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Evaluation Of Genetic Diversity In Wheat Genotypes (*Triticum aestivum* L.)

Naresh Pal[1], Akash Singh[1], Aastha[2], Arun Kumar[2] and Mohit Sirohi[1]
[1]Department of Genetics and Plant Breeding
[2]Department of Agricultural Biotechnology
Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut (U.P.) -250110

ABSTRACT

In any crop improvement program, the presence of genetic divergence is an important entry point for selection and hybridization. Genetic divergences were estimated using Mahalonobis D^2-statistics and principal component analysis. A trial was executed using ninety wheat genotypes with the objective of determining the genetic divergence in wheat crop. The studies were carried out in during the rabi 2014-15 cropping season using a randomized complete block design with three replications. The genotypes were grouped into 10 clusters namely cluster I (34 genotypes), cluster II (44 genotypes), cluster III (genotypes), cluster IV (1 genotype), cluster V (1 genotype) cluster VI (1 genotype) cluster VII (1 genotype) cluster VIII (4 genotypes) cluster IX (1 genotype) and cluster X (2 genotypes). This indicates that the genotypes grouped within a particular cluster are more or less genetically similar to each other and apparent wide diversity is mainly due to the remaining genotype distributed over rest of the other clusters. The maximum intra cluster distance exhibited for cluster VIII (124.718) and lowest for cluster VI (111.063). The maximum inter cluster distance was showed between cluster VI and I (649.474) whereas, minimum between clusters III and II (104.941). The hybridization between the genotypes HUW 658, K-9265 and PBW-533 with Unnat halna, HD- 2932 and DBW 16 would produce heterotic hybrids and wide spectrum of variability in subsequent generations. The grain yield per plant followed by plant height, spike length, days to maturity, number of tiller per plant, dry gluten content, number of spikelet per spike, biological yield per plant and days to 50% flowering contributed most towards genetic divergence.
Key Words: Tritium aestivum, genetic divergence

INTRODUCTION

Wheat (*Triticum aestivum* L) is one of the most important cereal crops of the world as a source of human diet and largest energy rich cereal crop also called as the 'King of cereals. The major breeding objective in bread wheat is to create new improved genotypes with features that contribute to greater yield potential, increased yield stability and improved product quality to hybridize and synthesize high yielding genotypes. To make effective crossing programme, parents should belong to different genetic clusters with high genetic distance. The present studies also confirm the results of earlier workers such as on the yield aspects in different environments. The D^2 statistics (Mahalonobis, 1936) is one of the most important biometrical techniques to estimate genetic divergence present in a population. Selection of parents based on extent of genetic divergence has been successfully utilized in several crops. This experiment was laid with the objectives to identify genetically divergent bread wheat parents genotypes was done. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability. Mahalanobis D^2statistics has extensively been used by several workers to study the genetic diversity in different agronomic crops and to identify the characters or characters responsible for such type of divergence. Using Mahalanobis D^2-statistics, the population can be classified in to different groups. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in a collection of spring wheat genotypes by multivariate analysis (1).

MATERIALS AND METHODS

Ninety diverse accession of wheat were evaluated for grain yield and its component traits in randomized block design with three replications during *rabi*-2014-15 season at crop research center, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each entry was sown in a single row of 2 m length with inter and intra row spacing of 22.5 cm and 10 cm, respectively. Observations on twelve quantitative characters namely days to 50 per cent flowering, plant height, spike length, number of tiller per plant, number of spikelets per spike, days to maturity, biological yield, harvest index, 1000- test weight, gluten content number of grain per spike and grain yield per plant were recorded from five plants in each replication. The mean values were transformed in to uncorrelated linear function for Mahalanobis D^2 analysis [4]. The genotypes were grouped in to different clusters per Tocher's method [5], whereas intra and inter cluster distances were computed.

RESULTS AND DISCUSSION

In the present study ninety genotypes of wheat were subjected to D^2 analysis using twelve component characters. Out of the 10 clusters, cluster I, II, III, IV, V, VI,VII, VIII, IX and X had 34, 44, 1, 1, 1, 1, 1, 4, 1 and 2 genotypes, respectively (Table 2). It was concluded that in general, there was parallelism between genetic and geographic diversity. Genetic diversity is generally associated with geographical diversity. The genotypes within the same cluster although formed specific clusters but were collected from different places, which indicated that the geographical distribution and genetic divergence did not follow the same trend. . The maximum intra cluster distance exhibited for cluster VIII (124.718) and lowest for cluster VI (111.063). The maximum inter cluster distance was showed between cluster VI and VIII (649.474) whereas, minimum between clusters III and I (104.941) Table 1. The maximum intra cluster distance was because of wide genetic diversity among its genotypes.[8] The chance of developing good segregate by crossing to genotypes for the same cluster exhibited low value of intra cluster distances. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding wheat varieties. However, results showed that cluster analysis based on PCA is a more precise indicator of differences among wheat genotypes than cluster analysis (not based on PCA). Evaluation of genetic diversity can be useful for the selection of the most efficient genotypes. Accordingly, if such efforts result in the reduction of diversity, production of plants with higher uniformity may guarantee the production of enough food for the world increasing population. However, so far the breeding strategies have not resulted very much in the reduction of genetic (allelic) diversity. This result is similar finding by (6). The maximum inter cluster distance was revealed between cluster VI and I (649.474) followed by cluster VIII and I (557.823) cluster VI and IV (522.935), cluster VIII and IV (419.032), cluster VII and I (402.319), cluster VI and V (380.393) cluster IX and VI (362.852) and cluster III and cluster II (352.350) (Table-1). These result observed similarity by (7 and 2). The clearly indicates that the genotypes included in this clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of wheat for improving grain yield. The least inter cluster distance was between clusters V and I (176.318) followed by cluster V and IV (447.346) and cluster II and I (412.977). As a consequence, the trait constellation might be associated with particular region and in nature loosed their individuality under human interference. However, in some cases, effect of geographical origin influenced clustering. So, geographic distribution was not the sole criterion of genetic diversity. This suggests that it is not necessary to choose diverse parents from diverse geographic regions for hybridization. Thus the crosses between the genetically diverse genotypes of cluster VI characterized by spike length, number of spikelet per spike, grain yield per plant and gluten content with genotypes RAJ-4120 and cluster IX characterized by plant height, harvest index and grain per spike with these genotypes like K-607 are expected to exhibit high heterosis and are also likely to produce new combination with desired characters to get desirable segregates with higher yield for developing superior variety of wheat. The cluster mean calculated for eleven characters under study have been presented in Table-3. Days to 50% flowering showed highest mean for cluster number III (82.04) and lowest mean for cluster number II (76.60). Days to maturity revealed highest mean for cluster number I (132.76) and lowest mean for cluster number X (121.93). Plant height expressed highest mean for cluster number IX (97.58) and lowest mean for cluster number I (75.18). Spike length exhibited highest mean for cluster number VI (11.03) and lowest mean for cluster number IV (7.40). Number of tillers per plant had highest mean for cluster number II (8.62) and lowest mean for cluster I (7.91).Number of spikelet per spike recorded highest mean for cluster number VI (19.53) and lowest mean for cluster number IV (15.36). Biological yield per plant estimated highest mean for cluster number II (48.48) and lowest mean for cluster number I (39.81). Harvest Index noted highest mean for cluster number IX (39.64) and lowest mean for cluster number II (34.38). Grain per spike was found

highest mean for cluster number IX (53.37) and lowest mean for cluster number IV (42.01). 1000 grain weight observed highest mean for cluster number I (40.76) and lowest mean for cluster number IV (36.75). Grain yield per plant exhibited highest mean for cluster number VI (16.89) and lowest mean for cluster number IV (15.27). Gluten content showed highest mean for culture number VI (8.56) and lowest mean for cluster number III (7.64). The percent contribution of number of grain yield per plant (16.01) followed by plant height (13.60), spike length (12.53), days to maturity (8.86) number of tiller per plant (7.70), dry gluten content (8.86) number of spikelet per spike (6.55) and biological yield per plant (5.82) contributed most towards genetic divergence (Table 4). Remaining characters contributed very little or did not contribute at all towards genetic divergence. These result of similar finding by (3). Based on the genetic diversity and superiority with respect to any of the traits the genotypes may be identified and may be involved in crossing for obtaining high heterotic population, segregants and also may be exploited for development of hybrids wheat.

Table-1 Average intra and inter cluster (D² value) distance in ninety of wheat.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**63.119**	132.782	170.452	115.512	176.318	649.474	402.319	557.823	259.236	322.110
II		**64.017**	104.941	125.377	122.402	333.676	224.326	352.350	170.542	207.394
III			**78.707**	108.159	123.673	337.744	190.155	293.978	119.980	128.848
IV				**65.642**	144.792	522.935	259.234	419.032	125.096	194.870
V					**79.018**	380.393	196.202	250.842	132.343	146.322
VI						**111.063**	217.538	219.893	362.852	284.404
VII							**73.779**	158.555	131.575	152.315
VIII								**124.718**	238.381	168.923
IX									**69.557**	113.664
X										**83.571**

Bold values are intra cluster distances

Table-2 Distribution of ninety genotypes of wheat

Clusters number	No. of genotypes	Genotypes
I	34	LN-15-C,WCW-985,AAI-15-36,AAI-16,PBW-590,K-4014,PBW-343,K-911,K-402,UNNAT HALNA,HUW-658,K-9265,LN-15-B,NW-1014,HD-3086,WH-841,K-427,K-452,K-8962,UP-2765,K-9144,PBW-39,K-910-30,H-985,RAJ-3765,UNNAT HAHANA,K-9162,NW-1076,AAI-11,DBW-6215,UP-2425 PBW-373,HUW-213,K-9423
II	44	HD-2864,HD-2733,HD-3095,HD-2932,LN-26-A,PBW-550,HD-2985,UP-2792,K-8434,MP-3336,K-6525,HUW-251,PBW-533,K-60,WH-1101,K-9107,DBW-16,PBW-98-4,W-1105,W-95-3,K-802,K-9533,HD-3076,WCW-984,HUW-835,PBW-502,PBW-656,LN-12,K-903,RAJ-4246,W-1120,K-710,PBW-226,HD-3068,K-616,NW-4035,HD-2967,MP-4010,MP-1248,HD-2285,PBW-435, ,WH-1021,K-1250,K-991
III	1	WCW-95-5
IV	1	DBW-17
V	1	NW-2636
VI	1	RAJ-4120
VII	1	K-424
VIII	4	DBW-72, CBW-38,NW-5019,HUW-647
IX	1	K-607
X	2	C-306,K-906
Total	**90**	

Table-3 Cluster means values for twelve characters in wheat.

Character \ Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
Gluten content	8.04	8.30	7.64*	8.16	8.09	8.56**	8.16	8.32	8.11	8.18
Grain yield/plant	15.28	16.39	16.10	15.27*	15.71	16.89**	16.44	16.84	16.05	15.35
1000 grain Weight (g)	40.76**	37.35	39.11	36.75*	38.20	39.67	40.16	37.18	39.40	38.70
Grains /spike	43.97	47.07	47.01	42.01*	45.50	52.76	49.86	49.45	53.37**	43.76
Harvest index (%)	39.11	34.38*	36.94	35.45	37.66	39.13	36.72	39.22	39.64**	35.04
Biological yield/	39.81*	48.48**	43.60	43.21	42.08	43.11	45.23	42.92	41.12	44.40
Number of spikelet's/spike	16.61	17.04	17.70	15.36*	16.75	19.53**	18.67	18.37	19.51	16.36
Tillers/plant	7.91*	8.62**	8.08	7.40*	8.36	8.15	8.55	8.44	8.24	8.27
Spike length (cm)	7.74	8.65	9.20	8.22	8.59	11.03**	9.98	9.96	10.47	8.88
Plant height (cm)	75.18*	91.21	81.26	79.48	81.69	89.45	85.73	87.64	97.58**	95.17
Days to maturity	132.76**	123.13	130.83	130.48	126.25	126.79	129.12	124.55	122.11	121.93*
Days to 50% flowering	81.85	76.60*	82.04**	80.03	79.25	81.08	81.75	79.80	79.33	77.36

*, ** represent minimum and maximum values, respectively

Table-4 Contribution of different characters in creating diversity in wheat based on Mahalanobis's *D*² analysis.

Character	Contribution
Gluten content (%)	7.06 %
Grain yield/plant	16.01 %
1000 grain weight (g)	4.07 %
Grains /spike	4.02 %
Harvest index (%)	2.95 %
Biological yield/ plant (g)	5.82 %
Number of spikelet's/spike	6.55 %
Tillers/plant	7.70 %
Spike length (cm)	12.53 %
Plant height (cm)	13.60 %
Days to maturity	8.86 %
Days to 50% flowering	4.77 %

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