

ASSESSING GENETIC DIVERSITY FOR YIELD AND QUALITY TRAITS IN GERMPLASM LINES OF BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

Seventy eight germplasm of bread wheat used to study the nature and magnitude of genetic divergence using Mahalanobis's D² statistics. The data for eight important quantitative traits recorded from the genotypes raised in Randomized Block Design having two replications. The seventy eight genotypes were grouped into eleven clusters. Cluster I was largest with twenty seven genotypes followed by cluster II with twenty five genotypes. The maximum inter-cluster distance was observed between cluster III and IV, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Noteworthy is that cluster VII and VIII exhibited high cluster means for seed yield per plot, spikelets per spike; cluster XI for protein content and cluster X for sedimentation value. Among the eight traits studied, maximum contribution was made by plant height (38.49%), followed by grain yield (32.77%) and sedimentation value (11.59%). Hence, plant height, grain yield and sedimentation value together contribute 82.85 percent towards total divergence. Therefore, these characters may be given importance during hybridization programme.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's leading cereal grain and in India it is the most important food crop next to rice. Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could be misleading. To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons. To achieve this target, the wheat production has to be increased at the rate of < 1 m.mt per annum (Sharma *et al.*, 2011) and this can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergent. The study of genetic variability reveals about the presence of variation in their genetic constitution and it is outmost important as it provide the basis of effective selection. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Kahrizi *et al.*, 2010). The importance of genetic diversity within the overall limits of fitness for realizing heterotic response in the F₁ and broad spectrum of variability in segregating generation has been emphasized by Joshi and Dhawan (1996) Murty and Arunachalam (1966), Bhatt (1970) and Shekhawat *et al.* (2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin, 1985). In order to assess the degree of diversity, D² statistic based on multivariate analysis developed by Mahalanobis (1960), has

been adopted by Jain *et al.* (1979), in hexaploid wheats and by Lee and Kaltsikes (1973). Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Pagnotta *et al.*, (2008) found a good amount of genetic variability for both evaluated agro-morphological and molecular traits and concluded that the variability does not change proportionally. Hence, selection within the clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through intervarietal hybridization (Joshi *et al.*, 2008). In views of these facts, the present experiment was carried out to determine the magnitude of genetic variability parameters for various yield and quality traits in bread wheat.

MATERIALS AND METHODS

The experimental material comprising seventy eight germplasm of bread wheat grown during *rabi* 2012 at All India Coordinated Wheat Improvement Project, University of Agriculture Sciences Dharwad. These were planted in paired row plot of 3m length in RBD with two replications. Data were recorded on five randomly tagged plants for quantitative traits, *viz.*, days to maturity, plant height, spike length, number of spikelets per spike, thousand grain weight, plot yield and

quality traits *viz.*, protein content and sedimentation value. Wilks (1932) criteria were used to test the significance differences in mean values of all the eight characters.

Statistical analysis

Mahalanobis (1936) defined the distance between two populations as D^2 , which was obtained by Tochers method, described by Rao (1952). Contribution of individual characters towards divergence was estimated according to the method described by Singh and Choudhary (1985). Grouping of variety into various clusters was done and average intra and inter cluster distance were estimated. The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez, 1984) and lastly to find out the significance mean difference between varieties different genetic parameters were estimated.

RESULTS AND DISCUSSION

Based on Mahalanobis' D^2 analysis, seventy eight genotypes were grouped into eleven clusters with variables number of genotypes suggesting considerable amount of genetic diversity in the material. The cluster I had maximum 27 genotypes followed by II and III having 25 and 10 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. Cluster IV and V had seven and three genotypes respectively while, the remaining clusters were represented by only single genotype (Table 1). The

genotypes falling in the same cluster are more closely related and hence the clusters having the maximum number of genotypes, reflected narrow genetic diversity (Kumar *et al.*, 2014). The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region (Verma and Mehta, 1976). The intra-cluster D^2 value ranged from 0 to 9.41 while, inter-cluster D^2 value ranged from 9.8 to 22.98 (Table 2). The maximum intra cluster distance was exhibited by the genotype of cluster III (9.41) followed by cluster IV (9.27) and cluster II (8.70). The maximum inter-cluster distance was observed between cluster I and IV (25.50) followed by between clusters I and VIII (22.98) suggesting wide diversity between them and germplasm in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. Similar findings have been reported by Kumar *et al.*, 2014, Vinod kumar *et al.*, 2014 and Garje *et al.*, 2013. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Zaman *et al.*, 2005, Saxesena *et al.*, 2013). Many workers 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.

Table 1: Distribution pattern of 78 genotypes of bread wheat into eleven clusters based on D^2 statistics

Sl. No.	Cluster number	No of genotypes	Genotypes
1	Cluster1	27	WH542, HI1531, PBW579, PBW533, HD2402, HD2864, LOK1, RAJ4037, UAS316, MACS6295, PBW343, WH147, Local collection, C306, HD2687, ANNUJELLO, PBW17, HW5207, PBW343, MACS6222, UP2744, HD2985, AKAW4627, HD2687, HD2285, HD2932, UAS304
2	Cluster2	25	NIAW917, HS420, MACS6274, HS240, HW2036, HD1913, HD2781, RAJ4083, HD2733, PBW638, PBW17, PBW16, HD2733, VL829, MACS6273, UAS320, HS277, NI5439, VL876, MP4107, PBW596, HI977, HD2987, PBW581, HW1085
3	Cluster3	10	C591, HI1500, MACS6145, HW2004, HD2888, K-9107, HW1014, VL804, HI1563, SONALIKA
4	Cluster4	7	BINNU, DATALINE, DRYDALE, JANZ, GLADUS, WYALKATCHEN, YITPI
5	Cluster5	3	BAXTER, SUNLIN, CARNMAH
6	Cluster6	1	LOK45
7	Cluster7	1	HB2987
8	Cluster8	1	MP4080
9	Cluster9	1	C-518
10	Cluster10	1	HUW468
11	Cluster11	1	VL616

Table 2: Average intra and inter cluster D^2 values among 11 clusters for 78 Genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	8.07	11.28	15.19	15.28	15.31	10.88	12.44	11.47	12.92	15.53	12.55
Cluster II		8.7	15.91	17.41	11.57	11.51	15.97	15.09	15.79	12.32	14.47
Cluster III			9.41	25.5	20.69	16.1	11.58	22.98	11.49	22.19	11.95
Cluster IV				9.27	15.32	19.59	20.97	13.14	20.18	19.85	19.04
Cluster V					7.64	17.62	20.64	18.51	17.82	15.95	16.84
Cluster VI						0	14.78	13.43	16.47	9.25	17.13
Cluster VII							0	18.92	9.8	21.27	8.21
Cluster VIII								0	21.13	14.83	19.25
Cluster IX									0	22.79	9.98
Cluster X										0	21.93
Cluster XI											0

Table 3: Cluster means for yield and quality characters in wheat genotypes

	Days to heading	Plant height (cm)	Spike length(cm)	Spikelets/spike	Thousand grain weight (g)	Protein content (%)	Sedimentation value (ml)	Grain yield per plot (g)
Cluster I	58.47	74.02	9.01	16.41	42.81	13.86	41.07	564.13
Cluster II	61.08	71.70	9.39	17.42	38.84	14.75	58.06	684.10
Cluster III	58.05	91.31	9.28	16.03	43.89	15.06	53.35	632.00
Cluster IV	70.68	66.31	9.37	18.83	28.82	14.13	33.43	144.92
Cluster V	71.67	70.83	11.26	17.78	27.78	14.43	63.50	185.17
Cluster VI	60.50	76.84	7.67	13.84	51.23	12.85	47.00	1344.00
Cluster VII	60.00	91.50	8.34	26.00	32.48	15.13	37.00	837.00
Cluster VIII	53.50	59.00	9.59	16.34	46.10	13.90	31.00	772.00
Cluster IX	68.00	93.00	7.92	18.50	36.80	12.95	44.00	153.00
Cluster X	61.50	66.34	8.92	16.34	40.63	12.90	58.50	1529.00
Cluster XI	65.00	89.84	13.25	20.84	32.98	16.85	43.00	387.00

Table 4: Per cent contribution of yield and quality characters towards diversity in wheat

Sl. No.	Characters	No. of first rank	% Contribution
1	Days to heading	303	10.09%
2	Plant height	1156	38.49%
3	Spike length	6	0.20%
4	Spikelets/spike	5	0.17%
5	Thousand grain weight	123	4.10%
6	Grain yield per plot	984	32.77%
7	Protein content	78	2.60%
8	Sedimentation value	348	11.59%
	Total	3003	100%

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 3). Cluster VIII bears lowest mean value for days to heading (53.50). Similarly for plant height cluster IV bears lowest value (66.31) and cluster IX consists of tall type plants with mean value 99.00. Cluster XI consists of genotypes with longest spikes having mean value 13.25. Cluster VII consists of genotypes bearing maximum grains per spike with mean value of 613.84. Thousand grain weight was found to be maximum for cluster VI with mean value of 51.23 followed by cluster VIII (46.10). Same observation was also carried out by Ahmad *et al.*, (2008) and Jaiswal *et al.*, (2010). Protein content was highest in cluster XI (16.85) followed by cluster VII (15.13) and III (15.06). For sedimentation value, the highest mean value was exhibited by cluster V (63.50), whereas minimum was found in cluster VIII (31.00). Eivazi *et al.*, (2007) grouped the wheat genotypes into two clusters for quality characters. The diverse values of different characters for different clusters shows that there exists a moderate level of divergence among genotypes studied. However, for certain characters like protein content, starch content and zeleny value, the diversity amongst all the clusters was found to be minimum, i.e. the mean values do not differ very much. Pagnotta *et al.*, (2008) found a good amount of genetic variability for both evaluated agro-morphological and molecular traits and concluded that the variability does not change proportionally. Noteworthy is that cluster VI, VII and VIII reflected high cluster means for seed yield per plot, number of spikelets per spike and test weight those might be utilized in hybridization-selection breeding programme for wheat

genotypes. Similar findings have also been reported by Tsegaye *et al.*, 2012, Kumar *et al.*, 2013 and Vinod kumar *et al.*, 2014. Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.

The maximum contribution towards the total divergence (Table 4) was exhibited by plant height (38.49%) followed by grain yield (32.77%) and sedimentation value (11.59%). The minimum percentage of contribution was observed in spikelets per spike (0.17%) followed by spike length (0.20%) and protein content (2.60%). The traits *viz.*, plant height, grain yield and sedimentation value contributed 82.85 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and quality traits. Thus the characters which show more percent contribution towards the total divergence should be considered during selection (Kumar *et al.*, 2013). Hybridization between the genotypes of different clusters can give high amount of hybrid vigour and good recombination. Therefore, measuring genetic divergence by biometrical analysis should be more helpful in proper choice of parents for crop improvement programme.

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