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RESEARCH ARTICLE

AGRO-MORPHOLOGICAL AND GENETIC DIVERSITY AMONG ELITE WHEAT GENOTYPES GROWN UNDER KASHMIR CONDITIONS

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ABSTRACT

Genetic divergence was studied using Mahalanobis D^2 statistics in a set of 68 bread wheat genotypes using 14 quantitative traits. On the basis of which, these genotypes were grouped into 10 clusters. Inter-cluster distances ranged from 4.67 (cluster III and VI) to 15.33 (cluster VIII and IX) and were more than intra-cluster distances which ranged from 0 (cluster X) to 9.25 (cluster II). Based on degree of inter-cluster distances, clusters II, V, VI, VII, IX, and X were regarded as diverse clusters, however, the maximum inter-cluster distance was observed between clusters VIII and IX (15.33) followed by clusters V and IX (14.60) and VII and IX (13.78). This indicates that the genotypes included in these clusters have wide genetic diversity and could be used in hybridization programme which may be aimed at either combination breeding or for exploitation of heterosis. Traits like number of productive tillers per running meter, 1000 grain weight and grain yield had high contribution towards genetic divergence, hence these traits are major determinants of genetic diversity in the present set of genotypes. The presence of significant genetic variability among the evaluated wheat genotypes suggests an opportunity for improvement of grain yield through hybridization of genotypes from different clusters and subsequent selection from the segregating generations.

INTRODUCTION

Wheat (*Triticum aestivum* L.) on account of its wide adaptation to various agro climatic conditions has a prominent position among the grain crops in the world both in area and production. It is the leading grain crop of the temperate climate of the world just as rice is the leading grain crop in the tropics. Globally wheat occupies 216 million hectares area with a production of 650 million tonnes and productivity 30 q ha^{-1} (FAO, 2012). At global level India ranks as second largest wheat producing country, contributing about one-tenth of the global wheat production. The area under wheat cultivation in India is 29.25 million hectares with a production of 85.93 million metric tonnes and a productivity of 29.38 q ha^{-1}. In India, wheat ranks second in area under cultivation after rice. During last five years, the productivity of wheat has increased @ 1.75 per cent while the gross production has gone up by 3.67 per cent (Anonymous, 2012). In Jammu and Kashmir, wheat ranks third both in area and productivity after rice and maize and occupied an area of 0.278 million hectares with a total production of 0.496 million tonnes and a productivity of 17.35 q ha^{-1} (Anonymous, 2010). In Kashmir, wheat is grown on a limited area of 0.96 thousand hectares while in Jammu it occupies an area of 273 thousand hectares. Jammu and Kashmir has been recognized as a food deficit state, necessitating large import of food grains exceeding more than 5 lac tones per annum.

Introduction, evaluation and identification of potentially useful germplasm, is the first and foremost step in a crop improvement programme. The high yielding genotypes with good adaptation and agronomically desirable attributes could be directly utilized for general cultivation. However, an effective and massive hybridization programme would be a viable approach and for such a hybridization programme to be successful, the characterization and variability pattern of the available germplasm holds a promise. To sustain the high productivity level of wheat, genetic variability existing in nature or created through crop breeding is of immense value. Genetic uniformity within a crop is readily brought about by using the same gene or gene complexes during breeding programmes. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it. To overcome the menace of this uniformity, it is essential that genetic variability, present in both the cultivated and wild species, is systematically exploited and used to generate new gene complexes for higher grain yield and tolerance to biotic

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and abiotic stresses. The effectiveness of selection depends upon the range of genetic variability already existing in the population in respect of important economic characters. The progress of breeding is conditioned, primarily by the magnitude, nature and inters relationship of genetic variation for various plant characters in such a population.

Before attempting diversity analysis, it is pertinent to understand some basic concepts. The variability present among different genotypes of a species is known as genetic diversity. Genetic diversity in crops arises due to mutation, recombination, and geographical separation or due to genetic barriers to crossability. Variability differs from diversity in the sense that the former has observable phenotypic differences whereas; the latter may or may not have such an expression. Genetic divergence refers to degree of diversification with regard to component traits and determines the relative proportion of each such trait to the total divergence. Phenotypic variability is the observable variation present in a population, it includes both genotypic and environmental components of variation and, as a result its magnitude differs under different environmental conditions. Genotypic variation on the other hand is the component of variation which is due to the genotype differences among individuals within a population and is the main concern of the plant breeder. Phenotypic plasticity is the consequence of efficient physiological mechanisms which compensates for the disturbances due to environment. Genetic control of development of a line in such a manner that it is able to adjust to the recurrent fluctuations in the environment so that the vital functions of line continue unimpaired. It is responsible for genotypic variability by minimizing the effects of natural selection. Quantitative traits are highly influenced by the environment. Consequently it becomes difficult to determine heritable genetic differences on the basis of phenotype of a plant. Therefore, quantitative assessment of degree of divergence in parental varieties entering the crosses is essential.

Understanding of genetic diversity in a crop species is a key to its improvement under changing environments (Sajjad *et al.,* 2011). Evaluation of genetic diversity among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. Knowledge about germplasm diversity and genetic relationships among breeding materials could be an invaluable aid in crop improvement strategies (Mohammadi and Prasanna, 2003) and study of the genetic diversity in bread wheat is important to breeding and genetic resource conservation programs (Zhang *et al*., 2011). Hence, a technique which can provide direct and reliable estimates of diversity at genotypic level will be more useful. D2 proposed by Mahalnobis (1936) based on multivariate analysis is most appropriate method for selecting the parents as it furnishes a measure of actual divergence between any pair of population (Rao, 1952). Keeping the above facts in view, present study was conducted to determine genotypic divergence for different characters in wheat genotypes.

MATERIALS AND METHODS

Experimental plant material comprised sixty eight eco-geographically and genetically divergent genotypes of bread wheat differing in pedigree and yield potential. These genotypes were obtained from Wheat Breeder, CSK Himachal Pradesh Krishi Vishwavidyalaya, Wheat and Rice Research Station, Malan, Kangra (H.P India) and were grown in randomized block design with three replications each at Mountain Research Centre for Field Crops, SKUAST-Kashmir, Khudwani, situated at latitude 34^0 E, 74^0 N and at an altitude of 1560m amsl (above mean sea level) during *Rabi* 2011-12. Each plot consisted of 3 rows of three meter length spaced 23.0 cm apart while keeping plant to plant distance of 5-6 cm in each row in each replication . Observations were recorded on 10 randomly selected competitive plants for 14 morpho-physiological traits related to adaptation and yield. The traits spike length (cm), plant height (cm), number of spikelets per spike, number of grains per spike, flag leaf length (cm), flag leaf width (cm), leaf area (cm^2) were recorded on ten randomly selected plants from each genotype and replication while biological yield per plot (g), grain yield per plot (g), days to 50% flowering and, days to maturity (DM) were recorded on plot basis. However, harvest index (%) was calculated from mean values of grain and biological yields whereas thousand grain weights (g) was measured by counting 1000 grains random sample from each genotypes taking three replicates. The mean values of above traits were subjected to statistical analysis following standard procedures detailed below and interpretations were made accordingly.

Genetic Divergence Analysis

In order to quantify the genetic distance between any two genotypes, Mahalanalobis (1936) D^2 statistics as described by Rao (1952) was employed. The variance and covariances were subjected to multivariate analysis. The original inter-mated variables (x's) were first transformed into set of mutually uncorrelated variable (y's as linear function of x's) and the D^2 values were worked out. Pivotal condensation method was used to compute inverse matrix of the error dispersion matrix (Rao, 1952). The generalized distance function (D^2) between two genotypes is simply the sum of square of differences in y's i.e.

$$D2 = \sum_{i=1}^{p} (Y1i - Y2i)\ 2$$

The value between the variables on the basis of P character is:

$$DP2 = \sum_{i=1}^{P} \sum_{j=1}^{P} S\ (Wij\ didj)$$

Where, DP2 = D2 value between the variables on the basis of P character.

Wij= Inverse matrix of pooled common dispersion obtained from error matrix

'd'= Difference of mean value for the character of respective genotypes as indicated by i and j.

Determination of Group Constellations

The D^2 values for all combinations presented in the matrix form were arranged in increasing order of magnitude and clustering was according to method suggested by Tocher (Rao,

1952). At first, two most closely associated genotypes were chosen and then third genotype was located which had the smallest D^2 value with the 1st two genotypes. This procedure was continued. The new genotypes were added so long as increase in average D^2 value become abruptly high, then this genotype was not included in the former group. The genotypes of 1st cluster were omitted and rests were treated similarly for constructing new clusters. A few genotypes which had comparatively very high D^2 value from the others formed independent clusters.

Intra and Inter-Cluster Distances

The intra cluster D^2 value was calculated as the sum of n (n-1)/2. D^2 values among the genotypes within a cluster divided by n (n-1)/2. Single Genotype always has zero intra cluster D^2 value. For calculating the inter cluster D^2 value all possible D^2 values between genotypes of the clusters were added and then divided by n1 x n2, where n1 and n2 are number of genotypes in first and second cluster, respectively. The intra and inter cluster distances were calculated by taking the squares root of respective D^2 value between genotypes of a particular cluster and between genotypes belonging to two clusters, respectively.

Cluster Mean Value

The cluster mean of a particular character is the summation of mean value of genotypes included in a cluster, divided by number of genotypes in the same cluster.

RESULTS

Genetic Divergence

In order to select genetically divergent parents for hybridization, D^2 statistic was computed for clustering genotypes based on genotypic divergence following Tocher' s method (Rao, 1952). The magnitude of genetic divergence among the 68 genotypes varied to differences in character expression.

Clustering of Genotypes

Sixty eight wheat genotypes were classified (Table 2) into 10 clusters. The cluster I possessed the largest number of genotypes (32) followed by cluster II (13) and cluster IV (10). Cluster IX (3). Clusters III, V and VI, VII and VII included 2 genotypes each and cluster X having only one genotype.

Table 1. Name of genotype and their pedigree used in divergence study

Name	Pedigree	Name	Pedigree
MNS 44	IBWSN 3090	MNS154	SUNCO.6//TNMU/TUI
MNS57	SERI 1B2/3/KAUZ Z/BOW//KAUZ/ 4/PBW343 KUKUNA	MNS28	MAXICAN WHEAT EC635554
MNS 206	AUG116(08-09)41PBWSN-408	MNS173	WWM68(EC 582270)
MNS 117	HPW 89XVL801P1	MNS141	PBW 65 X UP 2335
MNS 206	AUG1(9-10)26 SAWSN-3021	MNS38	IBWSN-3037
MNS 178	WW6XHPW152P4	MNS39	IBWSN-3047
MNS79	TUKURU//BAV92/RAYONO	MNS54	KIRITATI/4/2 SERI 1B2/3/KAUZ 2/BOW
MNS40	IBWSN-3048	MNS61	CIRCUS/ELVIRA//PFAU/WEAVER
MNS218	SAWSN-3063	MNS71	*T.DICOCCUM* P 194625/*AE. SQUIROSSA* (372)//TUI
MNS3	SAWSN-3062	MNS58	PBW 343 2/KUKUNA/5/CN079//PF70354/MU/3/PASTOR/4/
MNS135	PBW 343 X WH 601	MNS91	VL 616XPBW443
MNS194	KIRITATI//HUW 234+LR34 /PRINIA099M-39Y-OB	MNS37	IBWSN-1135
MNS230	IBWSN1065	MNS160	WHEAR//2PRL/2 PASTOR
MNS6	26SAWSN -3101	MNS25	EC 635535
MNS219	IBWSN1047(07-08)	MNS92	VL 616XPBW343
MNS60	PRL/2PASTOR/4/CHO1X/STAR/3/E1/ 3CN079//2SERI	MNS47	SAMNYT-5
MNS43	IBWSN 3071	MNS116	WW5 X HPW 155 P2
MNS132	UP2338XHD2618	MNS133	UP2338 X HD2618
MNS158	PBW343 2/KUKUNA/ /PBW343 2/KUKUNA(ESWYT509)	ESW X T 8-09-10	KIRITATI/4/2 SERI 1B 2/3/KAUZ 2/BOW//KAUZ
MNS96	VHW 4167 P2-1	ESW X T 71-09-10	WA X WING 2/KIRITATI
MNS224	SAWSN 3183	ESW X T89-09-10	WBLL 1. 2/KIRITATI
MNS41	IBWSN-3052	ESW X T33-09-10	PRL/2 PASTOR/4/CHOIX/STAR/3/HE1/3 CNO79//2.SERI
MNS216	IBWSN 348(07-08)	ESW X T38-09-10	CNDO/R143//ENTE/MEXL2/3/AE.SQUIROSSA (TAUS)/4
MNS180	WW6XHPW152P6	ESW X T37-09-10	ELVIRA/5/CNDO/R143//ENTE/MEX175 /3/AE. SQUIROSSA 4/2OCI/6/VEE
MNS137	UP2338XHD2618	ESW X T32-09-10	PRL/2 PASTOR/4/CHOIX/STAR/3/HE1/3 CNO79//2.SERI
MNS222	IBWSN-1067	ESW X T19-09-10	SERI 1B2/3/KAUZ 2/BOW//KAUZ/4/PBW343. 2 KUKUNA
MNS179	WW6XHPW152P5	ESW X T45-09-10	WA X WING 2/VIVITSI
MNS147	WW 6 XHPW152P1	ESW X T60-09-10	PRL/2 PASTOR
MNS168	T.DICOCCUM P 194625/AE. SQUIRROSA (372)//TUI	ESW X T34-09-10	PFAU/MILAN/5/CHEN/AE.SQUIROSSA (TAUS)//BCN/3
MNS153	WHEAR/VIVITS//WHEAR	ESW X T11-09-10	WEAVER/TSC//WEAVER/3/WEAVER/4/2 WAXWING
MNS53	KIRITATI//2 PBW65/2 SERI 1B	ESW X T7-09-10	KIRITATI//2 PBW65/2 SERI 1B
MNS87	PBW65XUP 2335	ESW X T12-09-10	WAXWING//PFAU/WEAVER
MNS4	26SAWSN -3171	ESW X T88-09-10	SERI.1B 2/3/KAUZ.2/BOW//KAUZ
MNS199	CHIBIA/PRL11/CM65531/3/SKAUZ/BAV9-YR/LR/LB	HPW 42	VEE'S'/4/WN'S'/CBB//CNO'S'/3/JAR/ORZ'S'

Table 2. Clustering pattern of wheat genotypes

CLUSTER NO	No. of genotypes	GENOTYPE
I	31	MNS 44, MNS57, MNS 206, MNS 117, MNS 206, MNS 178, MNS79, MNS40, MNS218, MNS3, MNS135, MNS194, MNS230 MNS6, MNS219, MNS60, MNS43, MNS132, MNS158, MNS96, MNS224, MNS41, MNS216, MNS180, MNS137, MNS222, MNS179, MNS147, MNS168, MNS141 and MNS92
II	13	MNS153, MNS53, MNS87, MNS4, MNS199, MNS154, MNS28, MNS173, MNS38, MNS39 , MNS54, MNS61, MNS91
III	2	ESW X T33-09-10 and ESW X T11-09-10
IV	10	MNS71 , MNS58 , MNS37, MNS160, MNS25, MNS47, MNS116, MNS133, ESW X T 8-09-10 and ESW X T19-09-10
V	2	ESW X T7-09-10, ESW X T12-09-10
VI	2	ESW X T60-09-10 and ESW X T88-09-10
VII	2	ESW X T34-09-10 and HPW 42
VIII	2	ESW X T89-09-10 and ESW X T37-09-10
IX	3	ESW X T89-09-10, ESW X T38-09-10 and ESW X T32-09-10
X	1	ESW X T45-09-10
Total	68	

Table 3. Intra (diagonal) and inter cluster distances for 10 clusters in wheat genotypes

Cluster no	1	2	3	4	5	6	7	8	9	10
1	**8.118**	8.798	6.647	9.513	7.999	7.642	8.108	7.728	13.237	10.140
2		**9.259**	6.892	9.608	8.653	8.012	8.123	8.833	12.352	9.742
3			**2.861**	7.578	4.814	4.675	5.649	6.400	11.546	7.949
4				**10.407**	8.926	8.186	8.590	9.088	12.851	9.828
5					**3.717**	5.107	7.134	6.245	14.605	9.776
6						**4.107**	5.224	5.524	13.727	6.757
7							**4.255**	6.141	13.785	4.784
8								**5.548**	15.338	8.274
9									**8.031**	14.162
10										**0.000**

Table 4. Cluster mean for 14 characters under study

CL\CHR	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
I	180.27	252.24	105.03	95.56	18.10	0.85	15.39	8.96	43.87	**39.67**	412.37	50.65	51.47	434.39
II	179.21	251.87	94.15	103.02	16.42	0.82	13.43	8.38	41.69	37.77	382.05	50.26	50.22	396.84
III	178.33	252.00	93.40	99.83	17.74	0.76	13.55	6.83	39.50	34.27	383.33	48.40	52.22	377.03
IV	182.53	253.50	102.05	102.64	16.90	0.86	14.62	8.09	39.30	34.01	330.00	50.71	48.39	346.23
V	178.50	249.33	107.60	89.93	17.31	0.76	13.05	7.75	42.50	30.67	283.33	53.23	53.85	307.58
VI	183.50	258.50	90.00	89.38	16.50	0.96	15.82	5.83	41.00	32.73	308.33	46.35	50.27	293.19
VII	182.83	257.00	72.23	90.61	13.63	0.77	10.37	8.02	39.00	33.57	300.00	47.36	45.97	291.21
VIII	185.33	259.83	115.90	81.43	16.20	0.77	12.38	8.15	41.50	36.80	325.00	44.49	49.28	298.99
IX	183.89	234.56	97.56	143.77	16.78	0.91	15.26	7.86	44.00	**38.09**	477.78	56.88	49.20	561.36
X	185.67	255.00	67.07	92.43	10.85	0.92	9.85	5.40	34.00	29.87	300.00	43.71	42.53	272.04

Where, X1= Days to 50% flowering, X2=Days to maturity, X3= plant height (cm), X4= No. of tillers /meter, X5= Flag leaf length (cm), X6= Flag leaf width (cm), X7= flag leaf area (cm), X8= Spike length, X9= No. of spike lets, X10= No. of grains/ spike, X11= Biomass yield (gm), X12= Harvest index, X13= 1000 seed weight (gm) and X14= Grain yield/plot

Intra and Intercluster D^2 Values

Genotypes grouped in the same cluster (intra cluster) are expected to be genetically more similar to each other while genotypes grouped in different clusters (inter clusters) as genetically more divergent. The clusters which are separated by greatest statistical distance showed maximum divergence. Intra cluster D2 values amongst various clusters (Table 3). Inter-cluster distances ranged from 4.67 (cluster III and VI) to 15.33 (cluster VIII and IX) and were more than intra-cluster distances which ranged from 0 (cluster X) to 9.25 (cluster II).

Cluster Means

Under normal Kashmir conditions the highest and lowest cluster means (Table 4) respectively for different traits were observed *i.e.* for Days to 50% flowering (III and X), Days to maturity (VIII and IX), plant height (VIII and X), No. of tillers /meter (IX and VIII), Flag leaf length (I and X), Flag leaf width (X and V), flag leaf area (VI and X), Spike length (I and X), No. of spike lets (IX and X), No. of grains/ spike (I and X), Biomass yield (IX and V), Harvest index (IX and X),1000 seed weight (V and X) and Grain yield/plot (IX and X)

Difference was observed in proportion of contribution of each character to total diversity (Table 5). No of tiller per running meter contributed highest (25.15%) towards diversity. This was followed by 1000 grain weight (17.60%), grain yield per plot (16.94%) and spike length (8.86%) number grain per spike(6.93%), harvest index (5.83%), flag leaf width(4.78%), flag leaf length(4.12%), biomass yield(2.41%), days to flowering (2.23%), number of spikelet per spike (2.20%), plant height (1.88%) and days to maturity recorded (0.20%) . value.

Table 5. Per cent contribution of different traits towards total diversity

Source	Ranked first (no. of times)	Contribution %
Days to 50% flowering	51	2.23
Days to maturity	5	0.21
plant height(cm)	43	1.88
No. of tillers /meter	573	25.15
Flag leaf length(cm)	94	4.12
Flag leaf width(cm)	109	4.78
flag leaf area (cms)	20	0.87
Spike length	200	8.77
No. of spike lets	50	2.20
No. of grains/ spike	158	6.93
Biomass yield(gm)	55	2.41
Harvest index	133	5.83
1000 seed weight(gm)	401	17.60
Grain yield/plot	386	16.94
TOTAL	2278	100

DISCUSSION

In breeding self pollinated crops like wheat, usually the concept of pure line and progeny selection is practiced. Unlike allogamous crops, this system of mating and breeding imposes a restriction on population for its genetic expansion as inbreeding leads to rapid fixation, precludes free exchange of favourable genes and greatly prevents emergence of desirable gene constellation (Joshi and Singh, 1979). Moreover, the germplasm in self pollinated crops is available in the form of multitude of pure lines and the genes of interest are scattered over these lines. Assembling such gene constellations determining traits related to phenology, adaptation, biological and grain yield etc., followed by establishing the recombinants as pure lines is main strategy for the improvement of self pollinated crops. This situation warrants for critical choice of the parents in breeding programme, particularly if the aim is improvement of complex quantitative traits. Such work would be facilitated if breeder is able to broadly classify the germplasm on the basis of given set of characters and then to pick up parents for hybridization either to exploit heterosis or for transgressive segregants in subsequent generations (Chandra, 1977). Therefore choice of parents for hybridization should be based not only on agronomic performance but also on genetic variances, genetic divergence (Bhatt, 1973) as it would help in understanding genetic potentiality of populations to yield desirable genotypes. Therefore, D2 statistics proposed by based on multivariate analysis (Mahalnobis, 1936) being one of the most appropriate method for selecting the parents is used in present study to determine genetic divergence among 68 wheat genotypes for grouping them into different cluster using Tocher method (Rao,1952). Fang *et al*. (1996) clustered 120 genotypes of durum wheat into five groups based on maturity date, plant height, spike length, number of seed per spike, 1000-seed weight and spike seed yield. Contrary to this, the grains/spike, 1000 gain weight, spike length, biological yield and gain yield were minimum in these genotypes. Gashaw *et al.* (2007) clustered indigenous durum wheat genotypes of diverse origin into homogenous groups based on estimates of genetic divergence (D^2) for the hybridization programme. They found that there was no correspondence between geographic and genetic distances i.e. germplasm collected from the same geographic area were placed into different cluster groups and those collected from different geographic regions were placed into the same cluster. According to Rahim *et al*. (2010) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Ali *et al.* (2008) and Singh and Dwivedi (2002) also reported that cluster analysis can be useful for finding high yielding wheat genotypes, the results of this study showed the presence of a high genetic divergence among wheat genotypes. There is significant genetic variability among tested genotypes that indicates the presence of excellent opportunity to bring about improvement through wide hybridization by crossing genotypes in different clusters. The results of the present study indicate the presence of genetic diversity among the tested bread wheat genotypes. Parents from divergent clusters can be used for hybridization in order to isolate useful recombinants in the segregating generations. This information might be used in the genetics and breeding programmes for improvement of bread wheat in Kashmir conditions

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