Genetic Divergence of Exotic Germplasm Lines in Wheat (Triticum aestivum L.)

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One hundred fifty three exotic wheat genotypes were evaluated alongwith three checks for quantitative characters to study genetic divergence by employing D^2 analysis. The genotypes were grouped in to 13 diverse clusters. Clustering pattern of genotypes showed no definite relationship between genetic divergence and geographical distribution of genotypes. The highest genetic divergence was observed between cluster V and VIII, whereas, cluster I and II were closest one. On the basis of genetic divergence and mean performance, nine diverse and superior genotypes, being exceptionally good for one or more traits and reasonable for other, comparison to checks, were selected and these genotypes may be useful in multiple crossing or diallel selective mating system to recover transgressive segregants.

Key words: Wheat, Genetic divergence, Exotic lines

The success of any crop-breeding programme depends on the nature and amount of genetic variability available in the germplasm collections. Germplasm serves as the most valuable natural resources in providing needed attributes for engineering successful varieties (Hawkes, 1981). The indigenous as well as exotic materials obtained from other countries constitute the germplasm collections of a crop available to a breeder. The classification of germplasm collection is a prerequisite for distinguishing genetically close and divergent types for various plant breeding programme. By using advance biometrical techniques such as multivariate analysis based on Mahalanobis's D² statistics (Mahalanobis, 1936) it has now become possible to quantify the degree of genetic divergence amongst biological populations and assessing of relative contribution of various desirable attributes of breeding and agronomic value to the total divergence.

Materials and Methods

One hundred fifty three exotic lines of wheat germplasm alongwith three checks (HP 1731, PBW 343 and NW 2036) were evaluated in an augmented design at Main Experiment Station of ND University of Agriculture and Technology, Kumarganj, Faizabad during *rabi* 2003-04. Each genotype was accommodated in two rows plot of 2.5 m long with inter- and intra-row spacing of 25 cm and 5 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were recorded on 5 randomly selected competitive plants from each plot on twelve quantitative characters namely, growth habit, days to heading, days to maturity, plant height, tillers per plant, ear length, spike weight, grains per spike, 1000 grain weight, biological yield per plant. harvest index and grain yield per plant. The data recorded on above characters were subjected to D^2 analysis of Mahalanobis (1936) and Rao, 1952.

Results and Discussion

Based on D^2 statistics, 153 genotypes were grouped in to 13 non-overlapped clusters (Table 1). Cluster I had maximum 24 genotypes, followed by cluster II, XI and VII having 23. 22 and 21 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity.

The maximum inter cluster distance was observed between cluster VIII and V. Cluster VIII also recorded very high inter cluster distances from clusters indicating thereby, highly diverse nature of the members of cluster VIII with the members of cluster VI. VII, III, IX and XI. Therefore, hybridization of desirable genotypes belonging to cluster VIII in those of clusters VI VII, III, IX and XI may be recommended for isolating transgressive segregants. The minimum inter cluster distance was observed between clustery VII and VIII and followed by cluster III and VIII and cluster. VII and XI which showed existence of less diversity between these cluster pairs (Table 2).

The average intra cluster distance in cluster X was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves, however, in all cases, the inter-cluster distances were greater than the intra cluster distances implying presence of greater degree of genetic diversity between the genotypes of two cluster than the genotypes present within the cluster.

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Table 1. Clustering pattern	of 153 genotypes on the basis of Non-	hierarchical Euclidean Cluster analysis for 13 characters

Cluster No.	Number of Genotypes	Genotypes
1	24	35 th IBWSN-5, 35 ¹⁺¹ IBWSN-21, 35 th IBWSN-42, 35 th IBWSN-45, 35 th IBWSN-162, 35 ^{dl} IBWSN-163, 35 ¹⁺¹ IBWSN-170, 35 th IBWSN-193, 35 th IBWSN-210, 35 ¹⁺¹ IBWSN-269, 35 th IBWSN-301, 20 th SAWSH-23, 20 th SAWSH-202, 10 th SAWYT-33, 23 rd ESWYT-43, 10 th HTWYT-14, 10 th HTWYT-39, 10 th HTWYT-50, 13 th HRWSN-99, 13 th HRWSN-124, 13 th HRWSN-303, 35 th IBWSN-416, 20 th SAWSN-18, 13 th HRWSN-147.
IT	23	35 ^{U1} IBWSN-27, 35 th IBWSN-37, 35 th IBWSN-176, 35 ^{U1} TBWSN-410, 20 ^{H1} SAWSN-41, 20 th SAWSN-227, 20 th SAWSN-334, 20 th SAWSN-338, 10 th SAWYT-18, 13 th HRWSN-36, 13 th HRWSN-116, 13 th HRWSN-211, 3 rd IAT-24, RWCB 03-5, RWCB 03-20, RWCB 13-29, RWCB 03-33, 3 rd RWYT-MR-9, 11 th HMN-9, 23 rd ESWYT-3, 23 rd ESWYT-15, 13 th HRWSN-141.
HI	9	35 th IBWSN-375, 20 th SAWSN-109, 10 th SAWYT-15, 23 rd ESWYT-48, 10 th HTWYT-40, 6 th EGPSN-3, 6 th EGPSN-24, 6 th EGPSN- 142, 1 1 th HMN-6.
IV	15	35 th IBWSN-294, 20 th SAWSN-48, 13 th HRWSN-7, 13 th HRWSN-17, 13 th HRWSN-21, 13 th HRWSN-126, 13 th HRWSN-126, 13 th HRWSN-168, 13 th HRWSN-216, 10 th HRWYT-23, 3 rd IAT-78, 3 rd IAT-80, RWCB-03-12, 13 th HRWSN-127, 3 rd IAT-31, HP-1731.
v	5	10th HTWYT-8, 13th SRWSN-13, 6th EGPSN-45, 6th EGPSN-131, 6th EGPSN-133.
VI	8	35"' IBWSN-415, 20" SAWSN-31, 20" SAWSN-70, 20"' SAWSN-1 16, 10"' HRWYT-19, 10" HRWYT-30, 6" EGPSN-147, RWCB 03-9.
VII	5	13th HRWSN-101, 10th HRWYT-19, 6th EGPSN-132, 3rd RWYT-MR-4, 1 1th HMN-22.
VIII	1	3ª IAT-9
IX	6	35 th IBWSN-364, 35 th IBWSN-367, 20 th SAWSN-34, 6 th EGPSN-41, 2 nd HLWSN-182, 35 th IBWSN-535.
х	5	20 th SAWSN-43, 20 th SAWSN-57, 10 ¹¹ ' HTWYT-42, 2 nd HLWSN-18, 3 nd 1AT-44.
XI	22	35 th IBWSN-39, 35 th IBWSN-84, 35 th IBWSN-85, 35 ¹¹¹ IBWSN-265, 20 th SAWSN-71, 20 ¹¹¹ SAWSN-102, 20 th SAWSN-108, 20 th SAWSN-1 10, 20 th SAWSN-1 11, 20 th SAWSN-1 13, 20 th SAWSN-1 17, 20 th SAWSN-1 19, 20 th SAWSN-138, 10 th HTWYT-3, 13 th HRWSN-149, 10 th HRWYT-37, 6 ¹¹¹ EGPSN-30, 6 th EGPSN-137, 6 th EGPSN-143, 6 th EGPSN-145, 3 rd IAT-33, NW 2036.
хи	21	35 th IBWSN-365, 35 th IBWSN-366, 35 th IBWSN-369, 35 th IBWSN-374, 35 th IBWSN-403, 20 th SAWSN-45, 20 th SAWSN-62, 23 rd ESWYT-27, 10 ¹¹¹ HTWYT-15, 10 th HTWYT-22. 10 th HTWYT-30, 13 th HRWSN-33, 13 th HRWSN-108, 13 th HRWSN-118, 13 th HRWSN-119, 13 th HRWSN-221, 13 ¹¹¹ HRWSN-307, 3 rd IAT-54, RWCB 03-49, 3 rd IAT-34, PBW -343
XIII	9	35 th IBWSN-33, 20 th SAWSN-225, 10° SAWYT-20, 10 th SAWYT-48, 10 th HTWYT-11, 13 th HRWSN-125, 10 th HRWYT-21, 3 rd IAT-43, RWCB 03-10

Table 2. Estimates of a	average intra	and inter	cluster di	istances for	the 13	cluster in	wheat
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Cluster No.	I	<u> </u>	111	ĩ۷	v	VI	VII	VIII	IX	x	XI	XII	XIII
1	1.706	2.272	2.604	2.820	3.998	3.310	5.568	9.403	4.359	4.326	2.465	1.879	3.685
11		1.709	3.808	2.114	3.857	4.372	4.278	8.468	5.729	5.385	2.435	2.345	4.528
HI			2.229	4.623	4.910	3.768	6.136	10.077	3.336	3.775	2.664	2.858	4.673
IV				2.082	2.803	3.669	3.865	8.936	6.423	5.739	3.001	2.533	4.286
v					1.742	3.938	3.435	11.129	7.167	7.061	3.009	4.267	5.584
VI						2.612	6.378	10.914	4.789	5.255	3.831	3.143	2.988
VII							2.772	10.095	8.774	7.533	3.941	5.177	7.665
VIII								0.000	10.068	9.292	10.053	8.596	9.332
IX									2.749	4.942	5.289	4.485	4.327
х										3.194	5.790	5.231	3.701
XI											2.198	3.689	2.583
XII												1.951	5.141
XIII													1.923

Bold figures represent intra-cluster distance

The cluster IX showed the highest cluster means for ear length, grains per spike, spike weight and grain yield along with second highest mean for biological yield per plant. Cluster VIII recorded highest mean for tillers per plant and biological yield per plant. The entries exhibited early flowering and maturity were concentrated in cluster V and VI, respectively. Plant height and harvest index resulted highest mean in cluster X. 1000 grain weight was exhibited higher mean in cluster III. The differential contribution to total divergence was observed in different yield attributes (Table 3). The germplasm lines were divergent mainly on the basis of ear length, grains per spike and spike weight as these traits contributed largely to divergence as compared to other traits.

Cluster No./Characters	I	11	111	IV	v	VI	VII	VIII	IX	x	XI	XII	XIII
Days to heading	84.62	87.83	82.47	87.00	79.92	83.07	83.96	106.00	85.30	88.88	81.93	86.90	87.53
Days to maturity	119.17	121.16	119.56	119.68	115.44	114.70	120.48	146.40	121.60	122.64	118.16	121.23	120.82
Tiller per plant	9.31	10.50	10.62	12.07	12.88	17.17	10.48	10.20	11.90	9.28	9.68	11.23	18.18
Plant height (cm)	84.85	82.91	92.56	82.40	75.99	92.24	79.26	86.08	101.50	106.96	90.67	94.68	83.88
Ear length (cm)	10.16	9.82	11.49	9.06	8.76	10.36	8.84	10.12	12.18	11.27	10.15	10.78	10.49
Grains per spike	56.32	50.00	58.82	42.76	39.28	52.93	29.88	48.60	63.24	61.32	48.70	50.88	56.53
Spike weight (g)	2.70	2.36	2.99	2.02	1.89	2.41	1.65	2.14	3.38	3.27	2.32	2.43	2.78
1000 grain weight	36.27	34.97	44.68	34.54	41.22	38.44	42.81	35.64	43.99	40.96	41.55	36.49	33.85
Biological yield (g)	31.93	22.85	29.49	29.77	28.37	38.27	12.35	30.48	42.33	31.61	23.03	30.87	45.71
Harvest index (%)	33.68	28.52	32.91	34.87	33.66	37.96	33.38	32.18	29.03	46.94	30.02	36.02	33.65
Grain yield per plant (g)	10.01	7.84	8.89	8.65	8.37	11.47	3.82	9.47	15.08	6.94	7.82	9.12	13.66

Table 4. Diverse and superior genotypes with desirable characters selected from different clusters

Genotype	Cluster number	Desirable characters
2 nd HLWSN 182	IX	Plant height, ear length, grains per spike, spike weight and grain yield per plant
RWCB 03-9	VI	Days to maturity and tillers per plant
2ndHLWSN183	x	Ear length, grains per spike and harvest index
20 th SAWSN34	IX	Spike weight, grains per spike and 1000 grain weight
20thSAWSN31	VI	Biological yield and grain yield per plant
35 th IBWSN 415	VI	Grain yield per plant, harvest index and tillers per plant
20th SAWSN 225	XIII	Grain yield
RWCB 03-10	XIII	Tiller per plant, grain yield per plant and biological yield
10 th HTWYTII	XIII	Grain yield and biological yield

The data on inter cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotypes among 153 genotypes. The genotypes, exceptionally good in respect to one or more characters and atleast comparable in respect to other to the checks, were deemed desirable. On the basis of nine genetically diverse genotypes, superior genotypes were selected (Table 4); they belong to different four clusters. Intermating of divergent groups would lead to greater opportunity for crossing over which release latent variability by breaking linkage and progenies derived from cross are expected to show broad spectrum of genetic variability providing a greater scope for isolating transgressive segregants in the advance generation. So, these genotypes may be used in a multiple crossing programme or in diallel selective mating system to recover transgressants.

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