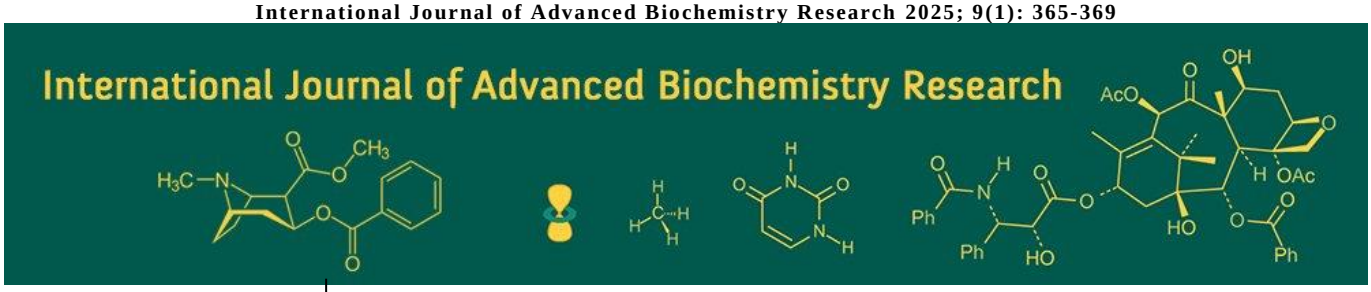

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; 9(1): 365-369
www.biochemjournal.com
Received: 18-10-2024
Accepted: 24-11-2024

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Deciphering genetic diversity and variability in wheat (*Triticum aestivum* L.) for sustainable crop improvement

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DOI: https://doi.org/10.33545/26174693.2025.v9.i1e.3511

Abstract
This study was conducted at the N.E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, India, during the rabi seasons of 2022, to assess genetic divergence and variability. A total of 30 genotypes (27 entries and 3 checks) were evaluated for thirteen traits. Analysis revealed significant contributions of different traits like flag leaf area and spike length to genetic diversity. For all the traits, analysis of variance indicated substantial genetic variability among genotypes. Cluster analysis grouped the genotypes into 4 clusters for 2020. Among different clusters, Cluster I included the maximum number of genotypes, with 27 genotypes grouped together, followed by Cluster II, Cluster III and Cluster IV that contains single genotype each, respectively. Maximum genetic divergence was observed between Clusters I and III (1842.13). Based on inter-cluster distances, cluster mean values, and per se performance, several promising genotypes were identified for improving yield, such as GW 1339, IC 296729, and HI 1619. WAPD 1519 and GW 527 found to be in different clusters in both the environment hence it validates that the genotypes are highly diverse and can be used as a donor in a hybridization programme. Genotypes that are having the higher mean value as well as lying in different clusters and are superior over the check are also one of the important donors for the yield improvement.

Keywords: Wheat, genetic diversity, cluster, variability

Introduction
Wheat (*Triticum aestivum* L. em. Thell) is one of the most important cereal crops of the world both in terms of area and production. Wheat belongs to family Poaceae, the largest family within the monocotyledonous plants. It is allohexaploid (2n = 6x = 42) with three genetically related genomes A, B, and D. A major factor in the country becoming a food surplus nation was the green revolution symbolized by wheat cultivation. Wheat is a self-pollinating crop that belongs to the Poaceae family. Since repetitive DNA sequences make up more than 80% of the bread wheat genome, the plant's enormous genome is the product of extensive duplications and polyploidy (Smith and Flavell, 1976) [5]. Twenty-five times larger than the average rice chromosome, the wheat chromosome is approximately 810 MB in size. The phenotype of wheat plants is regulated by about 30,000 genes, according to recent studies.

Across the world, wheat ranks first in terms of area (222.14 Mha), second in terms of production (779.3 Mmt), and yields an average of 35.1 q/ha. Leading wheat-producing countries include China, India, USA, France, Russia, Canada, Pakistan, and Australia. After China, India is the world's second-largest producer of wheat. In India, wheat is ranked second among staple food crops, right after rice. During (2023-24) a total of 30.54 million hectares area planted to wheat, with an average national productivity of 3484 kg per hectare and a production of 106.84 million metric tons. States like Uttar Pradesh (34.16 million tons), Madhya Pradesh (22.42 million tons), Punjab (14.46 million tons), Haryana (10.62 million tons), Rajasthan (9.19 million tons), and Bihar (5.60 million tons) are significant producers of wheat in India (ICAR-IIWBR, 2022) [6].

Genetic diversity forms the backbone of any breeding program, providing the variability needed to develop high-performing genotypes capable of withstanding various biotic and abiotic stresses.

A broader genetic base ensures the flexibility to respond to emerging challenges such as climate change, pest outbreaks, and soil degradation.

Materials and Methods

The present investigation was conducted during the rabi seasons of 2020-21at the N.E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand. The experimental material consisted of 30 wheat genotypes, provided by G.B. Pant University of Agriculture and Technology, Pantnagar, along with three commercial check varieties (UP 2855, UP 2844 and DBW 187) (Table 3). These genotypes represent a broad genetic base and were evaluated for their performance across multiple traits to identify promising lines for future breeding programs. The experiment was conducted using a Randomized Block Design (RBD) with three replications in which each replication contains 30 genotypes with each genotype planted in 3 meter long 4 row plots. The row to row spacing was kept 20cm apart. Observations were made on five randomly selected plants per genotype for the following traits: flag leaf area (cm^2), plant height (cm), spike length (cm), peduncle length (cm), number of spikelets per spike, number of grains per spike, thousand grain weight (g), harvest index (%), days to heading, days to maturity, number of effective tillers per meter, biological yield (g) and grain yield (g). The replication-wise mean values of different entries were subjected to Randomized Block Design analysis of variance. Both genotypic and phenotypic coefficients of variability was computed as per the method suggested by Burton and Devane (1953) [3]. Genetic advance over mean was calculated by the following formula as suggested by Johnson, Robinson and Comstock (1955) [7]. Heritability in broad sense was estimated as per Allard (1960) [1]. Genetic divergence between 30 wheat genotypes was calculated by analysing the data of thirteen characters through D^2 statistics (Mahalanobis, 1936) [9]. Genotypes were classified into various clusters by using Tocher's methods (Rao, 1952) [11]. Singh and Chaudhary (1977) [13] gave the formula for average intra cluster and inter-cluster distance.

Results and Discussion

Genetic Variability

The analysis of variance (ANOVA) for different traits under study revealed highly significant mean sum of squares for all traits viz., days to heading, days to maturity, number of effective tillers per meter, flag leaf area, plant height, peduncle length, spike length, thousand grain weight, biological yield, grain yield and harvest index and were presented in Table: 1.

Table 1: ANOVA for RBD using 30 wheat genotypes

	Mean sum of square		
	Replication	**Genotype**	**Error**
Degree of freedom	2.00	29.00	58.00
Days to heading	3.70	5.07**	0.67
Days to maturity	1.41	16.38**	2.16
Number of effective tillers per meter	128.41	146.18**	33.84
Flag leaf area (cm^2)	16.34	181.76**	8.20
Plant height (cm)	41.64	285.92**	41.59
Peduncle length (cm)	34.90	61.18**	6.09
Spike length (cm)	0.30	6.43**	0.60
Thousand grain weight (g)	56.36	53.61**	8.42
Biological yield (g)	360750.00	1272216.90**	200477.59
Grain yield (g)	40982.34	85723.60**	17179.06
Harvest index (%)	52.70	154.22**	18.56

Estimation of genetic variability, heritability (h2) and genetic advance

Phenotypic coefficient of variation ranged from moderate to high for most of the characters with highest for harvest index (26.32%) followed by biological yield (22.18%) and minimum for days to heading (1.68%) followed by days to maturity (2.05%). Genotypic coefficient of variation ranged from moderate to high for most of the characters with highest for harvest index (22.16%) followed by flag leaf area (20.32%) and minimum for days to heading (1.39%) followed by days to maturity (1.70%). Environmental coefficient of variation ranged from low to moderate for most of the characters with highest for harvest index (14.20%) followed by biological yield (13.29%) and minimum for days to heading (0.94%) followed by days to maturity (1.14%). Results of the study were in agreement with the reports of Singh *et al.* (2020) [12] and Naveen *et al.* (2023) [10].

Heritability represents the extent of variation in a trait that can be transmitted from one generation to the next. It serves as a key tool in distinguishing whether the observed phenotypic differences among individuals arise from genetic factors or environmental influences (Comstock and Robinson, 1955) [7].

The critical estimate of the results revealed that high heritability coupled with high genetic advance as per cent of mean was found for the flag leaf area H^2 (87.6%) and GAM (39.17%) followed by harvest index H^2(70.9%) and GAM (38.44%). Results showed that there are characters which have high heritability with high genetic advance as per cent of mean, which indicated that there is an additive type of gene action whereas characters present showed high heritability and low genetic advance as per cent of mean have the dominant type of gene action. Selection for the characters with additive type of gene action will be helpful as the additive type of gene action is heritable and fixable.

Table 2: PCV, GCV, ECV, heritability, genetic advance and genetic advance as per cent of mean for different characters under study in wheat.

S. No.	Character	PCV (%)	GCV (%)	ECV (%)	h^2 (b) (%)	GA (%)	GA as % of mean
1	Days to Heading	1.685	1.398	0.942	68.79	2.069	2.388
2	Days to Maturity	2.052	1.701	1.148	68.7	3.718	2.904
3	Effective tillers per meter	7.681	5.567	5.292	52.5	9.137	8.312
4	Flag leaf area (cm^2)	21.714	20.322	7.650	87.6	14.664	39.179
5	Plant height (cm)	11.904	9.686	6.921	66.2	15.126	16.234
6	Peduncle length (cm)	14.747	12.779	7.360	75.1	7.649	22.811
7	Spike length (cm)	14.902	13.036	7.220	76.5	2.512	23.491
8	Thousand grain weight (g)	14.266	11.425	8.543	64.1	6.403	18.849
9	Biological yield (g)	22.180	17.752	13.298	64.1	985.429	29.267
10	Grain yield (g)	20.239	15.291	13.259	57.1	235.256	23.798
11	Harvest index (%)	26.322	22.163	14.200	70.9	11.664	38.442

Table 3: List of genotypes

SI.	Genotype
1	AKAW 4901
2	DBW 252
3	HI 1619
4	HS 645
5	GW 1339
6	DM 6
7	DBW 221
8	TAW 186
9	GW 322
10	HI 1634
11	UASNG 326
12	WH 730
13	RWP 2014-2018
14	WAPD 1519
15	DM 7
16	UAS 462
17	GW 492
18	DBW 107
19	GW 527
20	MACS 4059
21	HI 1544
22	IC- 296729
23	DBW 278
24	PBW 777
25	IC- 529962
26	DBW 246
27	HS 661

Genetic Divergence

The study assessed genetic divergence among 30 wheat genotypes, including 3 checks, using Hierarchical Cluster Analysis (HCA) based on Torcher's method. The results reveal a substantial genetic diversity, vital for improving yield and other agronomic traits in wheat.

Cluster Formation

In 2020, On the bases of diversity analysis 30 genotypes of wheat were clustered into 4 different clusters using Torcher's method (Rao, 1952) [11]. Genotypes distribution among different clusters is presented in the Table 4 and dendrogram (visual presentation) in fig 1. Among different clusters, Cluster I included the maximum number of genotypes, with 27 genotypes grouped together, followed by Cluster II, Cluster III and Cluster IV that contains single genotype each, respectively.

Table 4: Cluster composition of thirty wheat genotypes

Cluster	Number of genotypes	Name of the genotypes
I	27	WH 730, RWP 2014-18, DBW 107, DBW 278, DBW 252, DBW 187, GW 492, UP 2855, PBW 777, DBW 246, UASNG 326, HI 1619, DM 6, DM 7, GW 1339, GW 322, UAS 462, AKAW 4901, UP 2844, HS 645, TAW 186, HI 1634, HI 1544, IC 296729, IC 529962, HS 661, DBW 221
II	1	WAPD 1519
III	1	GW 527
IV	1	MACS 4059

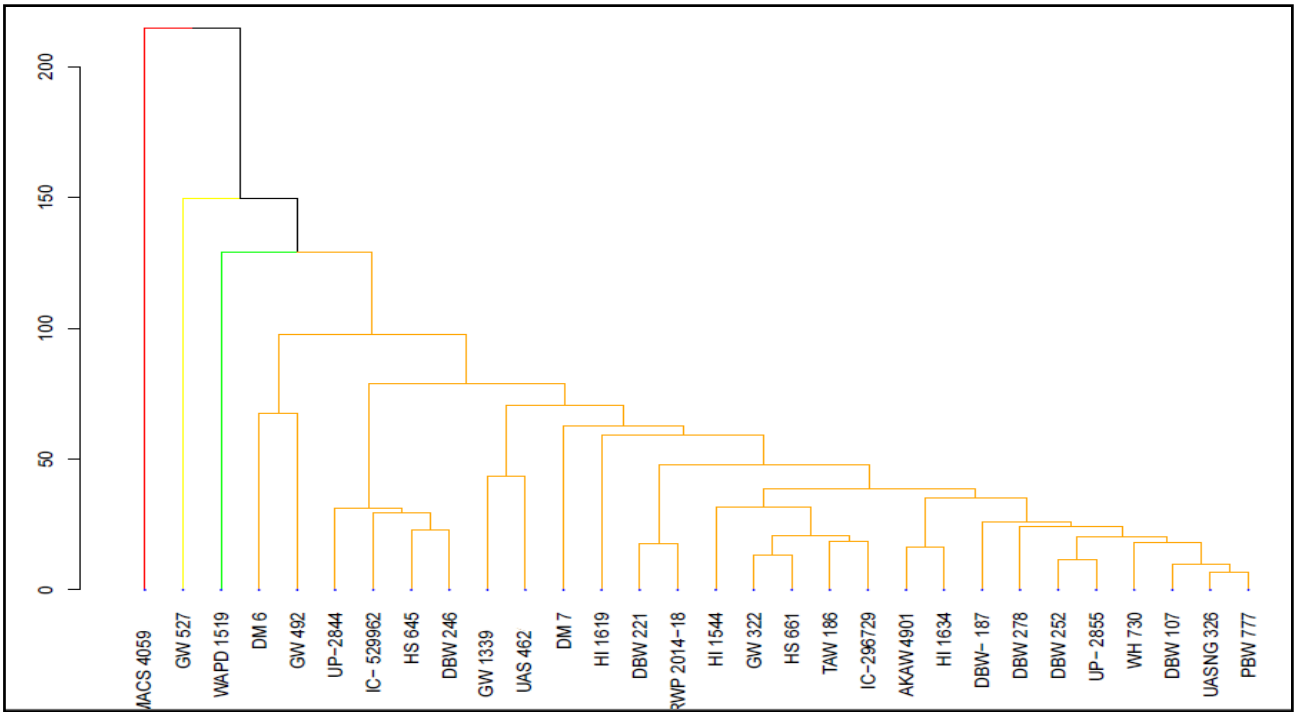

Fig 1: Dendrogram showing different clusters obtained by using Tocher's method of classification

This distribution indicates that the majority of genotypes exhibit genetic similarity, especially in the larger clusters. However, the presence of smaller clusters shows sufficient genetic divergence, essential for enhancing heterosis in future breeding programs.

Intra- and Inter-Cluster Distances

Cluster numbers indicate the groups into which genotypes are categorized. The extent of diversification between clusters is measured by the distance separating them. A greater distance between clusters corresponds to higher genetic divergence, whereas a smaller distance indicates lower divergence. Genotypes within the same cluster are more closely related to each other compared to those belonging to different clusters. Inter and Intra cluster distance for different clusters is presented in table 5.

Table 5: Intra cluster (diagonal) and inter-cluster distances for four clusters

	C1	C2	C3	C4
C1	623.399	1392.48	1842.13	1328
C2		0	587.483	276.341
C3			0	520.915
C4				0

- For Pantnagar data analysis the highest intra cluster distance was found for the Cluster I (623.399. Whereas, the lowest intra-cluster distance was observed for Clusters II, III and IV (0.00).
- The highest inter-cluster distance was found for the Cluster I and III (1842.13) followed by cluster I and II (1392.48). Whereas, the lowest inter- cluster distance was observed for the Clusters II and IV (276.341) followed by cluster III and IV (520.915).

These results suggest that crossing genotypes from clusters with higher inter-cluster distances (e.g., Clusters I and III or Clusters I and II) will likely yield hybrids with superior heterosis and variability. Similar results were reported by Singh *et al.*, (2022) [14], Yadav *et al.*, (2023) [16] and Kumar *et al.*, (2024) [8].

Relative Contribution of different characters towards divergence

Towards divergence the contribution of each character is presented in Table 6. In E1 it was concluded that flag leaf area (19.60%) contributed maximum towards divergence followed by spike length (12.65%), peduncle length (11.367%), harvest index (10.129%), days to heading (8.492%), days to maturity (8.422%), thousand grain weight (6.917%), grain yield (6.083%), plant height (6.065%), effective tillers per meter (5.322%) and biological yield (4.951%). Results of the study were in agreement with the reports of Thungo *et al.* (2021) [15], Bendjama *et al.* (2022) [2] and Chaudhary *et al.* (2022) [4].

Table 6: Per cent contribution of different characters towards diversity for 30 genotypes

Traits	Contribution
Days to heading	8.492
Days to maturity	8.422
Effective tillers per meter	5.322
Flag leaf area (cm^2)	19.600
Plant height (cm)	6.065
Peduncle length (cm)	11.367
Spike length (cm)	12.650
Thousand grain weight (g)	6.917
Biological yield (g)	4.951
Grain yield (g)	6.083
Harvest index (%)	10.129

Suitable Donors for Breeding

Through critical examination of genetic diversity, several genotypes were identified as superior donors for key agronomic traits. These genotypes exhibit favorable performance for traits such as days to heading, plant height, spike length, grain yield and other yield-contributing traits. Examples of suitable donors include:

- **Early Heading:** DBW 221 and DBW 225
- **Plant Height:** DM 6 and WAPD 1519
- **Spike length:** IC 296729 and HI 1634
- **Grain Yield per plot:** GW 1339 and UP 2855

These genotypes represent valuable genetic resources that can be incorporated into breeding programs to improve wheat yield and resilience.

Conclusion

The study revealed significant genetic diversity among 30 wheat genotypes, underscoring the potential for genetic improvement through hybridization. Hierarchical Cluster Analysis (HCA) grouped the genotypes into distinct clusters, with Cluster IV. In addition, the study found that there is no direct correlation between geographical isolation and genetic diversity, as genotypes from different regions were placed in the same clusters. This highlights the need to consider genetic diversity rather than geographical origin when selecting parents for hybridization. By leveraging the genetic diversity identified in this study, breeders can develop high-yielding, resilient wheat varieties better suited to the climatic and agronomic conditions in India. Future research should focus on utilizing these genetically diverse parents to enhance wheat productivity and sustainability.

Acknowledgements

The authors sincerely express their profound gratitude to all individuals who contributed to the successful completion of this research, either through direct support or indirect encouragement. The authors also extend heartfelt thanks to the Department of Genetics and Plant Breeding, Govind Ballabh Pant University of Agriculture and Technology (GBPUA&T), Pantnagar, for providing the necessary infrastructure, research facilities, and academic guidance throughout the course of this investigation. Lastly, the authors acknowledge the moral support and encouragement from their families and friends, which served as a constant source of motivation during this study.

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