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Sreevani Gownipalli
Department of Genetics and
Plant Breeding, School of
Agriculture, Lovely Professional
University, Phagwara, Punjab,
India

Harshal Ashok Avinash
Department of Genetics and
Plant Breeding, School of
Agriculture, Lovely Professional
University, Phagwara, Punjab,
India

Nidhi Dubey
Department of Genetics and
Plant Breeding, School of
Agriculture, Lovely Professional
University, Phagwara, Punjab,
India

**Doddipatla Hari Sri Prasanna
Kumar**
Department of Genetics and
Plant Breeding, School of
Agriculture, Lovely Professional
University, Phagwara, Punjab,
India

Corresponding Author:
Sreevani Gownipalli
Department of Genetics and
Plant Breeding, School of
Agriculture, Lovely Professional
University, Phagwara, Punjab,
India

Analysis of genetic diversity, variability, heritability and genetic advance for yield and its attributing traits in Wheat (*Triticum aestivum* L.)

Sreevani Gownipalli, Harshal Ashok Avinash, Nidhi Dubey, Doddipatla Hari Sri Prasanna Kumar

Abstract

The study analysed 129 wheat genotypes (Segregating population) of F₅ generation using an augmented design with six blocks and four checks in the Research Fields of Genetics & Plant Breeding, School of Agriculture, “Lovely Professional University, Phagwara, Punjab.” Among the seven Clusters, Cluster 1 was the largest cluster containing fifty-nine genotypes whereas Clusters 2 and 4 were filled with fourteen genotypes, Cluster 9 with eight genotypes, and Cluster 3 and 7 with seven genotypes whereas the remaining Clusters viz. Clusters 5 and 7 with only four and five genotypes respectively and the genotypes within these clusters exhibited significant differences and show immense potential as parental candidates for crossbreeding. The inter-Cluster D² values varies from 15.749 (Cluster 1 and 3) to 70.316 (Cluster 2 and 5) indicating the presence of a broad spectrum of genetic diversity among the genotypes present in the Clusters. Intra cluster D² values ranged from 8.8579 (cluster 10) to 21.7595 (cluster 4). The analysis indicates that the genotypes grouped within each cluster exhibit limited diversity, suggesting that selecting parents from the same cluster for the hybridization program may not be a favourable approach. “The current study shows that the phenotypic coefficient of variation is greater than the genotypic coefficient of variation may be due to the influence of interaction” between the genotype and the environment for all the phenotypically expressed traits of the wheat plant. Harvest index recorded the highest GCV (17.29) and PCV (21.76) respectively while Single plant yield had the highest heritability h² (89.29%). However, 1000 grain weight (30.63) and plant height (22.71) showed the highest “genetic advance as a per cent mean (GAM).

Keywords: Genetic divergence, clusters, principal component analysis, inter-cluster, intra-cluster, and variability

Introduction

Wheat is a hexaploid plant with a chromosome number of 42 (2n=6x), and it primarily undergoes self-pollination with an annual growth cycle having AABBDD genome, and it belongs to the family Gramineae (Poaceae) and genus *Triticum aestivum* (Mollasadeghi *et al.*, 2011) [19]. It is the Largest and Most Predominantly farmed food crop in the world. It is India's second most significant primary food crop after rice; because of its size, great productivity, and prominent geographical location, it is referred to as the “King of Cereals (Curtis, 2002) [4]. It serves as a staple diet for more than one-third of all people on Earth in various forms. With more than 35% of the cereal calories consumed in the developing world, 74% in the developed world, and 41% consumed directly worldwide, it is one of the most important staple crops for ensuring global food security (Shiferaw *et al.*, 2013) [5]. When it comes to production and consumption, wheat holds a crucial position as one of the most important grain export crops globally, including in Ethiopia (Ranjana and Kumar, 2013) [21]. During the growing season of 2012/13, Ethiopia emerged as the largest wheat producer in Sub-Saharan Africa, with a harvested area spanning 1.51 million hectares, a total production of 3.78 million tonnes, and an average yield of 2.5 tonnes per hectare. It's worth noting that this average yield was approximately 45% lower than the global average. Following Ethiopia, South Africa ranked second in wheat production in Sub-Saharan Africa, while Ethiopia secured the fourth position in wheat production across the entire African continent. (CSA, 2012; Degewione and Alamerew, 2013) [6, 8]. Improved varieties are now less resilient to biotic and abiotic stress as a result of their limited genetic diversity.

Genetic variability measurements, such as genotypic and phenotypic coefficients of variation (GCV, PCV), broad sense heritability (h²b), and genetic advance (GA), was carefully

examined in order to accurately assess the level of genetic variety existing in a population. According to (Johnson *et al.*, 1955) ^[11], heredity affects the selection programme and demonstrates the relative efficacy of selection based on the phenotypic variance of a variable. Predicting the true value of selection when heritability was combined with genetic advancement is more advantageous. Because Grain Yield in cereals is a complex polygenic character, identifying prospective cultivars depends critically on understanding the degree of correlation between yield and the linked features. Plant breeders use an indirect selection of independent variables that could exhibit closely associated responses with other associated traits to increase yield to meet the growing demands of the global population (Zafarnaderi *et al.*, 2013) ^[25]. The character association was estimated using variance and covariance components as given by (Fisher, 1954) ^[9] and (Miller *et al.*, 1958) ^[2].

Therefore, knowledge of the level of genetic diversity and divergence in wheat aids in choosing the parents for the development of superior varieties. Genetic diversity plays a crucial part in a breeding program's success because, as we know, a plant with greater variation or variability has a higher possibility of being exploited to produce fruitful recombination and a broad range of variability in segregating generations during genetic improvement. Heritability estimations were used in this study in order to predict the potential advancement that may be achieved by enhancing the selection procedure. In order to make selection effective, genetic advance estimates provide a clear picture of segregating generations (Saleem *et al.*, 2016) ^[22]. The study of heritability provides more information regarding a specific character that can be passed down from one generation to the next. A plant breeder can forecast future generations' conduct and their response to selection by using knowledge of a trait's heritability. Heritability values can be used as a scale for evaluating the association of genes between parents and offspring (Memon *et al.*, 2007) ^[17].

The ability to use the best genetic stock for crop improvement is made possible by heritability and genetic advancement (Mangi *et al.*, 2008) ^[15]. High heritability estimates and high genetic progress provide the best conditions for selection. Any breeding program's success depends on the amount of genetic variety present in the germplasm, thus it's essential to have a solid understanding of the heritability and genetic advancement within the many yield-related characteristics (Waqar-ul Haq *et al.*, 2008) ^[24].

The assessment of genetic diversity using biometric methods like Mahalanobis (D₂) statistics has enabled the selection of genetically distinct parents. Recent studies have demonstrated the usefulness of Mahalanobis generalized distance (D₂ statistic) in estimating qualitative traits within genetic diversity (Mahalanobis, 1936) ^[14].

Materials and Methods

The present experiment was at the Research Farm of the department of Genetics & Plant Breeding, "School of Agriculture, Lovely Professional University, Phagwara, Punjab". The study evaluates 129 Segregating populations (F₅ generation) selected from the superior F₄ Segregating population and 4 Checks. The 129 genotypes were sown in 6 blocks, each block with 20 genotypes with 4 checks, and each genotype is sown in 2 lines In Augmented Block Design with 22.5 cm of the row-to-row spacing with a row length of 2

meters with 5 cm space within the row, and also standard agronomic practices are carried out for better crop growth.

In the experimental trial, we selected five random plants of each genotype from 129 segregating populations along with four check varieties and tagged them for the data collection. In addition, observations were taken for the quantitative traits *viz.*, days for 50% heading, days to maturity, plant height (cm), number of productive tillers, number of spikelets per spike, spike length, number of grains per spike, spike weight, 1000 grain weight, number of grains per plant, biological yield for the plant, harvest index (%) and chlorophyll content of the plant.

The data mentioned above were subjected to statistical analysis using Analysis of Variance (ANOVA) at a 0.05% probability level. The software used for this analysis was SPSS Version 16.0 (SPSS, Chicago, USA). Variability and heritability (h²) were estimated based on the approach suggested by Hanson and Johnson in 1995 ^[11], allowing for the assessment of genetic advance.

Furthermore, correlation analysis was conducted to determine the degree and direction of association between different traits. Path analysis was employed to identify the direct and indirect effects of component traits on yield, enabling the identification of traits that significantly contribute to overall yield.

Results and Discussion

Grouping of genotypes into various Clusters

Upon examination of the outcomes concerning the categorization of genotypes (Fig.1 and Table 1), it was observed that the 129 genotypes were classified into Ten Clusters. This classification was achieved by applying agglomerative hierarchical clustering with complete linkage, utilizing Mahalanobis distance to determine the relative magnitudes of D₂ values ^[8]. The genotypes fitting to similar Cluster had an average minor D² value than those fitting to diverse Clusters. Among the Ten Clusters, Cluster 1 was major one including of fifty-nine genotypes trailed by Cluster 2 and 4 with fourteen genotypes, Cluster 9 by eight genotypes, Cluster 3 and 7 with seven genotypes and cluster 8 with five genotypes whereas remaining Clusters *viz.* Cluster 6 and 10 with only four genotypes respectively.

Compared to genotypes within the same cluster, those within distinct clusters exhibited a greater degree of diversity. Additionally, genotypes from the same geographical location were distributed across various clusters, indicating that the clustering of genotypes did not correspond with their geographical distribution. These findings are consistent with previous reports found in references ^[9-12].

Average intra and inter-Cluster D² value

Examining the distances between clusters (Table 2) reveals a wide range of inter-cluster D₂ values, from 12.5376 (between Cluster 4 and Cluster 5) to 53.7539 (between Cluster 2 and Cluster 6). This indicates that there is a substantial amount of genetic diversity among the genotypes within the clusters. The largest inter-cluster distance was observed between Cluster 2 and Cluster 6 (53.7539), followed by Cluster 6 and Cluster 9 (53.7305), Cluster 8 and Cluster 10 (52.7159), and Cluster 3 and Cluster 6 (51.6844), indicating that genotypes from these clusters exhibited high divergence and have the potential to serve as hybridization parents. It is anticipated that hybridization between genotypes from these distant

clusters will result in increased variability and transgressive segregates, given that the greater the distance between clusters, the greater the genetic diversity among genotypes. In contrast, the smallest inter-cluster distance (12.5376) was observed between clusters 4 and 5, indicating their close relationship and similarity in the examined characteristics.

Inter-cluster distances were found to be greater than intra-cluster distances, indicating that the genotypes exhibit substantial diversity. This result is consistent with previous wheat-related reports by [13]. The intra-cluster D2 values varied between 8.8579 (for cluster 10) and 21.7595 (for cluster 4). The intra-cluster distance was greatest for Cluster 4, followed by Cluster 1 (20.684) and Cluster 2 (19.2992), with the remaining clusters exhibiting ordinary intra-cluster distances. This suggests that genotypes within the same cluster have a low level of genetic diversity; therefore, selecting progenitors from within a cluster for a hybridization program may not be the most effective strategy.

Cluster means

Cluster means depict the average performance of all genotypes within each cluster, providing valuable information regarding potential parents for trait improvement. The study's results revealed substantial variation between clusters for all of the analyzed characteristics. Table 3 provides the cluster means for grain yield and nutritional characteristics, indicating significant differences between clusters for these traits.

Cluster mean standards for DTH were maximum in cluster 10 (93.75) and lowest in cluster 6 (89.75). Cluster mean for DM (days to maturity) was highest in cluster 10 (128.75) and lowest in cluster 6 (124.75), while for PH it was highest in cluster 8 (114.7) and lowest in cluster 10 (68.18). NPT was highest in Cluster 5 (5.667) and lowest in Cluster 2 (4.948) while EL was highest in Cluster 8 (8.708) and lowest in Cluster 10 (7.865). Further, NSPE was highest in cluster 8 (17.56) and lowest in cluster 2 (14.871). EW was highest in Cluster 5 (2.663) and lowest in cluster 6 (2.303). NGPE was highest in cluster 5 (46.864) and lowest in cluster 3 (35.771). Similarly, TGW was highest in cluster 8 (52.68) and lowest in cluster 9 (33.8). BYP was highest in cluster 3 (24.164) and lowest in cluster 7 (13.314). GYP was highest in cluster 5 (11.506) and lowest in cluster 9 (7.157). While HI was highest in cluster 6 (81.801) and lowest in cluster 3 (34.112) and CC mean was highest in cluster 10 (44.667) and lowest in cluster 8 (34.841)

The cluster means represent the average performance of all genotypes within each cluster, which provides valuable information regarding potential progenitors for trait improvement. The results of the investigation revealed significant variation between clusters for all analysed characteristics. The cluster means for grain yield and nutritional characteristics are provided in Table 3, indicating that there are significant differences between clusters for these variables.

Variability, Heritability, and Genetic Advance

The result tabulated in Table 4 presents the genotypic and phenotypic variances, heritability, GCV, PCV, genetic advance, and genetic advance as a percentage (%) of the mean (GAM%) for the entire yield contributing characters.

Genetic variability: The basic prerequisite for carrying out

any crop enhancement effort is the presence of sufficient genetic heterogeneity. Generally, PCV values will be maximum than their particular GCV values representing slight environmental influences.

Genotypic coefficient of variation (GCV)

The genotypic coefficient of variation medium GCV values was observed in harvest index (17.29), 1000 grain weight (15.86), plant height (12.51), and chlorophyll content (11.39). Low GCV values were observed in biological yield per plant (8.22), number of grains per ear (6.38), number of spikelets per ear (6.31), ear length (4.59), ear weight (4.05), days to 50% heading (3.34), maturity days (2.41) and no. of productive tillers per plant (2.35).

Phenotypic coefficient of variation (PCV)

High PCV value was observed in the harvest index (21.76) and biological yield per plant (21.01). Medium PCV values were grain yield per plant (19.81), 1000 grain weight (16.94), ear weight (16.91), plant height (14.21) and chlorophyll content (12.97) whereas low PCV values were recorded in number of spikelets per ear (9.87), ear length (9.61), number of grains per ear (9.47), number of productive tillers per plant (8.04), days to 50% heading (3.93) and days to maturity (2.80).

In this study, the phenotypic coefficients of variation were marginally greater than the genotypic coefficients of variation, indicating that the environment had some effect on the expression of the investigated trait. High values for GCV and PCV were recorded for Harvest index, single plant yield and 1000-grain weight. This suggested the possibilities for making further improvement using these traits observed the maximum magnitude of GCV and PCV biological yield. (Nithya *et al.*, 2020) [20] also report these findings for grain yield per plant and productive tillers per plant for the number of grains per panicle. Low GCV and PCV values of the traits indicated low variance and the results indicate that the environment has little effect on these characteristics, suggesting that phenotypic coefficients are more appropriate for evaluating them. These results align with those of (Sandeep *et al.*, 2018) [23] and (Amegan *et al.*, 2020) [3] regarding the number of days to 50% blossoming and the number of days to maturity.

Heritability h^2 (Broad Sense)

Higher heritability values were recorded in harvest index (89.29), 1000 grain weight (87.67), plant height (77.47), chlorophyll content (77.39), ear length (76.69), days to maturity (73.99), grain yield per plant (73.29), days to 50% heading (72.45), biological yield per plant (65.31) and number of grains per ear (62.58). Moderate heritability values were observed in a no. of productive tillers per plant (58.57), ear weight (55.35) and number of spikelets per ear (40.87). This indicates that the trait is further influenced by ecological influences then administered by non-additive gene action. These results were in accordance with the results of (Akshay *et al.*, 2022) [1].

Genetic Advance as Percent Mean (GAM)

High GAM values were recorded in 1000 grain weight (30.63) and plant height (22.71). Medium standards of genetic advance as a percent of the mean were detected in chlorophyll content (14.29) whereas low values of genetic advance as a

percent (%) of the mean were observed in number of spikelets per spike (8.32), grain yield per plant (7.39), biological yield per plant (6.63), days to 50% heading (5.87), harvest index (5.26), ear length (4.86), days to maturity (4.27), number of

grains per ear (3.28), ear weight (2.00), number of productive tillers per plant (1.42). Following results are in accordance with the results of (Kumar *et al.*, 2020)^[12] and (Naveen *et al.*, 2023)^[18].

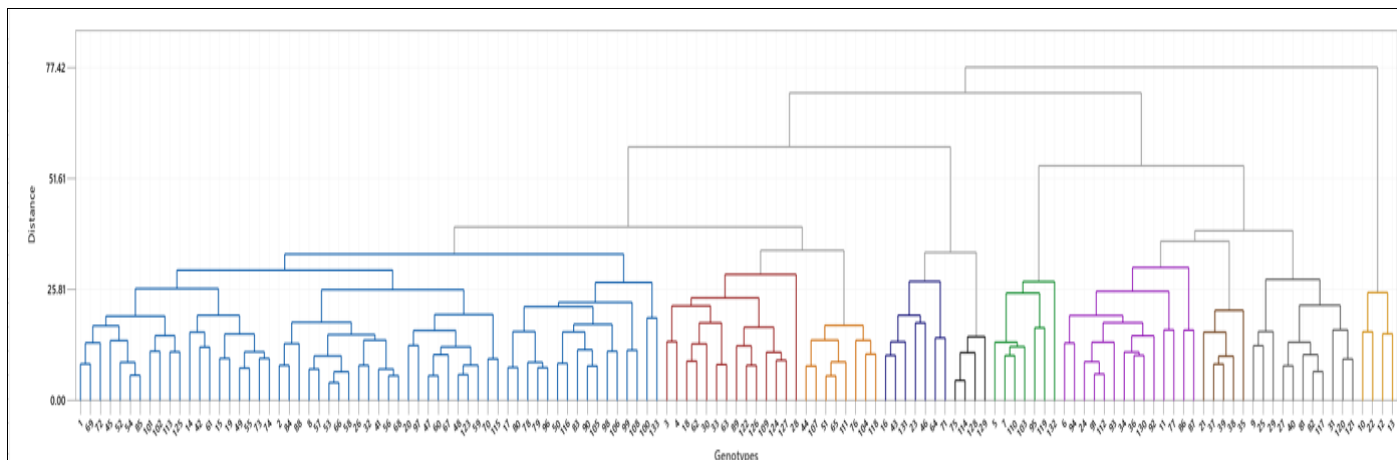


Fig 1: Dendrogram describing war linkage, Euclidean distance

Table 1: Shows is cluster name, number of genotypes average distance and maximum distance

Cluster Name	Number of genotypes	Average distance	Maximum distance
Cluster1	59	10443.6	12.8503
Cluster2	14	2055.1	11.6935
Cluster3	7	1238.1	12.9566
Cluster4	14	2328.7	12.3424
Cluster5	11	1532.1	11.428
Cluster6	4	637.4	12.573
Cluster7	7	1278.1	13.1814
Cluster8	5	452.5	9.0222
Cluster9	8	569.7	8.2956
Cluster10	4	187.5	6.5692

Table 2: Inter and Intra cluster distance

Cluster	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9	Cluster10
Cluster1	20.684	14.2296	28.3554	20.928	15.3914	43.0003	24.2036	40.1278	16.8871	16.4419
Cluster2		19.2992	23.3638	25.579	20.8473	53.7539	37.0591	41.9762	11.7966	23.7686
Cluster3			18.3145	19.312	24.17	51.6843	48.482	28.4666	17.8569	43.2485
Cluster4				21.7595	12.5376	33.227	33.4477	21.7355	23.0189	35.0614
Cluster5					18.24	36.3553	28.1804	26.5428	22.0174	27.8852
Cluster6						13.9844	31.8812	37.0063	53.7305	48.3823
Cluster7							18.1437	48.2058	40.7082	20.6657
Cluster8								13.8616	39.7729	52.7159
Cluster9									10.2764	30.8129
Cluster10										8.8579

Table 3: Cluster Mean

Variable	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9	Cluster10
DTH	90.644	91.857	90.429	90.5	91	89.75	90.143	93.4	90.75	93.75
DTM	125.695	127.929	126.857	126.071	126.455	124.75	125.143	128.4	126.375	128.75
PH	79.471	77.071	97.025	99.896	90.476	111.675	80.247	114.7	82.237	68.18
NPT	5.236	4.948	5.057	5.362	5.667	5.017	5.229	5.853	5.242	5.05
EL	8.21	8.284	8.146	8.356	8.458	7.895	7.946	8.708	8.218	7.865
NSPE	15.668	14.871	15.171	16.943	17	15.975	15.686	17.56	15.475	15.15
EW	2.368	2.507	2.399	2.525	2.663	2.303	2.455	2.462	2.5	2.352
NGPE	41.58	40.007	35.771	41.693	46.864	44.45	42.929	45.48	40.412	41.05
TGW	36.442	38.893	39.603	38.514	44.143	40.455	40.019	52.68	33.8	37.422
CC	38.813	43.538	36.214	37.935	37.206	37.767	38.842	34.841	36.304	44.667
BYP	17.405	21.798	24.164	19.938	21.675	15.075	13.314	22.002	18.875	16.1
HI	54.027	42.222	34.112	51.424	53.477	81.801	77.527	48.327	38.048	63.275
GYP	9.36	9.152	8.175	10.183	11.506	12.139	10.353	10.662	7.157	10.213

Table 4: Genotypic and phenotypic variance, GCV, PCV, Heritability (Broad sense), genetic advance (%) and Genetic advance at mean (GAM %)

Characters	Range		Mean	Co-Variance		h ² bs (%)	GA	GA% Mean
	Minimum	Maximum		GCV (%)	PCV (%)			
Days to heading	80.79	101.54	91.27	3.34	3.93	72.45	5.36	5.87
Days to maturity	119.17	136.92	126.26	2.41	2.80	73.99	5.39	4.27
Plant height (cm)	64.50	126.26	85.60	12.51	14.21	77.47	19.44	22.71
Number of productive tillers per plant	3.40	6.42	5.25	2.35	8.04	58.57	0.07	1.42
Ear length (cm)	5.74	11.47	8.18	4.59	9.61	76.69	3.68	4.86
Number of Spike lets per spike	13.19	24.49	15.82	6.31	9.87	40.87	1.32	8.32
Ear weight (gm)	1.08	3.67	2.39	4.05	16.91	55.35	0.05	2.00
Number of grains per ear	28.32	56.19	42.49	6.38	9.47	62.58	1.58	3.28
1000 Grain weight (gm)	24.53	57.21	38.32	15.86	16.94	87.67	11.74	30.63
Chlorophyll content	25.06	63.92	38.20	11.39	12.97	77.39	10.39	14.29
Biological yield per plant	11.14	32.59	18.50	8.22	21.01	65.31	1.23	6.63
Harvest index (%)	28.87	89.92	52.76	17.29	21.76	89.29	4.49	5.26
Grain yield per plant	5.46	15.17	9.55	11.49	19.81	73.29	5.79	7.39

The result of analysis of heritability and genetic advance for 129 genotypes, based on 143 morphological traits and yield components data revealed that heritability estimates were highest for the Harvest index (89.29) and 1000 grain weight (87.67)

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