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D^2 analysis in certain promising genotypes of wheat (*Triticum aestivum* L. em. Thell)

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Abstract

A field experiment was carried out with 104 diverse indigenous elite genotypes of bread wheat along with four checks for genetic variability, character association and divergence analysis in Augmented Block Design, divided into 5 blocks of equal size. Each block had 24 plots of test entries along with 4 checks (*viz*., LOK-1, WH-147, HD-2009 and DBW-17). The trial was conducted at Main Experiment Station Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.) during *Rabi* 2013-14. The observations were recorded on eleven quantitative traits *viz*., days to 50% flowering, days to maturity, plant height, tillers / plant, spike length, flag leaf area, peduncle length, 1000-grain weight, biological yield / plant, harvest index and grain yield / plant. Results revealed that 100 indigenous lines and 4 check varieties of wheat were grouped into eleven distinct clusters by using non-hierarchical Euclidean cluster analysis. It indicated the existence of high degree of genetic diversity present in the varieties / lines. Therefore, these varieties / lines may serve as valuable source for selection of diverse parents. Maximum intra-cluster distance was found for cluster-VI followed by cluster-XI. On the other hand the minimum intra-cluster distance was recorded for cluster-VII followed by cluster-II. The highest inter-cluster distance was observed between cluster-IV and cluster-XI followed by cluster-III and cluster-XI. The lowest inter-cluster distance was observed between cluster-I and cluster-II followed by cluster-VII and cluster-IX. Hence, crosses should be made between these widely related genotypes located in intra and inter cluster distances, to get desirable extant of heterotic potential in order to increase the production and productivity of wheat in Northern Eastern Plain Zone of Uttar Pradesh.

Keywords: Wheat (*Triticum aestivum*), Genetic Diversity (D^2), Cluster

1. Introduction

Wheat, (*Triticum aestivum* L. *em.* Thell) the world’s largest cereal crop, belongs to Graminae (Poaceae) family of the genus *Triticum*. It has been described as the ‘King of cereals’ because of the acreage it occupies, high productivity and the prominent position in the international food grain trade.

India stands second rank in production and consumption next to china in the world. India’s share in world wheat production is about 14.13%. Wheat is only the crop where production increase more than fifteen fold during last sixty three years (6.5 million tonnes in 1950 to 95.91 million tonnes in 2014. (Anonymous; 2014) [1]

The world acreage under wheat crop during 2012-13 was 221.47 million ha with production of 654 million tonnes with an average yield of 31.50 q/ha. (Anonymous; 2014) [1]. In India, the total area for wheat crop during 2015-16 was 30.23 million hectares with the production of 93.50 million tonnes and average productivity was 30.93 q/ha. (Project Director’s Report 2015-16).

During the year 2015-16 in Uttar Pradesh ranked first with an area of 9.65 mha with the production of 26.87 million tonnes with average productivity of 27.86 q/ha. The productivity of wheat in other states is comparatively lower than that of Punjab and Haryana.

Wheat may be compared well with other cereals in nutritive value. It has good nutrition profile with 12.1 percent protein, 1.8 percent lipids, 1.8 percent ash, 2.0 percent reducing sugars, 6.7 percent pent sans, 59.2 percent starch, 70 percent total carbohydrates and provides 314K calper100g of food. It is also a good source of minerals and vitamins *viz*., calcium (37 mg/100g), iron (4.1 mg/100g), thiamine (0.45 mg/100g), riboflavin (0.13 mg/100g) and nicotinic acid (5.4 mg/100mg) (Lorenz and Kulp, 1991).

The technological packaging of improvement, wheat seed, chemical fertilizer with an overall supporting infrastructure and policy environment for agricultural transformation led to rapid wheat productivity and production of wheat increased to the tune of 263% and 711%, respectively by the year 2010-11 as compared to 1965-66 (Anonymous, 2011).

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Overall, there was 1.546% decrease in production while area sown to wheat increased by only 1.37% relative to previous crop season. In Haryana, there was increase in production by 5.2% with marginal increase in area *i.e*. 0.9%. However, Punjab recorded 3.0% increase in production with little decrease in area *i.e*. 0.7%. Although, the increase in production would be largely attributed to extended cool winter and cool weather and relatively high amount of rains during the crop season as compared to previous year.

During genetic improvement of yield in crop plants selection and hybridization techniques are utilized frequently. Selection is usually practiced for pooling favourable genes, while hybridization is predominantly utilized to accumulate favourable genes in a variety for obtaining better performance. For this purpose donor can be solved out from available germplasm, because germplasm severs as valuable natural reservoir providing several better attributes.

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. So, the knowledge of genetic diversity and relatedness in the germplasm is a pre-requisite for crop improvement programmes. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes. So precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation would help to select parents for evolving superior varieties. For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme. In the present study, 104 geographically diverse indigenous genotypes were used for assessing their genetic diversity considering yield as one of the important selection criterion and its practical utility for wheat improvement for target ecosystem.

Materials and Methods

The experiment was carried out during *Rabi* 2013-14 at Main Experiment Station Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.) This place is situated between $26^0.47^{per}$ N latitude, $82^0.12^{per}$ E longitude and at an altitude of 113 m above the mean sea level. The climate of district Faizabad is semi arid with hot summer and cold winter. Nearly 80% of total rainfall is received during the monsoon (only upto September) with a few showers in the winter. The soil type of experimental site was reclaimed salt affected soil (pH = 7.9) EC = 0.36 rich in potash and low in organic carbon, nitrogen and phosphorus.

The experiment was conducted to evaluate the 104 diverse wheat germplasm lines along with 4 checks (*viz*., LOK-1, WH-147, HD-2009 and DBW-17) in Augmented Block Design. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experimental field was divided into 5 blocks with 24 plots in each block (twenty test genotypes along with 4 checks). Each plot was consisted two rows of 2.5 m length with spacing of 5 cm within the rows and 25 cm between the rows.

The data were recorded on 5 randomly selected plants from each block for eleven characters *viz*., Days to 50% flowering, flag leaf area (cm^2), plant height (cm), spike length (cm), tillers per plant, peduncle length (cm), days to maturity, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g) and harvest index (%). Data recorded on the above characters were subjected to estimate the correlation coefficient (Searle, 1961) and Non-hierarchical Euclidian cluster analysis (Beale, 1969 and Spark, 1973) [13].

Results and Discussion

The study of genetic divergence among 100 indigenous genotypes of wheat along with 4 checks were assessed by employing Non-hierarchical Euclidean cluster analysis for eleven characters. The 104 genotypes were grouped in to 11 different non-overlapping clusters as presented in Table-1. Cluster I emerged with highest number of entries as it was constituted by 19 entries followed by cluster V, X having 12 genotype each, cluster IX contain 11 entries, cluster XI having 10 entries followed by cluster VIII having 9 entries and cluster VII contain 8 entries, cluster II, III, VI having 6 entries each, cluster IV contains 5 entries. The estimates of average intra-and inter-cluster distances for eleven characters were presented in Table-2. The highest intra cluster distance was observed in cluster V followed by cluster XI. The lowest intra cluster distance was observed in cluster VII. The highest inter-cluster distance was observed between cluster-IV and cluster-XI followed by cluster-III and cluster-XI. Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distances may yield high heterotic potential. These results corroborate the findings of…. The lowest inter-cluster distance was observed between cluster-I and cluster-II followed by cluster-VII and IX, which indicated that the genotypes belonging to these cluster pairs were genetically close to each other. The maximum intra-cluster distance was found for cluster-VI followed by cluster-XI, the minimum intra-cluster distance was recorded for cluster-VII followed by cluster-II. Cluster-I having 19 genotypes were responsible for highest cluster mean for spike length and showed moderate performance for remaining characters. Cluster-II having 6 genotypes resulting highest cluster mean for days to 50% flowering and test weight and showing moderate means for remaining characters. Cluster-III possessing 6 genotypes, showed lowest cluster mean for days to 50% flowering, tillers per plant, grain yield per plant and harvest index and average cluster mean for all the characters. The 5 genotypes of cluster-IV were characterized by highest cluster mean for days to 50% flowering and moderately perform for the other character. The 5 genotypes of cluster-IV were characterized by lowest cluster mean for plant height, peduncle length, biological yield, test weight and moderately performance for the other character. The 6 entries of cluster VI showed highest cluster mean for harvest index and grain yield and lowest cluster mean for flag leaf area and days to maturity. All the genotype of this cluster showing moderates performance for remaining characters. The cluster VIII, comprising 11 genotypes the highest cluster mean for days to maturity along with moderate performance in favor of other character. The 12 genotypes of cluster-X were responsible for highest cluster mean for flag leaf area. All the genotype of this cluster showing moderates performance for remaining characters. The cluster-XI constituted by 10 genotypes had highest cluster mean for plant height, tillers per plant, peduncle length and biological yield per plant along with moderate order cluster mean for rest of the character.

The above discussion clearly showed wide variation from one cluster to another in respect of cluster means for 11 characters, indicating that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distances and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in wheat to sustain the productivity level in NEP zone of Eastern Uttar Pradesh. These results are similar to those of

Table 1: Clustering pattern of 104 wheat genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 11 characters

Cluster number	No. of genotypes	Genotypes
I	19	AKAW-4731, DBPY-11-2(d), LBPY-2013-3, LBPY-2013-1, DBW-17, HD-2009, GW-2010-288, NIAW-2064, RAJ-4350, RAJ-4351, HI-8737, VW-20168, KB-2013-01, DBPY-11-4(d), GW-2010-278, WSM-55(d), NIAW-2349, RAJ-4393, LBPY-2013-4
II	6	GW-2010-285, LBPY-2013-5, GW-2010-282, DBPY-12-1(d), KB-2013-5, LBPY-2013-2
III	6	DBPY-11-1(d), DBPY-12-4(d), DBPY-12-6(d), DBPY-12-7(d), DBPY-12-1(d), JS-6-4
IV	5	DBPY-11-3(d), GW-2010-281, RAJ-4395, RAJ-4396, AKAW-4739
V	12	GW-2010-280, NIDW-846(d), GW-2010-286, GE-2010-429, HI-1588, GW-2011-354(d), HI-8750(d), HI-8758(d), HI-8756(d), RAJ-4392, RAJ-4394, GW-2011-361
VI	6	GW-2010-274, GW-2010-291, GW-2010-279, KLY-1090, VW-20145, NIDW-760
VII	8	GW-2010-294, GW-2010-297, VW-20169, DBPY-12-5(d), HI-8728(d), LBPY-2011-1, DBPY-12-8(d), GW-2010-298
VIII	9	GW-2010-277, GW-2010-284, HI-8726(d), RAJ-4265, GW-2010-296, NIDW-842(d), DBPY-2013-5(d), KLY-1035, KLY-1082
IX	11	GW-2010-275(d), GW-2010-292, GW-2010-272, LOK-1©, WH-147, GW-2010-287, GW-2011-362, LBPY-2011-7, GW-2010-283, LBPY-2011-6, LBPY-2011-8
X	12	DBPY-12-3(d), GW-2011-347, GW-2011-351(d), LBPY-2011-2, GW-2011-356, RAJ-4304, GW-2011-346, JS-6-1, DBPY-2013-4(d), LBPY-2011-10, WSM-57-13, GW-2012-436
XI	10	DBPY-2010-276, VW-20167, LBPY-2011-5, LBPY-2011-9, DBPY-2013-1(d), NIDW-2268, DBPY-2013-2(d), GW-2012-421, GW-2010-290, DBPY-2013-3(d)

Table 2: Estimates of average intra- and inter-cluster distances for 11 clusters in wheat

	Cluster 1	**2 Cluster**	**3 Cluster**	**4 Cluster**	**5 Cluster**	**6 Cluster**	**7 Cluster**	**8 Cluster**	**9 Cluster**	**10 Cluster**	**11 Cluster**
Cluster 1	10.948	15.121	23.227	17.584	16.75	28.818	19.173	24.084	17.093	23.341	36.642
2 Cluster		8.317	35.892	28.673	20.764	23.045	15.416	19.539	17.698	22.412	24.255
3 Cluster			12.756	28.048	21.757	41.500	26.979	40.558	24.734	21.865	43.621
4 Cluster				10.915	18.221	35.173	24.564	24.438	20.923	29.451	49.885
5 Cluster					12.908	34.241	20.378	23.422	17.404	17.247	33.990
6 Cluster						15.146	16.595	22.616	19.745	26.324	25.021
7 Cluster							7.312	15.497	15.144	15.490	22.142
8 Cluster								13.898	21.367	23.331	29.863
9 Cluster									9.975	15.200	22.817
10 Cluster										10.649	19.906
11 Cluster											14.520

Bold figures indicates Intra-cluster distance.

Table 3: Clusters means for 11 characters in wheat

	Days to 50% flowering	**Flag leaf area (cm^2)**	**Plant height (cm)**	**Days to maturity**	**Tillersper plant**	**Spike length (cm)**	**Peduncle length (cm)**	**Biological yieldper plant (g)**	**Grain yieldper plant (g)**	**Test weight (g)**	**Harvest index (%)**
1 Cluster	81.087	31.183	77.378	113.661	4.529	8.610**	16.526	19.027	7.445	41.290	38.882
2 Cluster	82.250**	28.523	84.143	114.417	5.567	8.070	15.422	26.487	10.695	44.602**	40.170
3 Cluster	73.750*	36.578	82.391	111.500	3.442*	7.134	21.548	15.563	5.256*	40.938	33.514*
4 Cluster	80.050	28.721	69.190*	113.900	5.350	7.554	14.615*	14.945*	5.802	31.441*	38.299
5 Cluster	80.688	34.630	78.170	115.104	5.025	6.574	17.954	20.240	6.976	38.655	34.007
6 Cluster	78.750	26.597*	83.760	110.000*	4.983	7.064	22.085	27.280	12.310**	34.682	44.636**
7 Cluster	75.250	27.600	75.626	113.000	5.400	6.451	19.662	25.608	10.526	40.706	41.266
8 Cluster	78.417	29.380	75.380	116.556**	5.567	7.144	17.758	27.973	11.170	33.105	40.548
9 Cluster	80.464	35.725	78.520	110.064	5.700	7.399	21.002	23.998	8.898	37.170	37.152
10 Cluster	76.979	45.332**	82.384	113.083	5.171	5.937*	22.880	25.178	9.051	39.846	35.822
11 Cluster	78.275	41.121	94.198**	112.350	6.650**	6.556	26.396**	30.145**	12.038	41.342	39.391

Minimum value-*
Maximum value-**

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