



ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(7): 770-773
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www.thepharmajournal.com
Received: 03-05-2021
Accepted: 09-06-2021

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Genetic divergence analysis in wheat germplasms (*Triticum aestivum* L.)

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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 19 plots of test entries along with 4 checks (*viz.* KRL-19, NW-1067, KRL-3-4 and KRL-1-4). 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, peduncle length, spike length, number of grain per spike, test weight/1000-grain weight, grain yield per plant, biological yield per plant and harvest index. Results revealed that 105 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 V and cluster VIII. The minimum intra-cluster distance was recorded for cluster VI followed by cluster II. The highest inter-cluster distance was observed between clusters V and VIII, followed by cluster V and VIII, cluster III and IX. The lowest inter-cluster distance was observed between cluster I and IV followed by cluster VI and VII. 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.) 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.

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.

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, 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, 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 109 wheat

germplasm lines along with 4 checks (namely KRL-19, NW-1067, KRL-3-4 and KRL-1-4) 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), Number of productive tillers per plant, Spike length (cm), Peduncle length (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 Euclidian cluster analysis (Beale, 1969 and Spark, 1973) [5, 22].

Results and Discussion

The study of genetic divergence among 105 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 importance of genetic diversity for selecting parents for recombination breeding in an autogamous crop such as wheat to recover transgressive segregates has been also repeatedly emphasized (Verma *et al.*, 2006; Tsegaye *et al.*, 2012; Singh and Upadhyay, 2013; Verma *et al.*, 2013; Dejene *et al.*, 2016; Pandey *et al.*, 2017; Singh *et al.*, 2017) [24, 23, 17, 25, 9, 14, 21].

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 IX followed by cluster V and cluster VIII. The minimum intra-cluster distance was recorded for cluster VI followed by cluster II. The highest inter-cluster distance was observed between clusters V and VIII, followed by cluster V and VIII, cluster III and IX. 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 I and IV followed by cluster VI and VII, which indicated that the genotypes belonging to these cluster pairs were genetically close to each other.

The six genotypes of cluster-I were responsible for lowest cluster mean for biological yield/plant and showing moderates performance for remaining characters. Cluster-II having 18 genotypes resulting lowest cluster mean for days to maturity, Test weight and showing moderate means for remaining characters. Cluster-III having two genotypes, showed highest

cluster mean for days to Peduncle length and showed lowest cluster mean for grain yield/plant and average cluster mean for all other characters. Cluster-IV was characterized by highest cluster mean for days to 50% flowering, plant height, and moderately performs for the other character with eight genotypes. The cluster-V having the lowest cluster means for tillers/plant, with 13 genotypes and recorded average performance for all the other characters. Cluster-VI having seven genotypes, showed highest cluster mean for days to test weight, No. of grain/spike, biological yield/plant showed lowest cluster mean for spike length, and average cluster mean for all other characters. The cluster VII, comprising eight genotypes, showed lowest average cluster mean for harvest index, and rests are moderates characters. The cluster VIII, comprising 15 genotypes, showed lowest average cluster mean for days to 50% flowering and rests are moderates characters. Cluster IX having 16 genotypes, showed highest cluster mean for days to maturity and showed lowest cluster

mean for plant height and average cluster mean for all other characters. Cluster X having eight genotypes, showed highest cluster mean for tillers/plant, spike length, harvest index, grain yield/plant and average cluster mean for all other characters. Cluster XI having eight genotypes, showed average cluster mean for all other 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	6	HD-2824, PBW-154, PBW-502, K-0307, KRL-35, KC-975
II	18	SATSN-16, SATSN-28, SATSN-8, SATSN-36, SATSN-30, NW-5054, HD-3086, HD-2643, PBW-343, DBW-107, HP-1731, UP-2425, RAJ-4120, CHIRYA-3, LOK-1, FLW-15, FLW-8, KRL3-4 (c)
III	2	SATSN-C29, PBW-443
IV	8	SATSN-11, SATSN-17, SATSN-21, HD-2967, PBW-550, FLW-6, GW-273, KRL19 (c)
V	13	SATSN-12, SATSN-23, SATSN-N10, SATSN-18, SATSN-6, SATSN-27, K-307, SATSN-20, AKAW-4927, NW-4018, DBW-17, RAJ-3765, KRL-99
VI	7	SATSN-13, SATSN-34, HD-2307, KRL-210, HDR-77, RAJ-3777, NW1067 (c)
VII	8	SATSN-N1, K-8027, K-9107, HP-1633, HP-1761, UP-2338, HALNA, FLW-4
VIII	15	SATSN-31, SATSN-5, SATSN-22, SATSN-N24, SATSN-14, SATSN-35, NW-1014, HI-3118, DBW-14, DBW-39, KRL-213, RAJ-3077, HUW-234, FLW-12, DBW-11
IX	16	SATSN-C25, SATSN-3, SATSN-26, SATSN-33, NW-2036, HD-2733, HD-2329, PBW-373, K-9006, HP-1744, UP-2621, CBW-38, SONALIKA, FLW-3, DBW-22, K-8962
X	8	SATSN-19, SATSN-7, NW-1012, NW-7049, FLW-1, CHIRYA-7, KRL-20, KRL1-4 (c)
XI	8	SATSN-15, SATSN-9, SATSN-4, SATSN-2, NW-1076, DBW-187, HUW-468, FLW-5

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	11.002	15.804	19.383	14.677	22.063	23.885	21.314	23.490	29.757	25.115	20.968
2 Cluster		6.564	20.623	15.970	27.949	16.246	18.061	21.280	24.879	24.846	27.632
3 Cluster			13.770	20.620	23.931	21.373	21.274	25.394	33.965	31.106	26.097
4 Cluster				6.978	18.360	16.509	20.848	24.024	23.742	18.510	20.306
5 Cluster					16.926	31.030	36.770	33.992	30.106	24.407	25.353
6 Cluster						1.438	15.149	28.277	23.288	26.744	26.755
7 Cluster							13.889	23.572	28.760	30.132	26.992
8 Cluster								16.596	26.069	23.401	26.410
9 Cluster									19.550	25.232	28.626
10 Cluster										14.309	20.508
11 Cluster											15.354

Table 3: Clusters means for 11 characters in wheat

	Days To 50% Flowering	No of Grain Per Spike	Plant Height (Cm)	Days To Maturity	Tillers /Plant	Spike Length (Cm)	Peduncle Length (Cm)	Biological Yield/Plant (G)	Test Weight (G)	Harvest Index (%)	Grain Yield/Plant (G)
1 Cluster	82.73	42.42	86.24	121.73	6.08	14.73	19.62	30.53*	38.57	40.32	12.30
2 Cluster	82.40	40.21	81.42	120.60*	6.68	13.76	17.80	33.51	35.04*	37.02	12.39
3 Cluster	78.00	42.67	84.90	121.71	6.25	12.68	25.70**	31.70	40.02	38.05	12.06*
4 Cluster	83.16**	37.47*	86.96**	122.38	6.60	13.43	18.57	32.23	40.71	43.03	13.87
5 Cluster	81.75	40.32	80.95	121.00	5.62*	13.17	23.15	31.19	41.35	46.14	14.38
6 Cluster	80.00	49.97**	86.42	122.00	6.81	12.68*	17.54*	36.16**	41.68**	37.21	13.45
7 Cluster	81.83	45.57	86.72	123.75	6.89	14.25	22.49	34.30	38.83	35.53*	12.18
8 Cluster	77.06*	43.69	81.12	124.00	7.04	14.73	21.80	31.45	35.27	41.19	12.96
9 Cluster	81.25	46.99	79.61*	124.62**	6.35	13.66	19.16	34.42	35.76	43.32	14.86
10 Cluster	81.42	44.42	80.88	121.57	7.17**	14.94**	22.00	32.07	39.14	46.82**	14.99**
11 Cluster	81.45	48.72	89.67	121.81	6.47	14.69	24.60	31.58	37.25	44.95	14.45

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