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Genetic diversity analysis for morpho-physiological, yield and quality traits in bread bread wheat under irrigated condition

B.A. Veeresha*[1] and V. Rudra Naik[2]

[1]Department of Genetics and Plant Breeding, [2]Principal Scientist (Plant Breeding), All India Coordinated Wheat Improvement Project, University of Agricultural Sciences, Dharwad-580005, Karnataka, India

***e-mail:** ambavee@gmail.com

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Abstract: In the present study, one hundred bread wheat genotypes were evaluated for assessing the nature and magnitude of genetic divergence using Mahalanobis's D^2 statistics. The data for twenty five quantitative traits recorded from the genotypes raised in alpha lattice design with two replications. All the genotypes were grouped into eight clusters. Cluster IV was largest with twenty six genotypes followed by cluster II with twenty four genotypes. The maximum inter-cluster distance was observed between cluster V and VI, suggesting that the genetic makeup of the genotypes in one cluster differ entirely from those included in other clusters. Thus, hybridization among these cluster pairs is recommended for getting high transgressive segregants in F_2 generation. Noteworthy is that both cluster III and II exhibited high cluster means for grain yield (kg/ha) and number of grains per spike, cluster VIII for thousand grain weight, number of spikelets per spike and sedimentation value and cluster VII for protein content. Cluster VII bears highest mean value for chlorophyll content at anthesis (49.40) and during grain filling (after anthesis, 48.28), whereas, Cluster V bears highest mean value for leaf vegetation at anthesis (0.69) and during grain filling (0.50). Similarly Cluster VIII has the lowest mean value for canopy temperature before anthesis (22.90), at anthesis (24.58) and during grain filling (27.20). Among the traits studied, maximum contribution was made by sedimentation value (45.29%), followed by days to maturity (18.59%), relative water content (16.24%) and thousand grain weight (8.42%). Hence, sedimentation value, days to maturity, relative water content and thousand grain weight together contribute 88.54% towards total divergence. Therefore, these traits may be given importance during hybridization programme. Noteworthy is that cluster II, IV, VI and VIII reflected high cluster means for grain yield, spike length, number grains per spike, protein content, number spikelets per spike, thousand grain weight, sedimentation value, and these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

Key words: D^2 statistics, Genetic divergence, Morpho-physiological traits, Bread wheat

Introduction

Wheat (*Triticum aestivum* L.) is an important staple food crop in the world and occupies a unique position as used for the preparation of a wide range of food stuffs. To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons and hence, there is an immediate need to increase to achieve this target (Sharma *et al.,* 2011). This can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergence. In plant breeding programme, direct selection for yield as such could be misleading. 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. The knowledge of genetic variability of yield and yield attributing traits helps in the improvement of grain yield and planning of the future breeding programme. Besides these, the degree of divergence and relative contribution of different components to total divergence helps in identification of selection parameters to be used as criteria for the improvement of yield in wheat (Kumar *et al.,* 2014). Several workers have emphasized the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996). The importance of genetic diversity for realizing heterotic response in the F_1 and broad spectrum of variability in segregating generation has been emphasized by 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). 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 diversity and association of morpho-physiological traits with grain yield. 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). The success of any crop breeding program depends on the nature and magnitude of genetic variability available in the germplasm. The genetic diversity analysis helps in selecting genetically diverse parents. Genetically diverse parents belonging to different genetic backgrounds when brought together in hybridization provide an opportunity to combine genes of diverse nature. They would offer promising segregant derivatives which often result due to complementary interaction of divergent genes in

parents. Along with yield improvement there is added emphasis on improvement in quality of bread wheat to have better quality end products like bread, biscuits and chapatti. Evaluation of germplasm collections is an essential preliminary step to utilize them in further breeding program, using the diversity analysis tools we can quantify the degree of genetic divergence amongst different populations (Jaiswal *et al.,* 2010). Therefore, the present investigation is aimed at estimating the nature and magnitude of genetic diversity for various morpho-physiological, yield and quality traits in bread wheat.

Materials and Methods

The present experiment was conducted to assess the genetic divergence in bread wheat genotypes based on D^2 statistics. One hundred bread wheat genotypes were sown under timely sown irrigated condition in alpha lattice design with two replications during *rabi* 2014-2015 at All India Coordinated Wheat Improvement Project, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad. The crop was raised with all the recommended package of practices. Data were recorded on five randomly selected plants for morpho-physiological traits, *viz.,* chlorophyll content before anthesis (SPAD-1), chlorophyll content at anthesis (SPAD-2), chlorophyll content after anthesis (SPAD-3), normalized difference vegetation index before anthesis (NDVI-1), normalized difference vegetation index at anthesis (NDVI-2), normalized difference vegetation index after anthesis (NDVI-3), canopy temperature before anthesis (°C), canopy temperature at anthesis (°C), canopy temperature after anthesis (°C), flag leaf length (cm), flag leaf width (cm), flag leaf area (cm^2), relative water content (%), leaf waxyness, days to fifty percent flowering, days to maturity, plant height (cm), spike length (cm), number of productive tillers per meter, number spikelets per spike, number grains per spike, thousand grain weight (g), grain yield (kg/ha) and quality traits *viz.,* protein content (%) and sedimentation value (cm).

Genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936). The simultaneous test of differences between mean values of the character studies was done by using Wilks criterion (Rao, 1952). Treating D^2 as the square of generalized distance, all genotype were grouped into a number of clusters, according to the method described by Tocher (Rao, 1952). The average intra-cluster and inter cluster distances and the per cent contribution of characters towards genetic divergence were calculated according to the method described by Singh and Chaudhary (1985).

Results and Discussion

The genetic divergence analysis of twenty five quantitative traits was carried out based on Mahalanobis' D^2 analysis. All the hundred genotypes were grouped into eight clusters with variables number of genotypes under each cluster suggesting considerable amount of genetic diversity in the genetic material. The cluster IV had maximum of twenty six genotypes followed by cluster II with twenty four and cluster I having nineteen genotypes. Cluster III, VI

Table-1: Composition of bread wheat genotypes in different clusters under timely sown irrigated condition

Clusternumber	No ofgenotypes	Genotypes
Cluster I	19	CG 1012, C 591, LOCAL COLLECTION, QCSN-35, RAJ 1482, QCSN-33, PBW 581, MP 4107, NIAW 1994, MP 1293, MACS 6648, GW 322, HB 2987, HW 5207, RAJ 4386, RAJ 4032, HD 2864, UAS 304, UAS 320
Cluster II	24	PBW 721, PBW 396, HI 1531, MP 3288, HD 2781, UAS 365, QCSN-34, UAS 347 QCSN-36, MACS 6274, WH 1166, QCSN-30, HUW 689, QCSN-22, SONALIKA, MP 4080, DHARWAD DRY, GLADUS, K 9644, WH 1080, MACS 6607, LOK 1, HS 240, HD 3172
Cluster III	14	NIAW 2325, HD 1913, HUW 468, LOK 15, HD 2932, DBW 17, AKAW4627, DBW 173, UAS 315, K 1316, NIAW 917, NW 6035, MACS 6222, MP 1292
Cluster IV	26	PBW 343, C 306, HD 2888, NIAW 1415, HD 2329, SONARA 64, PBW 16, UAS 316, WH 147, PBW 533, MP 3424, PBW 638, MACS 6295, PBW 579, JANZ, UP 2744, HI 1500, HS 277, HD 2987, HD 2733, HS 420, DRYDALE, NIAW 2030, HI 1563, HD 3090, HW 1085
Cluster V	4	PBW 596, AKAW 4692, HD 2402, UAS 324
Cluster VI	11	CARNMAH, WYALKATCHEN, DATALINE, BINNU, MACS 6273, SUNLIN, PBW 720, BAXTER, HD 2967, AKAW 3717, YITPI
Cluster VII	1	ANNUELLO
Cluster VIII	1	HI 977

Table-2: Average intra and inter cluster D^2 values under timely sown irrigated condition in bread wheat genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	25.75	39.99	34.67	37.08	40.15	54.73	38.20	49.39
Cluster II		29.18	46.02	49.12	60.43	44.41	61.34	46.35
Cluster III			31.93	50.37	44.58	67.03	41.57	38.59
Cluster IV				31.61	55.17	48.43	43.20	64.17
Cluster V					36.74	79.61	48.86	65.20
Cluster VI						29.74	69.43	69.15
Cluster VII							0.00	55.32
Cluster VIII								0.00

Table-3: Cluster means for different characters under timely sown irrigated condition and their contribution to total divergence in bread wheat genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	% Contribution
X 1	43.99	43.27	42.40	44.68	42.44	44.88	45.70	43.10	0.01%
X 2	47.71	46.95	46.01	48.47	46.10	48.47	49.40	46.55	0.01
X 3	47.71	45.69	44.40	47.54	48.12	45.07	48.28	42.58	0.02%
X 4	0.60	0.58	0.61	0.59	0.60	0.59	0.60	0.58	0.01%
X 5	0.67	0.66	0.68	0.66	0.69	0.66	0.68	0.65	0.01%
X 6	0.50	0.47	0.46	0.44	0.50	0.43	0.40	0.42	0.03%
X 7	23.81	23.29	23.39	23.23	23.64	23.22	23.68	22.90	0.01%
X 8	25.78	25.17	25.69	25.24	24.93	25.18	25.00	24.58	0.01%
X 9	27.08	28.07	27.99	29.50	27.77	29.01	30.95	27.20	0.02%
X10	20.16	20.12	21.90	19.06	19.87	16.83	24.11	24.60	0.12%
X 11	1.05	1.06	1.08	0.93	0.97	0.77	1.15	1.33	0.04%
X12	15.86	16.25	17.67	13.65	14.41	9.83	20.53	24.22	0.02%
X 13	71.52	69.83	60.17	69.36	82.90	68.74	51.35	42.15	16.24%
X 14	2.61	4.02	1.79	2.71	1.50	3.73	2.00	1.00	2.48%
X 15	55.45	58.98	51.89	64.00	47.50	70.18	55.50	52.50	3.35%
X 16	97.76	100.58	94.21	104.94	90.25	110.32	98.50	96.50	18.59%
X 17	76.00	75.05	78.18	75.56	77.12	70.93	74.04	73.75	0.79%
X 18	8.71	8.66	8.58	9.24	8.93	8.60	7.56	8.55	0.36%
X 19	113.82	100.70	94.07	102.79	88.38	115.57	137.50	123.75	1.21%
X 20	17.21	16.77	16.11	17.65	16.19	17.85	16.25	18.55	0.00%
X 21	42.97	43.61	43.82	44.57	40.10	40.35	33.90	40.03	2.95%
X 22	37.28	36.63	40.74	36.92	40.96	29.71	34.58	46.43	8.42%
X 23	3818.55	3970.83	3994.46	3874.04	3512.50	3145.11	3236.25	3800.00	0.08%
X 24	14.58	14.80	14.44	15.08	14.85	15.45	15.80	14.70	0.04%
X 25	58.76	74.33	62.61	52.73	49.25	72.23	48.50	78.50	45.29%

X1 = Chlorophyll content before anthesis (SPAD-1), X2 = Chlorophyll content at anthesis (SPAD-2), X3 = Chlorophyll content after anthesis (SPAD-3), X4 = Leaf vegetation before anthesis (NDVI-1), X5 = Leaf vegetation at anthesis (NDVI-2), X6 = Leaf vegetation after anthesis (NDVI-3), X7 = Canopy temperature before anthesis (^oC), X8 = Canopy temperature at anthesis (^oC), X9 = Canopy temperature after anthesis (^oC), X10 = Flag leaf length (cm), X11 = Flag leaf width (cm), X12 = Flag leaf area (cm^2), X13 = Relative water content (%), X14 = Leaf Waxyness, X15 = Days to fifty percent flowering, X16 = Days to maturity, X17 = Plant height (cm), X18 = Spike length (cm), X19 = Number of productive tillers per meter, X20 = Number spikelets per spike, X21 = Number grains per spike, X22 = Thousand grain weight (g), X23 = Grain yield (kg/ha), X24 = Protein content (%), X25 = Sedimentation value (cm)

and V had fourteen, eleven and four genotypes respectively. While, the remaining clusters VII and VIII were represented by only one 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. The genotypes in cluster VI represent the combination of genotypes of different geographical origin. 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 (Kumar *et al.,* 2014). The intra-cluster D^2 value ranged from 0 to 36.74 while, inter-cluster D^2 value ranged from 34.67 to 79.61 (Table 2). The maximum intra cluster distance was exhibited by the genotypes of cluster V (36.74) followed by cluster III (31.93) and cluster IV (31.61). The maximum inter-cluster distance was observed between cluster V and VI (79.61) followed by between clusters VI and VIII (69.43) suggesting wide diversity between these clusters and they could be used as parents in hybridization programme to obtain desirable segregants. Similar findings have been made by Kumar *et al.,* 2014 and Vinod Kumar *et al.,* 2014. When genetically diverse lines are crossed the chances of getting transgressive segregants are more and hence, selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability in segregating generations (Zaman *et al.,* 2005, Saxesena *et al.,* 2013).

The comparison of cluster means revealed considerable differences among the clusters of different quantitative traits (Table 3). Cluster VI bears highest mean value for chlorophyll content before anthesis (44.88) and Cluster VII bears highest mean value for chlorophyll content at anthesis (49.40) and during grain filling (after anthesis, 48.28), whereas, Cluster V bears highest mean value for normalized difference vegetation index at anthesis (0.69) and during grain filling (0.50). Similarly Cluster VIII has the lowest mean value for canopy temperature before anthesis (22.90), at anthesis (24.58) and after anthesis (27.20). The lowest mean value for days to heading (47.50) and days to maturity (90.25) was seen in cluster V, the same cluster has shown highest mean value for relative water content (82.90). Cluster VIII bears highest flag leaf area (24.22), more number of spikelets per spike (18.55) high thousand grain weight (46.43) and sedimentation value (78.50) and lowest mean value for leaf waxyness (1.00). Similarly for grain yield (kg/ha) cluster III bears highest mean value (3994.46) with mean protein content of 14.44 percent. Cluster VII consists of genotypes with more number of productive tillers per meter (137.50)

and maximum protein content (15.80). The leaf waxyness was found to be highest for cluster II with mean value of 4.02. Cluster IV consists of genotypes bearing maximum grains per spike with mean value of 44.57 and longest spikes having mean value of 9.24. Similar observations were made by Ahmad *et al.,* (2008) and Jaiswal *et al.,* (2010). The genetic divergence for these morpho-physiological traits indicates that these genotypes can be used in breeding for water stress environment. Eivazi *et al.,* (2007) reported moderate level of divergence among genotypes for different traits like protein content, starch content and zeleny value. Pagnotta *et al.,* (2008) reported good amount of genetic variability for both agro-morphological and molecular traits and concluded that the variability does not change proportionally. Noteworthy is that cluster III and VIII reflected high cluster means for grain yield (kg/ha), number of spikelets per spike, thousand grain weight and sedimentation value. Hence, those might be utilized in hybridization followed by selection for the development of wheat genotypes with high grain yield and sedimentation value. Similar findings have also been reported by Tsegaye *et al.,* 2012, Kumar *et al.,* 2013 and Vinod Kumar *et al.,* 2014.

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. Among the characters studied, maximum contribution was made by sedimentation value (45.29%) followed by days to maturity (18.59%), relative water content (16.24%) and thousand grain weight (8.42%). The percentage of contribution observed for spikelets per spike was zero and minimum was for protein content (0.04%). The traits *viz.,* sedimentation value, days to maturity, relative water content and thousand grain weight together contributed 88.54 percent towards total divergence. Therefore, these traits may 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 (Jagadev *et al.* 1991and Kumar *et al.,* 2013).

Thus it is concluded from the present study that, hybridization between the genotypes of divergent clusters can give high amount of hybrid vigour and good recombination. As per the mean values of different characters for different clusters, it can be said that genotypes belonging to these clusters can be used in breeding program for improvement of various yield as well as quality traits. Grain yield, spike length, number grains per spike, protein content, number spikelets per spike, relative water content, thousand grain weight and sedimentation value were important components and these should be taken into account and improvement program involving measuring genetic divergence by biometrical analysis is more helpful in choice of parents for breeding in wheat.

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