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Mahesh Jarman

JNKVV, Zonal Agricultural
Research Station, Powarkheda,
Narmadapuram, Madhya Pradesh,
India

Animesh Chatterjee

JNKVV, Zonal Agricultural
Research Station, Powarkheda,
Narmadapuram, Madhya Pradesh,
India

Vinod Kumar

JNKVV, Zonal Agricultural
Research Station, Powarkheda,
Narmadapuram, Madhya Pradesh,
India

Yogendra Singh

Department of Plant Breeding &
Genetics, JNKVV, Jabalpur,
Madhya Pradesh, India

Corresponding Author:

Mahesh Jarman

JNKVV, Zonal Agricultural
Research Station, Powarkheda,
Narmadapuram, Madhya Pradesh,
India

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Selection of elite cross combination and genotype through genetic divergence analysis in bread wheat (*Triticum aestivum* L.)

Mahesh Jarman, Animesh Chatterjee, Vinod Kumar and Yogendra Singh

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Abstract

Genetic divergence study on bread wheat (*Triticum aestivum* L.) consisted 12 genotypes of diverse sources and 45 F_1 's. The experiment was conducted at Zonal Agricultural Research Station, Powarkheda, Narmadapuram (M.P.) in Rabi 2022-23 in Randomized Complete Block design in three replications. Standard package and practices were given to raise healthy crop. Results of analysis revealed their association into seven clusters. Approximate configurations of the clusters based on the D^2 values. According to Mahalanobis' D^2 statistic it can be concluded that, days to heading, days to maturity, plant height, peduncle length, effective tiller /plant, spike length, number of spike per plant, number of spikelets/spike, number of grains/spike, 1000-grain weight, biological yield per plant, harvest index, and grain yield per plant contributed the most towards genetic diversity. 57 genotypes clustered into 7 distinct groups, indicating substantial genetic variation for breeding programs. Genotypes spread across most clusters, allowing selection of parents with complementary traits for hybridization. Cluster III ideal for breeding as it has the highest average grain yield. While Cluster IV valuable for breeding due to high average 1000-grain weight and number of grains/spikes. Cluster VI useful for breeding as it has the highest average number of tillers and spikelets. Large inter-cluster distances (VI-VII, IV-V) indicate significant genetic variation, perfect for breeding programs. Even within clusters (e.g., V), high maximum intra-cluster distances suggest good diversity for parent selection. Selecting parents from diverse clusters creates a broad spectrum of variability in offspring. This allows breeders to select the best combinations of traits for developing new and improved wheat varieties with enhanced yield, quality, and other characteristics.

Keywords: *Triticum aestivum* L., genetic divergence, multivariate analysis, D^2 -statistics

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide, providing a staple food source for a significant portion of the global population. The increasing demand for wheat, coupled with challenges such as climate change, disease pressures, and the need for sustainable agricultural practices, underscores the necessity for continuous improvement of wheat varieties. The development of elite genotypes with superior agronomic traits is pivotal to enhancing yield, quality, and resilience of wheat crops.

Genetic divergence analysis is a critical tool in plant breeding, enabling researchers to assess genetic variability among different genotypes. This variability is essential for identifying potential parents for breeding programs, as it provides the genetic basis for selecting traits that can be combined to produce superior progeny. By examining genetic divergence, breeders can pinpoint combinations that maximize heterosis (hybrid vigor) and produce high-performing wheat varieties.

Genetic diversity is the basic for genetic improvement. It is widely accepted that information on genotypes diversity and genetic relatedness among elite breeding materials are fundamental elements in plant breeding (Mukhtar *et al.* 2002) [9]. Genetic diversity is important factor for any hybridization programme especially in self- pollinated crops (Joshi and Dhawan 1966) [4]. Recent studies have highlighted the significance of genetic diversity in improving wheat. For instance, Singh *et al.* (2022) [13] demonstrated the effectiveness of using genetic divergence analysis to identify promising parental combinations in wheat breeding programs. Similarly,

Sharma *et al.* (2023) [11] emphasized the importance of utilizing diverse germplasm to enhance the genetic base of wheat, which is crucial for developing resilient and high-performing varieties. The selection of elite cross combinations through genetic divergence analysis involves evaluating a wide range of genotypes to determine their genetic distance. This process helps in identifying diverse parental lines that, when crossed, are likely to exhibit desirable traits such as increased yield, improved disease resistance, and better adaptability to environmental stresses.

Materials and Methods

Keeping in view the importance of genetic diversity in breeding for 10 high yielding varieties studies on genetic divergence of bread wheat were carried out at Zonal Agricultural Research Station, Powarkheda, Narmadapuram in Rabi 2022-23. The experiment was laid in completely randomized block design with three replications. Each genotype was accommodated in a double row plot of 2.5 m length with row to row and plant to plant spacing of 20 and 5 cm respectively. The sowing was done on 10th November 2022 by dibbling the seeds in rows. The experiment was conducted under irrigated and high fertility conditions. Proper care was taken to keep only one plant at each spot. Five plants were selected randomly from each plot and observations were recorded for the following characters:

- (A) **Pre- harvest observations:** (1) Days to flowering (2) Days to maturity
 (B) **Post- harvest observation:** (3) Plant height (cm), (4) Peduncle length (cm), (5) Effective tillers /plant, (6) Spike length (cm), (7) Number of spikes per plant, (8) Number of spikelet's per spike, (9) Number of grains per spike, (10) Biological yield per plant, (11) Harvest index (%), (12) 1000-grain weight, (13) Grain yield per plot (g) were recorded as per recommended protocols.

Analysis of variance of plot means for different characters were calculated as per standard procedures. To study the genetic diversity in the above characters the data were processed further by using Mahalanobis D² statistics describe by Rao (1952) [10]. The simultaneous test of differences between mean values of the character studies was done by using Wilks criterion (Rao 1952) [10]. Treating D² as the square of generalized distance, all genotype were grouped into a few clusters, according to the method described by Tocher (Rao 1952) [10]. The average intra-cluster and inter cluster distances were calculated following the method described by Singh and Chaudhary (1977) [14].

Results and Discussion

The present study was undertaken to evaluate the performance of bread wheat genotypes for yield and its attributes.

Multivariate analysis of divergence

The quantitative assessment of genetic divergence was carried out for all the 13 morphological characters, using Mahalanobis' D² statistic. To estimate the D values, correlated means of characters were transformed to standard uncorrelated characters, using pivotal condensation method. The statistical distance between pairs of treatments was obtained as the sum of squares of the differences between the pair of corresponding uncorrelated values of any two treatments considered at a time.

Clustering pattern in genotypes

Genotypes are the specific genetic makeup of an organism. Clustering in this context refers to grouping genotypes together based on how similar their genetic makeup is. This analysis helps researchers understand the genetic relationships between different individuals within a species or population. A set of 57 genotypes of wheat were subjected to D² analysis for thirteen characters. Based on D² values seven clusters were formed (Table1). This indicated that substantial diversity exists in the available genotypes of wheat. Results of cluster analysis revealed that the cluster II was the largest group consisting of 13 genotypes followed by cluster I (12 genotypes), clusters VI (8 genotypes), clusters III and VII (7 genotypes), clusters V (6 genotypes) and clusters IV (4 genotypes). From the clustering pattern, it was found that the wheat genotypes were genetically divers to each other. Hence, the genotypes studied are reliable enough for hybridization and selection. 57 genotypes are also distributed over VII clusters, clusters I and cluster II indicating there is little role of geographical origin in genetic diversity. So, the role of geographical origin cannot be overruled in cluster composition. Present result confirms the finding of previous workers Kumar *et al.* (2009) [5], Ferdous *et al.* (2011) [3], Ajmal *et al.* (2013) [1], Kumar *et al.* (2013) [6], Verma *et al.* (2013) [15], Yadav *et al.* (2014) [18].

Table 1: Inter and Intra cluster distance of genotypes in wheat

Cluster	Number of Genotypes	Cluster Members
I	12	11, 13, 14, 21, 22, 23, 24, 32, 36, 49, 50, 55
II	13	20, 25, 28, 30, 40, 41, 48, 51, 52, 53, 54, 56, 57
III	7	15, 16, 17, 18, 27, 29, 35
IV	4	31, 37, 38, 39
V	6	1, 2, 3, 4, 5, 19
VI	8	26, 33, 34, 42, 43, 44, 46, 47
VII	7	6, 7, 8, 9, 10, 12, 45

Components of cluster mean

All the genotypes were grouped into seven clusters to study the genetic variability existing among the lines. Tocher's procedure (Singh and Chaudhary, 1977) [14] was adopted for grouping. The distribution of line into clusters and their mean values have been presented in Table: 2a and 2b, respectively.

Table 2a: Mean performance of genotypes in individual cluster for seed yield and its components in bread wheat genotypes

Clusters	Genotypes	DH	DM	PH	PL	ET	SL	NOS/P
I	12	63.49	113.46	72.58	31.47	14.99	9.1	7.38
II	13	68.95	112.67	74.26	33.89	15.64	9.6	7.77
III	7	62.45	111.45	71.14	34.39	16.64	7.83	7.00
IV	4	62.83	113.54	75.92	34.18	15.04	9.75	9.66
V	6	58.06	113.25	85.39	33.4	14.06	7.94	7.19
VI	8	67.25	111.69	83.75	33.98	18.56	9.75	8.69
VII	7	65.86	118.07	85.45	32.44	14.74	8.71	7.29

Table 2b: Mean performance of genotypes in individual cluster for seed yield and its components in bread wheat genotypes

Clusters	Genotypes	NOSL/S	NOG/S	1000-TGW	BY/P	HI %	GY/P
I	12	18.21	50.28	43.85	65.90	32.75	21.61
II	13	18.72	54.18	45.46	64.39	36.93	23.77
III	7	18.76	46.81	43.98	67.39	37.31	25.07
IV	4	18.25	59.08	47.21	63.61	36.00	23.01
V	6	16.75	40.08	43.56	60.58	26.47	16.12
VI	8	21.46	56.17	45.15	64.00	38.59	24.69
VII	7	17.33	37.33	41.02	61.63	28.57	17.55

Here, Days to heading (DH), Days to maturity (DM), Plant height (cm) (PH), Peduncle length (cm) (PL), Effective tillers per plant (ET), Spike length (SL), Number of spike per plant (NSPP), Number of spikelet's per spike (NSPS), Number of grains per spike (NGPS), 1000 grain weight (g) (TW), Biological yield per plant (g) (BYPP), Harvest index (%) and Grain yield per plant (GYPP)

The comparison of cluster mean revealed considerable difference among the clusters of different quantitative characters (Table 2a and table 2b). The cluster III had the highest mean value for grain yield per plant (25.07) and peduncle length (34.39), similarly, genotype included in cluster IV recorded the highest mean value for 1000-grain weight (47.21), number of grains per plant (59.08), number of spikes per plant (9.66), and spike length (9.75). The cluster VI exhibited highest mean value for effective tillers per plant (18.56), spike length (9.75) and number of spikelet's per spike (21.46). Cluster II had highest days to heading (68.95). Whereas, cluster VII had highest mean

value for days to maturity (118.07) and plant height (85.45).

These findings suggest that breeding programs can potentially select lines from these clusters to combine desirable traits. For example, lines from cluster III with high grain yield and peduncle length could be crossed with lines from cluster IV that have high 1000-grain weight, number of grains per plant, number of spikes per plant, and spike length. This could lead to the development of new varieties with improved grain yield and other beneficial traits. Present results confirms the finding of previous workers Kumar *et al.* (2009)^[5], Kumar *et al.* (2013)^[6], Verma *et al.* (2013)^[15], Yadav *et al.* (2014)^[18] and Singh *et al.* (2014)^[16].

Intra and Inter cluster divergence D² Values

The average D² values within (intra) and between (inter) clusters were calculated as per the procedure given by Singh and Chaudhary (1977)^[14] and have been presented in Table- 3.

Table 3: Inter and intra relation between cluster (Pooled)

Clusters	I	II	III	IV	V	VI	VII
I	3.501						
II	2.935	3.415					
III	3.450	3.886	3.192				
IV	4.323	3.336	4.992	2.817			
V	4.778	5.399	5.454	5.919	3.716		
VI	4.686	3.186	4.743	4.465	6.592	3.510	
VII	3.863	4.699	5.223	5.753	3.576	5.683	3.038

The maximum inter cluster distance was observed in between cluster VI and Cluster VII (6.565) followed by Cluster IV and cluster V (5.919), cluster IV and VII (5.753), VI and VII (5.683), cluster V and III (5.454), cluster V and II (5.399). This suggested that the hybridization programme involving from the diverse clusters is expected to produce better desirable segregants for development of useful genetic stocks or varieties. The lowest inter cluster distance was noticed between cluster II and I (2.935) followed by cluster VI and II (3.186), cluster III and I (3.450), cluster V and VII (3.576) The maximum intra cluster distance were observed in cluster V (3.716) followed by cluster VI (3.510), cluster I (3.501) and cluster II (3.415). The selection of divergent genotypes from above clusters would produce a broad spectrum of variability for quantitative traits studied, which an able future for selection and improvement. The minimum intra cluster distance was observed in cluster IV (2.817). Present result confirms the finding of previous worker Singh *et al.* (2014)^[16]. Many researchers in different crops have also reported that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability in segregating generations. Heterosis is generally attributed to genetic divergence among the parental lines involved in the cross. Nevertheless, the genetic divergence for the maximum expression of the heterotic effects has a limit as suggested by Moll *et al* (1965)^[8] and Arunachalam and

Bandyopadhyay (1984)^[2].

Conclusion

This study reveals that significant genetic diversity among the 57 wheat genotypes evaluated across 13 characters. The spread of genotypes across all clusters (except cluster IV) suggests a good balance of diversity. This is beneficial for breeding as it allows selection of parents for hybridization and crosses for further selection of superior plant from various clusters with complementary traits. Breeders can strategically select parents and cross combinations from these clusters based on their strengths. Cluster III (high grain yield and peduncle length) could be crossed with Cluster IV (high 1000-grain weight, number of grains/plant, spikes/plant, and spike length). The significant inter-cluster distances, particularly between VI & VII (6.565), indicate a high degree of genetic divergence between these clusters. This is highly desirable for breeding as it suggests these clusters harbor contrasting and potentially complementary traits. By strategically selecting parents from clusters with high inter-cluster distances and considering intra-cluster diversity, breeders can maximize the chances of generating offspring with a rich pool of genetic variations. This, in turn, allows for the selection of desirable segregants for developing new and improved wheat varieties with enhanced yield, quality, and other agronomic characteristics. Select the best-performing hybrids for

further development and potential commercial release. breeders can enhance their ability to develop superior F₁ hybrids, ultimately contributing to improved crop productivity and sustainability.

Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. *J Wheat Res.* 2014;6(1):154-159.

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