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Estimation of genetic variability and diversity in bread wheat (*Triticum aestivum* L.) for yield and yield contributing traits

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Abstract
An experiment was carried out to study genetic variability and genetic divergence for 12 traits in 50 diverse genotypes of bread wheat under normal sown condition. The analysis of variance revealed highly significant differences among the mean square due to genotypes for all the characters studied. High genotypic and phenotypic coefficient of variation was observed for grain weight per main spike followed by biological yield per plant, 1000-grain weight and grain yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for 1000-grain weight, grain weight per main spike, number of grains per main spike, biological yield per plant and grain yield per plant. Genetic divergence was assessed by Mahalanobis D^2 statistic, which grouped 50 genotypes into ten clusters. Maximum genetic divergence was observed between cluster VII and IX followed by between cluster IV and VII. The attributes, *viz.*, 1000-grain weight, biological yield per plant, number of grains per main spike, days to maturity and grain weight per main spike had highest contribution towards total genetic divergence.

Keywords: Bread wheat, genetic variability, heritability, genetic advance, genetic divergence, D^2-statistics, clustering

Introduction
Wheat is the second most important food crop after rice in terms of both area and production, India contributes 12 per cent to the world wheat pool. In India, during 2018-19 area under wheat cultivation was 29.56 m ha with the annual production of 101.20 million tonnes with an average productivity of 34.24 kg/ha (Anon., 2019) [2]. In Gujarat, it occupied an area of 0.94 m ha with production of 2.77 million tonnes with an average productivity of 2946 kg/ha (Anon., 2019) [2]. Major wheat producing states are Punjab, Haryana, Uttar Pradesh, Bihar and Rajasthan which are located in the Indo-Gangetic Plains and accounts for 85 per cent of total wheat production in the India.

Availability of sufficient genetic variability is very important in a crop improvement programme. Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be of a great importance in planning a successful breeding programme (Mary and Gopalan, 2006) [16]. The choice of parents is of paramount importance in breeding programme. For effective selection, information on nature and magnitude of variation in population, association of characters with yield and among themselves and the extent of environmental influence on the expression of these characters are necessary (Yagdi, 2009) [28]. Therefore, it is essential for a breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence, these above said parameters give the information regarding the availability of genetic variability for different characters in germplasm. Therefore, study of genetic variability of grain yield and its component characters among different varieties provides a strong basis for selection of desirable genotypes for augmentation of yield and other agronomic characters.

The choice of genetically divergent parents for hybridization under transgressive breeding programme is also dependent upon categorization of breeding materials on the basis of appropriate criteria. Mahalanobis D^2 technique is one of the potent tools for measuring genetic divergence. In plant breeding, genetic diversity play an important role because hybrids between lines of diverse origin, generally, display greater heterosis than those between closely related parents and may generate broad spectrum of genetic variability in segregating populations (Arunachalam, 1981) [4].

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Materials and Methods

The study was carried out at Wheat Research Station, Junagadh Agricultural University, Junagadh during *Rabi* 2018-19. The experimental material consisted of 50 diverse genotypes of wheat (*T. aestivum* L.). Fifty genotypes of bread wheat were sown in a Randomized Block Design with two replications at Wheat Research Station, Junagadh Agricultural University, Junagadh. Each line was sown in a single row plot of 2.50 m × 1.20 m length with a spacing of 20 cm × 10 cm. The genotypes were randomly allotted to the plots in each replication. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of the crop. The characters studied was days to 50% flowering, grain filling period, days to maturity, plant height, number of productive tillers per plant, spike length, number of grains per main spike, grain weight per main spike, grain yield per plant, biological yield per plant, harvest index and 1000-grain weight. The replication-wise mean values of five randomly selected plants in each entry were used for the statistical analysis for different character under study. Analysis of variance was estimated as suggested by Panse and Sukhatme (1985) [20], Coefficient of variation was calculated as suggested by Sivasubramanian and Menon (1973) [25] to estimate the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), heritability in broad sense was estimated according to the formulae proposed by Burton and De Vane (1952), genetic advance (GA) was calculated according to the formulae given by Johnson *et al.* (1955) [10]. The statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics (Mahalanobis, 1936) and clustering of genotypes was done using Tocher method (Rao, 1952) [21].

Results and Discussion
Genetic Variability

Analysis of variance revealed that mean square due to genotypes was highly significant for all the traits as shown in Table 1, indicating the presence of sufficient amount of genetic variability among the genotypes for all the 12 characters studied (Alam *et al.*, 2013; Wolde *et al.*, 2016 and Ibrahim 2019) [1, 27, 9]. The various components taken under study are presented in Table 2. Close relationship between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for all the characters. The magnitude of PCV was slightly greater than GCV revealed a very little influence of environmental variation for their expression. This indicated that phenotypic variability may be considered as reliable measure of genotypic variability. Similar results have also been reported by Anzer *et al.* (2017) [3]; Kumar *et al.* (2018) [13]; Rathwa *et al.* (2018) [22] and Gaur (2019) [8].

The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for grain weight per main spike followed by biological yield per plant, 1000-grain weight and grain yield per plant. The high genotypic coefficient of variation indicated the presence of wide variation for the characters under study to allow selection for individual traits. High value of genotypic and phenotypic coefficient of variation for traits like grain weight per main spike, biological yield per plant, 1000-grain weight and grain yield per plant were reported by Sidharthan and Malik, 2007 [24]; Zarkti *et al.,* 2012 [29]; Nusrat *et al.*, 2015 [18]; Anzer *et al.,* 2017 [3]; Kumar *et al.,* 2018 [13]; Gaur 2019 [8] and Ibrahim, 2019 [9].

Heritability estimates reported here was based on broad sense only and hence the total genetic variance may include dominance and epistatic components which are not available for selection. In present study, high heritability in broad sense estimates were observed for 1000-grain weight (98.52%), grain weight per main spike (96.48%), number of grains per main spike (93.79%), biological yield per plant (93.52%), grain yield per plant (86.48%), days to maturity (86.02%), days to 50% flowering (81.76%), number of productive tillers per plant (79.70%), spike length (71.47%) and plant height (68.81%). Similar results were reported by Sidharthan and Malik, 2007 [24]; Majumder *et al.,* 2008 [15]; Kamboj, 2010 [11]; Alam *et al.,* 2013 [1]; Kumar *et al.,* 2014 [12]; Subhashchandra *et al.,* 2014; Wolde *et al.,* 2016 [27] and Bhanu *et al.,* 2018 [5]. The genetic advance expressed as per cent of mean was highest for grain weight per main spike (61.08%), biological yield per plant (54.49%), 1000-grain weight (47.02%), grain yield per plant (39.40%) and number of grains per main spike (32.28%). Similar findings were reported by Rathwa *et al.,* 2018 [22] and Guar, 2019 [8]. High heritability coupled with high genetic advance expressed as percentage of mean was more valuable in predicting the effect of selection (Johnson *et al.*, 1955) [10].

Genetic Diversity

In the present investigation, ten different clusters are made from 50 genotypes which are shown in Table 3. Dendrogram showing distribution of 50 genotypes among 10 clusters by using complete linkage and Euclidean distance is shown in Figure 1. On the basis of D^2-values, ten clusters were formed from 50 genotypes. The cluster II and cluster III having largest number of genotypes (10) followed by cluster VII (9), cluster I (8), cluster V (6) and cluster VIII (3). On the other hand, cluster IV, cluster VI, cluster IX and cluster X are solitary clusters. In general, intra cluster distances were lower than the inter-cluster distances and this was in accordance with Alam *et al.* (2013) [1] and Santosh *et al.* (2019) [23]. Thus, the genotypes included within a cluster tended to less diverse from one another. The intra-cluster distance (D) ranged from 4.51 (cluster-I) to 8.25 (cluster-VIII). High intra-cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of bread wheat. The intra and inter-cluster distances are shown in Table 4. The maximum inter-cluster distance was found between cluster VII and IX (D=29.05) followed by that between IV and VII (D=25.64). The minimum inter-cluster distance was observed between cluster IV and IX (D=5.56). D^2 analysis indicated wider genetic diversity among 50 genotypes of bread wheat which were grouped into ten clusters. Maximum genetic divergence was observed between cluster VII and IX followed by between cluster IV and VII. The attributes, *viz.,* 1000-grain weight, biological yield per plant, number of grains per main spike, days to maturity and grain weight per main spike had highest contribution towards total genetic divergence. Hence, selection for divergent parents based on these five characters would be useful for exploitation of heterosis breeding in bread wheat if commercially feasible. On the basis of cluster means, cluster X had the highest mean values for days to 50% flowering (51.50 days) and days to maturity (91.50 days), while cluster VI had desirable rating for grain filling period (64.50 days) and dwarfness (71.90 cm). The cluster IX had the highest mean values for number of productive tillers per plant (7.20); spike length (12.10 cm); number of grains per main spike (50.90); grain weight per main spike (4.80 g); grain yield per

plant (19.10 g); biological yield per plant (53.10 g); and 1000-grain weight (57.60 g). The maximum mean values for harvest index (39.90 %) were observed in cluster II.

The cluster means for 12 characters are presented in Table 6. The perusal of the Table 5 revealed that the 1000-grain weight contributed maximum (60.41%) as the first ranker towards the total divergence in yield with its average ranging from 28.07 for cluster VII to 57.60 for cluster IX. Biological yield per plant (9.06%), number of grains per main spike (8.57%), days to maturity (7.76%) and grain weight per main spike (7.43%) were the next important traits contributed to total genetic divergence. A considerable diversity of 93.23% was observed due to these five characters. Hence, selection for divergent parents based on these five characters would be useful for heterosis breeding in bread wheat. Similar findings were reported by Nimbalkar et al., 2002 [17] and Chapla et al., 2008 [7]. Days to 50% flowering, number of productive tillers per plant and harvest index contributed 5.14% towards total genetic divergence. On the other hand, grain yield per plant,

grain filling period, and plant height and spike length contributed low genetic divergence towards total divergence. Low genetic diversity for these traits in such diverse group of genotypes may also suggest high degree of consistency and moderate to low heritability of these traits.

In the present study, the cluster X differed from other clusters in respect of days to 50% flowering and days to maturity, while cluster VI had desirable rating for grain filling period and dwarfness. The cluster IX had the highest mean values for number of productive tillers per plant, spike length, number of grains per main spike, grain weight per main spike, grain yield per plant, biological yield per plant and 1000-grain weight. The maximum mean values for harvest index were observed in cluster II. Therefore, intercrossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters, and their rational improvement for increasing grain yield in bread wheat.

Table 1: Analysis of variance for various characters in 50 bread wheat genotypes

Source	d.f.	Days to 50% flowering (days)	Grain filling period (days)	Days to maturity(days)	Plant height (cm)	Number of productive tillers per plant	Spike length (cm)
Replications	1	2.56	3.61	0.64	0.02	0.02	0.97
Genotypes	49	8.66**	4.94**	23.27**	56.24**	0.57**	1.83**
Error	49	1.58	2.06	3.25	17.54	0.11	0.52

Source	d.f.	Number of grains per main spike	Grain weight per main spike (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)	1000 grain weight (g)
Replications	1	1.39	0.07	1.30	3.39	4.91	7.67
Genotypes	49	86.53**	1.80**	14.09**	169.52**	42.46**	174.32**
Error	49	5.38	0.06	1.90	10.98	19.68	2.57

*, ** Significant at 5% and 1% levels, respectively.

Table 2: Phenotypic range, coefficient of range, phenotypic (PCV %) and genotypic (GCV %) coefficients of variation, heritability, genetic advance and genetic advance expressed as a percent of mean for various characters in bread wheat

Sr. No.	Characters	Phenotypic range	Coefficient of range (%)	Mean ± S.E.	PCV (%)	GCV (%)	Heritability in broad sense (%)	Genetic advance	G. A. expressed as per cent of mean
1	Days to 50% flowering	51.50-59.50	7.21	55.88 ±0.88	3.72	3.37	81.76	3.51	6.27
2	Grain filling period (days)	61.00-68.50	5.79	65.65±1.01	2.40	1.83	58.35	1.89	2.87
3	Days to maturity	91.50-109.00	8.73	98.72±1.27	3.46	3.20	86.02	6.04	6.12
4	Plant height (cm)	71.90-98.10	15.41	82.92±2.96	6.39	5.30	68.81	7.52	9.06
5	No. of productive tillers per plant	4.70-7.20	21.01	6.03 ±0.23	8.81	7.87	79.70	0.87	14.47
6	Spike length (cm)	7.40-12.10	24.10	9.31 ±0.51	10.26	8.68	71.47	1.41	15.11
7	No. of grains per main spike	25.40-50.90	33.42	39.37 ±1.64	16.71	16.18	93.79	12.70	32.28
8	Grain weight per main spike (g)	1.60-4.80	50.00	3.09±0.18	30.73	30.19	96.48	1.89	61.08
9	Grain yield per plant (g)	5.80-19.10	53.41	12.00±0.98	22.11	20.56	86.48	4.72	39.40
10	Biological yield per plant (g)	16.60-53.10	52.37	32.55±2.34	28.28	27.35	93.52	17.74	54.49
11	Harvest index (%)	27.44-53.15	31.90	37.73 ±3.14	12.21	8.94	53.65	5.09	13.49
12	1000-grain weight (g)	21.50-58.4	46.18	40.29±1.13	23.17	22.99	98.52	18.95	47.02

Table 3: Grouping of 50 genotypes of bread wheat in various clusters on the basis of D^2 statistic

| Cluster	No. of genotypes	Name of genotypes
I	8	JAU-2018-10, JAU-2018-21, JAU-2018-20, JAU-2018-42, JAU-2018-16, JAU-2018-27, JAU-2018-37, JAU-2018-48
II	10	JAU-2018-5, JAU-2018-22, JAU-2018-4, JAU-2018-47, JAU-2018-26, JAU-2018-30, JAU-2018-45, JAU-2018-29, JAU-2018-2, JAU-2018-23
III	10	JAU-2018-6, JAU-2018-35, JAU-2018-46, JAU-2018-38, JAU-2018-31, JAU-2018-19, JAU-2018-32, JAU-2018-24, JAU-2018-33, JAU-2018-1(GW 366)
IV	1	JAU-2018-18
V	6	JAU-2018-39, JAU-2018-44, JAU-2018-12, JAU-2018-50, JAU-2018-41, JAU-2018-14
VI	1	JAU-2018-11
VII	9	JAU-2018-7, JAU-2018-15, JAU-2018-36, JAU-2018-3, JAU-2018-25, JAU-2018-13, JAU-2018-43, JAU-2018-40, JAU-2018-28
VIII	3	JAU-2018-8, JAU-2018-9, JAU-2018-34
IX	1	JAU-2018-17
X	1	JAU-2018-49
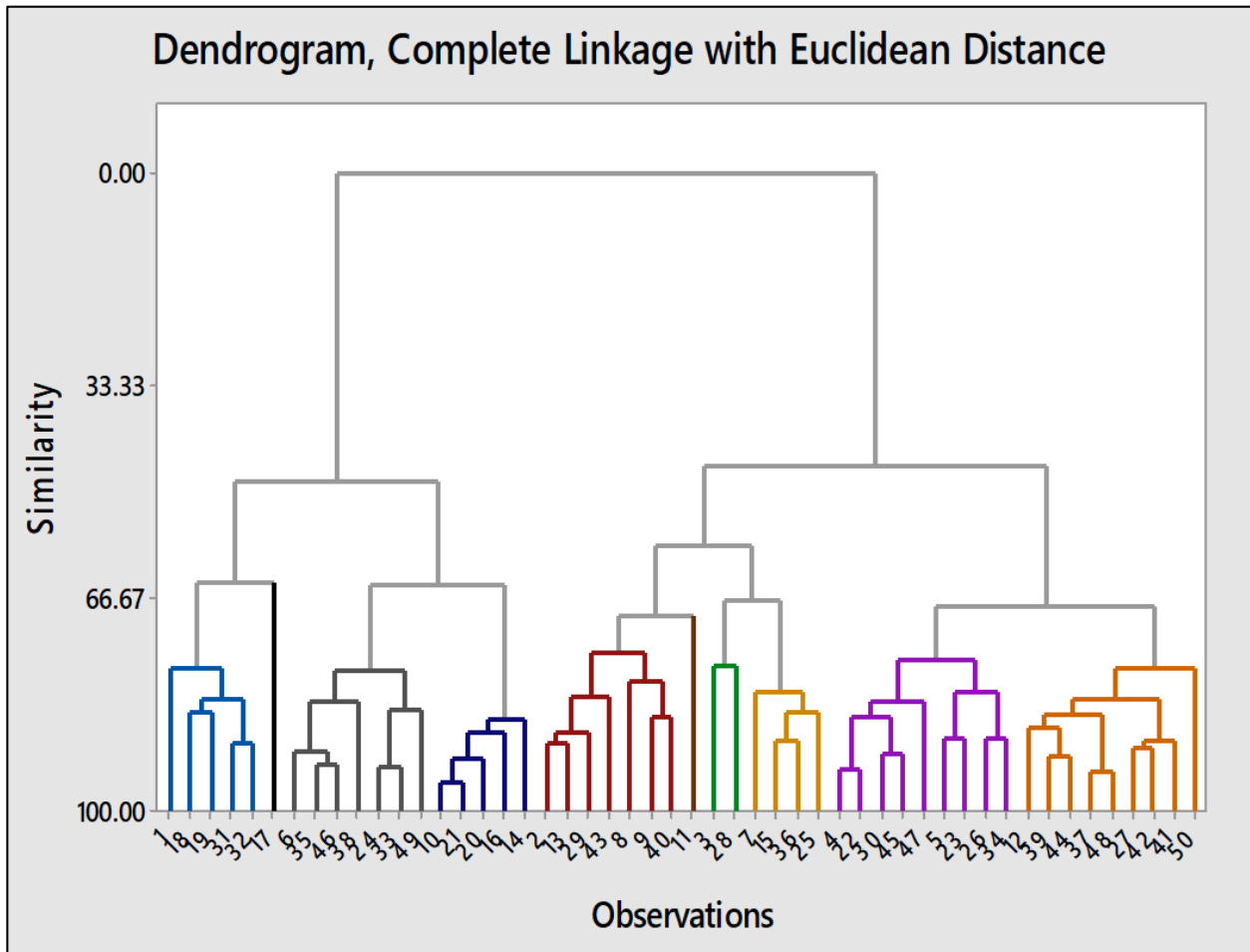
Fig 1: Dendrogram showing distribution of 50 bread wheat genotypes into 10 different clusters

Table 4: Average intra and inter-cluster distances between ten cluster in bread wheat

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	4.51	7.60	12.40	13.61	7.13	9.13	13.63	9.10	17.08	15.51
II		5.65	17.68	19.14	11.51	7.77	9.51	8.69	22.09	20.60
III			6.57	7.83	9.30	16.54	23.31	16.65	12.13	7.58
IV				0.00	11.88	19.05	25.64	19.61	5.56	11.48
V					6.31	10.79	16.85	10.63	15.96	11.30
VI						0.00	10.67	8.58	22.89	18.85
VII							8.10	10.82	29.05	25.37
VIII								8.25	23.54	17.82
IX									0.00	15.89
X										0.00

Table 5: Contribution of various traits towards total genetic divergence in bread wheat

Sr. No	Characters	Time ranked first	Contribution (%)
1.	Days to 50% flowering	29	2.37
2.	Grain filling period (days)	7	0.57
3.	Days to maturity	95	7.76
4.	Plant height (cm)	3	0.24
5.	Number of productive tillers per plant	20	1.63
6.	Spike length (cm)	2	0.16
7.	Number of grains per main spike	105	8.57
8.	Grain weight per main spike (g)	91	7.43
9.	Grain yield per plant (g)	8	0.65
10.	Biological yield per plant (g)	111	9.06
11.	Harvest index (%)	14	1.14
12.	1000-grain weight (g)	740	60.41

Table 6: Cluster mean values of 12 characters in 10 clusters in 50 bread wheat genotypes

Sr. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
1.	Days to 50% flowering	56.88	57.45	55.20	57.50	55.25	56.50	55.28	52.83	59.50	51.50
2.	Grain filling period (days)	66.44	66.55	65.10	67.00	64.83	64.50	65.44	64.67	66.00	65.00
3.	Days to maturity	100.50	100.80	97.80	103.50	97.58	97.50	97.28	94.50	109.00	91.50
4.	Plant height (cm)	84.24	80.90	86.80	91.60	83.78	71.90	77.19	82.81	98.10	87.90
5.	Number of productive tillers per plant	6.06	5.80	6.39	7.00	6.22	6.10	5.39	6.22	7.20	6.50
6.	Spike length (cm)	9.55	9.05	10.07	10.80	9.52	8.10	8.08	8.93	12.10	10.70
7.	Number of grains per main spike	42.11	36.77	45.88	47.60	42.37	31.10	30.11	34.93	50.90	45.70
8.	Grain weight per main spike (g)	3.21	2.50	4.18	4.30	3.68	2.60	1.76	2.70	4.80	4.30
9.	Grain yield per plant (g)	12.11	10.84	14.68	17.30	12.47	11.30	8.76	10.60	19.10	15.00
10.	Biological yield per plant (g)	34.02	27.25	43.09	52.10	33.67	21.40	22.21	27.27	53.10	41.60
11.	Harvest index (%)	35.82	39.90	34.48	33.17	37.53	53.15	39.49	39.08	36.04	36.10
12.	1000-grain weight (g)	40.13	34.85	52.27	55.40	43.92	37.90	28.07	34.30	57.60	52.80

Conclusion

Genetic variability is the basic requirement for crop improvement as it provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable. In the present investigation, the estimates of high heritability coupled with high GCV and genetic advance expressed as percentage of mean was observed for 1000-grain weight, grain weight per main spike, biological yield and grain yield per plant. These characters may have contributed to preponderance of additive gene action and selection pressure could profitably be applied on these characters for their rationale improvement (Panse, 1957). It has been well established fact that more the genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981) [4]. Therefore, in the present study, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster IX with the genotypes of cluster VII and cluster X, which may lead to broad spectrum of favorable genetic variability for yield improvement in bread wheat.

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