71	2.79	High	52
44	6T 6450	49.2	2.67	2.55	High	51
45	AC Copia	59.3	3.83	3.85	Low	70

46	AC Alta	63.1	3.73	3.82	Low	63
47	AC Certa	57.6	3.42	3.52	Medium	63
48	Berkshire	57.8	3.78	3.84	Low	66
49	Bogong	61.8	3.77	3.81	Low	65
50	Cananea	59.5	3.77	3.81	Low	66
51	Nutriseed	57.4	3.41	3.51	Medium	62
52	Tritigold	59.7	3.78	3.82	Low	65
53	WB-UW 36	57.8	3.42	3.52	Medium	61
54	Grillo “S”	64.4	3.74	3.83	Low	64
55	UM 940	62.4	3.75	3.84	Low	66
56	Frank	48.9	3.00	3.03	Medium	55
57	Wapiti*	49.1	2.67	2.89	High	50
58	OAC Trillium	48.1	2.89	3.01	High	49
59	TL 2942	81.5	3.85	3.96	Very Low	71
60	TL 2951	81.6	3.86	3.97	Very Low	74
61	AN 31*	81.4	3.84	3.95	Very Low	71
62	AN 34*	81.6	3.83	3.97	Very Low	72
63	Breakwell	81.7	3.88	3.96	Very Low	73
64	Endeavour	81.4	3.89	3.94	Very Low	72
65	Canobolas	81.7	3.84	3.98	Very Low	70
66	Chopper	81.3	3.85	3.98	Very Low	71
67	Florico	71.6	3.00	3.05	Medium	63
68	TL 6714	70.2	2.65	2.89	High	51
69	Hawkeye	74.9	2.72	2.77	High	51
70	Sandro	67.6	2.47	2.76	High	52
71	T 3048	69.4	2.68	2.71	High	54
72	Grace	69.7	2.71	2.69	High	52
73	Tl 6804	69.6	2.69	2.71	High	53
74	Pronghorn	69.7	2.68	2.73	High	54
75	NGSN 23	46.2	3.00	3.02	High	51
76	Springfest	46.2	3.00	3.02	High	51
77	Carman	66.3	3.84	3.89	Low	68
78	TL 6437	66.3	3.84	3.89	Low	68
79	T 3021	69.8	4.12	4.22	Very Low	74
80	T 3065	69.7	4.14	4.23	Very Low	74
81	AC Ultima*	69.7	4.13	4.2	Very Low	73
82	Welsh	69.9	4.11	4.21	Very Low	74

* - Winter Triticales

replaced in 8 triticales, 2R and 5R in 4 varieties, 2R and 4R/7R in 4 varieties, 3R and 5R in 2 varieties, 4R/7R and 5R in 2 triticales, and 4R/7R and 6R were replaced in 4 triticale genotypes. Overall, either individually or in combination with other substitutions, the frequency of replacement of rye chromosomes by wheat chromosomes as follows: 2R in 32 triticales; 3R in 6 triticales, 4R/7R in 25 triticales, 5R in 11 triticales, 6R in 4 triticales; and 7R/4R in 4 triticales.

The data on various kernel characters including seed shriveling 100-grain weight, volume of water displaced by 100-grains, test weight and seed setting in all 82 hexaploid triticale varieties were recorded (Table 1). In 12 triticale varieties the kernel shriveling was 'very low'; in 10 triticale genotypes it was 'low'; in 31 triticale genotypes it was 'medium' and in the remaining 29 triticales it was 'high'. The results obtained from other parameters revealed that the values of these parameters were high in triticales with low shriveling and were low in genotypes with high shriveling. The data on average seed set in all 82 triticale varieties revealed that 9 triticales had 'low seed set'; 35 had 'medium seed set' and the remaining 38 had 'high seed set'.

Giemsa banding technique is found more reliable over simple karyotypic features where size of the chromosome, arms and position of centromere differs due to contraction of chromosomes (Lukaszewski, 2006; Rybka, 2003). It was found that at least one to three D genome chromosomes were substituted in most of the secondary hexaploid triticales. In the present study, in total, 24 hexaploid lines showed full complement of rye chromosome without any R/D substitution. In an earlier study (Sapra and Stewart, 2004), 11 hexaploid triticales showed full complement of rye chromosome.

Out of 82 hexaploid triticales analyzed, rye chromosome 2R was replaced in maximum number of triticales followed by 5R (in 11 triticales), 4R/7R (in 25 triticales). 3R and 7R/4R in 4 triticales each and 6R was replaced in 4 triticales. The 1R chromosome was not replaced in any of the triticale varieties studied.

It was found that 2R/2D substitution resulted in higher seed set and that 4R/7R substitution had an intermediate effect. The role of interaction between wheat and rye genes and chromosomes on various morphological, agronomical and yield characters in triticales were also indicated. The R/D substitutions having agronomic importance may be used in breeding program by the breeders.

Authors' contribution

Conceptualization of research (DS, VRK); Designing of the experiments (DS, VRK); Contribution of experimental materials (DS, VRK); Execution of field/ lab experiments and data collection (DS, VRK); Analysis of data and interpretation (DS, VRK); Preparation of manuscript (DS, VRK).

Declaration

The authors declare no conflict of interest.

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