



Genetic Divergence Analysis of Wheat (*Triticum aestivum* L.) Genotypes

Jay Singh^{a++}, C.L. Maurya^{a#}, Rishabh Gupta^{b+++*},
Sunil Kumar^{c†}, Shivam Chaturvedi^{a++},
Ajay Pratap Singh^{a++} and Dhruvendra Singh Sachan^{d++}

^a Department of Seed Science and Technology, Chandra Shekhar Azad University, Agriculture and Technology, Kanpur, Uttar Pradesh, 208002, India.

^b Department of Genetics and Plant Breeding, Acharya Narendra Deva University, Agriculture and Technology, Kumarganj Ayodhya, Uttar Pradesh, 208002, India.

^c Uttar Pradesh State Seed Certification Agency, Lucknow, Uttar Pradesh, India.

^d Department of Agronomy, Chandra Shekhar Azad University, Agriculture and Technology, Kanpur, Uttar Pradesh, 208002, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

A laboratory experiment was carried out with 30 indigenous genotypes of bread wheat along with three checks in a complete randomized design for divergence analysis. The trial was conducted at Seed Technology laboratory of Acharya Narendra Deva University of Agriculture and Technology Kumarganj, Ayodhya during 2020-21. The observations were recorded on thirteen-character Test weight (1000-grain weight), seed width (mm), seed length (mm), shoot length, root length, seedling

⁺⁺ Research Scholar;

[#] Professor and Head;

[†] Scientist Assistant;

*Corresponding author: E-mail: rishabhgupta5575@gmail.com;

length, seedling dry weight, germination (%), first count, final count, vigour index-I, vigour index-II. The 30 genotypes grouped into 5 clusters resulted in cluster I and V emerging with highest number of entries as both were constituted by 9 entries followed by Cluster III having 6 genotypes and cluster II and VI having 4 genotypes respectively. The maximum intra cluster distance was estimated in the case of Cluster II (2.630) followed by cluster I (2.618), Cluster III (2.545), cluster IV (2.512), and cluster V (2.148). The highest inter-cluster distance was observed between clusters III and IV (6.062) Followed by clusters III and V (4.632), II and IV (4.489), cluster II and V (4.304). The minimum inter cluster was observed between II and III (3.317) followed by cluster IV and V (3.337) and cluster I and V (3.404). The cluster mean of 13 different characters for most of the character's highest cluster mean was observed in clusters IV and V and lowest cluster mean observed in cluster III and II.

Keywords: Character; divergence; seedling; vigour.

1. INTRODUCTION

Wheat is a cereal crop. It is predominantly present in the world; it provides food for people. In India mostly found in Haryana, Punjab, Madhya Pradesh, Uttar Pradesh, Rajasthan, Chattisgarh etc. Globally, wheat (*Triticum spp.*) is grown in about 223.04 million hectares holding the position of highest estate among all crops with annual production hovering around 784.91 million tons. In India, it's grown in an area of 31.40 million hectares with a production of 110.55 million metric tons and output of 3.52 metric tons/hectares correspondingly In India uppermost area under wheat cultivation 9.54 million hectares [1]. In India Uttar Pradesh has production approximately 32.75 million tonnes and productivity 3432 kg/hectare. The highest productivity 5183 kg/hectare in Punjab and the lowest productivity 1666 kg/hectare in Maharashtra [2]. The globe chief wheat producing countries are China, India, USA, Russia, Australia, Germany, France, Pakistan, Argentina, Turkey, Iran and Italy. With the increasing world population, demand of wheat crop is projected to extend by 60% by 2050, if this increment influences up to 9.7 billion obviously by the United Nations [3]. Constant increase in agriculture production and productivity essentially requires continuous expansion of recent and improved types of crops and efficient scheme of production and offer of seed to farmers. Seed quality within the sum of these qualities which differentiate the seed from the grain. The important seed quality attributes are genetic purity, physical purity, germination, moisture, well-being and vigour. In additionally to above quality seed should be of unchanging size and will own good. Germination capacity of superiority seed portion should be high for gaining the specified crop supernumerary this sector. Using seed of low germination will diminish the sphere establishment or stand and

thus the yields will be dropped. Seed germination is rested low with a range of things which is compulsory to the seed during its formation, maturing, ripening, like infection with the paste and pathogen. Sub ideal condition of nutrients and water and precocious rains or frost at the maturity stage. In additionally, post-harvest operations and management of the seed lots during marketing or supply are answerable for affecting the seed quality.

2. MATERIALS AND METHODS

The experiment was carried out during 2020-21 at Acharya Narendra Deva University of Agriculture and Technology Kumarganj Ayodhya (U.P.) Laboratory Department of Seed Science and Technology. The experiment was conducted to evaluate the 30 germplasm with three checks (PBW-343, NW-1014, NW-5054) in a completely randomized design. The genotypes exhibited wide spectrum variation for various seed quality and morphological characters. The data was recorded on 10 randomly selected seeds and seedlings for thirteen characters viz. 1000-seed weight (g), Seed length (mm), Seed breadth (mm), Shoot length (cm), Root length (cm), Seedling length (cm), Seedling Dry Weight (mg), Speed of germination, Germination (%), Vigour index-I, Vigour Index-II, First count (%), Final count (%). Data recorded on the above characters were subjected to estimate the Genetic divergence analysis.

1. Non-hierarchical Euclidean cluster analysis (Genetic divergence analysis) by following Beale,[4] and Spark, [5]; Mahalanobis [6] D^2 statistic.

3. RESULTS AND DISCUSSION

The non-hierarchical Euclidean cluster analysis was labouring to study the genetic divergence existing among 30 mustard genotype collections

based on 13 seed-quality characters. The pseudo-F-test revealed that 5 cluster arrangements were most appropriate for grouping the 30 genotypes.

The cluster mean for 13 characters is subjected in Table 1. The maximum cluster mean for 1000 Seed Weight(g) was recorded for cluster II (43.29) the lowest cluster mean was recorded in the case of cluster I (38.97) while the remaining showed a moderate mean for 1000 Seed Weight (g). The highest cluster mean for Seed Length (mm) was observed in the case of cluster III (6.75) followed by cluster V (6.55) and cluster IV (6.46), and the lowest cluster mean for Seed Length (mm) was recorded in cluster I (5.82). The cluster III (3.89) was observed as the highest cluster mean for Seed Width (mm) and the lowest cluster mean was recorded in cluster I (2.97). The rest of the cluster was recorded as a medium cluster mean for Seed Width (mm).

The maximum cluster mean for Shoot Length (cm) was recorded for cluster III (11.58) the lowest cluster mean was recorded in the case of cluster IV (8.12) while the remaining showed a moderate mean for Shoot Length (cm). The maximum cluster mean for Root Length (cm) was recorded for cluster III (15.05) the lowest cluster mean was recorded in the case of cluster IV (11.08) while the remaining showed a moderate mean for Root Length (cm). The maximum cluster mean for Seedling Length (cm) was recorded for cluster III (26.83) the lowest cluster mean was recorded in the case of cluster IV (19.40) while the remaining showed a moderate mean for Seedling Length (cm). The maximum cluster mean for Speed of germination was recorded for cluster II (20.88) the lowest cluster mean was recorded in case of cluster V (18.16) while remaining showed moderate mean for Speed of germination. The maximum cluster mean for Seedling Dry Weight (mg) was recorded for cluster II (154.75) the lowest cluster mean was recorded in case of cluster IV (138.20) while remaining showed moderate mean for Seedling Dry Weight (mg). The maximum cluster mean for First Count was recorded for cluster III (83.00) the lowest cluster mean was recorded in case of cluster V (78.89) while remaining showed moderate mean for First Count. The maximum cluster mean for Final Count was recorded for cluster II (91.50) the lowest cluster mean was recorded in case of cluster V (85.11) while remaining showed moderate mean for Final Count. The maximum cluster mean for Germination Percentage was recorded for cluster

II (92.19) the lowest cluster mean was recorded in case of cluster V (86.41) while remaining showed moderate mean for Germination Percentage. The maximum cluster mean for Vigour Index - 1st was recorded for cluster III (2557.9) the lowest cluster mean was recorded in case of cluster IV (1663.8) while remaining showed moderate mean for Vigour Index - 1st. The maximum cluster mean for Vigour Index - 2nd was recorded for cluster III (13418.7) the lowest cluster mean was recorded in case of cluster IV (11824.4) while remaining showed moderate mean for Vigour Index - 2nd. Cluster I and V emerged with highest number of entries as both were constituted by 9 entries followed by Cluster III having 6 genotypes, cluster II and VI having 4 genotypes respectively are presented in Table 3.

The estimate Inter and intra cluster distance for 5 cluster are presented in Table 2. The highest inter cluster distance was observed between the cluster III and IV (6.062) Followed by cluster III and V (4.632), II and IV (4.489), cluster II and V (4.304). The minimum inter cluster was observed between II and III (3.317) followed by cluster IV and V (3.337) and cluster I and V (3.404). The maximum intra cluster distance was estimated in case of Cluster II (2.630) followed by cluster I (2.618), Cluster III (2.545), cluster IV (2.512), cluster V (2.148). The result obtained under the present investigation following earlier reports- Examined nineteen advanced lines from the Semi-Arid Wheat Yield Trial (SAWYT) in addition to a locally grown cultivar (NIA-Amber), which was obtained from the International Maize and Wheat Improvement Centre (CIMMYT), Mexico, and was used as a control. The 17 genotypes were divided into two main groups (Cluster I and Cluster II) by the cluster analysis, however, genotype V1 stayed apart from the main clusters. In comparison to the other genotypes, the genotypes V6 and V19 produced the largest yields, and they grouped into a distinct clade reported by Arain et al., [7]. The results showed that non-hierarchical Euclidean cluster analysis was used to arrange 100 indigenous lines and 4 check types of wheat into eleven different groups. Cluster-VI had the greatest intra-cluster distance, followed by cluster-XI. However, cluster VII was found to have the lowest intra-cluster distance, followed by cluster II. Cluster-III and Cluster-XI had the second-highest inter-cluster distance, behind Cluster-IV and Cluster-XI. Cluster I and II had the smallest inter-cluster distance, followed by cluster VII and cluster IX reported by Singh et al., [8]. Using D2-Statistics,

Table 1. Cluster mean

Characters		1000 Seed Weight (g)	Seed Length (mm)	Seed Width (mm)	Shoot Length (cm)	Root Length (cm)	Seedling Length (cm)	Speed of germination	Seedling Dry Weight (mg)	First Count	Final Count	Germination Percentage	Vigour Index - 1st	Vigour Index - 2nd
I	Mean	38.97	5.82	2.97	10.21	14.99	25.41	19.74	139.67	81.33	87.56	88.91	2204.6	12116.0
	± SE	4.51	0.16	0.40	1.07	1.22	1.51	0.87	8.66	3.61	2.46	1.34	142.0	792.5
II	Mean	43.29	6.45	3.14	9.10	13.43	22.80	20.88	154.75	82.25	91.50	92.19	2087.4	13405.8
	± SE	0.86	0.46	0.40	0.87	1.46	1.27	1.34	12.01	3.59	2.08	2.14	147.1	1213.6
III	Mean	40.55	6.75	3.89	11.58	15.05	26.83	20.86	147.50	83.00	91.00	91.57	2557.9	13418.7
	± SE	2.77	0.51	0.18	0.93	1.01	1.65	0.76	5.96	3.10	2.10	2.11	532.6	518.7
IV	Mean	39.99	6.46	3.22	8.12	11.08	19.40	19.32	138.20	80.20	86.60	86.98	1663.8	11824.4
	± SE	4.68	0.55	0.43	1.49	1.07	1.57	0.69	9.50	3.11	0.89	0.85	132.2	607.8
V	Mean	39.01	6.55	3.82	9.13	13.93	23.31	18.16	151.11	78.89	85.11	86.41	1961.7	12726.7
	± SE	2.03	0.51	0.35	1.16	1.21	0.95	0.74	5.84	3.52	1.76	0.86	75.3	563.4

Table 2. Inter and intra-distances

Clusters	I	II	III	IV	V
I	2.618				
II	3.708	2.630			
III	3.763	3.317	2.545		
IV	4.071	4.489	6.062	2.512	
V	3.404	4.304	4.632	3.337	2.183

Table 3. Number of genotypes in each cluster

Clusters	No of genotypes	Genotypes
I	9	2,3,6,7,8,16,20,22,30
II	4	9,10,14,28
III	6	19,21,23,26,32,33
IV	4	15,17,24,29
V	9	4,5,11,12,13,18,25,27,31

fifteen genotypes were divided into five groups. The largest inter-cluster distance was found between clusters II and V, then II and III. This indicates that the genotypes that comprise these clusters have a high level of genetic diversity. Based on divergence and cluster mean, it may be hypothesised in a varietal improvement project that crosses between genotypes in clusters V, II, and III would result in desirable recombinants. Thus, crosses between the genetically diverse genotypes of cluster II, which includes genotypes CG-1707, CG-611, CG-1907, CG-1909, and CG-1043, and cluster V, which includes genotypes like CG1906, CG-1926, and Cluster III, CG-1931, are expected to show high heterosis as well as likely result in new recombinants with desired traits, as reported by Lakra et al. [9].

It is advised to try crossing the genotypes from cluster XII with cluster X genotypes based on the highest genetic distance, since this might result in the creation of a wide range of beneficial genetic diversity for yield increase in bread wheat, as described by Vora and Yusufzai [10]. The highest intra-cluster distance between the various genotypes was shown by cluster 2 in the divergence study, followed by cluster 1. Cluster 2 and 3 had the greatest inter-cluster distance, followed by cluster 2 and 7, while cluster 5 and 6 had the smallest inter-cluster distance, followed by cluster 1 and 3. According to the findings, varied genotypes from clusters 2 and 3 may be chosen to get the greatest number of transgressive recombinants from segregating generations to increase wheat crop reported by Patil et al. [11]. Five unique clusters that did not overlap were formed from the grouping of genotypes. With the greatest number of 8 genotypes, Cluster (II) was identified. Cluster (III) and cluster (V) had the most general inter-cluster distance (566.18), whereas cluster (IV) had the greatest intra-cluster distance (360.80). Therefore, crossing genotypes from cluster pairings that are separated by the previously described extremely large inter-cluster distances may produce the greatest amount of hybrid vigour and the greatest number of useful segregates found by Dvivedi et al. [12].

4. CONCLUSION

In conclusion, the overall results suggest that some of the data collected here will help select and improve the dominant genotype of wheat. The maximum intra-cluster distance was estimated in the case of cluster II (2.630)

followed by cluster I (2.618), Cluster III (2.545), cluster IV (2.512), and cluster V (2.148). The highest inter-cluster distance was observed between clusters III and IV (6.062) Followed by clusters III and V (4.632), II and IV (4.489), and clusters II and V (4.304).

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Anonymous, World agriculture production. United state department of agriculture, WAP. 2024;1-24.
2. Anonymous, Project directors report, ICAR-IIWBR, Karnal Haryana. 2020;1-3.
3. Anonymous, World population prospect report, United Nations; 2015.
4. Beale EML., Euclidean cluster analysis. A paper contributed to the 37th session of the International Statistical Institute; 1969.
5. Spark DN., Euclidean cluster analysis. Algorithm. As. 58. Appl. Stats. 1973;22: 126-130.
6. Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Ins. Sci. India. 1936;2(1):49-55.
7. Arain SM, Sial MA, Jamali KD, Laghari KA. Grain yield performance, correlation, and cluster analysis in elite bread wheat (*Triticum aestivum* L.) lines. Acta Agrobot. 2018;71(4): 1747. Available: <https://doi.org/10.5586/aa.1747>.
8. Singh T, Singh V, Singh KP, Verma OP, Mishra S, Srivastava A, Ahmad, R. D2 analysis in certain promising genotypes of wheat (*Triticum aestivum* L. em. Thell). J. Pharm. And Phyto. 2017;6(5):2714-2717.
9. Lakra A, Ekka RE, Sinha SK, Tigga K, Dinesh Thakur D. Genetic diversity analysis in wheat (*Triticum aestivum* L.) Journal of Pharmacognosy and Phytochemistry. 2020;9(6):117-119.
10. Vora Z, Yusufzai S, Genetic divergence analysis in bread wheat (*Triticum aestivum* L.)Life Sciences and Space Research. 2019;10(3):291-294.

11. Patil P, Shrivastav SP, Patil K, Landge R, Gurjar D., Genetic Variability, Heritability, Genetic Advance and Divergence Analysis in Wheat (*Triticum aestivum* L.) Indian Journal of Agricultural Research. 2022;A-6036:1-6.
12. Dvivedi RS, Singh B, Pathak VN, Verma SP, Panday KK. Genetic variability, character association and component analysis in wheat. Journal of Agri Search. 2023;10(3).

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