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Assessment of genetic diversity in bread wheat (*Triticum aestivum* L.) accessions

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Abstract
D^2 analysis was studied for yield and its component characters in 45 wheat genotypes using Mahalanobis D^2 statistic (1936) as described by Rao (1952). D^2 analysis indicated wider genetic diversity among 45 genotypes of wheat, which were grouped into twelve clusters. Maximum intra cluster distance was observed for cluster VI (7.12), whereas maximum inter cluster distance was observed between cluster II and XII (15.94). The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The genotypes belonging to the clusters separated by high genetic distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

Keywords: Wheat, D^2 statistics, genetic divergence, inter and intra cluster distance

Introduction
Wheat, a cereal grass of the poaceae family and of the genus Triticum, is the world's largest cereal crop. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. According to the earliest historic records, wheat was an important cultivated cereal in South-western Asia, its geographical centre of origin. Wheat is highly self-pollinated crop and amount of cross-pollination occurs less than 1%. It is the most important agricultural crop of the world and mainly of the area of temperate climates. In India mainly three species of wheat *viz*., bread wheat (*Triticumaestivum*L.), macaroni wheat (*Triticum durum*) and emmer wheat (*Triticumdicoccum*) are presently grown as commercial crop, covering 86, 12, and 2% of the total area, respectively. The bread wheat, a hexaploid with chromosome number 2n=42, is cultivated in the all wheat growing areas of the country. The macaroni or durum wheat (Tetraploid, 2n=28) is mostly grown in central and southern states, the emmer wheat (Tetraploid, 2n=28) is confirmed to the southern states (mainly Karnataka) and some parts of Gujarat. It ranks second among major cereals next to rice and ensure a vital role in food security of teeming hungry millions of India. India has also second largest area (26.3 m ha) under wheat cultivation in the world followed by China (22.5 m ha). The total wheat production for 2018-19 in India was approximately 99.12 million tonnes, which was higher than 97.11 million tonnes for 2017-18 (Anonymous, 2019b) [1]. The leading wheat producing countries are China, India, United States, France, and Russia Federation, (FAO, 2015) [2]. Over the years, wheat breeding has significantly contributed to increasing the yield potential throughout the world. Along with genetic potential, factors like heat, drought and disease also significantly affect ultimate yield. In addition, an average of 0.5 to 1.0% genetic gain of wheat per year is unable to keep pace with over 2% per year increased demand in developing countries.

Materials and Methods
Forty five bread wheat (Triticumaestivum L.) genotypes collected from the Wheat Research Station, Vijapur, Gujarat were used to evaluate in Randomized Block Design with three replications. Each plot consisting 3-meter length having three different genotypes with two rows of each keeping intra row spacing at 22.5cm. The experimental material was planted on16 November at Agronomy instructional farm, Sardarkrusinagar, to study yield and biochemical variability parameters among genotypes during crop season Rabi 2018-19. The observations were recorded on diverse biochemical and yield attributing traits, *viz*., initial plant population, days to heading, days to maturity, plant height (cm), number of tiller per meter, number of grain per spike, grain yield per plant (g), 1000 seed weight (g),

Leaf area per plant, zinc content (ppm), iron content (ppm), protein content (%), hectoliter weight (kg/hl), sedimentation value and harvest index (%)for conducting genetic diversity analysis. Recommended package of practices was followed to raise the crop. All the statistical analysis were performed at department of agricultural statistics using INDOSTAT v8.1 and biochemical analysis at wheat research station, Vijapur and Biochemistry Department, S.D.A.U. using standard protocols.

Results and Discussion

Mahalanobis's D^2 statistic was computed between all possible pairs of 45 Wheat genotypes and the genetic diversity present among the genotypes was estimated. For improving yield, selection of parents based on a number of characters having quantitative divergence is required which can be fulfilled by D^2 statistic developed by Mahalanobis (1936) [7] and Tocher's method as described by Rao (1952). The distance between two clusters is a measured of degree of diversification. The greater distance between two cluster the greater the divergence and vice versa. The genotypes falling in the same cluster were more closely related then those belonging to another cluster.

Distribution of genotypes into clusters

Forty five genotypes of wheat were grouped into main two clusters and sub divided in twelve clusters. The composition of clusters is given in Table 1 and Figure 1. The results indicate that a maximum number of diverse genotypes (29 genotypes) appeared in cluster I followed by cluster VII (6 genotypes) whereas clusters II, III, IV, V, VI, VIII, IX, X, XI and XII each with one genotype.

Intra and Inter cluster distances

The intra and inter cluster distances D^2 between all possible pairs of twelve clusters were computed and presented in Table 2. The clustering pattern showed that varieties from different source were clubbed into one group and also varieties of same source forming different cluster indicated no relationship between geographical and genetic divergence. The maximum inter cluster distance was observed between XII and II (D=15.94) followed by cluster XII and III (D=15.73), cluster XI and cluster X (D= 15.60), cluster XII and I (D=13.62), cluster VI and X (D=13.39), cluster XI and cluster I (D=13.30). The least inter cluster distance was observed between cluster X and II (D=3.40).

In the present study maximum intra cluster distance was observed for cluster VII (D^2=50.63) followed by cluster I (D^2=47.05) indicating more heterogeneous nature. The least intra cluster distance was observed for II, III, IV, V, VI, VIII, IX, X, XI and XII.

Cluster means for different characters

The mean performance of cluster values for all fourteen characters is presented in Table 3. The cluster mean observed for grain yield per plant was varied from 8.78(cluster IX) to 11.85 (cluster VI). The cluster IX (11.85) recorded the highest cluster mean for grain yield per plant followed by cluster IX (11.78) and cluster XII (11.29 cm). The lowest cluster mean for grain yield per plant was recorded by cluster IX (8.78). The genotypes of clusters IV (55.00 days) appeared to be early in flowering followed by cluster III, XI, XII (55.33), cluster II (55.67) and cluster IX (56.67) while the mean of cluster X (75.67) was highest indicating late flowering. Cluster mean for days to maturity revealed that cluster XII (91.33) was earlier to mature followed by cluster IX (92.00) and cluster IV (92.33), while cluster X (122.33) was late mature. The cluster VIII (37.87) recorded the maximum number of grains per spike followed by cluster IV (35.73). The cluster IX (46.52) recorded the higher mean for 1000 seed weight followed by cluster XII (45.84), cluster IX (4.5.40), while the cluster VIII (40.77) recorded minimum mean for 1000 seed weight. Therefore, inter-crossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the seed yield.

The genotypes in cluster XII and cluster II due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster XII and III and cluster XI and X. The lowest inter cluster distance was observed between cluster X and II followed by cluster IV and VI and cluster V and VIII showing these clusters were relatively less divergent and crossing between them cannot produce vigorous offspring (F1 progenies). Thus, genotypes included may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. The highest cluster mean for seed yield per plant (11.85) recorded by cluster VI appeared to be due to contribution of component characters *viz.*,days to heading (57.67), days to maturity (92.67), plant height (69.27), number of tillers per meter (91.67), number of grains per spike (25.47), 1000 seed weight (44.22), leaf area per plant (185.33), zinc content (28.73), iron content (38.23), protein content (12.43), hectolitre weight (80.28) and sedimentation value (40.53). High cluster means for similar characters were also reported by Mohanty *et al.* (2017) [8], Sapi *et al.* (2017) [10] and Patel (2018) [9]. The clustering pattern indicated that the geographical diversity need not necessarily be related to the genetic divergence, similar observations were noted by Kumar *et al*. (2013 a), Gurjar and Marker (2018) [3], Kalimullah *et al.*, (2012) [4, 5] and Patel (2018) [9].

Table 1: Distribution of genotypes evaluated for grain yield into different clusters of bread wheat

Cluster number	Number of genotypes included	Genotype (Cluster member)
I	29	27,40,16,22,20,23,29,39,26,17,19,37,13,35,34,8,30,7,9,24,33,45,41,18,11,25,1,12,28
II	1	21
III	1	42
IV	1	2
V	1	44
VI	1	16
VII	6	15,36,38,31,14,3
VII	1	32

IX	1	4
X	1	10
XI	1	43
XII	1	5

Table 2: Average intra and inter cluster D value of 45 genotypes of Bread wheat

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	6.86 (47.05)	8.89 (79.03)	9.75 (95.06)	8.38 (70.22)	8.61 (74.13)	8.84 (78.18)	9.96 (99.20)	9.38 (87.04	11.11 (123.43)	9.80 (96.04)	13.30 (176.89)	13.62 (190.99)
II		0.00	3.40 (11.56)	6.14 (37.69)	12.18 (148.35)	9.55 (91.20)	7.98 (60.52)	12.16 (147.86)	14.53 (211.12)	13.03 (169.78)	12.24 (149.81)	15.94 (254.08)
III			0.00	4.80 (23.04)	12.10 (146.41)	8.53 (72.76)	7.78 (60.22)	11.92 (142.08)	14.16 (200.50)	12.77 (163.07)	12.11 (146.65)	15.73 (247.53)
IV				0.00	8.14 (66.25)	5.79 (33.52)	6.19 (38.31)	8.75 (76.56)	10.18 (103.63)	10.56 (111.51)	10.01 (100.20)	12.31 (151.53)
V					0.00	7.64 (58.36)	9.54 (91.01)	5.42 (29.37)	5.58 (31.13)	8.21 (67.40)	10.93 (119.46)	7.77 (60.37)
VI						0.00	7.57 (53.30)	10.02 (100.40)	7.66 (58.67)	10.79 (116.42)	9.12 (83.17)	10.70 (114.49)
VII							7.12 (50.69)	10.30 (106.09)	10.97 (120.34)	11.70 (136.89)	9.05 (81.90)	12.36 (152.76)
VIII								0.00	8.93 (79.74)	5.59 (31.24)	13.99 (195.72)	11.47 (131.56)
IX									0.00	11.35 (128.82)	10.19 (103.83)	9.92 (98.40)
X										0.00	15.60 (243.36)	13.39 (179.29)
XI											0.00	11.83 (139.94)
XII												0.00

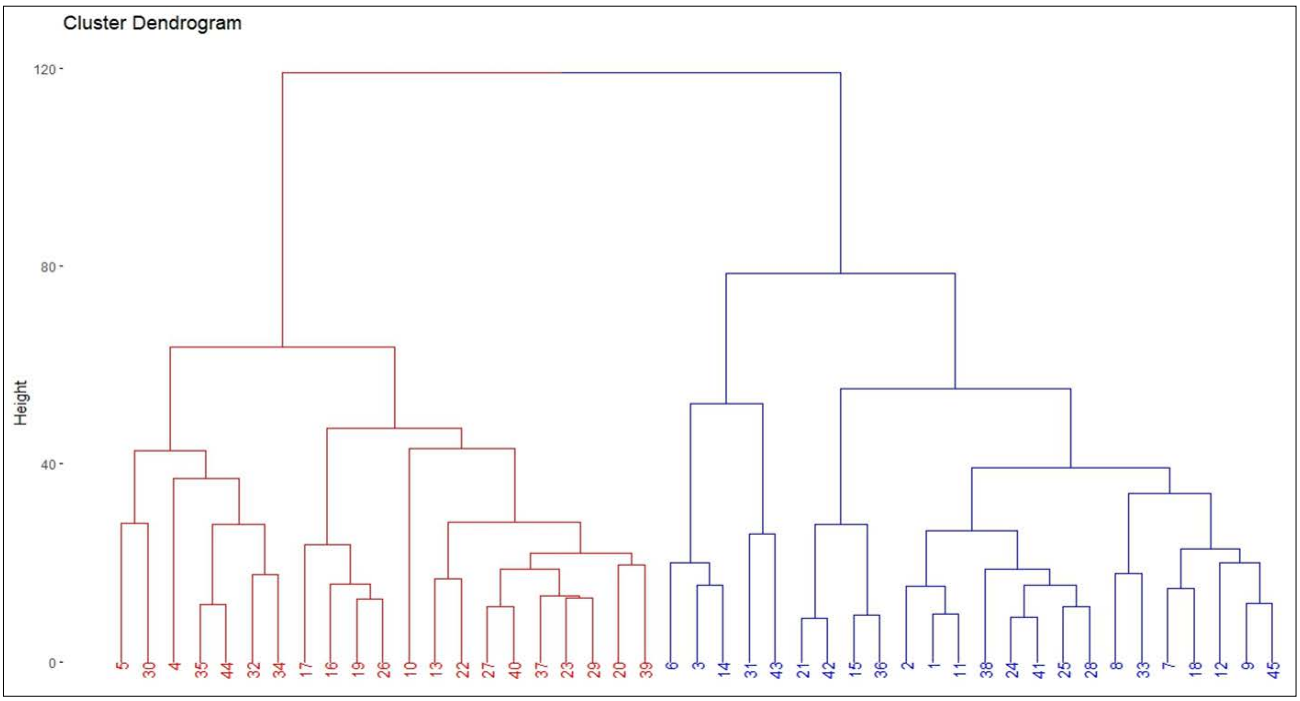

Fig 1: Tree diagram of 45 genotypes for 14 studied variables using hierarchical cluster analysis (ward's method and squared Euclidean distance)

Table 3: Average value of fourteen characters for each cluster

Characters														
Clusters	**Days to heading**	**Days to maturity**	**Plant height (cm)**	**Number of tillers per meter**	**Number of grain per spike**	**Grain yield per plant (g)**	**1000 seed weight (g)**	**Leaf area per plant**	**Zinc content (ppm)**	**Iron content (ppm)**	**Protein content (%)**	**Hectoliter Weight (kg/hl)**	**Sedimentation value (ml)**	**Harvest index (%)**
	58.56	96.01	68.87	67.80	28.69	9.32	41.68	153.21	30.03	36.16	12.29	79.96	41.22	48.78
	55.67	92.67	71.40	64.67	32.93	9.58	43.21	216.40	30.03	37.17	12.53	80.18	42.03	45.64
	55.33	94.67	74.40	69.67	34.73	10.19	42.95	221.65	28.80	39.53	12.97	80.02	43.43	52.64
	55.00	92.33	64.20	83.33	35.73	10.86	42.82	196.15	28.73	36.53	12.33	79.42	41.40	55.24
	58.33	97.00	64.93	93.67	33.67	10.98	43.48	129.80	31.03	37.70	11.90	80.24	39.03	54.20
	57.67	92.67	69.27	91.67	25.47	11.85	44.22	185.33	28.73	38.23	12.43	80.28	40.53	59.64
	60.94	97.11	70.89	95.33	31.17	9.68	41.10	198.88	30.76	35.21	11.98	79.98	40.09	50.89
	68.33	104.33	79.13	81.67	37.87	11.18	40.77	129.00	30.63	35.03	12.17	79.52	39.10	51.13
	56.67	92.00	72.87	111.67	28.67	11.78	45.40	133.53	26.67	32.93	12.23	80.14	38.57	56.19
	75.67	122.33	75.13	69.67	31.47	9.40	42.83	128.74	30.97	34.77	11.47	78.15	39.47	54.47
	55.33	94.00	58.60	123.67	28.40	8.78	46.62	202.71	27.83	41.30	11.60	78.21	36.80	50.62
	55.33	91.33	66.47	107.67	31.33	11.29	45.84	147.94	39.50	41.97	10.90	81.45	32.53	60.23
Mean	59.40	97.20	69.68	88.37	31.68	10.41	43.41	170.28	30.31	37.21	12.07	79.80	39.52	53.31

Conclusion

The results of D^2 statistics revealed wider genetic variability among the forty five genotypes which were grouped into twelve clusters. Moreover D^2 analysis corroborated the absence of relationship between geographic origin and genetic diversity, as genotypes from the same area scattered in different clusters and the genotypes of different area were grouped in the same clusters. Therefore, breeder must evaluate their material for genetic diversity and should not merely depend on their geographical diversity. The maximum inter cluster distance was observed between XII and II (D=15.94), thus genotypes included may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants.

References

1. Anonymous. Directorate of Economics and Statistics; c2019b. https://eands.dacnet.nic.in/
2. FAO. Food and Agriculture Organization of the United Nations online database; c2015 Accessed, 4th February. http:/www.fao.org/giews/
3. Gurjar D, Marker S. Evaluation of genetic divergence in wheat (*Triticum aestivum* L.) germplasm. Electronic Journal of Plant Breeding. 2018;9(1):361- 367.
4. Kalimullah SJ, Khan MI, Rahman, HU. Genetic variability, correlation and diversity studies in bread wheat (*Triticumaestivum* L.) germplasm. Journal of Animal and Plant Sciences. 2012;22(2):330-333.
5. Kalimullah SJ, Khan MI, Rahman H.U. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. J. Anim. and Plant Sci. 2012;22(2):330-333.
6. Kumar B, Singh CM, Jaiswal KK. Genetic variability association and diversity studies in bread wheat (*Triticum aestivum* L.). An International J. of Life Sci. 2013;(1):I43 I47
7. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Inst. Sci. 1936;2:49-55.
8. Mohanty S, Mukherjee S, Dash AP, Mandal AB. Genetic analysis for identification of terminal heat tolerant genotypes in wheat. Ind. J. Genet. 2017;77(1):160-162.
9. Patel NS. Selection criteria and genetic divergence of wheat (*Triticum aestivum* L.) under late and very late sown conditions. M.Sc. (Agri.) thesis submitted to Junagadh Agril. Uni, Junagadh; c2018.
10. Sapi S, Marker S, Bhattacharjee I. Evaluation of genetic divergence in bread wheat (*Triticum aestivum* L.) genotypes for yield parameters and heat tolerance traits. J. Pharmacognosy and Phytochem. 2017;6(4):253-257.