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GENETIC DIVERGENCE IN TRITICALE

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ABSTRACT

The genetic divergence among 25 elite lines of triticale along with Sonalika cultivar of bread wheat was assessed employing Mahalanobis' D^2 analysis based on 16 characters. Four clusters were formed. Cluster I was the largest with 23 lines. The remaining three clusters with one line each were highly diverse from one another. The spike length, days to heading and maturity, plant height, spikes per 0.5 m^2, grain hardiness, tillers per plant and grain yield had sizeable individual contribution towards genetic divergence among lines. Results revealed the narrow genetic base among elite lines in triticale. The need for widening the genetic base by integrating wheat germplasm into triticale crossing programme has been emphasized.

Key words: Cluster, D^2 statistic, genetic diversity, triticale.

The availability of genetically diverse germplasm is the basic need for progress in plant breeding. In a crop like triticale which is of recent origin with scarce information, studies on genetic diversity are important for planning effective hybridization programme. There is a high level of uniformity among most of the triticale lines because of extensive use of limited germplasm of rye and wheat in the synthesis of primary and secondary triticales. The present study was undertaken to assess genetic diversity among triticale lines.

MATERIALS AND METHODS

Twenty-five elite lines of triticale from International Triticale Yield Nurseries of CIMMYT, Mexico and Pantnagar along with Sonalika cultivar of breadwheat (*Triticum aestivum* L.) were evaluated in a randomized complete block design with three replications. Each plot consisted of six rows of 3 m length with inter- and intrarow spacings of 25 and 15 cm, respectively. Observations were recorded on 10 randomly selected plants for days to heading, flowering and maturity, spikes per 0.5 m^2, tillers per plant, plant height, spike

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length, number of spikelets and grains per spike, flag leaf area, general leaf area, 1000-grain weight, harvest index, grain plumpness, grain hardiness and grain yield.

Mahalanobis' D^2 statistic was employed to assess genetic diversity. Lines were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao [1].

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed significant differences among the lines for all the characters studied indicating sufficient scope for further improvement in these traits.

Based on Mahalanobis' D^2 statistic, lines were grouped into four clusters (Table 2). Cluster I was the largest comprising of 21 lines from CIMMYT and one line each from Australia (Aus 32) and Pantnagar (UPT 79339). The remaining three clusters had one line each. Out of 24 lines of triticale from CIMMYT, two lines (CIMM 2 and CIMM 5) had formed separate clusters. This pattern of distribution of lines into different clusters revealed that geographic origin was not adequate as an index of genetic diversity in triticale [2].

Table 1. Analysis of variance for sixteen characters in triticale

Character	Mean squares		
	replications (d.f.=2)	treatments (d.f.=25)	error (d.f.=50)
Days to heading	2.4	75.1**	1.0
Days to flowering	3.3	63.7**	1.2
Days to maturity	0.5	72.1**	0.6
Spikes per 0.5 m^2	24.5	1011.5**	41.4
Tillers per plant	1.2	3.8**	0.7
Plant height	17.6	252.6**	11.5
Spike length	0.1	6.9**	0.3
Spikelets per spike	0.6	44.1**	1.8
Grains per spike	4.9	394.5**	3.9
1000-grain weight	3.1	68.4**	2.2
Harvest index	0.7	136.4**	5.9
Grain plumpness	0.1	0.5**	0.1
Grain hardiness	0.2	3.7**	0.2
Flag leaf area	4.2	57.6**	3.9
General leaf area	0.3	34.1**	4.8
Grain yield	17.2	873.3**	15.9

**Significant at 1% level.

The maximum genetic divergence was observed between clusters II and IV, followed by III and IV, II and III, and I and IV (Table 3). Clusters I and II were the closest ones with genetic distance of 28.1. These two clusters accounted for 24 out of 25 triticale lines reflecting narrow genetic diversity among elite lines of triticale. The fixed selection criteria and similarity in parentage might be the cause of genetic uniformity among triticale lines [3]. Intense selection for agronomically important traits could narrow the genetic diversity to the extent that further progress might be difficult [4]. The extensive use of superior variety

Table 2. Distribution and parentage of triticale lines in different clusters

Cluster	Line	Parentage	Origin
I	CIMM 1	ABN'S'/ /Tejon/IRA/3/Panda 'R'	CIMMYT
	CIMM 3	F51018/Panda 'R'	CIMMYT
	CIMM 4	Panda 'S'/3/Gopher 'S'/2/IA/Bush	CIMMYT
	CIMM 6	Panda 'R'/Arabian/ / IA	CIMMYT
	CIMM 7	CIT 'S'/Spy/3/Inia/Turkey/CMH73A785	CIMMYT
	CIMM 8	CIT 'S'/Spy/3/Inia/Turkey // CMH73A785	CIMMYT
	CIMM 9	MN72130/Rye4/ /M2A/IRA/3/Polar 'S'	CIMMYT
	CIMM 10	Ocelot/Faion/4/M2A/Rahum/3/RM 'S'/IRA/5477	CIMMYT
	CIMM 11	Ocelot/Faion/4/M2A/Rahum/3/RM 'S'/IRA/5477	CIMMYT
	CIMM 12	IA/2*Tob/8156/ / CC/3/Inia/4/Spy/M2A/5/ Inia/Turkey/H616/71/3/Addax/MX	CIMMYT
	CIMM 13	Aus 32	Australia
	CIMM 14	Tesmo 'S'	CIMMYT
	CIMM 15	Panda 'S'/RM 'S'	CIMMYT
	CIMM 16	PTR 'S'/BCH 'S'/ / Panda 'S'	CIMMYT
	CIMM 17	Pika 'S'	CIMMYT
	CIMM 18	PTR 'S'/ / IGA/IRA	CIMMYT
	CIMM 19	Zebra 31	CIMMYT
	CIMM 20	Zebra 32	CIMMYT
	CIMM 21	BGL 'S'/CIN/ / MUS 'S'	CIMMYT
	CIMM 22	Panda 'S' /RAT 'S'	CIMMYT
	CIMM 23	Panda 'S' /RAT 'S'	CIMMYT
	CIMM 24	X 39860	CIMMYT
	UPT 79339	ZM/1531/3/CIN/PI/ / PTO/BGL	Pantnagar
II	CIMM 5	Panda 'R'/Arabian/ /IA	CIMMYT
III	CIMM 2	ABN 'S'/ /M2A/IRA/3/Panda 'R'	CIMMYT
IV	Sonalika	MIDA-U/K117A/ /2*TH/3/FN/4*TH/4/AN/5/ YT54/N10B/ /LR/6/B4946-A4-18-1/Y53/ /3*Y50	CIMMYT

like Armadillo in producing triticales at CIMMYT resulted in the narrow genetic base in triticale. Almost all the improved triticale germplasm at CIMMYT has Armadillo in its pedigree [5]. All the triticale lines were genetically diverse from Cluster IV (Sonalika) emphasizing the need to include wheat varieties as one of the parents for improvement of triticale. The breeding strategy for triticale should be to produce primary triticales (initial crosses between rye and wheat) by integrating diverse sources from rye and wheat germplasm followed by production of secondary triticales (crosses between primary triticale and wheat). Hexaploid wheat could play a significant role in the improvement of triticale through widening its genetic base [6, 7]. The intracluster divergence was zero for all the clusters except cluster I (21.2). On the basis of intercluster distance it was suggested that crosses between CIMM 5 and Sonalika, CIMM 2 and Sonalika, and CIMM 2 and CIMM 5 would be useful in generating transgressive segregates in later generations.

Table 3. Intracluster (in bold) and intercluster distances of triticale genotypes

Clusters	I	II	III	IV
I	**21.2**	28.1	28.7	33.0
II		**0.0**	34.0	41.3
III			**0.0**	37.6
IV				**0.0**

Underlined values are intracluster distances.

Cluster mean and the relative contribution of each character towards genetic divergence are given in Table 4. A perusal of cluster means revealed substantial differences among

Table 4. Cluster means for sixteen characters in triticale

Character	Cluster means				Mean contribution to genetic diversity (%)
	I	II	III	IV	
Days to heading	88.6	92.0	88.0	80.0	10.2
Days to flowering	94.6	98.3	93.7	85.0	0.9
Days to maturity	129.7	133.7	127.3	117.3	9.2
Spikes per 0.5 m^2	137.2	109.3	89.0	147.3	8.6
Tillers per plant	6.3	5.5	7.3	7.0	7.1
Plant height (cm)	107.4	98.6	109.5	92.7	9.2
Spike length (cm)	9.1	8.9	10.9	10.1	10.5
Spikelets per spike	22.1	22.2	26.1	15.0	1.9
Grains per spike	45.0	41.1	43.9	29.9	5.9
Flag leaf area (cm^2)	20.7	21.7	28.2	27.9	4.3
General leaf area (cm^2)	26.0	26.1	29.8	25.2	2.8
1000-grain weight (g)	38.5	34.3	39.2	56.3	3.7
Harvest index (%)	28.0	46.0	26.9	34.2	6.5
Grain plumpness	3.8	3.6	3.7	5.0	4.9
Grain hardiness (kg/cm^3)	9.4	7.8	10.5	10.0	7.4
Grain yield (g)	71.7	69.0	95.0	106.7	7.1

clusters for most of the characters studied. Spike length appeared to be the most important contributor towards divergence, followed by days to heading and maturity, plant height, number of spikes per 0.5 m^2, grain hardiness, number of tillers per plant and grain yield. Therefore, these traits could form the basis of selecting parents for crossing programme. Contribution to total divergence was negligible from days to flowering, number of spikelets per spikes and general leaf area. These results were in agreement with previous reports [2, 8].

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