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Genetic divergence analysis in wheat genotypes (*Triticum aestivum* L.) Under late sown condition

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Abstract

A field experiment was carried out with 100 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 6 blocks of equal size. Each block had 20 plots of test entries along with 4 checks (*viz.* NW-2036, DBW-14, NW-1014 and NW-1076). The trial was conducted at Main Experimental Station Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.) during *Rabi* 2019-20. The observations were recorded on eleven quantitative characters *viz.* days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, flag leaf area, spike length, number of spikelet per spike, test weight/(1000-grain weight), grain yield per plant, biological yield per plant and harvest index. Results revealed that 96 indigenous lines and 4 check varieties of wheat were grouped into eleven distinct clusters by using nonhierarchical 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. The maximum intra-cluster distance was found for cluster IX followed by cluster III and cluster II. The minimum intra-cluster distance was recorded for cluster IV followed by cluster I and cluster II. The highest inter-cluster distance was observed between clusters IX and V, followed by cluster IX and IV, cluster VIII and V. The lowest inter-cluster distance was observed between cluster VIII and VI followed by cluster VI and I, cluster IX and VI. 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 an important energy rich cereal for the majority of world's populations. Wheat attains unique position in agriculture and economy of our country because of being second most important food crop after rice.

The term "Wheat" is derived from many different locations, specifically from English, German and Welsh language. Wheat is most commonly defined by all cultures as "that which is white" due to its physical characteristics of light colored crops.

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. In the world during 2019-20, 216 million ha area was covered under wheat with a production of 764 million metric tonnes against year of 2018-19.

In India, during 2019-20, area under Wheat was 29.32 million ha with production of 103.60 million metric tonnes and yield of 3.53 metric tonnes per ha. Exports from India during 2019-20 were 0.2174 million metric tonnes as compared to 0.2262 million metric tonnes during 2018-19. India's closing stock in 2019-20 is estimated to be around 20.8 million tonnes whereas in 2018-19 it accounted for 1950 million tonnes. Indian wheat production in 2019-20 has made another landmark achievement by producing 107.18 mt with an average national productivity of 3508 kg/ha. During the past year production was also more than 100 million tonnes (103.60 million tonnes) and the current year production has witnessed a change of 3.58 million tonnes (+3.46%). The positive growth in production is attributed to the increased area by 4.21 per cent despite a fall in the crop yield marginally by - 0.72 percent. Increase in the support price by `85 per quintal in comparison to the recent past year and announced as `1925 per quintal of wheat, might have had a positive impact on the crop acreage (+1.24 million hectares). The crop area and productivity have increased in a majority of the states is a main reason behind the landmark production. States like Madhya Pradesh, Maharashtra, Gujarat and

Rajasthan have shown a significant increase in the crop area over the past year have resulted in a major quantum jump in overall wheat production. However, there existed regional variation in all the three variables in comparison to the previous year final estimates (2018-19).

Analysis on contribution of yield and/or area to the current year's overall wheat production indicated that the average national productivity has declined marginally by 0.72 per cent (-26 kg/ha) in 2019-20 but the significant increase in area (1.24 million hectares: 4.21%) has been the major reason for quantum jump and landmark production of 107.18 million tonnes. State wise estimates indicated that Bihar, Gujarat, Jharkhand, Karnataka, Madhya Pradesh, Maharashtra, Rajasthan, Uttarakhand and West Bengal registered a significant increase in the crop output. Similarly, with the exception of Assam, Bihar, Haryana, Himachal Pradesh, Rajasthan and Telangana, the rest of the states have witnessed an increase or maintained their productivity levels during the current season in comparison to the recent past. The crop yield varied across states and it ranged from as high as 5190 kg/ha in Punjab to 1250 kg/ha in Karnataka. Only Punjab and Haryana have registered yield levels much higher than the national average productivity of 3508 kg/ha. The increase in productivity during 2019-20 over the previous year was highest in the case of Uttarakhand (+262 kg/ha: +9.01%) and the highest reduction was noticed in the case of Haryana (-96 kg/ha: -1.95%). increase in area (1.24 million hectares: 4.21%) has been the major reason for quantum jump and landmark production of 107.18 million tonnes. State wise estimates indicated that Bihar, Gujarat, Jharkhand, Karnataka, Madhya Pradesh, Maharashtra, Rajasthan, Uttarakhand and West Bengal registered a significant increase in the crop output. Similarly, with the exception of Assam, Bihar, Haryana, Himachal Pradesh, Rajasthan and Telangana, the rest of the states have witnessed an increase or maintained their productivity levels during the current season in comparison to the recent past. The crop yield varied across states and it ranged from as high as 5190 kg/ha in Punjab to 1250 kg/ha in Karnataka. Only Punjab and Haryana have registered yield levels much higher than the national average productivity of 3508 kg/ha. The increase in productivity during 2019-20 over the previous year was highest in the case of Uttarakhand (+262 kg/ha: +9.01%) and the highest reduction was noticed in the case of Haryana (-96 kg/ha: -1.95%).

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 (Tsegaye *et al.*, 2012; Verma *et al.*, 2013; Dejene *et al.*, 2016; Pandey *et al.*, 2017; Singh *et al.*, 2017) [23, 25, 9, 14, 20]. 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, 109 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* 2019-20 at Main Experimental Station Research Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). This place is situated between 26^o.47'N latitude, 82^o.12' E longitude and at an altitude of 113 m above the mean sea level. The climate of district Ayodhya 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 meteorological data for the crop season have been given in Table-3.1. 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 100 wheat germplasm lines along with 4 checks (namely NW-2036, DBW-14, NW-1014 and NW-1076) in Augmented Block Design. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experimental field was divided into 6 blocks and 20 plots in each block (16 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 20 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), Number of productive tillers per plant, Spike length (cm), Flag leaf area (cm), Number of grains per spike, 1000-seed weight (g), Biological yield per plant (g), Harvest index (%), Grain yield per plant (g). Data recorded on the above characters were subjected to estimate the Non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973) [5, 22].

Results and Discussion

The study of genetic divergence among 96 indigenous varieties/lines of wheat along with 4 checks was assessed by employing Non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973) [5, 22] for eleven characters.

The 100 genotypes were grouped into 10 distinct and non-overlapping clusters. The discrimination of varieties/lines into so many discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the wheat materials (Deshmukh *et al.*, 1999; Roy *et al.*, 2004; Singh and Dwivedi, 2005; Verma *et al.*, 2006; Singh *et al.*, 2006; Iqbal *et al.*, 2007; Tsegaye *et al.*, 2012; Dhakar *et al.*; 2012; Toria *et al.*; 2011; Soni *et al.*, 2011) [24, 24, 23, 4, 21]. 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. In order to increase the possibility of isolating good segregates in the segregating generations it would be logical to attempt crosses between the diverse indigenous varieties/lines belonging to clusters separated by large inter-cluster distances.

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 IX followed by cluster III and cluster II. The minimum intra-cluster distance was recorded for cluster IV followed by cluster I and cluster II. The highest inter-cluster distance was observed between clusters IX and V, followed by cluster IX and V, cluster VIII

and V. 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 observed between cluster VIII and VI followed by cluster VI and I, and cluster IX and VI which indicated that the genotypes belonging to these cluster pairs were genetically close to each other.

The five genotypes of cluster-I were responsible for highest cluster mean for spikelets per spike (21.98), tillers /plant (7.08) and flag leaf area (17.32 cm) while showed moderate performance for remaining characters. Cluster-II having fifty eight genotypes showed moderates performance for all character. Cluster-III possessing twenty one genotypes, showed moderates performance for all characters. Cluster-IV were characterized by lowest cluster mean for number of spikelets per spike (17.46), days to maturity (115.00 days), flag leaf area (11.20 cm), biological yield per plant (25.40 g). It showed highest cluster mean for harvest index (40.16%) while remaining character showed moderate performance. It consist of one genotype. The One genotype of cluster-V were responsible for highest cluster mean for days to 50% flowering (83.00 days), and plant height (81.60 cm) and showed moderates performance for all remaining characters.

The One genotype of cluster-VI were responsible for highest cluster mean for days to maturity (122 days) while remaining characters showed moderate performance. The cluster-VII, comprising one genotype, showed highest average cluster mean for spike length (14.20 cm) and lowest average cluster mean for tillers /plant (5.60) while remaining characters showed moderate performance. The one genotype of cluster-VIII were responsible for highest cluster mean for biological yield per plant (47.60 g), grain yield per plant (14.80 g) and showed moderate performance for remaining characters. Cluster-IX having ten genotypes showed moderates performance for all characters. Cluster-X were characterized by lowest cluster mean for number of plant height (71.20 cm), spike length (8.80 cm), harvest index (26.71%) and grain yield per plant (7.80 g) while remaining characters of Cluster-X showed moderate performance.

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	5	HI-8777, KRL-370, HS-627, 50 th IBWSN 1269, RAJ-3765
II	58	AKAW-3713, PBW-777, UAS-459, DBW-88, WH-1310, 16 th HTWYT 12, WH-1216, DBW-71, HS-645, DBW-251, HW-5207, FLW-16, CG-1013, FLW-10, DWAP-1530, HS-646, DBW-110, RAJ-4083, DBW-778, PBW-725, VL-3014, 16 th HTWYT 45, AKAW-4901, HI-8737, HS-644, HI-8765, HI-1628, 38 th ESWYT 135, UASD DT-6, MP-1203, GJW-463, DHTW-60, PBW-756, HT-11, HI-1612, DBW-39, HD-3237, HS-626, PBW-780, NW-1076(C), 25 th SAWYT 319, DBW-129, K-1317, BRW-3723, DBW-179, HIKK-06, HS-611, HI-1621, NIAW-1994, NW-1014(C), HDW-439, HIKK-09, UAS-375, HI-1620, DBW-93, DWAP-1531, PWD-344, RAJ-3077
III	21	38 th ESWYT 114, VL-3013, 25 th HRWYT 238, HTW-9, HD-3086, HI-1619, WH-1127, HI-1609, WH-1080, HD-3118, HD-3171, AKAW-3717, 25 th SAWYT 337, MACS-3949, K-1006, HW-3631, KBRL-79-2, DDK-1051, NW-2036(C), FLW-22, 16 th HTWYT 27
IV	1	TLW-10
V	1	DWAP-15031
VI	1	DBW-107
VII	1	HD-3271
VIII	1	UAS-57
IX	10	HI-8708, COH-1105, BRB-3723, HD-3043, 38 th ESWYT 149, TL-3006, DBW-14(C), DBW-246, HTW-11, PBW-760
X	1	AKAW-4927

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
Cluster 1	48.12	215.54	299.17	382.62	483.37	145.73	202.47	182.93	247.89	410.69
2 Cluster		146.38	209.47	231.14	242.93	252.72	173.13	366.43	398.21	299.08
3 Cluster			165.04	263.40	324.30	394.37	269.49	480.83	463.26	334.05
4 Cluster				0.00	93.81	553.60	364.94	676.39	742.83	388.89
5 Cluster					0.00	569.10	349.32	697.29	747.98	371.32
6 Cluster						0.00	210.93	57.27	156.41	383.28
7 Cluster							0.00	244.25	398.08	504.78
8 Cluster								0.00	194.52	571.07
9 Cluster									203.01	417.52
10 Cluster										0.00

Table 3: Clusters means for 11 characters in wheat

	Days to 50% Flowering	Spikelets Per Spike	Plant Height (Cm)	Days to Maturity	Tillers /Plant	Spike Length (Cm)	Flag Leaf Area (Cm)	Biological Yield/Plant (G)	Test Weight (G)	Harvest Index (%)	Grain Yield/Plant (G)
1 Cluster	73.40*	21.98**	79.12	121.20	7.08**	13.80	17.32**	39.16	39.36	33.64	13.16
2 Cluster	79.91	19.61	77.79	120.93	6.70	11.78	13.61	33.38	36.86	37.69	12.53
3 Cluster	77.86	20.38	71.41	118.38	6.40	11.48	12.22	33.03	37.20	39.76	13.13
4 Cluster	75.00	17.46*	80.20	115.00*	6.80	13.60	11.20*	25.40*	34.60	40.16**	10.20
5 Cluster	83.00**	21.62	81.60**	115.00	6.80	13.60	11.60	25.60	31.40	39.84	10.20
6 Cluster	80.00	17.62	80.40	122.00**	6.20	10.40	13.80	44.20	37.60	30.77	13.60
7 Cluster	83.00	21.44	80.60	121.00	5.60*	14.20**	12.60	37.20	43.80	39.78	14.80
8 Cluster	79.00	20.68	81.20	117.00	6.60	10.40	13.40	47.60**	40.40	31.09	14.80**
9 Cluster	79.40	21.39	74.20	121.40	7.04	12.52	14.17	44.94	36.98	28.54	12.90
10 Cluster	82.00	18.64	71.20*	120.00	5.60	8.80*	13.80	29.20	34.20	26.71*	7.80*

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