

Diversity Analysis of Wheat Hybrids Grown under Timely and Late Sown condition

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ABSTRACT: To allow for more efficient genetic improvement, an assessment of genetic variance within various germplasm is required. Sixty- eight hybrid wheat genotypes including 10 CMS lines, 5 restorer and 3 checks were evaluated for 13 breeding traits in randomized block design in two environments to find out how much genetic variability there is between genotypes for grain yield and other agronomic traits. Average linkage cluster analysis classified 68 genotypes into four clusters. Higher inter-cluster distance was found between cluster III and II ($D^2 = 345.07$), followed by cluster IV and II ($D^2 = 319.31$), cluster IV and I ($D^2 = 196.69$), cluster II and I (166.17), cluster IV and III (150.02) and cluster III and I (131.79) indicating wider genetic diversity among these clusters. To improve the breeding traits for the enhancement of genetic gain, the parental lines may be crossed with the lines found higher inter cluster distance. Hybridization in between the genotypes of higher inter cluster distance possibility of the obtaining of good recombination with high breeding value. As a result, the goal of this study was to evaluate the level of genetic variation in hybrid wheat and its parental lines so that critical distinguishing breeding traits for future crop development could be identified.

Keywords: Hybrid wheat, Cluster analysis, Genetic distance, Genetic diversity.

INTRODUCTION

Wheat (*Triticum aestivum* L.) belongs to the family Gramineae (Poaceae) has been a staple food of the major civilizations for 8000 years. It is the world's most widely farmed cereal crop, accounting for 17 percent of global agricultural area, feeding roughly 40% of the world's population and providing 20% of total food calories and protein in human nutrition (Ajmal *et al.*, 2013; Getachew *et al.*, 2017; Kumar *et al.*, 2021). To feed an ever-increasing population, improved genotypes are needed to boost wheat production potential per unit area. This could be accomplished by making the most of wheat genetic material's genetic potential. With

109.52 million tonnes of wheat produced, India is the world's second-largest wheat producer. Madhya Pradesh is the world's second-largest wheat grower, with 6.69 million hectares, 17.58 million tonnes, and 2627 kilograms per hectare, respectively. (Anonymous, 2020-21). Analyzing the targeted wheat output at the national level in order to meet demand by 2025 AD could be difficult. As a result, hybrid breeding appears to be one of the options for meeting demand. Wheat's low cross-pollination capacity is a serious issue in hybrid seed production. Apart from the aforementioned issues, hybrid wheat development faces a number other challenges (Kumar *et al.*, 2021). The lack of genetic diversity among parents for harnessing heterosis, out-

crossing/natural crossing potential, complete fertility restoration and efficient and cost-effective hybrid seed production technology are notable (Goyal *et al.* 2020). Therefore, exploring genetic diversity in the available germplasm is a prerequisite in a breeding program to effectively utilize the superior genotypes. Genetic diversity is indispensable for species adaptation to variable environmental conditions, it is valuable for germplasm collection and conservation and, the information also helps to study heterosis (Virk *et al.* 2003; Duran *et al.* 2009). Plant breeding depends on the correct combination of specific alleles at the genetic loci present in a plants' genome (Hoisington *et al.* 1999). An assessment of genetic variation within varied germplasm is required to access alleles responsible for important agronomic features, allowing for more effective genetic improvement (Huassmann *et al.* 2004). As a result, the purpose of this study was to determine the level of genetic variety in hybrid wheat and its parental lines in order to identify essential distinct breeding traits for future crop improvement.

MATERIALS AND METHODS

The experimental materials comprised of 68 wheat hybrids including 10 CMS lines, 5 restorer lines and 3 checks which were raised under timely (E1) and late sown condition (E2) during *Rabi* season, 2020-21 in a randomized block design with three replications at research area of Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (Madhya Pradesh). The plot size was 2.5 × 0.80 m with row to row spacing of 20 cm. Observations for all the traits were recorded by taking five plants per plot basis. The data were recorded for

days to 50% flowering, days to maturity, plant height, number of effective tillers per plant, number of spike per plant, number of spikelets per spike, spike length, spike weight, number of grains per ear, thousand grain weight, biological yield per plant, harvest Index (%), and grain yield per plant. The pooled data from the sampled plants regarding different quantitative characters were used for various statistical analyses. The magnitude of genetic diversity among cytoplasmic lines of wheat was determined by using D^2 statistics Mahalanobis (1928). Hierarchical clustering using Tocher's method, as described by Rao (1952). The statistical tool INDOSTAT were utilized for data analysis.

RESULTS AND DISCUSSION

The level of genetic variation between parents determines how much genetic improvement can be achieved through hybridization and selection. Hailu *et al.* (2016); Birhanu *et al.* (2017); Kumar *et al.* (2021). The level of genetic diversity present among the genotypes could not be explained, despite the fact that the analysis of variance demonstrated substantial heterogeneity among the genotypes Kumar *et al.* (2021). Therefore, cluster analysis was performed to quantify the genetic divergence between any two genotypes or groups of genotypes.

Divergence analysis is performed using Mahalanobis (1928) D^2 distance to classify the diverse genotypes for hybridization purpose (Tables 2 and 3). The amount of genetic improvement achieved through hybridization and selection is determined by the genetic distance between parents.

Table 1: Distribution and grouping of 68 hybrid wheat genotypes into different diversity classes based on D^2 analysis.

Cluster No.	Number of genotypes	Genotypes included in the cluster
1.	42	JW 3382, CMS84A × Res 936, CMS86A × Res 936, CMS89A × Res 936, CMS96A × Res 936, CMS97A × Res 936, CMS2041A × Res 936, CMS84A × Res 902, CMS84A × Res 37, CMS85A × Res 37, CMS88A × Res 37, CMS89A × Res 37, CMS94A × Res 37, CMS96A × Res 37, CMS97A × Res 37, CMS2851A × Res 37, CMS84A × Res 9, CMS85A × Res 9, CMS88A × Res 936, CMS88A × Res 9, CMS94A × Res 9, CMS96A × Res 9, CMS97A × Res 9, CMS2041A × Res 9, CMS2851A × Res 936, CMS86A × Res 902, CMS88A × Res 902, CMS89A × Res 902, CMS94A × Res 902, CMS97A × Res 902, CMS2041A × Res 902, CMS2851A × Res 902, CMS85A × Res 2003, CMS86A × Res 2003, CMS88A × Res 2003, CMS94A × Res 2003, CMS96A × Res 2003, CMS97A × Res 2003, CMS2041A × Res 2003, CMS2851A × Res 2003, CMS85B × CMS96B
2.	12	CMS2041B, CMS2851B, Res 936, CMS94A × Res 936, Res 37, CMS96A × Res 902, CMS89B, CMS86B, CMS86A × Res 9, CMS89A × Res 9, Res 2003, CMS84B
3.	08	CMS85A × Res 936, Res 902, CMS88B, Res 9, CMS89A × Res 2003, CMS85A × Res 902, CMS94B, GW 322
4.	06	HI 1544, CMS2041A × Res 37, CMS86A × Res 37, CMS84A × Res 2003, CMS2851A × Res 9, CMS97B

The inter-cluster distances were greater than intra-cluster distances, which indicated the presence of a considerable amount of genetic diversity among the genotypes studied. The greater the magnitude of intra and inter cluster distance the higher the variability among the cluster and within the cluster and *vice versa*. The results are in concurrence with the findings of Kumar *et al.* (2021); Sen and De (2017). The highest intra cluster distance was recorded in Cluster I (56.76) followed by Cluster II (14.10). Inter-cluster distance values (D^2) between four clusters are presented in the (Table 2). The highest inter-cluster distance was exhibited between cluster III and II ($D^2 = 345.07$), followed by cluster IV and II ($D^2 = 319.31$), cluster IV and I ($D^2 = 196.69$), cluster II and I (166.17), cluster IV and III (150.02) and cluster III and I (131.79) indicating wider genetic divergence among the clusters. Thus, crossing of genotypes between members of cluster II with members of cluster III; members of cluster II with members of cluster IV; members of cluster I with members of cluster II, III and IV may produce high amount of heterotic expression in the F_1 's and broad spectrum of variability in segregating (F_2) populations. Genetic divergence in bread wheat genotypes reported by earlier workers Hailegiorgis *et al.* (2010); Degewione and Alamerew, (2013); Fellahi

et al. (2013); Ali *et al.* (2008).

The genotypes were grouped in such a way that cluster I had the largest member of all clusters with 42 (61.7%) genotypes, followed by cluster II with 12 (17.6%), cluster III with 8 (11.7%) and cluster IV with 6 (8.82%) genotypes (Table 1). The trait grain yield per plant contributed maximum to genetic divergence followed by number of spikelets per spike, days to 50% flowering, days to maturity, spike weight, plant height, harvest index, 1000 grain weight, biological yield per plant, number of spike per plant, spike length, number of grains per year and number of effective tillers per plant. The mean values of the 13 quantitative traits for each cluster are presented in Table 3. The highest cluster mean values were recorded for characters days to 50% flowering, plant height, number of effective tillers per plant, number of spikes per plant, number of spikelet's per plant, spike length, spike weight, number of grains per ear, biological yield per plant and grain yield per plant in cluster III, days to maturity, 1000 grain weight and harvest index in cluster IV (Table 3). As a result, these clusters may be superior for choosing genotypes as diverging parents. In hybridization programmes, distantly placed cluster genotypes are used to obtain a wide range of genetic diversity. (Kumar *et al.*, 2006; Devi *et al.*, 2010).

Table 2: Inter and intra cluster D^2 values for different clusters in hybrid wheat genotypes.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	56.76	166.17	131.79	196.69
Cluster II		14.10	345.07	319.31
Cluster III			0.00	150.02
Cluster IV				0.00

Table 3: Cluster mean for yield and yield contributing traits in hybrid wheat.

Characters	Cluster I	Cluster II	Cluster III	Cluster IV
Days to 50% flowering	63.12	39.67	63.33	46.83
Days to maturity	122.56	112.08	137.33	154.50
Plant height (cm)	86.58	69.25	88.83	76.00
Number of effective tillers per plant	15.24	15.58	24.83	18.00
Number of spikes per plant	13.92	13.50	24.17	14.50
Number of spikeletes per spike	16.98	10.33	22.00	14.00
Spike length (cm)	9.31	6.65	13.15	8.63
Spike weight (gm)	2.64	2.17	3.98	3.26
Number of grains per ear	36.84	31.92	53.17	33.00
1000 grain weight (g)	42.10	42.32	34.33	43.55
Biological yield per plant (gm)	38.79	33.25	54.93	25.98
Harvest index (%)	36.67	45.68	48.51	51.21
Grain yield per plant	14.13	15.03	26.66	13.28

CONCLUSION

Overall variability within a crop is due to heritable and non- heritable components. The present study comprised 68 hybrid wheat genotypes including 15 parental lines with 3 checks that were evaluated at two environments to study the genetic diversity. The highest inter-cluster distance was exhibited between cluster III and II ($D^2 = 345.07$), followed by cluster IV and II ($D^2 = 319.31$), cluster IV and I ($D^2 = 196.69$), cluster II and I (166.17), cluster IV and III (150.02) and

cluster III and I (131.79), indicating wider genetic diversity among the clusters. Therefore, initiating crossing program between parental lines of cluster II with members of cluster III; members of cluster II with members of cluster IV; members of cluster I with members of cluster II, III and IV may produce a high amount of heterotic expression in the F_1 's and broad spectrum of variability in segregating (F_2) populations. As a result, hybrids with a high inter cluster distance and intra cluster distance may be

investigated to determine which trait is responsible. These hybrids contribute to the high inter- and intra-cluster distances by being present in several clusters. We can plan to identify the parental lines based on distance, which hybrids provide greater distance hybrids, and which characteristic plays a big role in the production of diverse hybrids. These data could be used to develop a systematic breeding programme for wheat genetic improvement in the future.

FUTURE SCOPE

As a result, hybrids with a high inter cluster distance and intra cluster distance may be investigated to determine which trait is responsible. These hybrids contribute to the high inter- and intra-cluster distances by being present in several clusters. We can plan to identify the parental lines based on distance, which hybrids provide greater distance hybrids, and which characteristic plays a big role in the production of different hybrids. These data could be used to develop a systematic breeding programme for wheat genetic improvement in the future.

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Conflict of Interest. None.

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