

## Research Article

# Genetic Diversity Analysis for Seed Vigour, Yield and Its Component Traits in Bread Wheat (*Triticum aestivum* L.)

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## Abstract

An experiment was conducted to determine the genetic divergence for seed vigour, yield and its component traits. After standardizing data, cluster analysis was done with WARD method and Square Euclidean distance coefficient and 40 genotypes were grouped into 6 clusters. The intra cluster distance ranged from 0.000 (VI) to 7.242 (III) indicating considerable diversity between different clusters. The inter cluster distance ranged from 7.376 (between IV and V) to 10.475 (between II and VI). Cluster II had germination% (97.75%), seedling length (22.73 cm), vigour index-I (2220.93) and field emergence value (9.62%). Cluster III had vigour index-II (12242.82), seed density (1.16 g/cc), seedling establishment value (78.22%). Cluster V had highest grain yield (1014.4 g), harvest index (31.26%), number of tillers per meter (143.46), flag leaf length (29.72 cm), flag leaf area (41.51 cm<sup>2</sup>) and second highest plant drooping height. Thus; the genotypes of these clusters have excellent opportunities to bring about improvement through wide hybridization.

**Keywords:** Wheat Genotypes, Yield, Seed Vigour, Genetic Divergence, Cluster Analysis

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## Introduction

Wheat (*Triticum aestivum* L. em Thell.) is the first important cereal crop for the majority of world's populations. In India wheat is cultivated on 30.72mha, with a production 97.44 mt and productivity 31.72q/ha. Haryana with 11.14 mt production, 2.54 m ha area and 4.39 t/ha productivity ranks third in the country [1]. The major increase in the productivity of wheat has observed in the states of Haryana, Punjab and Uttar Pradesh. In India, wheat is grown under varied climatic conditions ranging from temperate Himalayan foothills to the hot areas of central and southern India and under subtropical environment during mild winter, which warms up towards the grain filling stage of the crop. Wheat constitutes about 22% of the world's food supplies [2]. With irregular and uncontrolled increase of world population it is predicted that the world it will reach 8 billion people by year 2020, from which 6.7 billion live in developing countries. Therefore, one of the politically, economically and socially major and important issues, especially in developing countries, is to supply for food requirements of vast human population [3]. Thus, development of high yielding wheat cultivars has always been a major objective of wheat breeding programmes throughout the world [4].

Genetic diversity is of major interest to plant breeders for developing cultivars with high grain yield. To carry out intensive breeding programme of varietal improvement, the knowledge of genetic diversity among parents and variability for important yield traits play a vital role in success of any hybridization programme. Genetic divergence analysis estimates the extent of diversity existed among selected genotypes [5]. Within a species, genetic distance can be used to estimate the divergence between different sub-species or different varieties of a species. Smaller genetic distances indicate a closely related species where as large genetic distances indicate a more distantly species. Knowledge about the nature and degree of genetic diversity helpful in hybridization programme to select the diverse parents by the breeder. Genetic variation decreases among the cultivars as result of conventional breeding practices affect the success varietal improvement of crops - particularly wheat.

Among different multi-variant analysis methods, principal components analysis, cluster analysis and principal coordinate analysis are the important methods [6]. Breeding specialist classify the different varieties to estimate their genetic distance and use their diversity in breeding program. Cluster analysis use mathematical formulas to classify the genotypes [7, 8]. Grouping the genotypes at the basis of studied characteristics can be used to estimate genetic dissimilarity and similarity in collections by Hierarchical cluster analysis. The present study was undertaken with the

objective of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme.

**Table 1** List of genotypes along with their pedigree

Sr. No.	Genotypes	Pedigree
1	WH 542	JUPATECO/BLUEJA/URES
2	WH 711	ALD 'S'/HAU//HD2285/3/HFW-17
3	WH 1021	NYOT95(GW296)/SONAK
4	WH 1025	C591/PBW231
5	WH 1080	PRL/2*PASTOR
6	WH 1081	PBW65/2*PASTOR
7	WH 1105	MILAN/S87230//BABAX
8	WH 1120	PRL/2*PASTOR
9	WH 1124	MUNIA/CHTO//AMSEL
10	WH 1126	WBLL1*2/VIVITSI
11	WH 1129	CS/TH.CS//3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHI
12	WH 1130	PRL/2*PASTOR/4/CHOIX/STAR/3/HE1*CN079
13	WH 1138	PBW65*2/PASTOR
14	WH 1142	CHEN/Ae.sq (TAUS)//FCT/3/2*WEAVER
15	WH 1154	WH337/HD2255//RAJ3077
16	WH 1163	HPW42/WH542
17	WH 1164	RL6043/4*NAC//2*PASTOR
18	WH 1166	HD29/*WEAVER/3/VEE/PJN//2*WEAVER/3/VEE/PJN//2*TUI/4/MILAN
19	WH 1167	WEAVEAR/VIVISI/3/C80.1/3*BATAVIA//2*WBLLI
20	WH 1168	ATTILA*2//CHIL/BUC*2/3/KUKUNA
21	WH 1169	KLDR/PEWITI/MILAN/DUCULA
22	WH 1170	LERKE/5/KAUZ/3/MYNA/VUL//BUC/FLK/4/MILLAN/6PROGRESOF2007
23	WH 1171	MILAN//PRL/2*PASTOR/4/CROC_1/AE.SQ(213)//PGO/3/BAV92
24	WH 1172	KLDR/PEWIT//MILAN/DUCULA
25	WH 1174	FILIN/IRENA/5/CNDOR/R143/ENIE/MEXI_2/3Ae.Sq/4/
26	WH 1175	FILIN/2*PASTOR//BERKUT/3/PASTOR/2*SITTA
27	WH 1177	HP1744/PBW443
28	WH 1178	CS//TH.86/3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHI
29	WH 1179	OASIS/SKAUZ//4*BCN/3/3*PASTOR
30	HD 2687	CPAN2009/HD2329
31	HD 2851	CPAN3004/WR426//HW2007
32	HD 2967	ALD/CUC//URES/HD2160/HD2278
33	PBW 343	ND/VG9144//KAL//BB/3//YCO 'S'/4/VEE#5 'S'
34	PBW 550	WH594/RAJ3856//W485
35	PBW 590	WH594/RAJ3814//W485
36	PBW 373	ND/VG9144//KAL//BB/3//YCO 'S'/4/VEE#5 'S'
37	DBW 17	CMH79A.95/3*CN079//RAJ3777
38	DPW 621- 50	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES
39	RAJ 3765	HD 2402/VL639
40	UP 2338	UP368/VL421//UP262

## Materials and Methods

A field experiment with 40 wheat genotypes was conducted under irrigated condition at CCSHAU, Hisar, India during winter (*Rabi*) season 2013-2014. The description of genotypes is given in **Table 1**. All the genotypes were grown in a randomized block design (RBD) with three replications in four rows of 2.5 meter length, keeping row to row distance of 20 cm. Observations for all the traits were recorded on five randomly selected plants for each genotype in each replication. Observations were recorded on the characteristics like days to 50% heading (DH), days to anthesis (DA), plant height (PH), flag leaf length (FL), flag leaf width (FB), flag leaf area (FLA), number of tillers per meter (T), spike length (SL), main spike weight (SW), spikelets per spike (SPS), grains per spike (GPS), grains weight per spike (GW), grain length (GL), grain breadth (GB), grain growth rate (GGR) at 14, 21 and 28 days after anthesis, biological yield (BY), grain yield (GY), thousand grains weight (TGW), harvest index (HI), standard

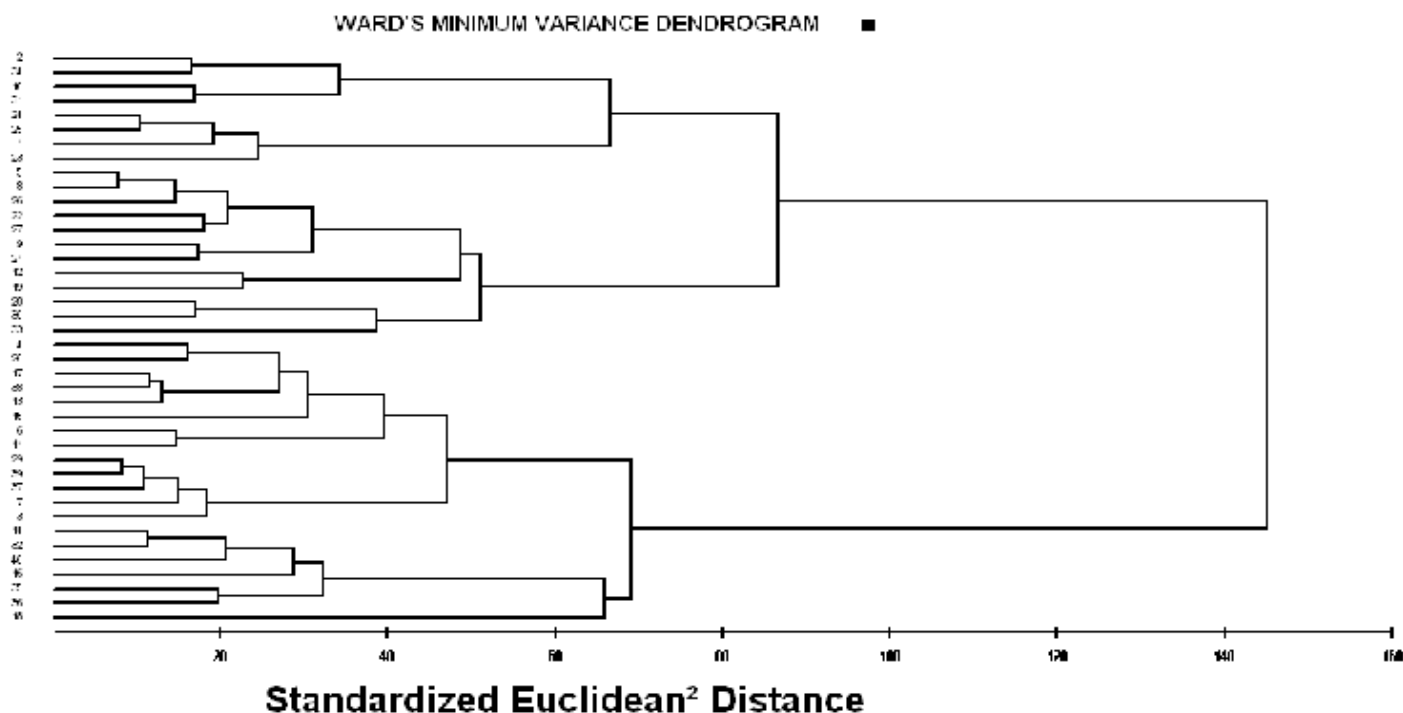
germination test (GM), seedling length (SLg), seedling dry weight (SD), vigour index-I (V-I), vigour index-II (V-II), seed density (Sd), plant straight height (SH) at 30 days, plant drooping height (Dr. H) at 30 days, field emergence index (FE) and seedling establishment (FS). Analysis of the observations recorded on different characters was carried out as per the standard procedure. To assess genetic diversity among the genotypes and genotypes were grouped on the basis of minimum genetic distance using the squared Euclidean and WARD method [9].

## Results and Discussion

In order to measure the genetic divergence between a number of genotypes, Euclidean cluster analysis was employed and the constellation of genotypes into clusters was done by Ward's minimum variance. Based on the divergence, 40 wheat genotypes involved in the present study were grouped into 6 clusters. Clustering pattern indicate the presence of considerable amount of genetic diversity in this material. In general, intercluster distances were relatively greater than intracluster distances indicating that genotypes included in different clusters were genetically more diverse than the genotypes included within a cluster. The cluster IV was the largest cluster consisting of 13 genotypes. This was followed by cluster III (12 genotypes), V (6 genotypes), cluster I (4 genotypes), II (4 genotypes) and cluster VI (1 genotype) as seen from **Table 2**.

**Table 2** Clustering of 40 genotypes of wheat

1 Cluster	4	WH 1163, WH 1172, PBW 550 and HD 2851
2 Cluster	4	WH 1129, WH 1179, WH 1080 and WH 1025
3 Cluster	12	WH 542, WH 1021, WH 1081, WH 1142, WH 1166, WH 1167, WH 1170, WH 1174, WH 1175, HD 2687, HD 2967 and DPW 621-50
4 Cluster	13	WH 711, WH 1124, WH 1126, WH 1130, WH 1154, WH 1164, WH 1168, WH 1169, WH 1171, WH 1177, WH 1178, PBW 343 and PBW 373
5 Cluster	6	WH 1105, WH 1120, WH 1138, DBW 17, PBW 590 and RAJ 3765
6 Cluster	1	UP 2338



**Figure 1** Dendrogram showing genetic relationship among 40 genotypes of wheat based on Euclidean distance

The intra cluster distance ranged from 0.000 (VI) to 7.242 (III) indicating considerable diversity between different clusters. Intra cluster distance was maximum for cluster III, followed by clusters I, V, IV and II and minimum for cluster VI which indicates the existenc of maximum variability within cluster III. The inter cluster distance ranged from 7.376 (between IV and V) to 10.475 (between II and VI) as shown in **Table 3**. [10-14] also reported the same. The higher intercluster distances exhibited the presence of more diversity among the genotypes involved in these clusters.

**Table 3** Intra (diagonal) and inter cluster distances values among grouped 40 genotypes of wheat

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	6.721	7.987	8.278	8.041	8.099	10.007
2 Cluster		6.014	7.926	8.478	9.245	10.475
3 Cluster			7.242	7.801	8.123	10.304
4 Cluster				6.484	7.376	9.721
5 Cluster					6.720	9.783
6 Cluster						0.000

If the genotypes possessing maximum genetic distance are used in hybridization programme, it is expected that more heterotic F<sub>1</sub>'s and most promising segregants in the segregating generations will be produced. This means that geographic diversity though important, may not be the only factor in determining genetic divergence whereas genetic diversity is the outcome of several factors, including geographical diversification. Therefore, for hybridization programme selection of varieties should be done based on genetic diversity rather than geographic diversity.

**Table 4** Mean values of different cluster for Yield and its component traits in wheat

	DH	DA	PH	FL	FB	FLA	T	SL	SW	SPS	GPS
Cluster 1	90.67	98.25	102.8	22.5	1.9	32.5	100.8	11.2	3.03	17.9	53
Cluster 2	101.6	109.4	109.9	23.4	1.8	31.7	106	12.8	2.91	19.4	52.5
Cluster 3	97.22	104.3	112.5	27.6	1.9	40	125.3	12.2	3.26	20.1	57.4
Cluster 4	94.82	102.5	108.3	27.6	1.9	39.6	125.8	11.2	3.33	17.8	52.4
Cluster 5	92.33	100.4	102.6	29.7	1.9	41.5	143.5	12.1	3.01	18.9	53
Cluster 6	92	100.7	131.7	25.1	1.5	27.8	121.9	11.7	3.5	20.1	57.8
Total mean	95.36	103	108.9	26.9	1.9	38.2	123.7	11.8	3.19	18.9	54.2
	GW	GL	GB	TGW	BY	GY	HI	GGR14	GGR21	GGR28	
Cluster 1	2.02	6.7	3.1	41.6	3438	840.4	24.8	6.97	11.83	14.26	
Cluster 2	2.01	6.9	3.2	41.76	3500	862.1	24.9	7.11	11.88	14.82	
Cluster 3	2.13	6.5	3.2	42.93	3590	941.4	26.5	6.34	12.47	16.37	
Cluster 4	2.33	6.8	3.4	47.04	3218	961.6	30.1	7.11	13.31	17.45	
Cluster 5	2.14	6.8	3.2	43.03	3250	1014	31.3	6.81	13.19	16.26	
Cluster 6	2.47	7.9	3	49.57	3917	883.3	22.6	7.37	14.03	15.83	
Total mean	2.18	6.8	3.3	44.2	3402	939.4	28	6.83	12.77	16.32	

**Table 5** Mean values of different cluster for seed vigour traits in wheat

	GM	SLg	SD	V-I	V-II	Sd	SH	Dr.H	FE	FS
Cluster 1	94.83	21.56	124.53	2042.75	11814.92	0.98	25.40	17.23	9.33	77.75
Cluster 2	97.75	22.73	122.16	2220.93	11943.08	1.08	19.95	11.96	9.62	75.58
Cluster 3	97.42	21.58	125.69	2102.20	12242.82	1.16	24.41	16.01	9.59	78.22
Cluster 4	95.92	21.56	126.80	2068.84	12170.77	1.01	24.20	15.35	9.46	76.23
Cluster 5	93.83	20.51	119.59	1922.04	11231.24	1.02	24.20	16.76	9.21	73.72
Cluster 6	96.00	19.77	103.33	1896.50	9919.67	1.07	26.93	16.07	9.40	64.00
Total mean	96.13	21.48	124.11	2065.12	11936.82	1.06	24.03	15.62	9.46	76.23

The mean values of different clusters for the 31 characters have been presented in **Table 4** and **5**. Cluster I was comprises of early genotypes with cluster mean of 90.67 for days to 50% heading, 98.25 for days to anthesis and had highest cluster mean value 17.23 cm for plant drooping height. Cluster II had highest spike length (12.78 cm), germination% (97.75%), seedling length (22.73 cm), vigour index-I (2220.93) and field emergence value (9.62%). Cluster III had highest spikelets per spike (20.13), flag leaf width (1.93 cm), vigour index-II (12242.82), seed density (1.16 g/cc), seedling establishment value (78.22%). Cluster IV had lowest biological yield (3217.9 g), spikelets per spike (17.82), grains per spike (52.36), seed density (1.01 g/cc) and highest grain breadth (3.40 mm), grain growth rate at 28 days (17.45 g/gr/day x 10<sup>4</sup>) and seed dry weight (126.80 g). Cluster V had highest grain yield (1014.4 g), harvest index (31.26%), number of tillers per meter (143.46), flag leaf length (29.72 cm), flag leaf area (41.51 cm<sup>2</sup>) and second highest plant drooping height. Cluster VI had highest biological yield (3916.7 g), 1000 grain weight (49.57 g), spike weight (3.500 g), grains per spike (57.77), grains weight per spike (2.47 g), plant height (131.73 cm), plant straight height (26.93 cm), grain growth rate at 14 and 21 days (7.37 and 14.03 g/gr/day x 10<sup>4</sup> respectively). Comparative study of cluster means values suggested that for improving specific trait the genotype

should be selected from cluster exhibited high mean value for that trait. Cluster II, III, IV and V exhibited the highest mean value for important seed vigour, yield and its attributing traits. Therefore, these four clusters were considered most desirable for selecting genotypes. Almost similar results were reported by [10], [11], [15] and [16].

## Conclusion

There is significant genetic variability present among tested genotypes that is important to select the genotypes with high genetic distance to bring about improvement by crossing. From this study, genotypes in clusters IV and V possess desirable combinations of yield and its components traits. In Clusters II and III the genotypes exhibited the combination of seed vigour and quality traits. Thus; the genotypes of these four clusters hold great promise as parents to obtain promising hetrotic F1's and may create considerable variability in the segregating populations.

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