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GENETIC DIVERGENCE OF WHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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ABSTRACT

An experiment was carried out with forty four genotypes of wheat (*Triticum aestivum* L.) collected from CIMMYT, Mexico in Randomized Block Design (RBD) with two replications under late sown condition to estimate the genetic diversity. Eight different morphological characters *viz.* plant height (cm), days to 50% heading, days to 50% flowering, 1000 seed weight (g), spike length (cm), number of effective tillers m⁻², number of grains spike⁻¹, grain yieldplant⁻¹ were considered for analysing the data. The D² analysis grouped the 44 genotypes into seven clusters indicating ample magnitude of diversity present in the experimental materials. The character plant height (cm) contributed maximum (28.01%) towards divergence followed by 1000 seed weight (24.31%), spike length (20.40%) and grains spike⁻¹ (13.95%). Highest inter cluster distance was observed between cluster V & III followed by III & VII and IV & VII, suggesting the genotypes selected from these clusters can be used for hybridization program to retrieve high potential desirable lines. Hybridization between accession 3045 of cluster III and accession 3056 from cluster V could give new recombination and transgressive segregants in the progenies produced desired from their crossing.

Key words : D² analysis, Genetic Diversity, Wheat.

Introduction

Wheat (*Triticum aestivum* L.) is one of the oldest and the second most important cereal crop grown after maize. Wheat belongs to Poaceae family having many species that come under the genus *Triticum*. Wheat is called as king of cereals as it is the staple diet for most of the population worldwide and can be cultivated under different kinds of climatic and soil conditions compared to any other grain crop. In India, the acreage under wheat was 303.06 lakh hectares during 2020-21 with production of 111.32 million tonnes and in West Bengal, it is 2.16 lakh hectares (DES; DWD, Gurugram, 2022). The largest wheat producing state is Uttar Pradesh with average production of 35.50 million tonnes (Directorate of Economics & Statistics, DAC&FW, 2020-21). China, India, Russia are the topmost wheat producing countries globally contributing to 41 percent of total world's wheat production. USA occupies fourth position in wheat production.

There is an increased demand for raising food grain production to feed the growing population globally. Various abiotic and biotic factors like salinity, water logging, heat stress, cold stress, droughts, pest and diseases affect severely the wheat grain production. In the present scenario for maintaining food security, wheat grain production is considered as major challenging task for countries worldwide (Curtis and Halford, 2014). Hence, availability of quality seed of improved genotypes is one of the most important aspects to be considered for increased grain production. Over the past century, selection of desirable parents for hybridization programme has been found effective in developing high yielding crop varieties. Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny. Genetic distance can be used to measure the genetic divergence

between different genotypes. Higher the genetic distance between parents, higher is the transgressive segregation that results into higher heterotic expression of the future generation. The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analysis of genetic relationships among breeding material (Mohammadi and Prasanna, 2003). Thus, the present study was undertaken to investigate the genetic diversity among the genotypes and identification of genotypes by cluster analysis for improvement of grain yield through future breeding program.

Materials and Methods

The present experiment was carried out during Rabi season in the year 2021-22 at AB Block farm, Bidhan Chandra Krishi Viswavidyalaya (BCKV), which is located at 23.5° North Latitude and 89.0° East Longitude with an altitude of 9.75 m above the mean sea level in Nadia, West Bengal, India. The experimental design was Randomized block design with two replications having plot size 1.2 m × 2.75 m. Row to row distance and plant to plant distance was 22.5cm and 10 cm respectively. Seeds of 44 genotypes including two checks (NADI#1 and DBW303) were collected from CIMMYT, Mexico. Eight morphological characters *viz.* plant height (cm), days to 50% heading, days to 50% flowering, 1000 seed weight (g), spike length (cm), number of effective tillers m², number of grains spike⁻¹, grain yield plant⁻¹ were considered for genetic divergence (D²) analysis. A basal dose of fertilizer N, P₂O₅ and K₂O @ 60:60:40 kg ha⁻¹ in the form of Urea, SSP and MOP was applied prior to sowing. Top dressing of N fertilizer @60 kg/ha⁻¹ was applied at 30 days after sowing. Irrigation, inter-culture operations and plant protection measures were followed as per necessity. Recording of data was done for randomly selected five plants in each plot and in both replications. Data analysis done using Mahalanobis D² statistics (Mahalanobis, 1936) and the average intra and inter cluster distances were evaluated according to the procedure summarized by Singh and Choudhary (1977) by using GENRES software.

Results and Discussion

Genetic Divergence

The degree of genetic diversity between parents determines the extent to which the genetic

improvement can be achieved through hybridization and selection (Hailu *et al.*, 2016). Furthermore, significant genetic variability was documented for grain yield and its component characteristics by Asif *et al.* (2004) and Kumar *et al.* (2009) in wheat. In present experiment, based on D² Analysis values, the 44 genotypes were grouped into 7 clusters using Agglomerative cluster methods as shown in Table 1.

Among the 7 clusters, cluster II and VII represented the largest group that comprised of 9 entries followed by cluster VI (8 entries) and cluster I and IV (7 entries) similar to work of Ali *et al.* (2017), where 8 clusters observed for 30 genotypes of wheat crop. Cluster III and V consisted of least number of entries (2 entries each). Entries within a cluster depicts narrow genetic diversity among them. Similar such experiments were reported by Juhi Pandey *et al.* (2021); Chaudhary *et al.* (2022). Both standard international and national checks were present in cluster I, indicating similarities between both the check entries (Fouad *et al.*, 2020).

Intra and Inter-Cluster Distances

The average intra and inter cluster distance as depicted in Table 2. revealed that among 44 entries, the maximum intra cluster distance (D²) was observed in cluster VII (31.851) followed by cluster VI (30.983) indicating the broad range of genetic diversity within these

Table 1 : Distribution of 44 genotypes into 7 clusters based on D² value.

Cluster	No. of genotypes	Accessions
I	7	3001(NADI#1),3002(DBW303),3003,3004,3005,3035,3036
II	9	3006,3007,3008,3009,3010,3012,3013,3023,3041
III	2	3043,3045
IV	7	3015, 3016,3019,3021 ,3022,3029,3039
V	2	3056,3058
VI	8	3024,3025,3028,3030,3031,3032,3038,3051
VII	9	3034,3040,3042,3046,3048,3053,3055,3057,3059

Table 2 : Average intra and inter cluster distances.

Cluster No.	I	II	III	IV	V	VI	VII
I	24.348	25.870	22.690*	30.495	33.288	28.228	32.547
II		26.378	27.893	32.666	30.639	28.720	29.408
III			6.694*	32.043	39.431**	30.272	35.898
IV				26.355	25.531	29.919	34.695
V					8.620	28.105	27.660
VI						30.983	31.550
VII							31.851**

Bold intra cluster distances, **highest, * lowest values.

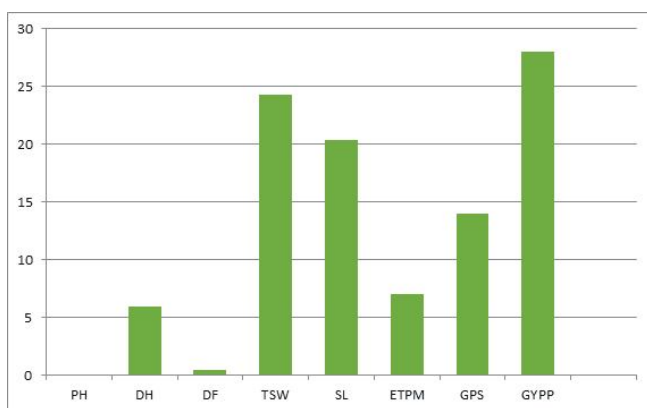


Fig. 1 : Percent contribution towards Genetic Divergence for different characters. **PH**- Plant height (cm), **DH**- days to 50% heading, **DF**- days to 50% flowering, **TSW**-1000 seed weight (g), **SL**-spike length (cm), **ETPM**-number of effective tillers m², **GPS**- number of grains spike⁻¹, **GYPP**- grain yield plant⁻¹.

Table 3 : Cluster means of 8 characters in D² analysis.

Character	PH	DH	DF	TSW	SL	EIPM	GPS	GYPP
Cluster I	72.547	62.514	71.143	26.066	16.857	224.929	37.071	6.096
Cluster II	73.800	60.722	69.222	24.930	16.325	266.944	33.667	6.381
Cluster III	72.825	66.500	74.750	24.825	16.200	333.500	48.500	4.965
Cluster IV	79.071	60.429	69.143	29.126	14.861	344.071	36.714	6.094
Cluster V	70.825	52.750	61.500	30.175	16.800	390.000	34.000	8.355
Cluster VI	79.087	58.375	68.938	27.382	16.829	311.875	35.563	6.384
Cluster VII	75.572	56.722	65.833	26.184	16.856	354.278	32.778	7.087

PH- Plant height (cm), **DH**- days to 50% heading, **DF**- days to 50% flowering, **TSW**-1000 seed weight (g), **SL**- spike length (cm), **ETPM**-number of effective tillers m², **GPS**- number of grains spike⁻¹, **GYPP**-grain yield plant⁻¹.

Table 4 : Relative character contribution towards Genetic Divergence.

Character	Times ranked First	% contribution to divergence	Cumulative percentage
PH	0	0.00	0.00
DH	56	5.9197	5.9197
DF	4	0.4228	6.3425
TSW	230	24.3129	30.6554
SL	193	20.4017	51.0571
EIPM	66	6.9767	58.0338
GPS	132	13.9535	71.9873
GYPP	265	28.0127	100
Total	946	100	

PH- Plant height (cm), **DH**- days to 50% heading, **DF**- days to 50% flowering, **TSW**- 1000 seed weight (g), **SL**- spike length (cm), **ETPM**- number of effective tillers m², **GPS**- number of grains spike⁻¹, **GYPP**-grain yield plant⁻¹.

clusters and minimum intracluster distance was observed in cluster III (6.694) representing lesser diversity under this cluster.

Inter-cluster distance is the main criterion for selection of genotypes using D² analysis (Khare *et al.*, 2015). The range of inter cluster distance was from 22.690 to 39.431. The maximum inter cluster distance was observed between cluster III and V (39.431) pursued by cluster III and VII (35.898) indicating the diversity of entries. When crossing of entries between higher inter cluster values is made, it is expected to show high heterotic response in successive generations. Least values of inter cluster distance was observed between cluster I and III (22.690).

Cluster Mean Values

Table 3 depicts the cluster means for all the morphological characters showing a significant difference across the groups. The highest cluster mean for the character grain yield plant⁻¹ was recorded undercluster V (8.355) chased by cluster VII (7.087) and least in

cluster III (4.965).

Cluster III (48.500) showed maximum cluster mean values followed by cluster I (37.071) for grains spike⁻¹. For the character number of effective tillers m², cluster V (390.000) showed highest cluster mean pursued by cluster VII (354.278). Cluster I (16.857) represented highest spike length followed by cluster VII (16.856). Highest cluster mean values for 1000 seed weight (g) was recorded in cluster V (30.175) followed by cluster IV (29.126). The cluster mean values for days to 50% flowering seem to be highest in cluster III (74.750) chased by cluster I (71.143). In case of days to 50% heading, cluster III (66.500) recorded highest cluster mean followed by cluster I (62.514). Plant height showed high cluster means in cluster VI (79.087) followed by cluster IV (79.071) and least value was observed in cluster V (70.825). Therefore, it is concluded that cluster VII genotypes with highest mean grain yield plant⁻¹ were considered for selection of parents.

Contribution towards genetic divergence

The percent contribution of characters towards

Table 5 : Desirable Genotypes for different characters.

Character	Rank I	Rank II	Rank III
PH	3051	3039	3016,3023
DH	3056,3034	3058	3051,3055,3057
DF	3034,3058,3056	3057	3055
TSW	3015	3042	3031
SL	3032	3034	3036
EIPM	3053	3046	3021
GPS	3031	3053	3045
GYPP	3057	3024	3040

PH- Plant height (cm), **DH**-days to 50% heading, **DF**-days to 50% flowering, **TSW**-1000 seed weight (g), **SL**-spike length (cm), **EIPM**-number of effective tillers m⁻², **GPS**- number of grains spike⁻¹, **GYPP**-grain yield plant⁻¹.

divergence is presented in Table 4 and its distribution is illustrated in Fig. 1. The character grain yield plant⁻¹ (28.0127) contributed maximum towards divergence followed by character 1000 seed weight (g) (24.3129), Spike length (20.4017), grains spike⁻¹ (13.9535), effective tillers m⁻² (6.9767), days to heading (5.9197) and days to flowering (0.4228).

Yield is an important economical character and the percent contribution towards genetic divergence was highest in grain yield plant⁻¹ compared to all other characters and hence selection based on yield character can be prioritized that may provide opportunity for higher genetic divergence. Similar reports have been observed in rice where yield contribution is more towards divergence (Dutta *et al.*, 2011; Jaiswal *et al.*, 2010). Hence, the percent contribution towards genetic divergence should be considered as one of the criteria for selecting the parents.

Conclusion

The diversity present between genotypes is the best source for selection of parents which upon crossing will lead to better transgressive segregates that remain heritably stable (Rathore *et al.*, 2022).

Based on inter cluster distance, accession 3045 (rank III) from cluster III and 3056 (rank I) as depicted in Table 5 from cluster V can be selected for hybridization programme for improvement of grain yield followed by entries from cluster III & VII and cluster IV and VII. Such crosses from above mentioned clusters can result in transgressive segregants from F₂ generation onwards since cluster V recorded maximum cluster mean value for number of effective tiller m⁻² character and cluster III recorded maximum cluster mean value for the character grain spike⁻¹. Both these characters can result in higher grain yield. The percent contribution towards genetic divergence is highest for grain yield plant⁻¹ compared to all other characters, thus selection based on

yield character can be prioritized, which provide opportunity for higher genetic divergence.

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