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Divergence analysis in certain genotypes of wheat (*Triticum aestivum* L. em. Thell)

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Abstract

A field experiment was carried out with 109 diverse indigenous genotypes of bread wheat along with four checks in Augmented Block Design for genetic variability, character association and divergence analysis, divided in to 7 blocks of equal size. Each block had 15 plots of test entries along with 4 checks (*viz.* LOK-1, HD-2009, WH-147 and DBW-17). The trial was conducted at Main Experimental Station Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.) during *Rabi* 2015-16. The observations were recorded on eleven quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height(cm), tillers per plant, spike length(cm), flag leaf area(cm), peduncle length(cm), 1000-grain weight(g), biological yield per plant(g), harvest index(%) and grain yield per plant(g). Results revealed that 105 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, 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 extent of heterotic potential in order to increase the production and productivity of wheat in North Eastern Plain Zone of Uttar Pradesh.

Keywords: Wheat (*Triticum aestivum*), genetic diversity (D^2), cluster

Introduction

Wheat, (*Triticum aestivum* L. em. Thell) is the world's largest cereal crop which belongs to Graminae 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. Wheat is consumed in a variety of ways such as bread chapatti, porridge, flour, suji etc.

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% of world's wheat production. Wheat is the only crop where production increase more than fifteen fold during last sixty three years (6.5 million tonnes in 1950 to 95.51 million tonnes in 2016-17 (Anonymous, 2016-17) [2].

In India, wheat covered about 29.72 mha during the recent past 2017-18 *Rabi* season and accounts for about 37 percent of the country's total food grains production as per the recent 3th Advance Estimates from Directorate of Economics and Statistics (DES), Ministry of Agriculture and Farmers Welfare (MoA&FW), India.

In India, during 2017-18 *Rabi* season the production of wheat 98.61million tonnes and average productivity was 33.18 q/ha, with the area of 29.72 million ha. During the year 2017-18 in Uttar Pradesh, the total wheat production was 31.98 million tonnes and average productivity was 32.69 q/ha., with the area of 9.786 million ha.

Wheat production in 2017-18 has made another record and hallmark level output of 98.61 mt with an average national all time highest productivity of 3318 kg/ha. The perusal of state wise production indicated that Uttar Pradesh tops the list with 31.99 mt, followed by Punjab (17.61mt), Madhya Pradesh (15.91 mt), Haryana (11.31 mt), Rajasthan (9.53 mt) and Bihar (4.58 mt). These top six states together contributed about 92 percent of the total production (Anonymous 2018) [3].

Wheat may be compared well with other cereals in nutritive value. It has good nutrition profile with 12.6 percent protein, 1.7 percent reducing sugars, 66.8 percent starch, 68.5 percent total carbohydrates and provides 314K cal/100g of food. It is also a good source of minerals and vitamins *viz.*, thiamin (0.30 mg/100g), riboflavin (0.07 mg/100g) and niacin (1.7 mg/100mg) (Kumar *et al.*, 2011).

For maintaining the sustainability and self sufficiency, the country need to target of 100 million tonnes by year 2030. 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. ?????

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 donors 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 (Singh *et al.*, 2010; Tsegaye *et al.*, 2012; Verma *et al.*, 2013; Dejene *et al.*, 2016; Pandey *et al.*, 2017; Singh *et al.*, 2017)^[19, 23, 25, 9, 14, 21]. 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, 105 geographically diverse indigenous genotypes were used for assessing the genetic diversity considering yield as one of the important selection criterion.

Material and Methods

A field experiment was carried out during *Rabi* 2015-16 at Main Experimental Station Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.). The experiment was conducted to evaluate the 109 wheat germplasm lines along with 4 checks (namely LOK-1, HD-2009, WH-147 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 7 blocks and 19 plots in each block (15 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 was recorded on 5 randomly selected plants from each plot for eleven characters *viz.* days to 50% flowering, days to maturity, plant height (cm), tillers per plant, spike length (cm), flag leaf area (cm²), peduncle length (cm), 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 Non-hierarchical Euclidian cluster analysis (Beale, 1969 and Spark, 1973)^[5, 22].

Results and Discussion

The 109 genotypes were grouped into 11 distinct and non-overlapping clusters Table-1. The estimates of average intra- and inter-cluster distances revealed that the genotypes present

in a cluster have little genetic divergence from each other with respect to aggregate effect of 11 characters under study, while much more genetic diversity was observed between the indigenous varieties/lines belonging to different clusters. Since, high or optimum genetic divergence is desired between the parents for hybridization plan for obtaining good segregants by crossing the little diverse genotypes belonging to same cluster are very low.

The estimates of average intra- and inter-cluster distances for eleven characters were presented in Table-2. The maximum intra-cluster distance was found for cluster VI followed by cluster XI and the minimum intra-cluster distance was recorded for cluster VII followed by cluster II. The highest inter-cluster distance was recorded between clusters IV and XI, followed by cluster III and XI.

Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distances, mentioned above, may through desirable transgressive segregants, which indicated that the genotype belonging to these cluster pairs separated by very high inter-cluster distances, mentioned above, may throw desirable transgressive segregants. The lowest inter-cluster distance was recorded between cluster I and II followed by cluster VII and IX, which indicated that the genotypes belonging to these cluster pairs were genetically close to each other.

Cluster-I having 19 genotypes were responsible for highest cluster mean for spike length and showing 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 performed for the other characters. The 5 genotypes of cluster-IV were characterized by lowest cluster mean for plant height, peduncle length, biological yield, test weight and moderately performed for the other characters. 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 characters. 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 characters.

The above discussion clearly shows 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 enhance the production and productivity of this crop in Northern Eastern Plain Zone.

Table 1: Clustering pattern of 109 wheat genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 11 characters

Cluster number	No. of genotypes	Genotypes
I	18	HI-1600, RAJ-4395, KB-2013-05, RAJ-4393, NIAW-2064, GW-2013-491, GW-2013-478, GW-2013-489, KB-2013-01, LBPY-2014-1, UP-2929, AKAW-4899, GW-2013-471, LBPY-2014-2, LBPY-2014-4, GW-2014-545, RAJ-4396, AKAW-4900,
II	8	LBPY-2014-3, GW-2014-582, NIAW-2809, RAJ-4478, GW-2013-482, AKAW-4901, DWAP-1539, DWAP-1540.
III	8	LBPY-2015-01, LBPY-2015-08, LBPY-2015-06, LBPY-2015-04, LBPY-2015-05, KV-2015-01, HI-1610, NIAW-2847,
IV	9	LBPY-2013-1, RAJ-4392, GW-2013-488, UP-3968, GW-2013-559, GW-2014-579, LBPY-2013-5, RAJ-4394, LBPY-2013-3,
V	9	RAJ-4351, LBPY-2014-10, HI-1608, HI-1609, HI-1607, LBPY-2014-8, LBPY-2014-12, UP-2970, NIAW-2844.
VI	9	NIAW-2349, LBPY-2014-7, LBPY-2014-9, AKAW-4923, DWAP-1534, RAJ-4441, HD-2009©, DBW-17©, WH-147©,
VII	9	LBPY-2014-6, RAJ-4444, DWAP-1530, RAJ-4472, DWAP-1532, GW-2014-547, GW-2014-573, RAJ-442, GW-2014-580.
VIII	9	LBPY-2013-2, DWAP-1535, KV-2015-02, UP-2928, GW-2014-546, NIAW-3023, RAJ-4479, NIAW-3033, RAJ-4480
IX	9	RAJ-4350, UP-2971, LBPY-2015-07, DWAP-1538, UP-2930, GW-2014-581, GW-2014-544, UP-2931, DWAP-1531.
X	11	LBPY-2014-15, RAJ-4443, RAJ-4445, DWAP-1536, DWAP-1541, LBPY-2015-03, RAJ-4481, GW-2014-563, GW-2014-575, GW-2014-574, LBPY-2015-02.
XI	10	LBPY-2014-5, LOK-1©, LBPY-2013-4, DWAP-1533, DWAP-1537, GW-2014-507, GW-2014-562, GW-2014-564, GW-2014-571, UP-2969.

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

Table 3: Clusters means for 11 characters in wheat

	Days to 50% flowering	Flag leaf area (cm ²)	Plant height (cm)	Days to maturity	Tillers per plant	Spike length (cm)	Peduncle length (cm)	Biological yield per plant (g)	Grain yield per 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

References

- Ali Y, Atta BM, Akhter J, Monneveux P, Zahid L. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. Pakistan J Bot. 2008; 40(5):2087-2097.
- Anonymous. Statistical data base, 2016. www.fao.org.
- Anonymous. Project Directorate Report, IIW&BR, Karnal, 2018.
- Azeem Akram Toria AI, Awan FS, Aziz-ur-Rehman Ahmad F, Malik A, Rao S. Genetic diversity in Indian sub-continental landrace cultivars of the genus *Triticum* L. African J Biotech. 2011; 11(44):10170-10175.
- Beale EML. Euclidean cluster analysis. A paper contribution to 37th Session of the International Statistical Institute, 1969.
- Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). Madras Agril. J. 2001; (7-0):457-461.

7. Bhushan B, Gaurav SS, Verma PN, Ali M, Meena MR. Character association and genetic divergence for quantitative traits in bread wheat (*Triticum aestivum* L.). *Annals of Bio.* 2014; 30(1):62-67.
8. Mishra CN, Tiwari V, Satish Kumar, Gupta V, Kumar A, Sharma I. Genetic diversity and genotype by trait analysis for agromorphological and physiological traits of wheat (*Triticum aestivum* L.) SABRAO J.I of Breeding and Genetics. 2015; 47(1):40-48.
9. Dejene K Mengistu, Yosef G Kidane, Carlo Fadda, Mario Enrico Pè. Genetic diversity in Ethiopian Durum Wheat (*Triticum turgidum* var *durum*) inferred from phenotypic variations. *Plant Genetic Resources*, 2016, 1-11.
10. Desheva G, Cholakov T. Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivum* L.). *Genetics and Plant Physiology*. 2015; 4(3-4):191-200.
11. Federer WI. Augmented design. *Hawaiian Planters Record*. 1956; 40:191-207.
12. Kulshrestha. Effect of environment on clustering pattern in bread wheat (*Triticum aestivum* L.). *Asian J. Environmental Sci.* 2009; 4(2):203-206.
13. Lal BK, Ruchi GM, Upadhyay A. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.) *Asian J Agril. Sci.* 2009; 1(1):4-6.
14. Manoj Kumar Pandey. Bind HN, Sanjeev Kumar, Singh BN. Genetic Divergence in Wheat (*Triticum aestivum* L. Thell.) Under Saline Sodic Condition. *Int. J Curr. Microbiol. App. Sci.* 2017; 6(5):181-189.
15. Ramya G, Madhusudan K, Pradeep PE, Kalappanavar IK, Sujay V. Multivariate analysis through D² statistic among free threshable mutants of tetraploid wheat (*Triticum sp.*) *Crop Res. (Hisar)*. 2012; 15(1):32-34.
16. Rizwana Maqbool, Sajjad Muhammad, Khaliq Ihsan, Rehman -Aziz-ur, Khan AS, Khan SH. Morphological diversity and traits association in bread wheat (*Triticum aestivum* L.) *American-Eurasian J Agril. and Environmental Sci.* 2010; 8(2):216-224.
17. Singh Bhuri, Upadhyay PK. Genetic divergence analysis in wheat (*Triticum aestivum* L.). *Internat. J Plant Sci.* 2013; 8(2):297-299.
18. Singh D, Singh SK, Singh KN. Diversity of salt resistance in a large germplasm collection of bread wheat (*Triticum aestivum* L.). *Crop Improvement*. 2009; 36(1):9-12.
19. Singh D, Singh SK, Singh KN. Genetic divergence in bread wheat (*Triticum aestivum* L.) germplasm under alkali soil. *Madras Agril. J.* 2010; 97(1-3):4-6.
20. Singh MK, Sharma PK, Tyagi BS. Genetic divergence and economic heterosis for yield component traits and protein content under normal and heat-stress environment in spring wheat. *Crop Improvement*. 2011; 38(2):163-170.
21. Singh T, Singh V, Singh KP, Verma OP, Mishra S, Srivastava A, Ahmad R. D² analysis in certain promising genotypes of wheat (*Triticum aestivum* L. em. Thell). *J. Pharmacognosy and Phytochemistry*. 2017; 6(5):2714-2717.
22. Spark DN. Euclidean cluster analysis. *Algorithm, A.* 58. *Applied Statistics*. 1973; 22:126-130.
23. Tsegaye D, Dessalegn T, Dessalegn Y, Share G. Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia. *African J Biotech.* 2012; 11(40):174-180.
24. Verma AK, Singh PK, Vishwakarma SR, Tripathi RM. Genetic divergence in wheat (*Triticum aestivum* L.). *Farm Sci. J.* 2006; 15(1):32-34.
25. Verma PN, Singh BN, Yadav RK. Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*T. aestivum* L.). *International J of Agril. Sci.* 2013; 3(2):395-399.