Plant Archives Vol. 25, Supplement 2, 2025 pp. 782-786 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-2.099

GENETIC DIVERGENCE ANALYSIS AND INSIGHTS OF DIVERSITY IN WHEAT

Dayanand Bana[1]*, S. D. Solanki[2], J. M. Patel[3], Sourabh Kumar[2] and H. N. Zala[2]
[1]Department of Plant Breeding and Genetics, Punjab Agricultural University,Ludhiana- 141004, Punjab, India
[2]Department of Genetics and Plant Breeding, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agriculture University, Sardarkrushinagar - 385506, Gujarat, India
[3]Wheat Research Station, Vijapur, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar – 385506
*Corresponding author E-mail: dayanandbana83@gmail.com

(Date of Receiving : 03-05-2025; Date of Acceptance : 10-07-2025)

ABSTRACT

During the rabi season of 2020-21, a study at the Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, investigated genetic diversity and stem rust resistance among 30 wheat genotypes. The trial was designed using a randomized block layout with four replications, evaluating 11 traits: grain yield per plant, days to heading, days to maturity, plant height, effective tillers per meter, grains per spike, spike length, 1000-grain weight, ear weight, biological yield per plant, and harvest index. Genetic divergence was analyzed using Mahalanobis' D^2 statistics and genotypes were grouped using the Tocher method. The analysis revealed that number of grains per spike contributed the most to genetic divergence, while days to heading and biological yield per plant contributed the least. Clustering showed Cluster-I with the highest number of genotypes (17), whereas Clusters-VI, VII, and VIII each contained only one genotype. Cluster-I exhibited the greatest intra-cluster distance (13.67), indicating significant genetic variation among its members. The largest inter-cluster distance was observed between Clusters-II and VIII (37.71) and smallest between Clusters-VI and VIII (17.06). Cluster-IV had the highest mean values for agronomic traits, including days to heading and spike length while Clusters-VIII and -II showed superior means for grain yield per plant and harvest index respectively. Genotypes with desirable traits from diverse clusters make use in future breeding programs to enhance wheat yield and physiological characteristics.

***Keywords*: Wheat, Diversity, Cluster distance, D^2 statistics.**

Introduction

Wheat (*Triticum aestivum* L.), a vital cereal grass from the *Poaceae* family and Triticum genus, stands as the world's leading cereal crop. Often hailed as the 'Cereal Monarch' due to its vast cultivation area, exceptional yield potential and significant role in global grain trade, wheat holds a unique place in agriculture. It serves as a primary source of nutrition and energy, forming the basis for diverse products such as bread, chapati, pasta, biscuits, and animal fodder. Globally, wheat is cultivated across 220.4 million hectares, yielding approximately 798.97 million tonnes annually. It supplies roughly 20% of the caloric intake for the global population FAO, (2023). In India, wheat spans 30.28 million hectares, producing 102.46 million tonnes DAC&FW (2022). Evolving lifestyles further challenge breeders to develop varieties with superior yield, high-quality seeds, and resilience against pests and environmental stresses Rana *et al.* (2013). However, like many plant species, wheat's genetic diversity is declining, reducing its adaptability and weakening traits due to natural selection and biological processes Allard (1996). Evaluating the scope and patterns of genetic variation in bread wheat is crucial for breeding programs and conserving genetic resources. Understanding genetic diversity enhances the potential for improving crop efficiency, which is vital for advancing breeding efforts and boosting food production Khodadadi *et al.* (2011). Greater genetic diversity increases opportunities for selecting and developing improved wheat varieties with desirable traits. Genetic diversity among genotypes does not solely depend on factors like geographic origin, release location, or ploidy level. Therefore, characterizing genotypes requires robust statistical approaches. Various methods, such as Mahalanobis' D²-statistics and hierarchical Euclidean cluster analysis, have been developed to evaluate genetic divergence by measuring similarity or dissimilarity based on the combined effect of key agronomic traits. Techniques like cluster analysis, principal component analysis (PCA), and factor analysis are effective for assessing genetic diversity, selecting parental lines, tracing crop evolutionary pathways, identifying centers of origin and diversity, and exploring genotype-environment interactions (Bhatt, 1970; Mohammadi and Prasanna, 2003). Accurate insights into the extent and nature of genetic divergence enable breeders to choose diverse parents for targeted hybridization Arunachalam, (1981). In self-pollinated crops, the success of yield improvement hinges on the magnitude and type of genetic variation available Joshi and Dhawan, (1966).

Material and Methods

In the rabi season of 2020-21, a trial was conducted at the Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, involving 30 wheat genotypes (Table 1). The experiment utilized a randomized block design with four replications. Each genotype was sown in a single-row plot, 3.0 meter long, with rows spaced 22.5 cm apart and plants within rows 10 cm apart. To reduce border effects, additional rows were planted around the plots. Recommended agronomic practices were followed to maintain a robust and competitive crop. Observations were recorded from five randomly selected competitive plants per genotype in each replication, covering 11 agro-morphological traits: days to heading, days to maturity, plant height (cm), effective tillers per meter, grains per spike, spike length (cm), 1000-grain weight (g), ear weight (g), biological yield per plant (g), harvest index (%), and grain yield per plant (g). Genetic divergence was analyzed using Mahalanobis' (1936) D² statistic, as outlined by Rao (1952), with genotypes clustered according to Tocher's method.

Result and Discussion

Using D²-statistics, 30 wheat genotypes were organized into eight clusters, ensuring that genotypes within each cluster exhibited lower D² values compared to those between clusters, reflecting closer genetic similarity within groups (Table 2). Cluster I contained the most genotypes (17), followed by clusters II and V (3 each) and cluster II and IV (2 each), while cluster VI, VII and had the fewest (1 each). Inter-cluster distances exceeded intra-cluster distances, indicating substantial genetic diversity among genotypes (Table 3). Inter-cluster distances ranged from 17.06 to 37.71, with the greatest distance between clusters II and VIII (37.71), suggesting significant genetic divergence. Conversely, the smallest inter-cluster distance was between clusters VI and VIII (17.06), indicating a closer genetic relationship that may limit breeding potential. Large inter-cluster distances highlight the potential for using genotypes from divergent clusters in hybridization programs to develop high-yielding wheat varieties, as they are likely to produce transgressive segregants. These findings are consistent with Vora *et al.* (2016), Arya *et al.* (2017), Pandey *et al.* (2017) and Ahmad *et al.* (2018). The highest intra-cluster distance was observed in cluster I (13.67), followed by clusters V (13.59), II (11.99), IV (11.58) and III (7.00) suggesting that genotypes within these clusters are more diverse and could yield valuable breeding material for achieving significant genetic gains, as supported by Ferdous *et al.* (2011) and Mustafa *et al.* (2019). In contrast, the smallest intra-cluster distances were found in clusters VI (0.00), VII (0.00), and VIII (0.00), indicating genetic uniformity within these groups, which may render selection less effective due to limited variation.

The mean values for 11 traits across clusters are summarized (Table 4), highlighting distinct performance among clusters. Cluster VII recorded the highest mean for days to days to maturity (109) and a notable spike length (9.90). Cluster IV excelled in days to maturity (108.99), plant height (96.29), 1000 grain weight (37.22) and had a highest spike length (10.81). Cluster III stood out for the maximum number of effective tillers per meter (90.99). Cluster VIII showed the highest biological yield per plant (16.39), grain yield per plant (8.21) and number of grains per spike (32.94). Cluster II led in ear weight (3.06) and harvest index (55.81). Cluster V exhibited high grain yield per plant (7.64) and number of effective tillers per meter (89.08). Cluster VI was distinguished solely by the high plant height (97.31). These findings align with prior research by Ferdous *et al.* (2011), Singh and upadhyay (2013), Kumar *et al.* (2013), Vora *et al.* (2016), Arya *et al.* (2017), Pandey *et al.* (2017), Ahmed *et al.* (2018) and Mustafa *et al.* (2019). These results shows that crosses between genotypes from different clusters with superior mean performance could enhance yield potential. Utilizing more divergent parents in hybridization may increase heterosis and generate greater genetic variability in segregating populations, facilitating the development of high-yielding wheat varieties.

Significant variation was observed across multiple traits among diverse wheat genotype clusters. The trait contributing most to genetic divergence was the number of grains per spike (23.67%), followed by spike length (21.83%), harvest index (17.70%), effective tillers per meter (15.17%), ear weight (14.71%), and 1000-grain weight (3.67%) (Table 5). These six traits accounted for 96.75% of the total genetic divergence, highlighting their importance. Selecting parental lines based on these traits could enhance genetic variation in wheat breeding programs. In contrast, days to maturity (2.29%), plant height (0.45%), and grain yield per plant contributed minimally (below 3%), while days to heading and biological yield per plant had negligible (zero) impact on divergence. The limited diversity in these traits, despite the diverse genotype group, suggests high consistency and potentially moderate to low heritability for these characteristics.

Based on the analysis of genetic divergence and cluster mean performance, crosses between genotypes from clusters I, II, and V are likely to yield maximum heterosis and valuable recombinants for wheat varietal improvement. Specifically, hybridizations involving cluster I genotypes (such as GW 322, GW 366, HD 2932 and HD 2864) with those from cluster V (including GW 451, GW 496 and VA 2019-37) are expected to produce high heterosis and generate novel recombinants with desirable agronomic traits.

Conclusion

The D² statistics analysis revealed significant genetic variation among 30 wheat genotypes, which were organized into eight clusters. The analysis indicated no correlation between geographic origin and genetic diversity, as genotypes from the same region were distributed across different clusters, while those from diverse areas grouped together. This suggests that breeders should assess genetic diversity directly rather than relying on geographical origins. Genotypes in Cluster VIII exhibited superior mean values for grains per spike, 1000-grain weight, biological yield per plant and grain yield per plant. Cluster IV genotypes showed elevated means for days to heading and spike length, while Cluster VII genotypes had high means for days to maturity. Cluster VI was notable for high plant height means, Cluster V for ear weight, and Clusters II and III for harvest index and effective tillers per meter, respectively. The greatest inter-cluster distance was observed between Clusters VII and II (D=37.71), followed by Clusters V and IV (D=37.08) and Clusters V and III (D=32.60). These genetically distant clusters offer potential for use in inter varietal hybridization programs to produce high-yielding recombinants through transgressive breeding.

Table 1 : List of genotypes

Sr. No.	Genotypes	Source	Sr. No.	Genotypes	Source
1	VA2019-02	SDAU, Vijapur, Gujarat	**16**	GW 366	SDAU, Vijapur, Gujarat
2	VA2019-03		**17**	GW 451	
3	VA2019-04		**18**	GW 496	
4	VA2019-17		**19**	GW 1339	
5	VA2019-18		**20**	HI 1544	
6	VA2019-19		**21**	HD 2932	
7	VA2019-34		**22**	HD 2864	
8	VA2019-35		**23**	LOK 1	
9	VA2019-36		**24**	MP 3288	
10	VA2019-37		**25**	DBW 110	
11	VA2016-22		**26**	GDW 1255	
12	VD2019-3		**27**	A-9-30-01	
13	VD2019-4		**28**	Agra Local	
14	VD2019-5		**29**	Lal Bahadur	
15	GW 322		**30**	A-206	

Table 2: Distribution of 30 genotypes of wheat into 8 clusters evaluated for grain yield

Cluster	Number of genotypes	Genotypes (Cluster member)
I	17	VA 2019-02. VA 2019-03, VA 2019-04, VA 2019-17, VA 2019-19, VA 2019-34, VA 2019-35, VD2019-3, VD2019-4, VD2019-5, GW 322, GW 366, GW 1339, HD 2932, HD 2864, LOK 1, LAL BAHADUR
II	3	VA 2019-18, VA 2019-36, A-9-30-01
III	2	VA 2016-22, A-206

IV	2	GDW-1255, AGRA LOCAL
V	3	VA 2019-37, GW-451, GW-496
VI	1	MP 3288
VII	1	DBW 110
VIII	1	HI 1544

Table 3 : Average intra and inter – cluster (D^2) value for thirty genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**186.93 (13.67)**	396.86 (19.92)	405.21 (20.12)	506.17 (22.49)	480.51 (21.92)	320.83 (17.91)	364.37 (19.08)	631.95 (25.13)
II		**143.88 11.99)**	857.71 (29.28)	541.57 (23.27)	930.91 (30.51)	650.52 (25.50)	515.23 (22.69)	**1422.30 (37.71)**
III			**49.08 (7.00)**	411.42 (20.28)	1062.78 (32.60)	377.86 (19.43)	666.48 (25.81)	614.09 (24.78)
IV				**134.21 (11.58)**	1375.54 (37.08)	349.84 (18.70)	321.95 (17.94)	920.17 (30.33)
V					**184.82 (13.59)**	719.21 (26.81)	657.27 (25.63)	621.65 (24.93)
VI						**0.00**	303.04 (17.40)	**291.09 (17.06)**
VII							**0.00**	536.10 (23.15)
VIII								**0.00**

(Note: - In bracket value of D and main values is of D^2 mention above table)

Table 4: Cluster mean value for 11 different characters in 30 genotypes of wheat

Cluster	DH	DM	PH	TIL/MTR	NGS	SL	GW	EW	BY	HI	GY
I	62.52	102.94	83.38	83.77	23.12	9.62	39.22	2.85	12.99	54.48	7.10
II	64.00	102.33	87.71	69.48	18.74	9.43	37.72	3.06	10.77	55.81	5.98
III	58.00	97.49	81.21	90.99	18.53	10.67	39.57	2.25	14.97	47.75	7.14
IV	71.50	108.99	96.29	64.50	20.38	10.81	37.22	2.34	14.36	47.30	6.79
V	56.33	98.00	76.61	89.08	29.78	8.49	41.11	3.53	13.74	55.49	7.64
VI	60.00	104.00	97.31	75.49	25.42	9.56	43.24	2.08	13.81	54.45	7.52
VII	70.00	109.00	96.91	64.00	27.25	9.90	37.38	3.18	15.65	45.66	7.15
VIII	59.00	100.00	93.21	84.25	32.94	10.33	43.54	2.55	16.39	50.07	8.21

Table 5: Contribution of various traits towards total genetic divergence

Sr. No.	Characters	Times ranked first	Contribution (%)
1.	Days to heading	0	0
2.	Days to maturity	10	2.29
3.	Plant height (cm)	2	0.45
4.	Number of effective tillers per meter	66	15.17
5.	Number of grains per spike	103	23.67
6.	Spike length (cm)	95	21.83
7.	1000 grain weight (g)	16	3.67
8.	Ear weight (g)	64	14.71
9.	Biological yield per plant (g)	0	0
10.	Harvest index (%)	77	17.70
11.	Grain yield per plant (g)	2	0.45

Acknowledgement

We are specially thanks to Wheat Research Station, Vijapur, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar for providing the experimental material, Agronomy Instructional Farm, sardarkrushinagar for provides resources, along with C P College of Agriculture for providing facilities for research trial.

References

Ahmad, T. Kumar, A. Pandey, D. and Prasad, B. (2018). Correlation and path coefficient analysis for yield and its attributing traits in bread wheat (*Triticum aestivum* L. em Thell). *Journal of Applied and Natural Science,* **10**, 1078-1078.

Allard, R. W. (1960). *Principles of Plant Breeding*. John Wiley and Sons, New York, p. 185.

Arunachalam, V. and Bandyopadhyay, A. (1989). On the method of classification using D square statistic and the importance of characters contributing to genetic divergence. *Indian Journal of Genetics and Plant Breeding,* **49**, 227-230.

Arya, V.K., Singh, J., Kumar, L., Kumar, R., Kumar, P. and Chand, P. (2017). Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Research,* **51**, 128-134.

Bhatt, G.M. (1970). Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self-pollinated crops. *Australian Journal of Agricultural Research,* 21, 1-7.

Food and Agricultural Organisation. QCL Crops and livestock products 2023. Available from, https,//www.fao.org/ faostat/ en/#data/QCL

Ferdous, M. Nath, U.K. and Islam, A. (2011). Genetic divergence and genetic gain in bread wheat through selection practices. *Journal of the Bangladesh Agricultural University* **9**, 1-4.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement in yield with special reference to self-fertilizing crops, 101-17.

Khodadadi, M., Fotokian, M.H. and Miransari, M. (2011). Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science*, **5**, 17-24.

Kumar, B., Singh, C.M. and Jaiswal, K.K. (2013). Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). *The Bioscan*, **8**, 143-147.

Mahalanobis, P. C. (1936). On the generalised distance in statistics. *Proceedings of the National Academy of Sciences, India* **2**, 49-55.

Mohammadi, S. A. and Prasanna, B. M. (2003). Analysis of genetic diversity in crop plants - salient statistical tools and considerations. *Crop Science,* **43**, 1235-1248.

Mustafa, S. G. Hossain, S. Sarker, M. M. Hossain, S. and Ansary, W. R. (2019). Character association and genetic divergence in spring wheat (*Triticum aestivum* L.). *Journal of Phytochemistry and Biochemistry* **3**, 2-2.

Pandey, M. K., Bind, H. N., Kumar, S. and Singh, B. N. (2017). Genetic divergence in wheat (*Triticum aestivum* L. Thell.) under saline sodic condition. *International Journal of Current Microbiology and Applied Sciences,* **6**, 181-189.

Rana, R. M., Rehman, S. U., Ahmed, J. and Bilal, M. (2013). A comprehensive overview of recent advances in drought stress tolerance research in wheat (*Triticum aestivum* L.). *Asian Journal of Agriculture and Biology,* **1**, 29-37.

Rao, C. R. (1952). *Advanced Statistical Methods in Biometrical Research*, Edition I. John Wiley and Sons, New York.

Singh, B. and Upadhyay, P. K. (2013). Genetic divergence analysis in wheat (Triticum aestivum L.). *International Journal of Plant Sciences (Muzaffarnagar),* **8**, 297-299.

The Department of Agriculture and Farmers Welfare. Agriculture statistics at a glance 2022. Available from, https,//agriwelfare.gov.in/en/Dept.

Vora, Z. N., Patel, J. B. and Pansuriya, A. G. (2017). Genetic divergence analysis in bread wheat (*Triticum aestivum* L.). *Research in Environment and Life Sciences* **10**, 291-294.