Indian J. Genet., **48**(3): 289–293 (1988)

RYE CHROMOSOME COMPOSITION AND KERNEL CHARACTERS IN DIFFERENT HEXAPLOID TRITICALES

V. R. K. REDDY*

Department of Agricultural Botany, Meerut University, Meerut

(Received: December 8, 1987; accepted: December 21, 1987)

ABSTRACT

The R/D substitutions was studied through Giemsa banding and their correlations with kernel characters determined in 64 hexaploid spring triticale strains/varieties. Karyotypic analysis revealed that 15 strains had full complement of rye chromosomes, while others had only replacements of one (in 35 strains) or two pairs of rye chromosomes. Preferential R/D substitutions were noticed with chromosome 2R being replaced in most cases, followed by 5R and 4R/7R. In none of the strains studied chromosome IR was replaced. Triticale strains with 4R/7R substitution exhibited lower degree of kernel shrivelling with higher values for test weight, 100-kernel weight and volume of water displaced by 100-kernels. But 2R, 3R, or 5R replacements resulted in high kernel shrivelling. Any two of these substitutions present together in one triticale, had cumulative effect. The 2R/2D substitution lines exhibited higher seed set, whereas 4R/4D substitution resulted in medium seed set. The seed set was considerably high when both 2R/2D and 4R/4D occurred together. Seed set was low when 3R and 5R were substituted alone or together.

Key words: Chromosome substitution, kernel characters, hexaploid triticale.

Large scale R/D substitutions have been reported in the secondary hexaploid triticales [1]. Initially the rye chromosomes in triticale were identified on the basis of karyotypic studies, but the identification of individual rye chromosomes has become easier with the availability of Giemsa staining technique. The heterochromatin content of rye chromosomes in triticales was negatively correlated with kernel shrivelling [2]. The present communication reports results of a study on R/D substitutions through Giemsa C-banding and their correlations with kernel characters in 64 hexaploid spring triticale strains.

MATERIALS AND METHODS

Seed material. Sixty four hexaploid triticale strains/varieties, obtained from different countries including USA, Mexico, Australia and India, were used (Table 1).

Identification of rye chromosomes by Giemsa staining method. For identification of rye chromosomes in different triticales, modified Giemsa banding technique [3] was employed. Rye chromosomes were classified according to Naranjo et al. [4].

Kernel characters in triticales. Data on the following kernel characters were recorded as means of five plants following Darvey [5]: i) average seed set: classified

*Present address: Department of Botany, Bharathiar University, Coimbatore 641046.

as low (< 50%), medium (50-65%), high (> 65%); ii) 100-kernel weight (g); iii) volume of water (ml) displaced by 100-kernels; iv) kernel shrivelling (visual observation): classified as very low, low, medium, and high; and v) test weight: measured as mass per 100 litres of bulk volume.

RESULTS

R/D SUBSTITUTIONS

The results of Giemsa staining in 64 hexaploid triticale genotypes for identification of rye chromosomes (Table 1) revealed that 15 strains had full complement of rye chromosomes (seven pairs, as revealed by 14 banded chromosomes). In the remaining 49 strains, there was replacement of one or two pairs of rye chromosomes. In the 35 triticale strains exhibiting substitutions for one pair of rye chromosomes, 2R was replaced in majority of strains, followed by 4R/7R, 5R and 3R. Even in the strains with substitutions for two pairs of rye chromosomes, 2R along with 5R was preferentially replaced in most cases. In none of the strains studied chromosome 1R was replaced. Chromosome 6R was substituted in only one strain.

Table 1. Data on different kernel characters of hexaploid triticales

Triticale strain or variety	Rye chromosomes replaced	Average seed set (%)	100-kernel weight (g)	Water displaced by 100-kernels (ml)	Kernel shrivelling	Test weight (kg/100 litres)
1	2	3	4	5	6	7
Beagle	None	79.4	3.04	3.41	Low	68
Carman	None	73.6	3.01	3.08	Low	64
Civet	None	62.4	2.49	3.04	Medium	57
DTS 216-8	None	53.7	2.38	2.69	High	56
DTS 702	None	54.4	2.52	2.71	High	53
DTS 829	None	51.4	2.63	2.84	High	57
DTS 1003	None	50.7	2.71	2.79	Medium	59
Panda 6	None	51.6	2.64	2.71	Medium	61
Rahum	None	49.9	2.57	2.69	Medium	59
T 527	None	57.7	2.49	2.80	Medium	60
UC 70	None	54.3	2.51	2.58	Medium	60
UC 72	None	52.4	2.52	2.65	Medium	59
UC 101	None	51.6	2.61	2.75	Medium	57
UC 103	None	52.3	2.49	2.54	Medium	52
UC 109	None	50.4	2.60	2.65	Medium	51
6 TA 531	2R	76.5	2.91	3.01	Medium	53
Beaver Arm	2R	75.6	2.68	2.78	High	53
Coorong	2R	86.8	2.71	3.22	Medium	56
DTS 6-1	2R	81.4	2.46	2.69	High	53
DTS 701	2R	75.5	3.01	3.21	High	54
DTS 703	2R	78.5	2.89	2.98	High	56
Mapache	2R	81.3	2.81	3.01	High	57
T 470	2R	76.4	2.61	2.84	High	55

Table 1. (contd.)

1	2	3	4	5	6	7
TL 319	2R	81.5	2.49	3.01	High	55
TL 419	2R	74.5	2.69	2.76	High	56
UC 56	2R	69.4	2.34	2.63	High	54
UC 105	2R	68.2	2.41	2.76	High	54
UC 125	2R	71.2	2.51	2.78	High	53
UPT 75132	2R	74.3	2.39	2.61	High	54
UC 60	3R	51.4	2.68	2.56	High	50
UC 63	3R	49.4	2.71	2.79	High	52
6TA 375	4R/7R	57.4	3.41	3.51	Medium	62
Bacum	4R/7R	59.3	3.83	3.85	Low	70
DTS 330	4R/7R	58.6	3.79	3.86	Low	68
DTS 222-12	4R/7R	59.6	3.86	3.91	Low	70
DTS 690	4R/7R	59.5	3.78	3.81	Low	69
DTS 840	4R/7R	65.4	3.74	3.83	Low	64
ELK 32	4R/7R	59.6	3.77	3.81	Low	66
Juanillo	4R/7R	59.8	3.76	3.85	Low	70
Maxitol	4R/7R	57.4	3.65	3.74	Low	68
T 40	4R/7R	55.6	3.59	3.70	Low	64
UC 48	4R/7R	57.8	3.78	3.84	Low	66
DTS 1019	4R/7R	60.2	2.69	3.75	Low	65
AM 133	5R	49.1	2.89	3.01	High	49
DTS 30	5R	51.6	2.80	2.85	High	52
TS 1–2	5R	48.9	3.00	3.03	Medium	55
UC 19	5R	54.1	2.67	2.89	High	50
UC 57	5R	52.1	2.68	2.79	High	52
UC 76	5R	61.9	2.98	3.01	High	52
UC 116	5R	49.4	2.89	3.00	High	51
DRIRA	2R, 4R/7R	81.7	3.83	3.97	Very low	69
DTS 357	2R, 5R	71.4	2.68	2.71	High	51
DTS 751	2R, 5R	83.6	3.01	3.05	Medium	53
JNK 192	2R, 5R	74.8	2.71	2.78	High	51
Siskiyou	2R, 5R	84.2	2.65	2.89	High	51
TLA 6311	2R, 5R	87.6	2.47	2.76	High	53
UC 34	2R, 5R	73.5	2.86	3.01	High	54
DTS 610	2R, 7R/4R	69.4	2.68	2.71	High	54
DTS 522	3R, 5R	48.3	2.38	2.45	High	51
JNK 6014	3R, 5R	46.2	3.00	3.02	High	51
JNK 0039	4R/7R, 5R	68.3	2.98	3.17	Medium	63
6TA 118	4R/7R, 5R	64.3	3.84	3.89	Low	68
UC 43	4R/7R, 5R	65.7	3.78	3.80	Low	67
T 116	4R/7R, 6R	69.9	4.11	4.21	Very low	71

KERNEL CHRACTERS VS. R/D SUBSTITUTIONS

The data on various kernel characters (Table 1) reveal that kernel shrivelling was medium to high in most triticale strains. Kernel shrivelling, in general, showed negative correlation with 100-kernel weight, volume of water displaced by 100 kernels, and test weight. Kernel shrivelling was comparatively lower in the strains carrying 4R/4D substitutions, and high in 2R/2D substitution lines. Seed set, in general, was medium to high in most strains. In all the strains where 2R, either alone or along with some other rye chromosome, was replaced, the seed set percentages were considerably high. On the other hand, substitutions for other rye chromosomes did not influence seed set noticeably.

DISCUSSION

There were at least 1–3 R/D substitutions in most of the secondary hexaploid triticales reported earlier [6, 7]. The results of the present study based on Giemsa staining technique confirm these observations. It was also observed that preferential substitution for certain rye chromosomes, e.g. 2R, was more frequent as compared to others. Other studies [8–10] also reported that majority of the triticales studied showed replacement of 2R, followed by 4R and 5R, but none of the strains lost chromosome 1R.

All R/D substitutions, with the exception of 4R/7R, have resulted in high kernel shrivelling, suggesting that 4R/4D substitution was more favourable for grain development. The improvement enhanced under combined substitution of 6R and 4R (T 1116). It was earlier reported tnat the most important rye chromosomes responsible for kernel shrivelling are 4R, 6R and 7R [11]. Loss of heterochromatin from these chromosomes leads to improvement in kernels, but once they have lost heterochromatin further loss of heterochromatin or substitution will not cause any improvement in the kernels. Positive relationship between 2R/2D substitution and high kernel shrivelling has been reported [11, 12]. The improvement in all kernel characters observed in the triticale varieties Beagle and Carman, despite the presence of full complement of rye chromosomes (Table 1) could be due to reduction in the total heterochromatin content without any substitution [11]. The presence of substitutions among A, B, and D genomes or translocations between A, B, R and D genome chromosomes might have also contributed to such improvement.

The 2R/2D substitution alone or in combination with additional substitutions resulted in higher seed set, suggesting that chromosome 2D is responsible for seed fertility. The presence of female fertility genes on chromosome 2D has already been reported [13]

ACKNOWLEDGEMENTS

The author is grateful to Dr. P. K. Gupta for suggestions made during the study, and to Indian Council of Agricultural Research, New Delhi, for financial help.

REFERENCES

1. B. Skovmand, P. N. Fox and R. L. Villarreal. 1984. Triticale in commercial agriculture: progress and promise. Adv. Agron., **37:** 1–45.

2. M. D. Bennett and J. P. Gustafson. 1982. The effect of telomeric heterochromatin of *Secale cereale* on triticale (×*Triticosecale*). II. The presence or absence of blocks of heterochromatin in isogenic backgrounds. Can. J. Genet. Cytol., **24:** 93–100.

3. B. S. Gill and G. Kimber. 1974. A Giemsa C-banded karyotype of rye. Proc. Natl. Acad. Sci., U.S.A., **71:** 1247–1249.

4. T. Naranjo, J. R. Lacadena and R. Giraldez. 1982. Interaction between wheat and rye genomes on homologous and homeologous pairing. Z. Pflanzenzuchtg., **82:** 285–305.

5. N. L. Darvey. 1973. Genetics of seed shrivelling in wheat and triticales. Proc. 4th Intern. Wheat Genet. Symp. Agricultural Station, Columbia, Missouri, U.S.A.: 155–160.

6. N. L. Darvey and J. P. Gustafson. 1975. Identification of rye chromosomes in wheat–rye addition lines and triticales by heterochromatin bands. Crop Sci., **15:** 239–243.

7. A. Merker. 1975. Chromosome composition of hexaploid triticale. Hereditas, **80:** 41–52.

8. J. P. Gustafson and F. J. Zillinsky. 1979. Influence of natural selection on the chromosome complement of hexaploid triticale. Proc. 5th Intern. Wheat Genet. Symp., 1978. New Delhi: 1201–1207.

9. W. Sowa and J. P. Gustafson. 1980. Relation between chromosomal constitution in triticale and several agronomic characters. Hod. Rosl. Akli. I Nasie., **24:** 390–397.

10. A. J. Luckaszewski, B. Apolinarska, J. P. Gustafson and K. D. Krolow. 1984. Chromosome constitution in tetraploid triticale. Z. Pflanzenzuchtg., **93:** 222–236.

11. J. P. Gustafson, A. J. Lukaszewski and B. Skovmand. 1984. Heterochromatin content and early endosperm development in 42-chromosome spring triticale. Can. J. Genet. Cytol., **26:** 85–90.

12. J. P. Gustafson. 1983. Cytogenetics of triticale. *In*: Cytogenetics of Crop Plants (eds. M. S. Swaminathan, P. K. Gupta and U. Sinha). MacMillan India Ltd., Delhi: 225–250.

13. R. Scarth and C. N. Law. 1984. The control of the daylength response in wheat by the group 2 chromosomes. Z. Pflanzenzuchtg., **92:** 140–150.