RESEARCH PAPER

Analysis of genetic diversity in wheat genotypes

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Abstract : D^2 analysis was studied for yield and its component characters in 169 wheat genotypes. Analysis was done using Mahalanobis's D^2 statistic (1936) as described by Rao (1952). Following the cluster analysis all the 169 genotypes showed that the genotypes were grouped into twelve clusters, with the variable number of genotypes in each cluster. The inter cluster distance was found to be highest between cluster VIII and XI; hence accessions from these clusters are suggested to obtain improvement in seed yield of wheat. Days to 50 per cent flowering, number of spike lets per spike, grain yield per plot and productive tillers per meter length are the most important characters contributing to total divergence.

Key Words : Genetic divergence, Cluster, Transgressive segregants

INTRODUCTION

Improvement of existing varieties is a continuous process in plant breeding. The selection of plants with high genetic variability is basic requirement in any successful hybridization programme. Wheat, a self-pollinating crop, has been bred for wide array of specific end-use quality traits and various adaptive characteristics, resulting in the development of distinct cultivars tailored to specialized end uses and specific production environments. Knowledge of genetic diversity in a crop species is fundamental to its improvement. Evaluation of genetic diversity levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. According to Franco *et al.* (2001) the study of phenotypic and genotypic diversity to identify groups with similar genotypes is important for conserving, evaluating and utilizing genetic resources; for studying the diversity of pre-breeding and breeding germplasm; and for determing the uniqueness and distinctness of the phenotypic and genetic constitutions of genotypes with the purpose of protecting a breeders intellectual property rights.

Genetic divergence analysis plays an important role in assessing the nature of diversity in order to identify the genetically diverse genotypes for their use in plant breeding programmes.

The multivariate analysis by means of Mahalanobis D^2 statistics is found to be an useful in identifying degree of divergence between biological population at genotypic level and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster level. Wheat is the most widely grown cereal in the world, it is the staple food for 35% of the world's population, and is becoming increasingly important in the developing world. To meet the demands for high yielding stress – resistance wheat cultivars desirable to increase the genetic phase of this crop.

MATERIAL AND METHODS

The material for the present investigation consisted of 169 wheat genotypes along with checks DWR 162 and Kalyansona,collected from Directorate of wheat research, Karnal. The experiment was laid out in an Simple lattice Design with two replications. Each genotype in each replication was grown in a plot of 3 rows of 2 meter length

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each with a spacing of 23 cm between rows, at Wheat Improvement Project, Main agricultural Research station Dharwad.

All the agronomic practices were followed during the crop growth period. Observations were recorded on five randomly selected competitive plants for eleven characters days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter, spike length, number of spikelets per spike, number of grains per spike, 1000 grain weight, protein content and grain yield per plot.

RESULTS AND DISCUSSION

Based on D^2 values 169 wheat genotypes were grouped in to twelve clusters. Among the clusters, cluster III was largest consisting of 28 genotypes followed by cluster II,IV,V,VI and VII with 26 genotypes while the cluster I had 6 genotypes. The remaining clusters VIII,IX ,XI and XII were solitary with the single genotype (Table 1). This revealed the presence of divergent genotypes within different clusters, The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. The inter cluster D^2 values also ranged widely with minimum value of 323.29 between cluster VII and IX and maximum value of 1450.95 between clusters VIII and XI indicated high diversity among the genotypes (Table 2). Cluster VIII and XI with single genotype each were the most divergent groups with a maximum inter cluster distance (1450.95). The genotype HI 8381(cluster VIII) had higher grain yield per plot, days to 50 per cent flowering , days to maturity. Whereas, the genotype HB208 in cluster XI had low plant height, peduncle length and higher 1000 grain weight. The results revealed that the mean value of each of the eleven characters showed that the different clusters were superior in respect of different characters (Table 3) It is desirable to select accessions from clusters showing high inter cluster distance (cluster VIII and cluster XI) and also with high grain yield as parents in recombination breeding programmes for obtaining desirable segregants. In conformity with this result earlier Sharma *et al.* (1998) also reported that the genotypes of heterogenous origin/place of release and of different ploidy levels often grouped together in the same cluster, suggesting some degree of ancestral relationship between the genotypes. But, Murthy and Arunachalam (1966) were of the opinion that the wide adaptability would be possible due to factors like heterogeneity, genetic architecture of populations, past selection history, developmental traits and degrees of general combining ability. It appeared that varieties having same geographical origin differed and possessed wide divergence factors, since rapid ecotype differentiation was taking place even in the absence of reproductive isolation (Bennet, 1970).

Table 1 : Clustering pattern of wheat genotypes

Cluster	Genotypes
1st	AJANTA*, AKW1071*, BIJAGA YELLOW+, BW11*, C 306*, CHHOTI LERMA*
2nd	NIAW 34*, UP 301*, NW2036*, HW 741*, UP 2338*, MOTIA*, WH711*, GW 322*, RAJ 911+, VL 829*, SAGARIKA*, NP165*, HS 1097-17*, DWR 137+, HD 1982*, K 8804*, NP 771*, DL 153-2*, JNK-4W-184+, HDR 27*, RIDLEY*, LOK 1*, HUW 234*, PBW 114*, HP 1633*, HD2687*
3rd	PBW 524*, NP 718*, PBW 443*, N59+, PBN 51*, RAJ 1482*, SHARBATI SONARA*, MACS 1967*, K8962*, VL 832*, UP 368*, HW 1085*, HUW 318*, K68*, HS 1138-6-4*, NP 823*, NIDW 15+, GW 405*, UP 2382*, VIJAY+, HI 977*, HD 2009*, DL 784-3*, CPAN 1676*, DWR 162*, HP 1731*, HD 2733*, KARCHIA 65*
4th	PBW 373*, SAFED LERMA*, NP761*, RAJ 821*, MONDHYA 3-2*, HW 657*, MLKS 11*, SONARA 64*, WH 896+, NP 890*, VL 804*, HD 4672+, HS 420*, NI 5749+, K 8027*, LERMA ROJO*, HD 2643*, J-1-7*, GW 273*, K 9644*, DDK 1009#, NW 1014*, HUW 213*, DWR 39*, UP 2121*, HI 8498+
5th	NI 5439*, PDW 215+, HW 2045*, K9107*, HD 2428*, UP 2003*, PBW 65*, VINATA*, K 53*, NP 825*, SONAK*, RAJ 3765*, NP 884*, WH 533*, NP 745*, HD 2824*, DWR 195*, DBW 14*, HUW 65*, HI 1500*, MACS 2694+, HUW 533*, HP 1761*, GW 503*, K7410*, KRL-19*,
6th	WH 542*, NP 836*, K 65*, NI 5643*, VL 401*, RAJ 4037+, HW 517*, HD 2501*, GW 1139+, K 9465*, KSML 3*, HYV 65*, MACS 2846+, DDK 1001#, UP2113*, HUW 206*, K 8020*, HD 2833*, HS 375*, SONALIKA*, PDW 233+, DWR 1006+, NP 760*, NW 1012*, DWR 16*, PBW 343*
7TH	HD 2135*, HI 1077*, DWR 185+, GW 496*, CPAN 1796*, K 852*, HUW 12*, HUW 468*, NIDW 295*, HD 2781*, HP 1744*, KRL 1-4*, RAJ 1555+, SKAML 1*, UP 1109*, NI 917*, WH 147*, NP 824*, JAY#, K 9006*, MACS 2496*, PBW 502*, UTKALIKA*, DL 803-3*, HW 2004*, PBN 142*,
8TH	HI 8381+
9TH	NP 737*
10TH	DT 46
11TH	HB 208*
12TH	KALYANA SONA*

*- T. aestivum   + - T. durum   # - T. dicoccum

Table 2 : Intra (diagonal) and inter cluster distances for 11 characters in wheat genotypes

	Grp1	Grp2	Grp3	Grp4	Grp5	Grp6	Grp7	Grp8	Grp9	Grp10	GRP11	Grp12
Grp1	6.494	750.96	577.43	744.43	748.04	751.47	740.57	1037.34	501.68	422.32	1189.08	606.45
Grp2		188.95	830.56	909.04	864.36	951.21	938.87	1181.43	796.32	652.54	1301.03	435.22
Grp3			157.64	853.92	815.37	776.01	786.08	1020.66	620.45	598.74	1255.92	719.22
Grp4				174.98	934.79	912.99	851.58	1154.81	695.48	723.42	505.42	843.82
Grp5					141.41	904.81	901.27	1125.86	693.77	360.57	1282.29	759.74
Grp6						205.49	937.01	349.52	772.56	728.42	1258.19	873.87
Grp7							169.57	1158.30	323.29	726.57	1226.21	827.98
Grp8								0.000	1030.51	997.42	1450.95	1120.04
Grp9									0.000	468.293	1112.92	659.49
Grp10										0.000	1139.82	526.43
GRP11											0.000	1238.56
Grp12												0.000

Table 3 : Cluster means for 11 characters in wheat

Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	Overall score	Rank
I	60.75 (11)	105.25 (11)	73.55 (3)	32.61 (11)	143.88 (9)	10.20 (2)	17.36 (11)	35.75 (9)	41.79 (8)	14.93 (8)	880.00 (7)	90	11
II	54.58 (4)	90.77 (4)	82.66 (10)	29.87 (8)	163.92 (2)	9.03 (6)	18.58 (4)	36.57 (7)	44.00 (3)	15.13 (3)	900.12 (4)	55	1
III	55.11 (5)	93.23 (5)	80.54 (7)	29.42 (5)	151.30 (8)	8.91 (7)	18.07 (8)	38.65 (2)	42.22 (6)	15.12 (4)	891.96 (5)	62	3
IV	55.44 (7)	93.79 (6)	79.33 (4)	28.77 (4)	157.35 (6)	9.16 (4)	18.81 (3)	40.10 (1)	40.67 (10)	14.97 (7)	858.27 (9)	61	2
V	55.58 (8)	95.19 (8)	82.41 (9)	29.71 (6)	157.80 (5)	9.35 (3)	18.23 (7)	37.68 (4)	42.47 (5)	15.02 (6)	889.40 (6)	67	5
VI	55.42 (6)	94.62 (7)	80.20 (6)	29.86 (7)	161.66 (3)	9.16 (4)	18.56 (5)	36.69 (6)	42.01 (7)	15.31 (2)	854.94 (11)	64	4
VII	56.17 (9)	97.46 (9)	81.70 (8)	30.04 (9)	157.14 (7)	9.09 (5)	17.97 (9)	36.97 (5)	42.83 (4)	14.65 (9)	945.21 (3)	77	8
VIII	69.00 (12)	107.00 (12)	70.33 (2)	28.00 (3)	158.40 (4)	7.60 (10)	18.83 (2)	38.50 (3)	48.33 (2)	13.15 (11)	995.00 (1)	62	3
IX	57.00 (10)	105.00 (10)	88.00 (12)	24.50 (1)	166.35 (1)	11.59 (1)	18.50 (6)	25.85 (11)	34.76 (12)	16.85 (1)	870.00 (8)	73	7
X	52.00 (2)	82.00 (2)	79.96 (5)	39.62 (12)	117.50 (12)	8.49 (9)	20.17 (1)	31.83 (10)	41.35 (9)	14.20 (10)	855.00 (10)	82	9
XI	54.00 (3)	74.00 (1)	62.20 (1)	26.90 (2)	135.55 (11)	6.50 (11)	16.33 (12)	25.50 (12)	56.04 (1)	15.05 (5)	805.00 (12)	71	6
XII	50.00 (1)	83.00 (3)	85.00 (11)	31.67 (10)	140.00 (10)	8.75 (8)	17.50 (10)	36.50 (8)	38.82 (11)	14.40 (9)	960.00 (2)	83	10

Table 4 : Per cent contribution of different traits towards total diversity

Source	Times ranked first	Contribution %
Days to 50% flowering	2156	15.19
Days to maturity	586	4.13
Plant height	1584	11.16
Peduncle length	603	4.25
Productive tillers per meter length	1672	11.78
Spike length	578	4.07
Spikelets per spike	2029	14.29
Grains per spike	759	5.35
1000-grain weight	1558	10.97
Protein content	658	4.64
Yield per plot	2013	14.18

Among 11characters studied, days to 50% flowering found to be most important character contributing to the divergence. The traits like number of spike lets per spike, grain yield per plot, productive tillers per meter length, plant height, 1000 grain weight, number of grains per spike, protein content, peduncle length, days to maturity and spike length were next in order (Table 4). These observations were in accordance with Walia and Garg (1996) for grain yield and number of tillers per unit length, Bergale *et al.* (2001) for plant height and Nimbalkar *et al.* (2002) for number of grains per spike,1000 grain weight and number of productive tillers.

Based on the cluster mean the clusters have been identified for selecting parents for future hybridization programme and accordingly, cluster IX with single genotype identified for selecting as a parent for incorporating dwarfness, number of productive tillers, spike length and protein content. Cluster V for grains per spike, cluster X for number of spike lets per spike and cluster VIII for yield per plot. The genotypes superior in the above cluster may be involved in a multiple crossing programme to recover transgressive segregants with high genetic yield potential.

So hybridization between genotypes of divergent clusters will lead to accumulation of favorable genes in a single varieties involving large number of divergent lines instead of closely related ones.

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