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Genetic diversity analysis for grain yield and associated traits in advanced lines of wheat (*Triticum aestivum* L.)

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Abstract

D² values between the pairs of genotypes, 23 genotypes were grouped into thirteen clusters. Cluster IV and IX was largest having three genotypes followed by II, V, VII, X, XII and XIII which had two genotypes in each cluster. There were four solitary clusters I, III, VI, VIII with genotypes K-9533, UP 2594, Raj 1555, NW 1012, K 9465, respectively. The mean values of each of the nine characters for the thirteen clusters showed that cluster XIII, which was most diverse, had high seed yield and number of siliquae per plant. Cluster VIII also represented entries with high seed, number of siliquae per plant and number of seeds per silique. Cluster IX had genotypes with highest test weight. These clusters could be regarded as useful sources of genes for seed yield. Cluster XI with the minimum number of days to maturity can be considered as a good source for earliness. The results revealed that 1000-seed weight contributed maximum to genetic divergence (61.03%) followed by effective tillers per plant (12.04%), spike weight (10.74%), peduncle length (7.87%) and harvest index (2.40%), which exhibited greatest contribution to genetic divergence, can be the basis of the selection of genetically diverse parents for hybridization.

Keywords: Divergence, D² distance, genotype, hybridization and wheat

Introduction

Wheat continues to retain pride in place among cereals due to its wide adaptation to various agro-climatic conditions. It also commands the prominent position in the international market for grain trade. In India wheat is the second most important food crop next to rice and is produced under conditions ranging from the temperate zone of Himalayan foot hills to the subtropical hot areas of central and southern India. The option for increasing wheat production by expanding the area under its cultivation has been exploited to almost its maximum and hence the only alternative left is to increase per unit production of the wheat plant through genetic improvement. So, continuous efforts are to be made to develop high yielding wheat genotypes. As for many field crops, the studies regarding the understanding and improvement of wheat are being conducted by the routine analysis of the genetic diversity among the genotypes because grain yield is a complex trait and is highly influenced by many genetic factors and environmental. Study on genetic divergence is very important in evaluating the variation in a breeding population. In addition genetic diversity is essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield (Joshi and Dhawn, 1966), wider adaptation, desirable quality, pest and disease resistance (Nevo *et al.*, 1982). In addition, genetic divergence is studied to identify specific parents for wider genetic variation and heterosis when they are crossed (Aditya, 1995). Mahalanobis D²-statistics 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 D²-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.

Materials and Methods

The experiment was laid out in a randomized complete block design (RCBD) with three replications at the field laboratory of department of Genetic and Plant Breeding, Agriculture Research Farm, Bhagwant University, Ajmer. This study was performed with 23 genotypes of wheat (Table-1) to assess the genetic diversity among the genotypes. Each replication was consisted of 25 plots and each of the plots was 2.0 m long with five rows. The spacing was 40 cm between rows and 5 cm between plants in a row. The space maintained between the plots

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was 80 cm and between the replication was one meter. Seeds were sown continuously by hand in rows and after complete emergence; 5 cm distance was maintained between plant after thinning and gap filling in a row of the plot. Urea, Triple Super Phosphate (TSP), Muriate of Potash (MP), Zypsum and Cowdung were applied at the rate of 220 Kg, 180 Kg, 50 Kg, 120 Kg and 6000 Kg/ha respectively. Data were recorded on individual plant basis from 10 randomly selected plants of

each genotype from the five rows per plot in each replication. Among the characters studied as reproductive traits, days to booting, days to heading, days to anthesis, days to maturity were recorded on plot basis and grain yield were recorded in the laboratory after harvesting. The genetic divergence among lines/varieties was estimated by Mahalanobis D²-statistics and the accessions were grouped into different clusters following Tocher's method (Rao, 1952)^[1].

Table 1: List of Indian mustard genotypes under study and their pedigree details

S. No.	Entry		Centre
1.	KALYANSONA		IARI, New Delhi
2.	UP-2594	SM4-HSN 24E /CPAN 2099	GBPUA&T, Pantnagar
3.	SONA LICA	II54-388/AN/3/ YF54/N10B/LR 64	IARI, New Delhi
4.	K-9533	HI 1077/HUW 234	CSAUA&T, Kanpur
5.	RAJ-1555	COCORIT'S / RAJ 911	RARI, Durgapura
6.	K-9106	K 8101 /K 68	CSAUA&T, Kanpur
7.	HD-2643,	VEE'S'/ HD2407 //HD 2329	IARI, New Delhi
8.	PBW-343	PBW343+Lr57/Yr40+ Lr37/Yr17	PAU, Ludhiana
9.	HD-2009	LR 64A /NAI 60	IARI, New Delhi
10.	K-9351,	K72/K8027//K72	CSAUA&T, Kanpur
11.	HUW -510	HD 2278/HUW 234/DL 230-16	BHU, Varanas
12.	K-68,	NP773/K 13	CSAUA&T, Kanpur
13.	K-9465,	HD 2160/K 68	CSAUA&T, Kanpur
14.	K-65	C591/NP773	CSAUA&T, Kanpur
15.	RAJ-6560	TOPDY 6	RARI, Durgapura
16.	HD -1981	E 5557/HD 845	IARI, New Delhi
17.	Seri-82		CIMMYT
18.	K-9162	K 7827/HD 2204	CSAUA&T, Kanpur
19.	Pavon-76		CIMMYT
20.	Sonara-64		CIMMYT
21.	NW 1012	PARANA#2//JUP/ BJV'S'/3/VEE#5'S'/JUN'S'	NDUAT, Faizabad
22.	NW 2036	BOW/CROW/BUC/PVN	NDUAT, Faizabad
23.	NW 1014	HAHN 'S'	NDUAT, Faizabad

Results and Discussion

The genetic divergence among 23 lines/varieties was estimated by Mahalanobis D²-statistics and the accessions were grouped into different clusters following Tocher's method (Rao, 1952)^[1]. Arunachalam and Ram (1967)^[3] advocated the use of equal number of strains from each region in order to find out a true picture of association existing between geographical and genetic divergence. It was not so in this study because the objective here was to pinpoint genetically diverse and desirable parents for the study of combining ability and heterosis.

Table 2: Distribution of eighty one genotypes of wheat in different clusters

Cluster No.	No. of genotypes	Genotypes
I	1	K-9533
II	2	Sonara-64, NW 2036,
III	1	UP-2594
IV	3	Kalyansona, HD 2643, HD 2009
V	2	PBW-343, HUW -510
VI	1	Raj 1555
VII	2	Seri-82, HD 1981
VIII	1	NW 1012
IX	3	K 9162, NW 1014, K 9351
X	2	K-68, Raj 650,
XI	1	K 9465,
XII	2	Sonalika, K 9106
XIII	2	K 65, Pavon-76

Based on the D² values between the pairs of genotypes, 23 genotypes were grouped into thirteen clusters (Table 2). Cluster IV and IX was largest having three genotypes followed by II, V, VII, X, XII and XIII which had two genotypes in each cluster. There were four solitary clusters I, III, VI, VIII with genotypes K-9533, UP 2594, Raj 1555, NW 1012, K 9465, respectively. The genotypes within the cluster had smaller D² value among themselves than the genotypes belonging to other cluster. Smaller D² values within cluster indicated that these genotypes were closely related. On the other hand genotypes belonging to two different clusters have large D² values, showing more genetic diversity with each other. Maximum intra-cluster distance was found in cluster III, which showed presence of diverse genotypes in this cluster. Cluster XI and XII were the most diverse, the inter-cluster distance between them (2072.84) being maximum. The cluster I and III had maximum inter-cluster proximity.

Average intra and inter cluster distance

The average intra and inter cluster D² and D values among different clusters are given in Table 3. The intra cluster distances ranged from 89.52 to 0.00 for cluster III and X/XI/XII/XIII, respectively. Cluster XI and XII were the most diverse, the inter cluster distance between them (2072.84) being maximum followed by cluster IX and XI (1949.45) and VI and IX (1337.50). The inter cluster proximity was maximum between cluster V and VIII (102.93) followed by I and III (103.02), hence they were closely related.

Table 3: Average intra- (in bold) and inter-cluster distances between different clusters of wheat genotypes.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	64.04 (8.00)	251.33 (15.85)	103.02 (10.15)	166.07 (12.89)	128.94 (11.36)	233.72 (15.29)	155.28 (12.46)	132.34 (11.50)	580.65 (24.10)	193.02 (13.89)	554.72 (23.55)	589.30 (24.28)	339.03 (18.41)
II		75.70 (8.70)	176.61 (13.29)	518.98 (22.78)	261.97 (16.19)	748.60 (27.36)	124.18 (11.14)	153.11 (12.37)	164.13 (12.81)	197.79 (14.06)	1204.87 (34.71)	231.10 (15.20)	125.10 (11.18)
III			89.52 (9.46)	215.95 (14.70)	154.22 (12.45)	345.2 (18.58)	151.6 (12.32)	154.69 (12.44)	454.23 (21.31)	162.55 (12.75)	676.55 (26.01)	495.46 (22.26)	289.35 (17.01)
IV				83.36 (9.13)	184.36 (13.58)	113.49 (10.65)	451.87 (21.26)	328.21 (18.12)	1019.80 (31.93)	311.55 (17.65)	245.78 (15.68)	1092.94 (33.06)	651.10 (25.52)
V					68.48 (8.28)	317.27 (17.18)	265.12 (16.28)	102.93 (10.15)	575.90 (24.00)	122.24 (11.06)	537.72 (23.19)	726.67 (26.96)	252.45 (15.89)
VI						77.39 (8.80)	575.34 (23.99)	475.13 (21.80)	1337.50 (36.57)	488.01 (22.09)	177.89 (13.39)	1320.98 (36.35)	896.01 (29.93)
VII							52.33 (7.23)	127.41 (11.29)	264.97 (16.28)	248.55 (15.77)	1098.46 (33.14)	206.07 (14.36)	199.57 (14.13)
VIII								72.88 (8.54)	360.46 (18.99)	161.34 (12.70)	852.61 (29.20)	424.33 (20.60)	141.05 (11.88)
IX									68.31 (8.26)	390.55 (19.76)	1949.45 (44.15)	153.07 (12.37)	154.54 (12.43)
X										0.00 (0.00)	750.08 (26.55)	621.94 (24.94)	145.45 (12.06)
XI											0.00 (0.00)	2072.84 (45.53)	1298.64 (36.04)
XII												0.00 (0.00)	333.32 (18.26)
XIII													0.00 (0.00)

Note: Values in parantheses are the group distance ($\sqrt{D^2}$)

Cluster mean

The perusal of Table 4 indicated that cluster XI, had very high mean for grain yield, (13.45 g) and peduncle length (27.67 cm) whereas it had lowest mean for effective tillers per plant (4.00). Cluster XII represented entries with ear length (8.55 cm), biological yield per plant (22.55 g). Cluster IX have entries with lowest spike weight (2.33). Cluster VII showed highest mean value for effective tillers per plant (7.00) 1000-seed weight (47.91 g) and lowest harvest index (23.67%). Cluster III have entries with high grains per spike and highest days to maturity. Cluster I had lowest days to maturity (58.77 days) whereas Cluster II have entries with highest highest spike weight (4.58 g) lowest biological yield per plant (5.32 g). Cluster IV have entries with highest biological yield per plant (28.02 g) and lowest plant height (95.66 cm). Cluster VI belongs to entries having traits of lowest 1000-seed weight (28.83) and highest highest harvest index 44.32%. Cluster V,

X and XIII had those genotypes which have highest plant height (122.77 cm), lowest peduncle length (14.00 cm) and lowest ear length (5.30 cm).

The mean values (table 4) of each of the nine characters for the thirteen clusters showed that cluster XIII, which was most diverse, had high seed yield and number of siliquae per plant. Cluster VIII also represented entries with high seed, number of siliquae per plant and number of seeds per siliqua. Cluster IX had genotypes with highest test weight. These clusters could be regarded as useful sources of genes for seed yield. Cluster XI with the minimum number of days to maturity can be considered as a good source for earliness.

The clustering pattern of different genotypes did not follow their geographical distribution, which showed that geographical diversity was not necessarily an index of genetic diversity. Singh *et al.* (2017)^[4] and Bhushan *et al.* (2014)^[5].

Table 4: Mean values of different characters in thirteen clusters of wheat

Clusters	Days to maturity	Plant Height (cm)	Effective tillers plant ⁻¹	Ear length (cm)	Peduncle length (cm)	Spike weigh (g)	Grains spike ⁻¹	1000-seed weight (g)	Biological Yield plant ⁻¹ (g):	Grain Yield Plant ⁻¹ (g)	Harvest Index (%)
I	58.77 ↑	101.22	4.19	5.33	14.57	2.56	48	41.05	19.33	8.45	34.65
II	81.44	98.03	5.39	6.32	16.81	4.58	55	44.29	15.32	10.69	25.86
III	78.13	113.52	5.54	7.06	17.13	3.71	62	31.37	35.06	5.89	28.93
IV	66.95	95.66	5.52	8.02	21.00 ↓	3.64	53	34.33	28.02	9.28	32.66
V	74.47	122.77	5.60	7.49	19.00	4.56	61	33.12	19.49	8.42	36.84
VI	84.75	116.56	6.00 ↑	6.36	20.25	3.02	55	28.83	26.36	9.82	44.32
VII	62.00	98.44	7.00 ↑	7.02	23.00	2.63	58	47.91	23.02	12.32	23.67
VIII	65.67	116.92	6.33	8.54	17.00	3.07	61	34.63	23.54	7.32	28.33
IX	69.83	95.13	5.17	7.21	18.83	2.33	45	45.18	21.21	11.22	31.92
X	71.33	96.67	5.67	7.68	14.00 ↑	4.20 ↓	53	41.56	19.68	8.98	39.63
XI	68.33	116.60	4.00 ↓	7.55 ↓	27.67	4.13	46	37.18	23.55 ↓	13.45	43.59
XII	73.33 ↓	97.00 ↑	6.67	8.55 ↑	21.33	3.00 ↑	52	33.09	22.55 ↑	11.67	29.43
XIII	71.67	112.50 ↓	5.67	5.30	19.67	4.57	55	35.40	26.30	7.86	34.37

Note: ↑ = Highest value, ↓ = Lowest value

The contribution of various characters towards genetic divergence is presented in Table 5. The results revealed that 1000-seed weight contributed maximum to genetic divergence (61.03%) followed by effective tillers per plant (12.04%), spike weight (10.74%), peduncle length (7.87%) and harvest index (2.40%), which exhibited greatest contribution to genetic divergence, can be the basis of the selection of genetically diverse parents for hybridization.

Table 5: Contribution of different characters towards genetic divergence in wheat genotypes

Characters	Per cent contribution towards divergence
Days to maturity	0.08
Plant height (cm)	1.45
Effective tillers plant ⁻¹	12.04
Ear length (cm)	0.06
Peduncle length (cm)	7.87
Spike weight (g)	10.74
Grains spike ⁻¹	0.62
1000-seed weight (g)	61.03
Biological Yield plant ⁻¹ (g):	1.79
Grain Yield Plant ⁻¹ (g)	2.20
Harvest Index (%)	2.40

The overall analysis showed that generally the cluster was quite divergent from one another except cluster I and III. Among these types of cluster, the selected genotypes for breeding programme/hybridization produce high heterotic response and release better segregants/lines in subsequent generation. However, caution should be exercised in selecting very divergent genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and its components are found to be higher in crosses between the parents in intermediate divergence classes than extreme ones (Singh and Upadhyay, 2013) [6].

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