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Evaluation of genetic divergence among elite wheat [*Triticum aestivum* (L.)] genotypes

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Abstract
Bread wheat (*Triticum aestivum* L.), an allohexaploid (2n=6x=42), is the premier food crop of worldwide importance. It is also a crop where conventional plant breeding has paid rich dividend as epitomized by the Green Revolution. The present investigation was conducted in *Rabi* season, 2021-2022 at Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The experimental materials for the present investigation comprised of 78 genotypes and three checks namely, Sonalika, HD2967 and HI8713. These genotypes were evaluated in an augmented block design and observations were recorded for twelve characters *viz.* days to 50% heading, days to 50% anthesis, days to maturity, plant height, number of tillers per meter, spike length, number of grains per spike, test weight, biological yield, grain yield, chlorophyll content and protein content. The maximum number of genotypes (45) were included in cluster-I followed by 26 genotypes in cluster-II, 8 genotypes in cluster-III and cluster-IV and cluster-V had one genotype each. The intra cluster distance ranged from 2439.39 (cluster-III) to 0.00 (cluster-IV and cluster-V). The maximum inter cluster distance (30499.17) was found between cluster-III and cluster-IV, whereas minimum distance (2154.75) was found between cluster-IV and cluster-V. So, Larger the distance between the clusters better the chance of getting transgressive segregants through crossing among these genotypes. The genotypes MACS5051, HI1612, DWAP1531, GW499, HD3249 and HI1633 performed well for grain yield and yield components, hence these genotypes can be used in future breeding programme to improve grain yield.

Keywords: Wheat, wheat, genetic divergence, inter-cluster and intra-cluster distance

Introduction
Wheat (*Triticum aestivum*) is number one cereal of the world and is grown on the largest area. As contrast to rice, wheat is grown in all the continents of the world. Domestication of wheat and the increase in ploidy (from *diploid* to *tetraploid* to *hexaploid*) had a great effect on its morphology and physiology. Modern wheat has larger leaves, reduced tillering phase, fewer but larger and heavier spikes and reduced to almost nil shattering Simmons (1987) [15]. Grain filling in modern wheat is more dependent on photosynthesis from leaves and stems than from spikes, and grain yield can be largely attributed to the greater distribution of the above ground mass to the grain. Jensen (1978) [7] also observed that a decline in plant height was associated with dwarf Mexican wheat, introduction of which led to the Green revolution, truly speaking wheat revolution India.

The cultivated wheat's of today constitute an alloploid series, diploids through hexaploid. From the study of morphological similarities between diploid wheat *T. monococcum L.* and tetraploid wheat *T. turgidum L.* It is clear that gene 'A' of the polyploidy wheat came from *T. monococcum.* Archaeological evidences also indicate that diploid wheat that contributed 'A' gene to the tetraploid was a wild form. The source of 'D' gene in hexaploids is *T. tauschi.* As regards 'B' gene there are different opinions and the donor could be *T. speltoides* Sarkar and Stebbins (1956) [18] or *T. longissimum* Feldman (1970, 1979) [6] or *T. urartu* Johnson (1975) [8].

Most wheat breeding and evaluation programmes aim to stabilize cultivar performance for high grain production over a wide range of conditions and broad adaptation. The genetic variations among wheat cultivars that influence yield are frequently muddled by interactions among cultivar and environment.

To assess yield potential throughout randomly occurring periods of normal and exceptional conditions, cultivars are typically evaluated across a wide number of environments or site years. However, some earlier research indicates that only high yielding conditions should be used for the selection of wheat cultivars with the highest yields. The number and location of testing sites are frequently not optimal due to time and resource limitations. This may result in the improper promotion of genetic material or the selection of inferior lines.

Genetic diversity is the variability that exists among the various genotypes of a species. It develops either as a result of genetic impermeability barriers or geographic isolation. A biometrical method called the D^2 statistic can be used to evaluate the genetic diversity that exists within a population. The D^2 statistic introduced by Mahalanobis in 1936 [9] quantifies genetic divergence at the intracluster and intercluster levels and aids in the). Selection of genetically diverse parents for use in crossing programmers. Plant breeding relies heavily on genetic diversity since hybrids between lines with different ancestries typically show high heterosis than those between closely related strains. For instance, increasing genetic variance between inbred lines in maize led to higher hybrid heterosis. The degree of genetic diversity between the parents was closely correlated with the degree of heterosis in cotton and alfalfa. The highest level of heterosis typically happens at the highest or middle level of diversity. The D^2 statistic has been used to assess crop variability in species like cotton, sorghum, pearl millet, wheat, and linseed (Moll and Stubber, 1974) [11].

The D2 technique measures the level of diversification and establishes the relative proportion from each constituent character that contributes to the total divergence thus aiding in the identification of divergent parents for hybridization. Compared to genotypes that are distributed among several clusters, those that are gathered together in a single cluster are less divergent. The clusters with the greatest statistical distance between them exhibit the highest degree of divergence. The following considerations should be made when choosing the parents for hybridization on the basis of the D2 statistic.

Materials and Methods

The present investigation was carried to estimate Evaluation of genetic divergence studies among elite wheat genotypes for quantitative characters at Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *Rabi* season of 2021-2022.

The experimental material for the present study comprised of 78 germplasm accessions of wheat received from National Genetic Stock Nursery, Indian Institute of Wheat and Barley Research, Karnal and 3 prominent checks (Sonalika, HD2967 and HI8713) were planted in an Augmented Block Design, considering each germplasm as a single plot, which consisted of 2 rows measuring 4m long with a spacing of 20 cm (row to row) and 10 cm (plant to plant) was maintained. These genotypes were evaluated in an augmented block design and observations were recorded for twelve characters *viz.* days to 50% heading, days to 50% anthesis, days to maturity, plant height, number of tillers per meter, spike length, number of grains per spike, test weight, biological yield, grain yield, chlorophyll content and protein content. Windostat V7.0 was taken in use to perform statistical analysis of the recorded data. D^2 statistics as proposed by Mahalanobis (1936) [9], was used to analyse genetic divergence among the considered 24 genotypes of bread wheat understudy and Tocher's approach, as suggested by Rao (1952) [13] grouped them into distinct clusters.

Results and Discussion

Clustering pattern of genotypes

Non-hierarchical Euclidean cluster analysis was used to compute the generalized distance for each pair of genotypes.

Group constellation

All the 78 test genotypes and 3 checks were classified into 5 clusters in such a way that average intra cluster distance remained minimum. Table 1 shows the clustering pattern of these genotypes. Cluster-I had 45 genotypes, whereas cluster-II comprised of 26

Table 1: Clustering pattern of all 81 genotypes of bread wheat.

Cluster group	Number of Genotypes	List of Genotypes
I	45	DBW222, HI1624, PBW763, MACS5053, HS627, GW2014-596, PBW757, FLW16, UP4000, UP3099, DBW107, V.30'3, TAW186, HD3249, RWP2014-18, HI1619, HD3271, HD3293, DBW71, DBW252, UP4001, AKAW4901, K1317, PBW800, HI1612, HI8713, DBW93, HI1609, HI1544, HI1633, DWAP1531, IC-27824, DBW221, PBW79-, HD3237, HI1628, PBW825, V.3020, DBW246, W-730, DM7, WAPD1505, PBW778, HD3317, HI1634
II	26	HS645, PBW777, PBW820, UP3016, HS611, DBW187, NIAW3170, UASNG326, DBW129, TAW185, DWAP1530, HD2967, DBW110, HS661, PBW760, DBW278, IC212176, DWAP1108, GW2010-288, DM6, HD3086, IC296729, GW322, SONALIKA, DBW150, WAPD1524
III	8	FLW22, GW499, MP1338, WAPD1508, GW492, RAJ3765, MACS5051, GW527
IV	1	DBW303
V	1	WAPD1519

Average intra and inter cluster distances

The average intra and inter cluster distances have been presented in Table 2. The maximum intra cluster distance was found for cluster-III (2439.39), which revealed maximum genetic diversity among its constituents, followed by the cluster I (1470.84), cluster-II (1407.36), cluster-IV (0.00) and cluster-V (0.00). Among the clusters, the cluster-IV and cluster-V had minimum intra cluster distance.

Inter cluster distance being maximum between cluster-III and cluster-IV (30499.17) followed by cluster-III and cluster-V (25499.40), cluster-II and cluster-III (16158.18), cluster-I and cluster-IV (13189.79), cluster-I and cluster-V (10426.71) indicated that the genotypes of cluster-III and cluster-IV, genotypes of cluster-III and cluster-V genotypes of cluster-II and cluster-III, genotypes of cluster-I and cluster-IV and the genotypes of cluster-I and cluster-V are distinctly related to each other. Minimum inter cluster distance between cluster-IV and cluster-V (2154.75) followed by cluster-II and cluster-V (3005.63), cluster-II and cluster-IV (3649.99), cluster-I and cluster-II (4856.58), cluster-I and cluster-III (5623.38) indicated that the genotypes of cluster-IV and cluster-V, the genotypes of cluster-II and cluster-V, genotypes of cluster-II and cluster-IV, genotypes of cluster-I and cluster-II and the genotypes of cluster-I and cluster-III possess genes which have same expression most of the time.

Table 2: Intra (bold) and inter cluster distance among the clusters

Cluster Distances					
	Cluster1	**Cluster2**	**Cluster3**	**Cluster4**	**Cluster5**
Cluster1	1470.84	4856.58	5625.38	13189.79	10426.71
Cluster2	4856.58	1407.36	16158.18	3649.99	3005.63
Cluster3	5625.38	16158.18	2439.39	30499.17	25499.4
Cluster4	13189.79	3649.99	30499.17	0	2154.75
Cluster5	10426.71	3005.63	25499.4	2154.75	0

Table 3: Cluster means of the all the clusters for all the characters studied.

Cluster Means: Torcher's method												
	Days to heading	**Days to Anthesis**	**Tillers/m**	**Spike length**	**Number Of grains perspike**	**Days to Maturity**	**Test weight**	**Biological yield (kg/plot)**	**Grain yield (kg/plot)**	**Plant height**	**Chlorophyll content**	**Protein content**
Cluster1	62.73	69.71	78.16	9.39	248.22	110.29	40.82	0.6	0.42	82.59	45.01	12.35
Cluster2	65.67	71.69	77.63	10.27	306.85	111.4	38.01	0.52	0.37	81.73	44.23	12.16
Cluster3	58.13	65.13	90	9.13	188.25	109.13	45.75	0.79	0.59	77.23	47.24	11.88
Cluster4	59	65	78	10	359	108	37.8	0.8	0.5	75.6	54.7	13.1
Cluster5	82	87	81	10.2	338	116	27.4	0.5	0.3	55.2	45.6	12.7

Contribution of different characters towards divergence

The relative contribution of different characters towards the expression of genetic divergence is given in Table 3.

Grain yield per plot contributed maximum (19.85%) towards genetic divergence followed by number of grains per spike (18.79%), number of tillers per meter (14.80%) and plant height (11.68%). Similar results were also confirmed by Nimbalkar *et al.* (2002) [12] for number of grains per spike and number tillers per meter, Vaithiyalingan (2005) [16] for plant height, Shahryari *et al.* (2011) [14] for grain yield and number of grains per spike and Vora Zarna *et al.* (2017) [17] for grain yield, number of grains per spike, plant height and number of tillers per meter.

Similar results were also confirmed by Chitralekha Shyam *et al.* (2020) [3] for spike length and biological yield, Manoj Kandel *et al.* (2018) [10] for days to 50% heading, test weight, days to 50% anthesis and days to maturity, Amit Lakra *et al.* (2020) [2] for spike length and days to maturity, Vora Zarna *et al.* (2020) [17], Dutamo *et al.* (2015) [4] and Amin *et al.* (2014) [1].

Table 4: Contribution of individual characters to total divergence and their rank.

Sr. No.	**Characters**	**Contribution%**	**Timesranked1st**
1	Days to heading	2.63	71
2	Days to Anthesis	2.86	77
3	Tillers/m	14.80	399
4	Spike length	9.61	259
5	Number of grain perspike	18.79	507
6	Days to Maturity	0.85	23
7	Test weight	1.92	52
8	Biological yield(kg/plot)	3.36	91
9	Grain yield(kg/plot)	19.85	535
10	Plant height	11.68	315
11	Chlorophyll content	3.74	101
12	Protein content	9.86	266

Conclusion

All the 81 genotypes were grouped into 5 non-overlapping clusters. Cluster-I had 45 genotypes, whereas cluster-II comprised of 26 genotypes, cluster-III comprised 8 genotypes and cluster-IV and cluster-V had 1 genotype each. The maximum intra cluster distance was

Found for cluster-III (2439.39), which revealed maximum genetic diversity among its constituents, followed by the cluster I (1470.84), cluster-II (1407.36), cluster-IV (0.00) and cluster-V (0.00). Among the clusters, the cluster-IV and cluster-V had minimum intra cluster distance. Inter cluster distance being maximum between cluster-III and cluster-IV (30499.17) followed by cluster-III and cluster-V (25499.40), cluster-II and cluster-III (16158.18), cluster-I and cluster-IV (13189.79), cluster-I and cluster-V (10426.71). Therefore, the crosses between the genotypes from these cluster pairs may give desirable transgressive sergeants. Grain yield per plot contributed maximum (19.85%) towards genetic divergence followed by number of grains per spike (18.79%), number of tillers per meter (14.80%) and plant height (11.68%). While, Characters like protein content (9.86%), spike length (9.61%), chlorophyll content (3.74) and biological yield per plot (3.36%) made moderate contribution towards genetic divergence and the traits like days to 50% anthesis (2.86%), days to heading (2.63%), test weight (1.92%) and days to maturity (0.85%) showed minimal contribution towards genetic divergence. On the basis of findings of study, six desirable donors for each character were identified on the basis of character mean. The most promising donors for grain yield were MACS5051 (1.01), HI1612 (0.71), DWAP1531 (0.71), GW499 (0.71), HD3249 (0.67) and HI1633 (0.67). These genotypes can be used for future breeding programme to improve the yield potential of the variety. For other characters, genotypes can be picked up from different groups, formed on the basis of ranking. The findings of present investigation might be useful to the future breeding programmers for developing improved genotypes.

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