MULTIVARIATE ANALYSIS OF DIVERGENCE IN TRITICALE

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ABSTRACT

The nature and magnitude of genetic divergence was assessed in 63 genotypes of triticale using D^2 - statistics. The population was grouped into 13 clusters. Cluster I, II, IX and VI were larger and included more than half of the total population. The geographical diversity has not been found related to genetic diversity. The varieties 'JNK 6T-234' and 'UPT 74546' belonging to clusters XII and XIII respectively having greater statistical distance between them may be selected for hybridization programme as they are expected to produce reasonably good heterotic effects.

KEY WORDS: Triticale, Genetic divergence.

The knowledge of nature and degree of divergence at inter and intra allelic level is very useful in understanding the course of evaluation of varieties and also in selecting of desirable parents for breeding programme. The more genetically diverse parents, greater are the chances of obtaining higher heterotic expression in F_1s and broad spectrum of variability in the segregating populations. A limited information (Kaltsikes, 1974 and Ahmed et al., 1980) is available on the genetic diversity in triticale.

MATERIALS AND METHODS

Sixty three genotypes were grown in a randomized block design with three replications in 1980-81. Each genotype had one row, each being 5 m in length. The spacing between and within lines was kept 45 and 15 cm respectively. Observations were recorded on 10 randomly selected plants from each row for plant height, tillers/plant, main spike length, spikelets/

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Table 1. Grouping of varieties into different clusters

Clusters	No. of varieties	Varieties
I	14	UPT 7530, UPT 7404, UPT 7511, UPT 74114, UPT 74293, UPT 75182, UPT 75233, UPT 75226. UPT 75203, DTS 280-7, DTS 30, TL 54 JNK 6T 206A-1 & JNK 6T 001A
II	11	UPT 75121, UPT 75162, UPT 75141, UPT 75231, UPT 75235, UPT 74294, UPT 75240, UPT 7406, UPT 75122, UPT 7620 & DTS 47-1
III	5	UPT 7546, UPT 7539, UPT 7542, UPT 75124 & TL 68
IV	2	TL 238 and JNK - 6T 243
V	4	UPT 75232, UPT 75234, JNK-6T 231 and JNK-6T 215
VI	6	UPT 7567, UPT 7578, UPT 7619, DTS 34-3, TL 63, JNK-6T 239
VII	2	UPT 75151 and TL 167
VIII	2	UPT 74524 and JNK-6T 220
IX	8	UPT 7621, UPT 74531, UPT 74547, UPT 74430, DTS 440-4, TL 174, JNK-6T-070, JNK-6T-212
X	3	UPT 74553, UPT 74551 and UPT 74548
XI	3	UPT 7535, UPT 74549 and DTS 551
XII	2	JNK-6T 243 and JNK-6T 139
XIII	1	UPT 74546

main spike, grains/main spike, yield/plant and 100-grain weight. The Mahalanobis's D^2 - statistics was used to measure the genetic divergence as suggested by Rao (1952). The grouping in various clusters was done by Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant difference in treatment means for all the characters except number of tiller/plant which was significant at 5% level. The entire population on the basis of D^2 statistics was grouped into 13 clusters (Table 1). Cluster I and II were the largest comprising of 14 and 11 genotypes respectively. The next cluster was IX which included 8 genotypes and followed by cluster VI with 6 genotypes. This indicated that the largest number of genotypes were genetically close to one another in these 4 clusters and the apparent wide diversity was mainly due to rest of the genotypes distributed in the remaining 9 clusters. The variety UPT 74546 from Pantnagar could not be grouped with any other variety and formed a separate cluster and thus proved to be the most genetically divergent. The other 8 clusters had varieties varying from 2 to 5. Varieties from the different locations were accommodated in the same cluster, while the varieties like DTS 551, DTS 34-3 and DTS 440-4 from Delhi and varieties from Pantnagar distributed to different clusters. The possible explanation for variability among the strains evolved in the same habitat may be due to directional selection for some agronomic characters and/ or genetically diverse nature of the parents used in synthesizing the genotypes. These results showed that the geographical diversity was not fully reflected in the genetic diversity as the clusters from the same origin have been grouped separately and from different origin in the same group. Such unparallelism between geographic and genetic diversity might be due to forces other than geographic distance such as ancestral relationship, genetic drift, free exchange of breeding material from one place to another and varied nature of selection in different regions. Genetic drift and selection in different environments could cause greater diversity than geographical distance. Singh and Bains (1968) and Singh and Gupta (1969) in cotton, Bhatt

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Table 2. Cluster means for seven Characters in Triticale

Cluster	Plant height	Tillers/ plant	Spikelets/ main spike	Spike length	Grains/main spike	Yield/ plant	100 grain weight
I	99.68	3.74	23.75	9.48	55.22	7.55	3.89
II	109.00	3.76	23.37	9.81	53.92	7.11	4.20
III	97.81	4.06	22.67	10.61	52.99	7.78	4.40
IV	88.75	4.64	24.13	10.93	70.06	9.20	4.01
V	102.92	4.40	22.66	9.25	50.08	7.77	3.95
VI	91.92	3.74	24.09	9.34	57.49	7.34	4.08
VII	91.88	3.90	24.80	9.59	60.59	6.38	3.01
VIII	108.86	4.29	25.29	10.88	68.79	9.28	3.53
IX	111.40	3.63	26.14	10.63	55.07	7.50	3.98
X	107.74	3.83	20.82	11.77	30.66	4.00	3.32
XI	104.25	3.61	22.47	11.26	51.39	7.77	4.03
XII	113.55	4.06	27.29	12.85	72.60	8.32	3.10
XIII	119.44	4.40	25.23	14.16	28.30	5.06	4.53

Table 3. Inter and intra-cluster distances

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	5.11	8.21	7.33	6.00	6.92	7.78	7.22	7.80	11.36	17.54	10.23	14.26	14.46
II		5.94	7.86	9.51	8.33	13.75	13.08	9.80	10.97	17.36	4.53	16.98	14.38
III			3.64	6.16	9.78	11.45	20.92	15.77	16.37	23.50	12.55	30.45	20.72
IV				2.51	9.12	9.41	13.33	19.40	18.75	33.04	23.35	43.85	54.25
V					8.14	14.23	15.14	15.95	16.21	23.82	18.54	32.98	30.82
VI						10.25	13.99	17.94	20.29	36.36	21.60	31.54	33.60
VII							3.39	12.53	18.79	39.77	32.49	27.77	77.36
VIII								4.94	14.33	38.79	26.57	8.13	66.11
IX									13.07	26.47	18.19	16.90	23.51
X										7.25	17.21	49.09	19.00
XI											28.69	41.12	41.56
XII												23.34	80.03
XIII													0

(1970) in self pollinated crops and Tewari (1975) in barley also deduced the same conclusion.

The analysis of mean values of clusters with respect to different clusters (Table 2) revealed overall wide differences among mean values of the clusters for all the characters. The maximum mean value for plant height was observed in cluster XIII, followed by cluster XII. The cluster XIII also showed the maximum mean value for length of main spike and 100-grain weight. Number of tillers/plant was found to be maximum in cluster IV followed by cluster V and VIII. The number of spikelets/main spike and grains/main spike were pronounced by the varieties grouped in cluster XII. The varieties included in the cluster VII were characterized by highest yield/plant. Population belonging to clusters IV and VII had also equally high yield/plant, while cluster X included poor yielders. The remaining clusters occupied intermediate position for this character.

Intra- and inter-cluster D^2 estimates are presented in Table 3. The intra-cluster distance varied from 2.57

(cluster IV) to 23.34 (cluster XII). The minimum intra-cluster were closest to one another than those in other clusters. Cluster XIII involved a single variety UPT 74546, which suggested that it has entirely a different genetic constitution from rest of the varieties included in other clusters. The inter-cluster distance ranged from 4.53 to 80.03, the minimum and maximum values being recorded between cluster II and XI, and VII and XII respectively. In cluster II and XI all the varieties except DTS 47-1 and DTS 551 were from Pantnagar, while in clusters VII and XIII recording the highest statistical distance between them involved varieties viz. UPT 75151 and TL 167 in cluster VII belonging to Pantnagar and Ludhiana respectively, and only variety UPT 74546 in cluster XIII from Pantnagar. These results indicated that the varieties included in cluster II are very much close to the varieties grouped in cluster XI, while the varieties belonging to clusters VII and XII had wide diversity between them. The genetic diversity among the parents to be included in the hybridization programme has been greatly emphasized but the

desirable diverse parents for hybridization need not necessarily be selected from distant geographic regions. The selection of the parents must be based on the inter-cluster distances as greater the distance between the two cluster, wider the genetic diversity and secondly, the well adopted varieties in a particular region should be utilized as they may impart in their progeny a high degree of adaptability in that particular region should be utilized as they may impart in their progeny a high degree of adaptability in that particular region and similar climatic conditions.

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