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EVALUATION OF GENETIC DIVERGENCE IN WHEAT (*TRITICUM AESTIVUM* L.) GERMPLASM

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ABSTRACT

The nature and magnitude of genetic diversity was assessed using non-hierarchical euclidean cluster analysis in 405 pure breeding lines of *T. aestivum* for grain yield and its associated traits. All the genotypes got grouped in 13 different clusters. The clustering pattern of the genotypes belonging to the same country revealed their distribution in more than one cluster showing nonparallelism between geographic and genetic diversity. Members of cluster IV and IX were highly diverse from each other. Cluster VI had high mean values for grain yield, biological yield, number of tillers/unit area and harvest index. A number of genotypes were also identified which may serve as potent genetic donors for some metric traits.

Key words: *Triticum aestivum*, nonhierarchical Euclidean cluster analysis, genetic divergence, germplasm evaluation.

Reduction in genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes [1]. Among the high yielding varieties of *Triticum aestivum*, most of the present day varieties are derived from six broad groups [2]. This situation of narrowing down of genetic base points towards the preservation, management, enhancement and evaluation of wide genetic variability. Mahalanobis' D^2 statistic described by Rao [3] has been utilized by a number of workers for estimating genetic divergence. Although D^2 statistic is a quantitative measure of genetic divergence, yet the clustering pattern of the genotypes is arbitrary [4]. In the present study, therefore, the genotypes subjected to nonhierarchical euclidean cluster analysis to overcome the limitation of D^2 statistic. Precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation could help to select parents for evolving superior varieties.

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MATERIALS AND METHODS

The experimental material comprised of 405 genotypes of wheat, selected on the basis of their agronomic and morphological characters from the germplasm collection maintained at the Department of Agricultural Botany, Institute of Advanced Studies, Meerut University, Meerut. The material was grown along with three check varieties in an augmented design at the Research Farm of the Department of Agricultural Botany. Each genotype was assigned to a single row, 3-m long plot, with 23 cm row-to-row distance with seed rate as recommended for commercial cultivation. From the centre using half meter long net plot out of the 3 meter long plot, five competitive plants were randomly taken to record observations on eight quantitative characters. To study genetic diversity, the data were analysed using nonhierarchical Euclidean cluster analysis [5].

RESULTS AND DISCUSSION

The analysis of variance showed that the blocks were homogenous and genetic differences existed for most of the traits among the check varieties. Maximum values of coefficient of variability (Table 1) were observed for grain yield/unit area, followed by biological yield/unit area and tillers/unit area. Therefore, these traits have higher contribution towards the total genetic divergence. The variability was observed to be moderate for ear length, 100-grain weight, plant height, harvest index, grains/ear and spikelets/ear.

Table 1. General mean, variance, coefficient of variability and range for different characters in wheat

Character	General mean	Variance	CV	Range
Days to flowering	83.4	16.3	4.8	72.6–94.6
Days to maturity	130.9	20.9	3.9	120.3–139.6
Plant height (cm)	92.7	181.2	14.5	42.6–120.9
Tillers per unit area	40.8	140.5	29.1	11.0–94.4
Spikelets per ear	18.3	5.9	13.3	8.1–27.5
Ear length (cm)	9.8	3.7	19.7	4.3–16.5
Grains per ear	54.7	56.6	13.8	30.9–80.5
100-grain weight (g)	3.8	0.5	18.3	1.8–5.5
Biological yield per unit area (g)	167.6	3098.3	33.2	42.2–372.9
Harvest index (%)	50.7	47.9	13.7	32.6–75.2
Grain yield per unit area (g)	84.2	788.1	33.3	22.1–197.1

The clustering pattern of the genotypes revealed that there were 13 clusters and the distribution of genotypes from different ecogeographical regions into these clusters was apparently random (Table 2). This tendency of genotypes to occur in cluster cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. Similar findings have also been made by earlier workers [6]. The maximum number of genotypes (38) was present in cluster VI and XII and the minimum number (19) in cluster IX. The mean performance of each cluster for traits studied is presented in Table 2. Cluster means showed appreciable differences for all the traits, particularly for plant height, tillers/unit area, biological yield per unit area and grain yield/unit area. The entries of cluster X showed the highest mean values for plant height (103.4 cm) and days to maturity (134.7). The lowest means for grain yield per unit area (46.3 g), grains/ear (43.8), ear length (6.7 cm) and tillers per unit area (28.5) were observed in cluster IX. Cluster IX had the highest coefficient of variability for plant height, grains/ear, 100-grain weight, and biological yield per unit area, whereas cluster XIII had the highest coefficient of variability for tillers per unit area, ear length, harvest index and grain yield per unit area. These results are reflected in intracluster distances as cluster IX and XIII had more intracluster distances (2.61 and 2.43, respectively).

Intra- and intercluster distances are given in Table 3. The magnitude of intracluster distances measure the extent of genetic diversity between the cultivars of the same cluster. Intracluster distance ranged from 2.10–2.61. Relatively lower values of intracluster distance suggested the presence of narrower genetic variation within a cluster.

Intercluster distance is a measure of genetic distance between two clusters. The maximum (5.91) intercluster distance was observed between clusters IV and IX and the minimum (2.25) between clusters II and VI. Cluster IV contained 25 genotypes,. viz., 6WA.737, BAU 2158, CC 505, CPAN 1885, CPAN 2004, CPAN 2024, CPAN 2043, CPAN 2074, CPAN 2088, CPAN 2093, CPAN 3002, CPAN 3041, CPAN 6062, CPAN 6112, Girija, HD 1952, HD 2119, HI 768, HI 8629, HW 868, K 8148, MUW 29, MUW 31, PBW 62, Sarbati Sonara, whereas cluster IX had 19 genotypes, namely, 6WA 740, BR 2104, BSM 159, CPAN 2036, CPAN 3037, CPAN 6098, HD 1925, HD 2190, HI 1270, HI 8757, JV 126, MACS 1963, MG 78-8-7, MUW 45, MUW 62, NI 875, NP 6115, Sr 948A and VL 490 (Table 4).

The parents for hybridization could be selected on the basis of their large intercluster distance for isolating useful recombinants in the segregating generations. A hybridization programme involving genotypes, viz., CC 505, CPAN 1885, CPAN 2024, CPAN 2074, CPAN 3041, CPAN 6062, HW 868, MUW 29 and Sarbati Sonara of cluster IV and BR 2104, CPAN 3037, HD 2190, HI 8757, JV 126, MACS 1963, MG 75 8-7, MUW 62 and Sr 948A of cluster IX could be undertaken to isolate high yielding segregants since these genotypes had high yield potential, long ear, bold grain, high spikelet fertility, high tillering capacity, and high harvest index with large genetic distance. The genotypes could also be utilized for introgressing their useful traits in the commercial wheat cultivars.

Table 2. Cluster mean, standard deviation, and coefficient of variability (CV%) of thirteen clusters for different characters in wheat

Character	Parameter	I (35)	II (29)	III (21)	IV (25)	V (34)	VI (38)	VII (35)	VIII (29)	IX (19)	X (37)	XI (35)	XII (38)	XIII (30)
Days to flowering	Mean	88.2	85.5	83.0	80.3	84.2	82.5	79.7	87.8	84.1	83.1	81.6	82.9	81.9
	SD	3.1	3.3	2.5	3.4	2.5	4.1	3.0	3.0	3.7	3.5	2.8	3.7	2.5
	CV	3.5	3.9	3.0	4.3	3.3	4.9	3.7	3.4	4.4	4.3	3.5	4.4	3.0
Days to maturity	Mean	129.4	134.5	132.2	130.9	132.0	127.0	125.6	131.3	128.6	134.7	133.7	132.0	129.5
	SD	4.8	3.4	3.1	4.2	3.2	3.7	2.5	3.9	3.9	3.2	3.1	4.6	3.7
	CV	3.7	2.5	2.3	3.2	2.4	2.9	2.0	3.0	3.1	2.3	2.3	3.5	2.9
Plant height (cm)	Mean	87.1	89.4	65.2	88.8	98.3	96.4	97.6	100.5	78.7	102.4	89.9	92.4	100.5
	SD	6.9	7.3	13.8	9.0	9.3	10.2	10.7	8.5	19.5	9.3	7.7	12.0	9.2
	CV	7.9	8.1	21.1	10.2	9.4	10.6	10.9	8.5	24.8	9.0	8.6	13.0	9.1
Tillers per unit area	Mean	39.4	56.1	43.8	41.8	42.6	55.5	31.1	44.3	28.5	38.3	29.2	45.2	30.3
	SD	7.4	10.8	10.1	8.2	9.2	8.9	7.6	7.4	8.5	5.2	5.7	7.1	9.5
	CV	18.7	19.2	23.0	19.6	21.7	16.0	24.4	16.8	30.0	13.6	19.6	15.7	31.4
Spikelets per ear	Mean	16.4	18.2	18.5	23.0	18.3	17.9	18.6	20.5	15.2	16.9	19.2	19.6	15.0
	SD	1.9	1.4	1.5	1.8	1.2	1.7	1.4	1.1	1.4	1.6	1.4	1.4	1.6
	CV	11.4	7.5	8.4	8.0	6.7	9.3	7.4	5.6	9.3	9.2	7.1	7.2	10.8
Ear length (cm)	Mean	9.8	8.8	9.5	10.9	10.0	9.2	9.3	10.5	6.7	9.4	11.0	11.7	8.9
	SD	1.5	1.7	1.5	1.9	1.6	1.5	1.5	1.2	1.2	1.6	1.1	1.9	2.0
	CV	15.1	19.9	16.1	17.3	15.9	16.6	16.1	11.4	17.9	17.1	10.1	16.5	22.9
Grains per ear	Mean	49.6	54.2	54.6	67.7	56.4	54.1	56.2	63.2	43.8	49.3	57.6	58.6	44.3
	SD	3.5	3.1	5.1	5.2	4.6	4.7	4.9	3.7	4.7	4.4	5.3	4.7	4.6
	CV	7.0	5.8	9.3	7.7	8.1	8.7	8.6	5.8	10.8	8.9	9.2	8.0	10.5
100-grain weight (g)	Mean	3.4	3.8	3.5	3.4	3.1	3.7	3.5	3.6	3.9	4.4	3.9	4.7	3.9
	SD	0.5	0.4	0.6	0.6	0.5	0.6	0.6	0.6	0.7	0.5	0.6	0.4	0.7
	CV	14.8	11.1	15.9	16.8	16.0	15.8	16.1	15.7	18.5	12.0	14.9	9.2	17.7
Biological yield per unit area (g)	Mean	127.4	204.7	141.3	187.8	157.7	242.4	136.1	212.9	87.9	168.1	115.8	227.9	123.8
	SD	22.8	43.1	25.9	42.1	26.1	38.1	24.3	31.3	24.8	24.3	30.3	43.7	30.2
	CV	17.9	21.1	18.3	22.4	16.6	15.7	17.9	14.7	28.2	14.4	26.2	19.2	24.4
Harvest index (%)	Mean	56.1	55.1	59.8	49.9	44.8	48.3	48.4	48.4	52.9	49.2	56.9	51.8	40.3
	SD	6.5	3.9	7.1	4.2	4.9	4.0	4.1	3.9	4.2	4.7	5.4	5.0	4.8
	CV	11.6	7.1	11.9	8.4	11.1	8.3	8.4	8.1	7.9	9.6	9.5	9.6	11.8
Grain yield per unit area (g)	Mean	71.0	111.0	83.7	93.8	70.1	117.1	65.9	102.7	46.3	82.3	65.3	117.1	50.2
	SD	12.9	21.8	14.0	22.2	10.9	20.7	13.2	15.4	12.5	11.0	16.2	19.6	14.7
	CV	18.2	19.6	16.8	23.7	15.5	17.7	20.0	15.0	27.1	13.4	24.8	16.8	29.4

Note. Number of genotypes in each cluster are given in parentheses.

Table 3. Inter- and intracluster (in bold) distances in wheat germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**2.31**	3.01	2.57	4.49	2.61	3.71	3.05	3.55	2.77	2.84	2.78	4.01	3.33
II		**2.31**	2.82	3.66	2.96	2.25	4.00	2.60	4.72	2.74	3.62	2.58	4.71
III			**2.44**	3.67	3.43	3.91	3.60	3.93	3.67	3.70	2.66	3.70	4.72
IV				**2.55**	3.07	3.59	3.27	2.48	5.91	4.19	3.17	2.95	5.42
V					**2.14**	3.02	2.29	2.41	4.10	2.53	2.77	3.49	3.01
VI						**2.48**	3.46	2.68	5.16	3.19	4.35	2.60	4.43
VII							**2.13**	3.51	3.50	2.97	2.55	3.85	2.79
VIII								**2.10**	5.54	3.26	3.50	2.37	4.83
IX									**2.61**	3.66	3.82	6.60	2.83
X										**2.15**	2.76	2.91	2.69
XI											**2.12**	3.39	3.85
XII												**2.56**	4.99
XIII													**2.43**

Table 4. Potent genetic donors in wheat identified from clusters IV and IX for different traits

Trait	Genotypes
High grain yield	BAU 2158, CC 505, CPAN 1885, CPAN 2004, CPAN 2024, CPAN 2043, CPAN 2074, CPAN 2088, CPAN 3004, CPAN 3041, CPAN 6062, CPAN 6112, HD 1952, HI 8629, HW 868, MJW 29, MUW 31, PBW 62, Sarbati Sonara.
Long ear	6WA 737, CPAN 1885, CPAN 2074, CPAN 2008, CPAN 6062, Girija, HD 2119, HI 768, HW 868, K 8148, PBW 62.
Bold grain	CPAN 3037, CPAN 6029, HI 8757, JV 126, MACS 1963, MG 75 8-7, MUW 62.
High spikelet fertility	6WA 737, BAU 2158, CC 505, CPAN 1885, CPAN 2004, CPAN 2024, CPAN 2043, CPAN 2070, CPAN 208, CPAN 2093, CPAN 3041, CPAN 6062, CPAN 6112, Girija, HD 1952, HD 2119, HI 768, HI 8629, K 8148, MUW 29, MUW 31, PBW 62, Sarbati Sonara.
High tillering capacity	6WA 737, CC 505, CPAN 1885, CPAN 2004, CPAN 2024, CPAN 3004, CPAN304, HD 2119, PBW 62.
High harvest index	BR 2104, CC 505, HD 2190, MG 78-8-7, HI 8757, HW 868, JV 126, MACS 1963, MUW 29, Sarbati Sonara, Sr9 48-A.

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