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GENETIC DIVERGENCE STUDIES IN WHEAT GERMPLASM USING NON- HIERARCHICAL EUCLIDEAN CLUSTER ANALYSIS

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Four hundred and forty-one wheat germplasm collections including important varieties and exotic and indigenous accessions were evaluated for 15 metric characters using non-hierarchical Euclidean cluster analysis. All the genotypes were grouped into 12 different clusters showing existence of high genetic diversity in the material. The genotypes of heterogeneous origin were grouped in the same cluster indicating non-parallelism between genetic and geographic diversity. The intra-cluster distance was maximum (2.90) in cluster II and minimum (2.10) in cluster V. Cluster IV and X were highly diverse (6.66) from each other. Genotypes of cluster IV were the highest yielders (X = 48.57 g, C.V. 23.80%). Several collections which may serve as good genetic donors for high spikelet fertility, dwarfness, long ear, bold grain, high number of ears and good source for multiple resistance against rusts and powdery mildew were identified.

Key words : Wheat, germplasm, divergence, cluster analysis

Multivariate analysis based on Mahalanobis D^2 statistic and canonical analysis have the limitations for classifying huge germplasm collections studies for several attributes (Arunachalam, 1981). Beale (1969) suggested the use of Non- Hierarchical Euclidean analysis to overcome these limitations. However, the utility of this analysis for choosing parents for generating good segregates has received very little attention. Hence, the present study was undertaken to study the nature and extent of genetic variability and divergence in the sufficiently large germplasm and also to identify the genetic stocks which may serve as potent donors for yield and yield contributing characters and resistance for common diseases.

MATERIALS AND METHODS

The experimental material consisted of 441 indigenous and exotic germplasm collections of wheat (*Triticum aestivum* L.) representing primitive

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cultivars, land races, old obsolete varieties, current cultivated varieties and special genetic stocks alongwith three check varieties, viz. Sonalika, UP 368 and HD 2329. The genotypes selected for the study were highly diverse geographically as well as genetically and exhibited wide range of variation for morphological, developmental and agronomic characters. These genotypes were evaluated in an augmented design under good fertility and irrigated conditions. Each plot consisted of two rows, each one meter long with 23 cm row to row and 10 cm plant to plant spacing. Observations were recorded on single plant basis on 15 yield and yield contributing characters. A separate nursery of the entire collection used in the above experiment was raised in hill plots for screening against the prevalent diseases.

Analysis of augmented design was done following Federer (1956). Genetic divergence was studied using method of Non-Heirarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973).

RESULTS AND DISCUSSION

The analysis of variance indicated that there was considerable inherent genetic differences between the check varieties and block effects were in general non-significant except for flag leaf area, plant height and extrusion peduncle length.

Table 1. The general means, variance, coefficient of variability and range for 15 quantitative characters

	Characters	mean	Variance	C.V. (%)	Range
1	Flag leaf area (cm^2)	41.65	117.69	26.05	14.17 - 75.55
2	Plant height (cm)	103.09	346.44	18.05	37.46 - 195.06
3	Grains per ear	64.17	246.37	24.46	26.62 - 11.62
4	Peduncle length (cm)	21.39	4.45	9.86	13.36 - 30.34
5	Extr. peduncle length (cm)	17.06	26.64	30.25	2.83 - 31.94
6	Ear length (cm)	13.29	4.03	15.10	4.71 - 22.39
7	Spikelets per ear	20.97	5.07	10.74	14.50 - 25.96
8	Grains per spikelet	4.51	0.53	16.14	2.74 - 8.87
9	Tillers per plant	23.06	54.76	32.09	4.37 - 56.67
10	Yield per ear (g)	2.73	0.82	33.17	0.55 - 6.65
11	100-grain weight (g)	4.19	0.83	21.74	1.87 - 8.76
12	Ears per plant	19.21	37.10	31.71	4.63 - 46.57
13	Biological yield (g)	102.29	2736.94	51.14	24.98 - 260.58
14	Harvest index (5)	33.47	58.87	22.92	6.19 - 50.91
15	Grain yield per plant (g)	33.75	200.37	41.94	6.68 - 94.11

The general means, variances, coefficient of variability and range for different characters are given in Table-1. Existence of sufficient variability in a crop is an inevitable requirement for effective breeding programme. High values of coefficient of variability were obtained for biological yield, grain yield per plant, yield per ear, tillers per plant, ears per plant and extrusion peduncle length. These results are corroborative with the findings of Randhawa *et al.* (1975) and Sharma *et al.* (1981). The relative contribution of yield *per se* and biological yield towards genetic diversity was very high. This suggests that choosing parental material for attempting crosses only on the basis of grain yield and biological yield is likely to throw useful transgressive segregants. Peduncle length and number of spikelets per ear exhibited the lowest coefficient of variability, while variability was moderate for flag leaf area, plant height, number of grains per ear, ear length, number of grains per spikelet, 100-grain weight and harvest index which indicated that more variability needs to be included or generated for these characters.

Non-hierarchical euclidean cluster analysis proved quite useful for estimating the genetic divergence utilizing the unreplicated data in the large germplasm collections. All the 441 wheat genotypes were grouped into 12 clusters (Table-2). This grouping indicated considerable amount of genetic

Table 2. Estimates of average intra - and inter-cluster distances

Cluster number	Number of genotypes	Mean grain yield (g)	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	42	24.13	(2.47)	5.45	3.98	4.50	3.46	3.86	3.01	2.86	2.39	4.66	3.35	3.23
II	49	48.17		(2.90)	5.41	2.92	2.78	3.83	4.78	3.03	6.99	2.73	4.04	3.31
III	20	31.55			(2.69)	4.37	3.89	4.42	4.32	4.70	5.43	4.23	4.32	3.32
IV	27	48.57				(2.42)	2.64	4.39	4.58	2.68	6.62	6.66	4.91	3.09
V	42	37.15					(2.10)	3.16	3.43	2.24	5.31	2.70	2.86	2.83
VI	35	29.72						(2.64)	5.05	3.28	5.16	4.85	3.36	3.17
VII	29	27.61							(2.64)	3.16	3.59	3.25	2.57	3.15
VIII	48	32.45								(2.49)	4.55	3.07	3.22	2.38
IX	37	18.77									(2.82)	6.14	3.87	4.56
X	26	47.47										(2.41)	3.71	2.71
XI	39	29.70											(2.50)	3.02
XII	47	32.94												(2.31)

Values in parenthesis are intra-cluster distances diversity in the germplasm. The genotypes of indigenous germplasm were scattered in more than one cluster and similarly the genotypes of exotic germplasm were distributed in different clusters, e.g. genotypes like, CPAN 1959, W 3422, HUW 100, HD 2285, SMR-44, B, H 256-13-7-1, HB-611-A, DL-181-10, OL-129-3, LoK-3, PBW-27, HP-1209, HI-617, J-392, NI-8365, HW-706, CPAN-2001 and UP-368 although had heterogeneous origin and/or region but were present in the same cluster X. Other clusters also behaved in similar fashion. Therefore, it is concluded that there is no parallelism between genetic and geographic diversity. These findings are, in general, agreement with the results obtained by Murty and Arunachalam (1966), Lee and kaltsikes (1973), Garg and Gautam (1988) and Walia and Garg (1996). However, in past, ecogeographical diversity has been largely relied upon as an index of genetic diversity (Griffing and Lindstorm, 1954). Further, the genotypes of the same cluster had little divergence from each other with respect to the aggregate effect of the fifteen characters examined. Therefore, the hybridization among the genotypes of the same cluster is not desirable for developing good segregates. Inter and intra-cluster distances provided index of genetic diversity among and within the cluster. Maximum genetic distance was observed between clusters IV and X. The crosses between the genotypes from these clusters may give putative transgressive segregates. The further choice of the genotypes may be done considering disease and insect reaction, quality and lodging resistance, etc. The genotypes occupying top positions in a superior cluster may further be assessed for their combining ability and gene effects following suitable mating desgins.

The screening of germplasm helped in identifying promising genetic stocks (Table 3) which may serve as good source of high spikelet fertility,

Table 3. Important genetic donors identified from exotic and indigenous germplasm for different characters

High spikelet fertility	CPAN 1842, Lr 25 ransee, HUW 100, CPAN 1947, K 7938, WSM-159-1, NI 8611, H-220-3-3-1, IC 31-6 & DL-214-1.
Long ear	H-256-36-5, Kleititan, CPAN 1997, Hope, NI 8611, IC-310-6, IC 23-3, HW 706, IC-29-1 & H 284-3-2B
Bold grain	Lok-1, CPAN 1885, Hy b 65, VL 493, BR 3087, HI 8-62, Mukta (HI 385), DL-205-1, H-264-30-3 & IC 143-3
High yield	WG 2009, SN 1198, Sr Tt 2, H-256-13-7-1-, CPAN 1969, DL 20-9, HW 838, HW 706, H-284-30-2B & DL-172-1
High ear number	Lr 25 Transee, CAPN 1581, W 3286, Maniton, Rai 1774, WG 357, H-220-20-1, HW 706, H-284-30-2B & DL 172-1.
Dwarfness	CPAN 1419, UP 301, D 6899, 3948 A1, Tordo 'S', Oleson Dwarf & Norin-10.

long ear, bold grain, high yielding types, high number of ears per plant and dwarf types. The germplasm expressed a wide range of variability for morphological characters also. Several rusts and powdery mildew stocks were identified. Accordingly, Rai 1865, CPAN 1959, H 263-106-6-1, CPAN 1991, UL 493, E 8163, UP 301, H 264-100-1-1, VL 608, HW 838, HW 865, K 7931, CPAN 2003, CPAN 2009 and CPAN 2010 may serve as good source for multiple resistance against rusts and powdery mildew in wheat. The germplasm used in the present study may have useful gene (S) for quality improvement and various edaphic and climatic stresses viz. water, salt, alkali and high temperature. Further screening of these materials for these attributes is thus suggested.

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