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Genetic Divergence Analysis Based on Seed Vigour Parameters in Wheat

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ABSTRACT: A study was conducted to evaluate the genetic divergence among thirty-four wheat varieties on the basis of seed vigour parameters. All the varieties were evaluated for their performance for different viability and vigour parameters *viz.* test weight, standard germination, seedling length, seedling dry weight, vigour index-I, vigour index-II, accelerated ageing test, electrical conductivity, tetrazolium test, dehydrogenase activity test, field emergence index and seedling establishment. Ward's Minimum Variance method was used to construct the dendrogram on the basis of these parameters. All the thirty-four genotypes were divided into two major clusters at a Standard Euclidean (L^2) distance of 170 and these two clusters were further divided into five sub major clusters at a distance 20. Cluster pattern revealed that, cluster 2 and cluster 4 were the largest group consisting of 8 genotypes each followed by cluster 5 (7 genotypes), cluster 3 (6 genotypes) and cluster 1 (5 genotypes). The cluster means revealed considerable differences among all the clusters. An examination of the varietal composition of the clusters indicated that the cluster 3 is composed of relatively high vigorous genotypes because of high mean values of most of the vigour parameters *viz.* seedling dry weight, vigour indices, accelerated ageing and dehydrogenase activity while the cluster 5 was consisted of low vigour genotypes.

Keywords: Euclidean distance, Seed vigour, Ward's minimum variance method

Wheat (*Triticum aestivum* L.) is one of the most important cereal crops which contribute substantially to the national food security by providing more than 50% calories to the people, who mainly depend on it. Bread wheat contributes 95% to total production, while another 4% comes from *T. durum* wheat and *T. dicoccum*'s share in wheat production is 1% [1]. The option for increasing wheat production by expanding area under cultivation has already been exploited to almost its maximum. However, the productivity can further be raised by developing the genotypes which are able to perform well even under unfavourable conditions and over marginal land and equally responsive to favourable conditions as well. In order to feed the growing population, we need to constantly improve wheat production on the limited arable land and use of vigorous seed provides an effective approach for enhancing crop unit production. Therefore, identification and development of high vigour genotypes is very important for improving agricultural yields as these genotypes have a great tendency to perform better under diverse environmental conditions [2].

Genetic diversity is simply originates in nature and for the varietal improvement, plant breeders create genetic recombination by crossing diverse parents. Selection of parents for varietal improvement programmes depends on the knowledge of available diversity [3]. Euclidean cluster analysis has been acknowledged as a powerful tool to assess the level of divergence between genotypes. There are numerous studies in literature related to genetic diversity analysis based on morphological and yield attributing characters but the studies based on seed vigour parameters are very few. Therefore, the present study has been

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undertaken to determine the nature and extent of genetic diversity with respect to seed vigour among thirty-four wheat genotypes.

MATERIALS AND METHODS

The study consisted of 34 varieties/genotypes comprising 30 genotypes of bread wheat and 4 genotypes of *durum* wheat. Seed material was obtained from Wheat and Barley Section, Department of Genetics and Plant Breeding, C.C.S. Haryana Agricultural University, Hisar in May, 2014. The vigour potential of these seeds was assessed by recording twelve parameters *viz.* test weight, standard germination, seedling length, seedling dry weight, vigour index-I, vigour index-II, accelerated ageing test, electrical conductivity, tetrazolium test, dehydrogenase activity test, field emergence index and seedling establishment. All these parameters were calculated in three replications of each.

For calculation of test weight, four replications of 1000 seeds were taken for each genotype, weighed and average (g) was calculated. Standard germination test was performed using between the papers (BP) method at 20°C as per ISTA [4]. Seedling length (root + shoot) was measured by taking ten randomly selected normal seedlings from standard germination samples and data was recorded in centimeters. For final calculation, average seedling length of these seedlings was taken. The same seedlings whose length was measured were dried in hot air oven for 24 hours at 80 ± 1°C and then their dry weight was measured. Average seedling dry weight of each genotype was calculated and expressed in milligrams.

The seedling vigour indices were calculated as per the method given by Abdul-Baki and Anderson [5] as follows:

Vigour Index-I = Standard germination (%) × Average seedling length (cm)

Vigour Index-II = Standard germination (%) × Average seedling dry weight (g)

Accelerated ageing and Electrical conductivity tests were carried out following the ISTA procedures [4]. Dehydrogenase activity (DHA) test was performed as per the method given by Kittock and Law [6] and Tetrazolium viability test was conducted as per the method suggested by Moore [7] and the data was expressed in percentage.

Field emergence index and field establishment was recorded by sowing one hundred seeds of all genotypes in three replications in a Randomized Block Design (RBD). The number of seedlings emerged were counted on each day up to seedling establishment. The field emergence index (speed of emergence) was calculated as described by Maguire [8]. The seedling establishment was determined by counting the total number of seedlings when the emergence was completed or when there was no further addition in total emergence.

Genetic divergence among 34 genotypes was studied through Non-hierarchical Euclidean cluster analysis [9-10] using the software SPSS Version 19.0 [11]. Thereafter, promising genotypes were selected from each cluster which have higher mean than the general mean and cluster mean for the standard germination and other associated seed vigour parameters.

RESULTS AND DISCUSSION

Group constellation based on Ward's Minimum Variance

All the thirty-four genotypes were divided into two major clusters at a Standard Euclidean^2 distance of 170 and these two clusters were further divided into five sub major clusters at a distance 20. The clusters were formed by grouping all the thirty-four genotypes in such a way that genotypes within each cluster had smaller D^2 value than those between clusters (Fig. 1).

Cluster pattern revealed that, cluster 2 and cluster 4 were the largest group consisting of 8 genotypes each which were followed by cluster 5 (7 genotypes), cluster 3 (6 genotypes) and cluster 1 (5 genotypes). The intra and inter cluster distances are given in table 1. A maximum difference among the genotypes within the same cluster was shown by cluster 5 (3.26). This was followed by cluster 2 and cluster 6 (3.00), cluster 1 (2.95) and cluster 4 (2.78). When diversity within clusters was studied, it showed a range of 2.78 to 3.26. Cluster 3 and cluster 5 showed maximum

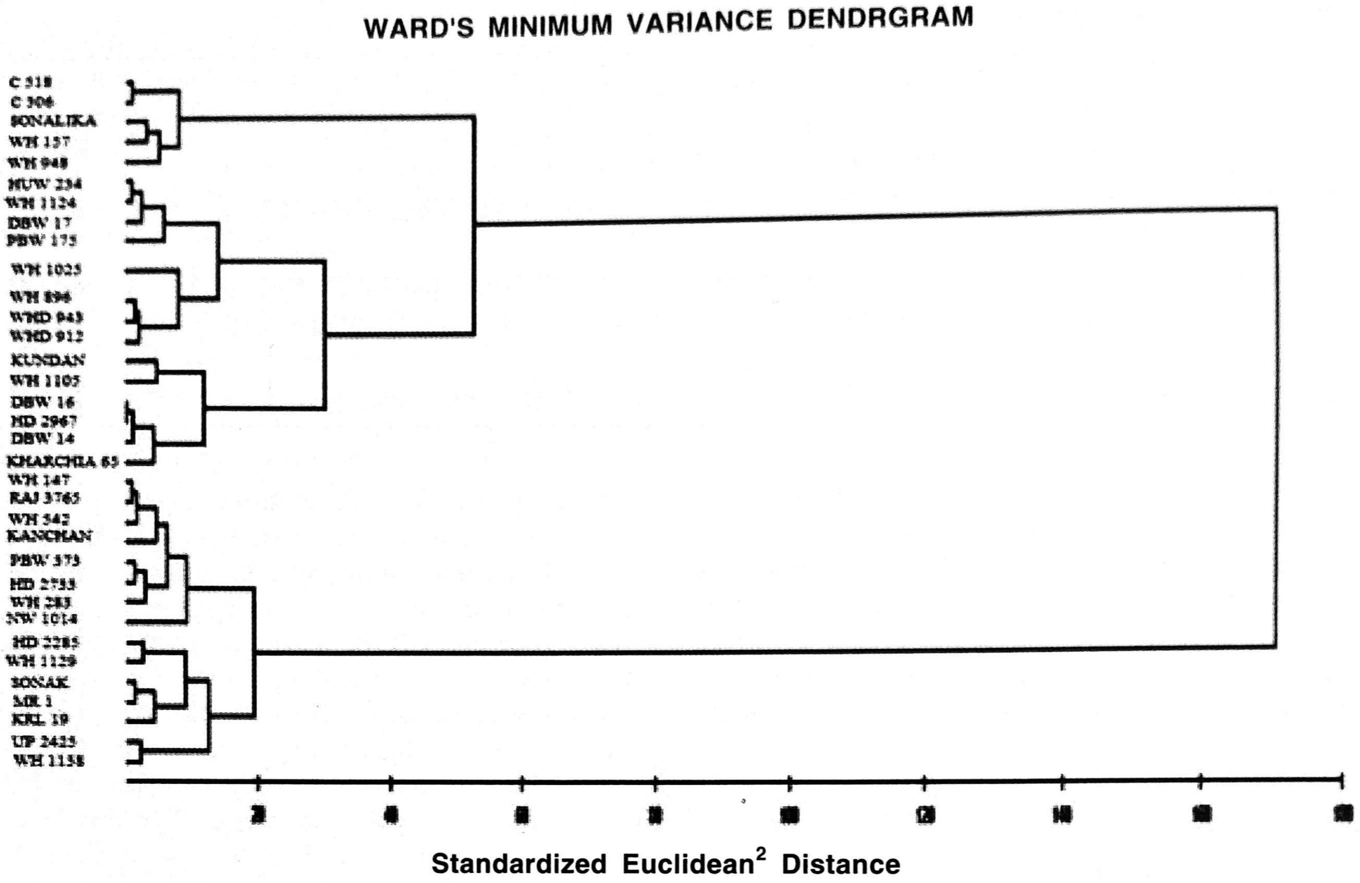

Fig. 1. Dendrogram showing the clustering pattern of thirty four varieties/genotypes based on seed vigour parameters

Table 1. Average inter and intra cluster distances

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	2.954	5.124	4.387	4.772	6.083
Cluster 2		3.004	4.018	4.658	6.244
Cluster 3			3.004	5.553	7.272
Cluster 4				2.779	3.627
Cluster 5					3.263

Diagonal values are intra cluster distances

inter cluster distance of 7.27, followed by that between cluster 2 and cluster 5 (6.24). The lowest inter cluster distance was observed between cluster 4 and cluster 5 (3.63), followed by that between cluster 2 and cluster 3 (4.02). The genotypes belonged to clusters which have more distance (3 and 5) are most divergent genetically (Table 2). So, it is clearly evident that genotypes C 518, C 306, SONALIKA, WH 157 and WHD 948 are quite dissimilar at genetic level as compared to genotypes HD 2285, WH 1129, SONAK, MR 1, KRL 19, UP 2425 and WH 1138. Critical analysis of varietal composition of these two clusters showed that cluster 1 mostly have older varieties and cluster 5 have newly developed varieties and advanced genotypes. Moreover, among four *durum* genotypes under the study, 3 genotypes grouped under cluster 2 and 1 genotype under cluster 1. This

Table 2. Clustering of wheat varieties/genotypes based on seed vigour parameters

	Names of genotypes	No. of genotypes
Cluster 1	C 518, C 306, SONALIKA, WH 157, WHD 948	5
Cluster 2	HUW 234, WH 1124, DBW 17, PBW 175, WH 1025, WH 896, WHD 943, WH 912	8
Cluster 3	KUNDAN, WH 1105, DBW 16, HD 2967, DBW 14, KHARCHIA 65	6
Cluster 4	WH 147, RAJ 3765, WH 542, KANCHAN, WH 157, HD 2733, WH 283, NW 1014	8
Cluster 5	HD 2285, WH 1129, SONAK, MR 1, KRL 19, UP 2425, WH 1138	7

pattern showed the genetic divergence between *durum* and *aestivum* genotypes for seed vigour traits. The group constellation based on the clustering showed that there is no correlation between groups formed and the geographical origin of these genotypes. There are many evidences for this in previous studies in wheat based on morphology [9, 10] and seed vigour traits [11].

Cluster means

The cluster means for the 12 characters studied in wheat genotypes revealed considerable differences among all the clusters. Cluster wise mean and over all cluster mean for the characters studied were presented in table 3 & 4. From the present data, it was evident that the mean value of test weight was the highest in cluster1 (49.48 gm) and lowest in cluster 5 (38.86 gm). The highest mean value of standard germination was present in cluster 2 (95.16%) and lowest in cluster 5 (78.71%). For seedling length cluster 1 (27.30cm) had the highest mean value and cluster 5 (19.37cm) had the lowest. In case of seedling dry weight cluster 3 and cluster 1 (178 mg) had the highest mean value and cluster 5 (120 mg) had lowest mean value. The vigour index-I had maximum value in cluster 3 (2565.39) and minimum mean value in cluster 5 (1525.40). For vigour index-II the maximum mean value was for cluster 3 (16.88) and minimum for cluster 5. For accelerated ageing cluster 3 (49.44%) had the highest mean values whereas, cluster 5 (40.48%) had the lowest mean value. Tetrazolium test had its highest mean value in cluster 2 (97.04%) and lowest in cluster 5 (85.91%). In case of electrical conductivity, the highest mean value was found in cluster 1 (171.20 µs/cm/seed) and lowest in cluster 2 (114.59 µs/cm/seed). The mean of dehydrogenase activity was highest for cluster 3 (0.40) and lowest for cluster 5 (0.21). For seedling establishment, the highest mean was observed for cluster 2 (82.58%) and lowest for cluster 5 (67.81%). Last is the case of field emergence index, the highest value of mean was found in cluster 2 (13.23) and lowest for cluster 4 (10.12). Singh *et al.* [11] found similar level of variability among durum wheat genotypes for seed vigour parameters.

Table 3. Mean values of various clusters for different parameters

	TW	SG	SL	SDW	VI I	VI II	AA	TZ	EC	DHA	SE	FEI
Cluster 1	49.48	87.20	27.30	178	2379.39	15.54	42.67	95.47	171.20	0.22	76.53	11.37
Cluster 2	45.32	95.16	21.82	135	2075.29	12.88	48.50	97.04	117.83	0.37	82.58	13.23
Cluster 3	42.86	95.00	26.98	178	2565.39	16.88	49.44	96.89	120.94	0.40	80.00	12.33
Cluster 4	42.14	85.33	20.98	130	1786.46	11.04	44.08	92.29	139.79	0.24	69.92	10.12
Cluster 5	38.86	78.71	19.37	120	1525.40	9.46	40.48	85.91	159.86	0.21	67.81	10.75

TW= Test Weight, SG= Standard Germination, SL= Seedling Length, SDW= Seedling Dry Weight, VI-I= Vigour Index I, VI-II= Vigour Index II, AA= Accelerated Ageing, TZ= Tetrazolium test, EC= Electrical Conductivity, DHA= Dehydrogenase Activity, FEI= Field Emergence Index, SE= Seedling Establishment

Table 4. Maximum mean values of different viability and vigour parameters for the 5 clusters

Cluster No.	Viability and vigour parameters
Cluster 1	Test weight, Seedling Length, Seedling Dry Weight, Electrical Conductivity
Cluster 2	Standard germination, Tetrazolium, Seedling Establishment, Field Emergence Index
Cluster 3	Seedling Dry Weight, Vigour Index-I, Vigour Index-II, Accelerated Ageing, Dehydrogenase Activity
Cluster 4	Good values of Accelerated Ageing, Tetrazolium
Cluster 5	High values of Electrical Conductivity

Table 5. Most promising genotypes identified from different clusters

Cluster No.	Genotypes	Parameters
1	WH 157, WHD 948	Standard Germination, Seedling Dry Weight
2	PBW 175, WH 1025, WH 896, WHD 943, WH 912	Standard Germination, Tetrazolium, Seedling Establishment, Field Emergence Index
3	KUNDAN, WH 1105, KHARCHIA 65 Activity	Standard Germination, Seedling Dry Weight, Vigour Index-I, Vigour Index-II, Accelerated Ageing, Dehydrogenase
4	WH 147, RAJ 3765, WH 542, WH 157	Standard Germination, Accelerated Ageing, Tetrazolium
5	HD 2285, WH 1129, SONAK, MR 1, WH 1138	Electrical Conductivity

Further examination of the varietal composition of the clusters indicated that the cluster 3 is composed of relatively vigorous genotypes because of high mean values of most of the vigour parameters *viz.* seedling dry weight, vigour indices, accelerated ageing and dehydrogenase activity. The cluster 5 was consisted of low vigour genotypes. Thus, the promising genotypes of these two clusters *i.e.* KUNDAN, WH 1105, KHARCHIA 65 (cluster 3) and WH 1129, SONAK, MR 1, WH 1138 (cluster 5) hold great promise as parents to obtain good hybrid combination and further breeding approaches like QTL analysis for seed vigour traits which can reveal the genetic basis of seed vigour (Table 5).

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