Genetic Divergence for the Morpho-agronomic Traits in Synthetic Hexaploid Wheats Derived from *Triticum turgidum* [(AABB) x *T. tauschii* (DD)]

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Forty-two synthetic hexaploid wheat (SHW) accessions were studied for their genetic divergence for a set of 10 morpho-agronomic characters using Mahalanobis D^2-statistic. The genotypes were grouped into three clusters with variable number of accessions. On the basis of the data on genetic divergence and cluster means, it is predicted that cluster III and cluster I were important for between cluster and cluster II was important for within cluster improvement. Therefore, this information may be useful to the breeders involved in wheat improvement by using these genotypes in multiple breeding programmes to recover transgressive segregants with desirable combinations of yield components.

Key Words: Cluster, Genetic Divergence, Synthetic Hexaploid Wheats

The germplasm evaluation for maintaining a wide genetic diversity is an urgency for realizing another quantum jump in wheat production. In this regard several workers evaluated germplasms of wheat for yield and its component traits (Joshi and Singh, 1979; Bari *et al.*, 1997; Kant *et al.*, 1999; Sorkhi *et al.*, 1999; Peer *et al.*, 2000). Identification of promising genotypes with good agronomic base and yield traits having resistance/tolerance to biotic/abiotic stresses is the pre-requisite for any plant breeding programme. It is also important that the considerable variability for morpho-agronomic traits must exist in the germplasm for exploitation using recombinant breeding programmes.

Synthetic hexaploid wheats (SHWs) ($2n=6x=42$) derived from the *Triticum turgidum* ($2n=4x=28$) x *T. tauschi* ($2n=2x=14$) developed at CIMMYT, Mexico, constituted relatively untapped germplasm for broadening the genetic base of common hexaploid wheat. Therefore, the present investigation was planned to study genetic divergence in SHWs for different morpho-agronomic traits.

Materials and Methods

The experimental materials consisted of 42 SHW accessions received from CIMMYT, Mexico. The pedigree of SHWs is given in Table 1.

The experiment was conducted in a randomized block design with three replications during the *rabi* season 1998-99 at Experimental Farm, Indian Agricultural Research Institute, New Delhi, India. Each accession was planted in three rows of 3 m length plot and the spacing between the rows was 23 cm and seed to seed distance of 10 cm. The recommended cultural and agronomical practices were followed to raise a good crop. The observations were recorded for 10 yield contributing characters *viz.*, days to anthesis, days to physiological maturity, plant height, culm length, leaf area, spike length, awn length, 1000-grain weight, number of grains/spike and yield/plant. Recording of data on morpho-agronomic characters was done using wheat descriptors of CIMMYT (1985) and IBPGR (1985). Ten plants were randomly selected for recording data from middle row of each test plot. The mean values were subjected to Mahalonobis D^2-statistic to measure genetic divergence as suggested by Rao (1952) and clusters were formed by Tocher's method (Rao, 1952).

Results and Discussion

The analysis of variance exhibited highly significant differences among the SHW accessions for all the 10 characters, indicating the existence of variation and scope for selection of desirable genotypes for use in breeding programmes aimed at enhancing the genetic potential of wheat germplasm.

On the basis of D^2 values, all the 42 accessions were grouped into three clusters (Table 2) with variable number of genotypes indicating the presence of sufficient amount of genetic diversity in the studied material. The maximum number of genotypes were present in cluster I (34 genotypes), while the cluster II accommodated seven genotypes and Syn. 50 was quite distinct from others and formed a separate cluster (cluster III). Cluster I had maximum number of genotypes mostly with same cross/pedigree. Pattern of clustering also indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence as genotypes developed from the different accessions of

Table 1. Cross/pedigrees of synthetic hexaploid wheats

S.No.	Synthetics	Name or Cross/pedigree/accession number
1.	Syn. 2	DOY1 / *Ae. Squarrosa* (188)
2.	Syn. 4	ALTAR 84 / *Ae. Squarrosa* (193)
3.	Syn. 5	ALTAR 84 / *Ae. Squarrosa* (198)
4.	Syn. 9	ALTAR 84 / *Ae. Squarrosa* (211)
5.	Syn. 12	ROK/KML / *Ae. Squarrosa* (214)
6.	Syn. 14	YUK / *Ae. Squarrosa* (217)
7.	Syn. 18	D67.2 / P66.270 // *Ae. Squarrosa* (220)
8.	Syn. 19	DVERD 2 / *Ae. Squarrosa* (221)
9.	Syn. 26	ACO 89 / *Ae. Squarrosa* (309)
10.	Syn. 27	GARZA / BOY // *Ae. Squarrosa* (311)
11.	Syn. 29	68.111 / RGB-U // WARD / 3 / *Ae. Squarrosa* (326)
12.	Syn. 33	YAV3/SCO // JO69 / CRA / 3 / YAV79 / 4 / *Ae. Squarrosa* (398)
13.	Syn. 35	68.11 / RGB-U // WARD / 3 / *Ae. Squarrosa* (511)
14.	Syn. 36	DOY 1 / *Ae. Squarrosa* (515)
15.	Syn. 37	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (629)
16.	Syn. 39	CROC / *Ae. Squarrosa* (725)
17.	Syn. 40	68.111 / RGB-U // WARDRESEL / 3 / STIL / 4 / *Ae. Squarrosa* (781)
18.	Syn. 41	68.111 / RGB-U // WARD / RESEL / 3 / STIL / 4 / *Ae. Squarrosa* (783)
19.	Syn. 42	YAR / *Ae. Squarrosa* (783)
20.	Syn. 43	YUK / *Ae. Squarrosa* (864)
21.	Syn. 44	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (878)
22.	Syn. 45	68.111 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (878)
23.	Syn. 46	CROC 1 / *Ae. Squarrosa* (879)
24.	Syn. 47	68.11 / RGB-U // WARD / 3 / FGO / 4 / RABI / 5 / *Ae. Squarrosa* (882)
25.	Syn. 48	SORA / *Ae. Squarrosa* (884)
26.	Syn. 50	CROC 1 / *Ae. Squarrosa* (518)
27.	Syn. 51	PBW 114 / *Ae. Squarrosa*
28.	Syn. 52	ALTAR 84 / *Ae. Squarrosa* (JBANGOR)
29.	Syn. 53	YAV2 / TEZ // *Ae. Squarrosa* (249)
30.	Syn. 55	GAN / *Ae. Squarrosa* (180)
31.	Syn. 56	D67.2 / P66.270 // *Ae. Squarrosa* (257)
32.	Syn. 59	SRN / *Ae. Squarrosa* (358)
33.	Syn. 60	SCOOPI / *Ae. Squarrosa* (358)
34.	Syn. 62	SCA / *Ae. Squarrosa* (518)
35.	Syn. 63	YAR / *Ae. Squarrosa* (518)
36.	Syn. 65	BOTNO / *Ae. Squarrosa* (620)
37.	Syn. 68	D67.2 / P66.270 // *Ae. Squarrosa* (633)
38.	Syn. 74	YAV2 / TEZ // *Ae. Squarrosa* (895)
39.	Syn. 75	ARLIN / *Ae. Squarrosa* (283)
40.	Syn. 86	DOY1 / *Ae. Squarrosa* (372)
41.	Syn. 88	CPI / GEDIZ / 3 / GOO // JO69 / CRA / 4 / *Ae. Squarrosa* (409)
42.	Syn. 90	ALTAR84 / *Ae. Squarrosa* (502)

Table 2. Group constellation of the 42 synthetic wheat genotypes based on Mahalanobis D^2-statistic

Cluster	Number of genotypes	Genotypes
I	34	Syn. 2,56,33,5,47,12,90,39,60,48,51,44,41,36, 14,27,68,35,65,59,86,45,62,88,40,42,63, 26,43,37,75,53,19 and 52
II	7	Syn. 4, 46,74,9,29, 55 and 18
III	1	Syn. 50

T. tauschii selected from diverse locations also clustered together. These findings are on consonance with Bhatt (1970) and Sharma *et al.* (1998) in wheat.

Table 3. Average inter and intra cluster distance D^2 values and distance ($\sqrt{D^2}$) for 10 characters

Cluster	I	II	III
I $D^2/\sqrt{D^2}$	346.97 (18.63)	790.99 (28.12)	9632.38 (98.14)
II $D^2/\sqrt{D^2}$		1071.06 (32.73)	8640.89 (92.96)
III $D^2/\sqrt{D^2}$			0.00 (0.00)

The intra- and inter-cluster divergence among the genotypes was of varying magnitude (Table 3). Cluster II with seven genotypes exhibited maximum intra-cluster distance (18.63) indicating that the genotypes in this cluster are more diverse than the other clusters. This was used to select genetically diverse and agronomically superior genotypes from the 42 genotypes studied. With regards to inter-cluster distance, cluster III showed maximum genetic distance from cluster I than the cluster II. The greater the genetic distance between the clusters, wider is the genetic diversity between genotypes.

The genetic divergence among clusters was well reflected in cluster means (Table 4). Cluster III (Syn. 50) exhibited higher mean values for awn length, number of grains/spike and yield/plant. Genotypes in cluster II performed well for plant height, culm length, leaf area, spike length and 1000-grain weight while cluster I showed the highest mean values for days to anthesis and days to physiological maturity. This indicated that none of the clusters contained genotypes with all the desirable characters, which could be directly selected and utilized in the breeding programmes. Hybridization between the genotypes of different clusters was necessary for the development of desirable genotypes, which accommodates genes from the two parents. The crosses involving cluster III and cluster II may generate a material where negative correlation between the grain number and grain weight is brokendown. Transgressive breeding between the genotypes of different clusters has also been suggested by Singh *et al.* (1996), Deshmukh *et al.* (1999) and Kant *et al.* (1999).

Table 5. Contribution of different characters to genetic divergence

Character	Per cent contribution
Days to anthesis	1.10
Days to physiological maturity	0.60
Plant height	15.22
Culm height	0.80
Leaf area	2.44
Spike length	13.24
Awn length	43.61
1000-grain weight	1.28
Number of grains/spike	18.12
Yield/plant	3.60

Table 4. Cluster means of 42 synthetic wheat genotypes for 10 characters

Cluster	Days to anthesis	Days to physiological maturity	Plant height (cm)	Culm length (cm)	Leaf area (sq. cm)	Spike length (cm)	Awn length (cm)	1000-grain weight (g)	No. of grain/ spike	Yield/ plant (g)
I	119.24	147.93	109.73	98.83	8.76	10.98	5.12	38.40	20.35	4.40
II	116.33	144.05	111.89	100.69	10.22	11.20	5.60	40.25	31.95	6.15
III	107.67	137.67	81.87	79.29	6.00	5.91	14.30	38.99	37.19	8.01

Contribution of different characters towards genetic divergence was presented in the Table 5. It can be seen from the table that awn length contributed maximum (43.61%) towards genetic divergence in these SHWs. Characters like, number of grains/spike (18.12%), plant height (15.22%), spike length (13.24%) and grain yield/ plant (3.60%) jointly contributed 50.18% to total genetic divergence. This is in conformity with the observations of Murty and Arunachalam (1966) for plant height in grain crops, Kanwal *et al.* (1983) and Kuruvadi (1988) for plant height and spike length, Das Gupta and Das (1984) for grains/ear and Singh and Singh (1998) for grains/ear and plant height.

On the basis of divergence for the components of grain yield, it is suggested that good recombinants could be obtained from these SHW accessions. This information may be useful to the breeders for varietal improvement by using this material as new source for genetic diversity for morpho-agronomic characters of wheat.

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