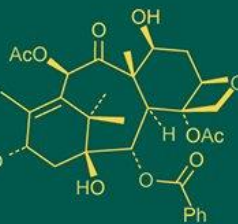
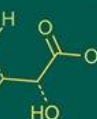
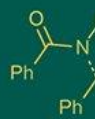


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Genetic diversity studies in bread wheat (*Triticum aestivum* L.) genotypes under timely sown irrigated condition

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Abstract

The present investigation was conducted on twenty-six wheat genotypes during the rabi season of 2024 at BTC College of Agriculture and Research Station, Bilaspur, Chhattisgarh, to assess genetic divergence in bread wheat genotypes. Genetic divergence analysis is the foundation for effective plant breeding, it is a valuable tool for identifying parents with complementary traits, which can be combined in hybridization programs to develop superior varieties. The objective of this study was to quantify the extent of genetic divergence to facilitate the selection of promising wheat genotypes for future breeding. The twenty six wheat genotypes were grouped into six distinct clusters. Cluster V was the largest with eight genotypes, followed by Cluster I (six genotypes), Cluster IV (five genotypes), Cluster VI (three genotypes), while Clusters II and III contained two genotypes each. The highest intra-cluster distance was observed in Cluster IV, followed by Cluster III, whereas the greatest inter-cluster distance was recorded between Clusters IV and VI. These results suggest that selecting parents from clusters with higher inter-cluster distances would increase the probability of generating superior segregants, thereby enhancing the chances of developing improved cultivars. Trait contribution analysis revealed that 1000-grain weight (g), grain yield per plot (kg), and biological yield per plot (kg) were the major contributors to overall genetic divergence. This highlights the importance of these traits in driving variability and suggests their potential as key selection criteria in wheat improvement programs.

Keywords: Wheat (*Triticum aestivum* L.), genetic divergence, Contribution of Traits to Divergence

Introduction

Wheat (*Triticum aestivum* L.) is a hexaploid cereal crop ($2n = 6x = 42$; AABBDD genomes), annual in nature, self-pollinated, and primarily grown as a cool-season rabi crop. It belongs to the tribe *Triticeae* under the family *Poaceae*. The complex genetic structure of wheat has endowed it with wide adaptability and substantial genetic diversity, enabling tolerance to diverse abiotic and biotic stresses arising from environmental fluctuations. Genetic diversity plays a crucial role in understanding patterns of variation within and among populations, which is essential for yield improvement and stress management. Estimating the extent and pattern of genetic divergence provides valuable insights for breeding and selection of desirable traits (Maniee *et al.*, 2009) [5]. Genetic divergence analysis is particularly important in breeding programs aimed at developing high-yielding, timely sown varieties that are resilient and perform consistently across environments. Crop improvement fundamentally relies on the availability of genetic diversity in plant genetic resources, which provides opportunities to develop new and improved cultivars with desirable attributes such as higher yield potential, larger seed size, and resistance to pests and diseases. The presence of variability within wheat genotypes allows breeders to identify superior lines, either for direct release as new varieties or as potential parents in hybridization programs. Genetic diversity between parents is essential to exploit heterosis and generate transgressive segregants. Furthermore, it enables breeders to develop varieties tailored for specific traits, including quality enhancement and tolerance to both biotic and abiotic stresses.

2. Materials and Methods

The present investigation was carried out during *rabi* season of 2024, at BTC college of Agriculture and Research Station, Bilaspur. Twenty six wheat genotypes with four checks *viz*, GW322 (C), HI8737(d) (C), HI8713(d) (C) and MACS6768 (C) were used. Experimental material were planted in randomized block design (RBD) with four replications. Each genotype was grown in a plot size of 8 m² for each entry in each replication. The observations were

recorded on five randomly selected plants from each plot in all the four replications of all the twelve characters *viz*, days to heading, days to maturity, plant height (cm), number of effective tillers/plant, spike length (cm), spike weight (g), total number of spikelet's/spike, peduncle length (cm), biological yield/plot (kg), grain yield/plot (kg), harvest index (%) and 1000 grains weight (g). Genetic divergence was estimated by Mahalanobis (1928), clustering was done by

Table 1: List of 26 wheat genotypes used in the present study along with place of origin

S. No.	Name of Genotypes	Place of Origin
1.	MACS4146(d)	ARI, Pune
2.	MACS4135(d)	ARI, Pune
3.	MACS6837	ARI, Pune
4.	HI8858(d)	IARI, Indore
5.	HI8849(d)	IARI, Indore
6.	HI88853(d)	IARI, Indore
7.	HI8854(d)	IARI, Indore
8.	HI1683	IARI, Indore
9.	HI8855(d)	IARI, Indore
10.	HI8850(d)	IARI, Indore
11.	GW561	SDAU, Vijaypur
12.	GW1369(d)	SDAU, Vijaypur
13.	GW554	JAU, Junagarh
14.	GW555	JAU, Junagarh
15.	MP3570	JNKVV, Powarkheda
16.	MPO1395(d)	JNKVV, Powarkheda
17.	MP1401	JNKVV, Jabalpur
18.	UAS485(d)	UAS, Dharwad
19.	AKDW5520(d)	PDKV, Akola
20.	WHD969(d)	HAU, Hisar
21.	DBW457	IWBR, Karnal
22.	DBW509B	IWBR, Karnal
23.	GW322 (Check)	RARS, Vijapur
24.	MACS6768 (Check)	ARI, Pune
25.	HI8737(d) (Check)	IARI RS, Indore
26.	HI8713(d) (Check)	IARI RS, Indore

3. Results and Discussion

3.1 Genetic divergence analysis

Genetic divergence analysis of 26 wheat genotypes were grouped in 6 clusters. cluster V was the largest cluster (8 genotypes) followed by cluster I (6 genotypes), cluster IV (5 genotype), cluster VI (3 genotype), cluster II and III had 2 genotypes. Cluster IV had the maximum intra-cluster distance, followed by cluster III. Cluster IV and VI had maximum inter cluster distances. This revealed that using parents from these clusters in a hybridization programme will result in a higher frequency of better segregants, which is important for the production of desired varieties. Similar results were observed by Lakra *et al.*, (2020) ^[4], Hazra *et al.* (2019) ^[1], Singh *et al.*, (2018) ^[8] and Yadav *et al.*, (2014) ^[9].

3.2 Contribution of Traits to Divergence

The contribution identifies the traits driving genetic divergence. For each pair of treatments, the trait contributing most to their D² distance was found. 'Times Ranked 1st' is a count of how many times each trait was the top contributor. 'Contribution (%)' in this count as a percentage of total pair wise comparisons. The trait contributing most to divergence was greatest for 1000 grains weight(g), grain yield/plot (kg) and biological yield/plot (kg). Similar results were observed by Jagdev (1993) ^[2] for 1000 grains weight (g) and grain yield/plot (kg), Nimbalkar *et al.*, (2002) ^[7] for 1000 grains weight (g) and Kumar *et al.*, (2017) ^[3] for grain yield/plot (kg).

Table 2: Wheat genotypes were grouped into 6 cluster

Cluster	Number of Genotypes	Genotypes
1	6	DBW457, GW322 (Check), MACS6768 (Check), MACS6837, MP1401, UAS485(d)
2	2	GW1369(d), HI8855(d)
3	2	HI88853(d), MACS4146(d)
4	5	HI8713(d) (Check), HI8854(d), HI8858(d), MPO1395(d), WHD969(d)
5	8	AKDW5520(d), DBW509B, GW554, HI8737(d) (Check), HI8849(d), HI8850(d), MACS4135(d), MP3570
6	3	GW555, GW561, HI1683

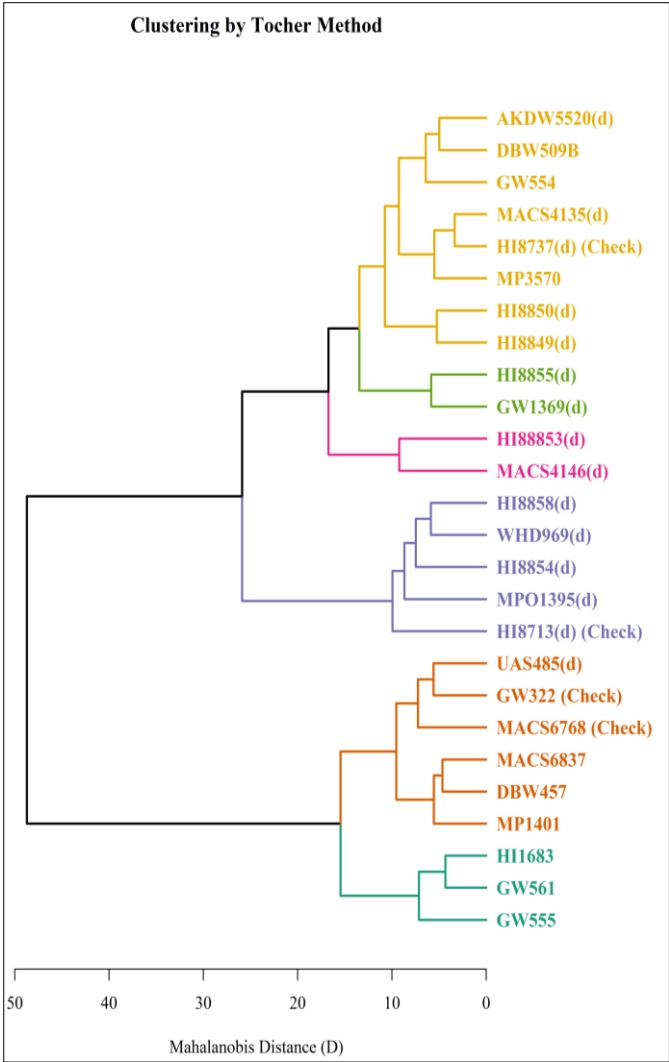


Fig 1: Clustering by Tocher Method

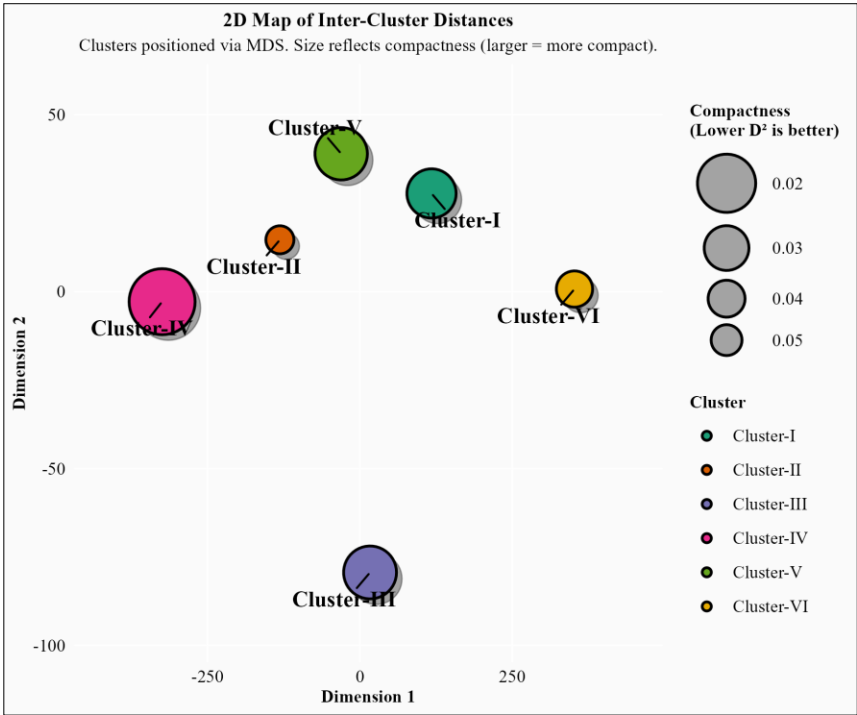


Fig 2: 2D Cluster Map

This plot spatially maps the clusters. Closer clusters are more similar based on their D² distance. Point size reflects internal compactness (larger points are more compact).

Table 3: Intra and inter-cluster distance in 26 wheat genotypes under 6 clusters

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	37.98	253.74	142.06	383.98	127.10	90.44
Cluster-II		17.07	174.16	106.59	86.26	453.58
Cluster-III			42.70	259.89	122.71	256.66
Cluster-IV				53.12	148.21	677.04
Cluster-V					42.11	291.63
Cluster-VI						23.33

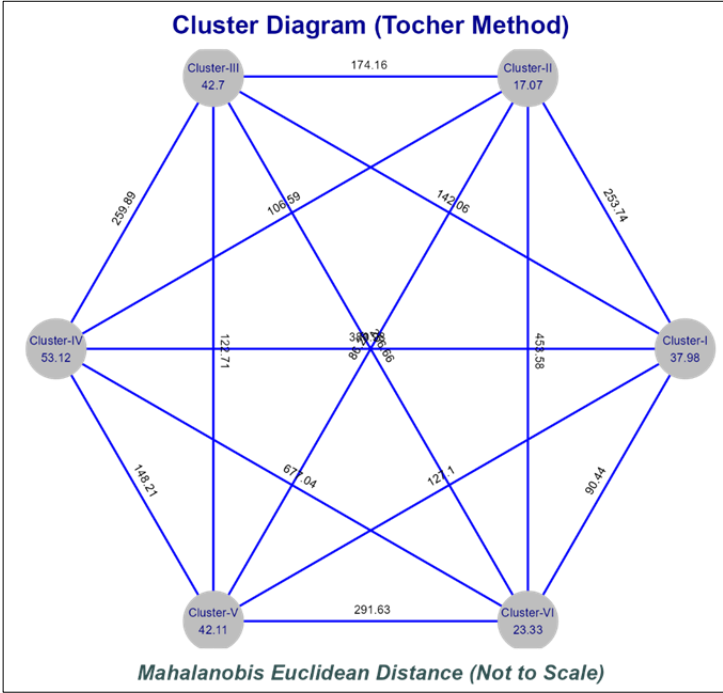


Fig 3: Diagrammatic presentation of inter and intra-cluster distances by using

The following diagram provides a schematic view of the D² distances between clusters. The values on the lines represent the distance between two clusters (inter-cluster distance), while the value inside each node represents that cluster's internal average distance (intra-cluster distance).

Table 4: Contribution of Traits to Divergence in percentages

Trait	Contribution (%)	Times Ranked 1st
TW	65.23	212
GYPP	11.38	37
BYPP	8.31	27
DM	5.23	17
HI	4.31	14
DH	1.85	6
SL	1.85	6
SW	0.92	3
PH	0.31	1
TNSPS	0.31	1
PL	0.31	1
ETPP	0.00	0

The charts below summarize these contributions. For clarity, traits with a contribution below 1% have been excluded. The pie chart shows the proportional share, while the bar chart allows for easier comparison of magnitudes.

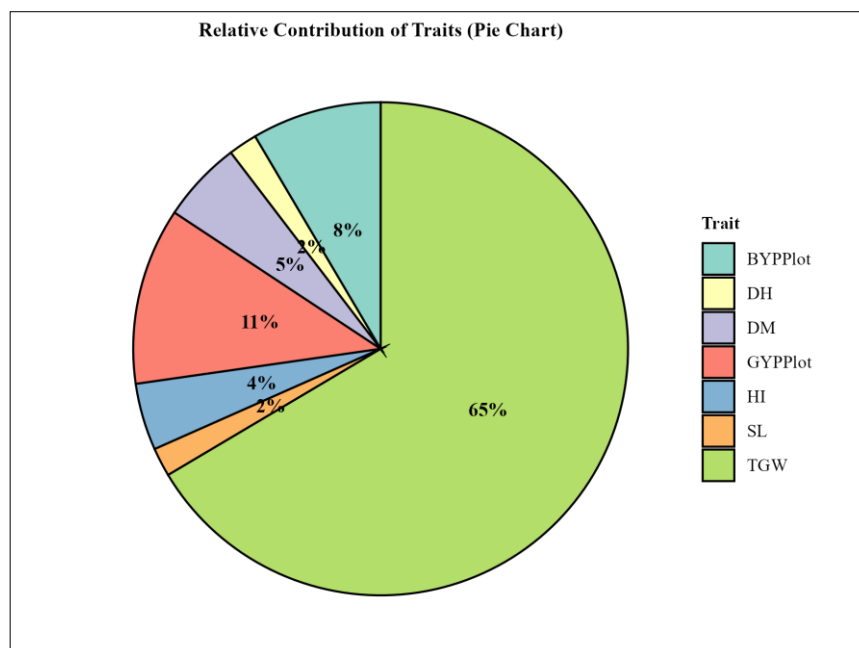


Fig 4: Contribution of Traits to Divergence (Visualizations)

4. Conclusion

Genetic divergence analysis of 26 wheat genotypes classified them into six distinct clusters, with Cluster V being the largest, comprising eight genotypes. The clustering pattern suggests that selecting parents from divergent clusters in hybridization programs would increase the likelihood of generating superior segregants, thereby facilitating the development of desirable varieties. Trait contribution analysis further highlighted the characters driving genetic divergence. For each pair of genotypes, the trait contributing most to the Mahalanobis D^2 distance was identified. The parameter '*Times Ranked 1st*' denoted how often a particular trait ranked as the highest contributor, while '*Contribution (%)*' represented its relative importance across all pairwise comparisons. The traits contributing most substantially to overall divergence were 1000-grain weight (g), grain yield per plot (kg), and biological yield per plot (kg), indicating their pivotal role in differentiating the wheat genotypes.

5. Acknowledgement

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6. Future Scope

1. Validation of genetic divergence results across multiple locations and years to assess stability and adaptability of genotypes.

2. Utilization of genetically diverse parents in hybridization programs to develop high-yielding, stress-tolerant cultivars.
3. Integration of molecular marker studies with divergence analysis to strengthen precision in identifying diverse genotypes.
4. Exploration of trait-specific diversity (e.g., quality, disease resistance, abiotic stress tolerance) for targeted breeding programs.
5. Development of a breeder-friendly core set of genotypes representing maximum diversity for use in future wheat improvement.

6. Conflict of Study

The authors declare that there is no conflict of interest associated with this study or its publication.

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