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Genetic variability and diversity analysis for identification of most divergent parents in relation to grain yield and its component traits in wheat (*Triticum aestivum* L. Em. Thell.)

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Abstract

An experiment was made to evaluate fifty wheat genotypes of different eco-geographic origin. Data on eight quantitative characters *viz*: Plant height, reproductive tillers/plant, length of spike, spikelets/spike, days to maturity, grains/spike, test weight and grain yield/plant were recorded. Analysis of variance (ANOVA) revealed significant differences among all the genotypes for almost all the traits under study. The genotypes showed moderate to high level of genotypic coefficients of variance (GCV) and phenotypic coefficients of variance (PCV). In general phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but the extent was quite small, indicating very less environmental influence on the expression of the characters. Higher estimate of GCV (15.55) was recorded for Length of spike followed by grain yield per plant (14.91). Divergence analysis is a tool to identify the divergent genotype for hybridization purpose. All the 50 genetically diverse genotypes were grouped into 8 clusters according to their closeness relationship values. Cluster I, II, III and VIII each had 7 genotypes, cluster IV and VI each had 4 genotypes, cluster V had 12 genotypes and cluster VII had 2 genotypes. Cluster V had maximum 12 genotypes, indicated that the genotypes involved in particular cluster are less divergent than genotype of other cluster. The maximum value of inter cluster distance was recorded between cluster I and VII (1755.86) followed by cluster IV and VII (1144.22). Inter cluster distance between cluster I and VII indicated that superior strains of cluster I may be used as parents for hybridization with superior genotypes selected from cluster IV in order to develop genetic variability in population for selection of the desirable recombinants.

Keywords: Genetic variability, diversity, *Triticum aestivum* L.

Introduction

Wheat (*Triticum aestivum* L.), a cereal of grass family, Graminae (Poaceae) is the world's largest cereal crop. It has been described as the 'King of Cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the food grain trade. It occupies an inimitable position in human life as it is the major source of food and energy with a large number of end use products like chapati, bread, biscuits and is also a good source of fodder for animals. Wheat was one of the first domesticated food crops and for 8000 years has been the basic staple food of the major civilizations of Europe, West Asia and North Africa. The majority of the cultivated wheat varieties belong to three main species of the genus *Triticum*. These are the hexaploid ($2n=42$), *T. aestivum* L. (bread wheat), the tetraploid ($2n=28$), *T. durum* and the diploid ($2n=14$), *T. dicoccum* and *T. monococcum*. Wheat covers an area of about 221.48 million hectares followed by corn 179.91 million hectares and rice 161.03 million hectares (Anonymous, 2014-15) [1]. In 2014-15 world production of wheat was 727.85 million metric tons making it the second most-produced cereal after maize (1,013.56 million metric tons) (Anonymous, 2014-15) [1]. It contains 70% carbohydrates, 22% crude fibers, 12% protein, 12% water 2% fat, and 1.8% minerals (Anonymous 2015) [2]. 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 disease and adverse climates changes. So precise information on the nature and degree of genetic diversity presents in wheat collections 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 programmes.

Keeping in view, the importance of genetic variability and diversity in the crop, present investigation has been taken.

Materials and Methods

The present investigation was carried out during Rabi 2016-17 at crop research farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.) using Randomized Complete Block Design with three replications to work out the status of genetic variability and diversity for seed yield and its contributing traits in fifty genotypes/lines of wheat. These lines were taken from the germplasm maintained, in the Genetics and Plant breeding department of the university. Each genotype was sown in two lines of 5.0 m long with 23 cm wide plot and 5 cm plant to plant distance. The observations were recorded on five randomly taken plants for eight quantitative characters viz., Plant height (cm), Number of reproductive tillers per plant, Length of spike (cm), Number of spikelets per spike, Days to maturity, Number of grains per spike, Test weight (gm), Grain yield per plant. Crop research farm is situated between 26.46070N latitude, 80.33340 E longitudes and at an altitude of 126 m above the mean sea level, near company bag, Kanpur. Kanpur district has humid sub-tropical climate and low temperature in winter season and high temperature in summer season. The experimental data collected in respect of eight characters on 50 wheat genotypes were compiled by taking the mean values of selected plants in each plot and subjected for Analysis of variance, GCV and PCV (Burton and de Vane 1953)^[4], Non-hierarchical Euclidean cluster analysis (Beale, 1969)^[3].

Results and Discussion

The assessment of genetic diversity using quantitative traits has been of prime importance in many contexts particularly in differentiating well defined populations. The germplasm in a self-pollinated crop can be considered as heterogeneous sets of groups, since each group being homozygous within its self. Selecting the parents for breeding programme in such crops is critical because, the success of such programme depends upon the segregants of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield. To help the breeder in the process to identify the parents that nick better, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives. Among them, Mahalanobis's generalized distance occupies a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the difference among several quantitative traits.

Darwin (1859)^[5] used the expression divergence in characters to denote variation in genera, species and varieties. Huxley (1955)^[6] used other term, genetic polymorphism, for this purpose, which means coexistence of different genetic forms in a population. Genetically diverse parents are preferred for use in hybridization programme because crosses involving divergent parents have been found to offer greater possibility of obtaining desirable segregants in segregating generations. The presence of potential genetic variability in early and advance generations is an important pre-requisite for the success of selection procedures in attaining objectives of breeding programmes.

Mahalanobis D² statistic has been widely used to determine extent of genetic diversity in the available material in different crops. Divergence analysis is a tool to identify the divergent genotype for hybridization purpose.

Genotypic composition of different clusters is given in table

1. Inter and intra cluster distance is given in table 2. And Cluster means for eight characters in wheat is given in table 3. All the 50 genetically diverse genotypes were grouped into 8 clusters according to their closeness relationship values. Cluster I, II and III each had 7 genotypes, cluster IV had 4 genotypes, cluster V had 12 genotypes, cluster VI had 4 genotypes cluster VII had 2 genotypes and cluster VIII had 7 genotypes. Cluster V had maximum 12 genotypes it indicated that the genotypes involved in particular cluster are less divergent than genotype of other cluster. The maximum value of inter cluster distance was recorded between cluster I and VII (1755.86) followed by cluster IV and VII (1144.22).

Inter cluster distance between cluster I and VII indicated that superior strains of cluster I may be used as parent for hybridization with superior genotypes selected from cluster IV in order to develop genetic variability in population for selection of the desirable recombinants. The lowest value of inter cluster distance was recorded between cluster II and III due to close relationship genotypes of these clusters would not be recommended for hybridization.

The comparison of cluster mean revealed considerable differences among the clusters for different characters, cluster I exhibited minimum value of cluster mean for test weight (32.34) and had not maximum value of any character for cluster mean. Therefore the genotypes K-906, K-9423, DBW-41, DBW-2594, K-9351, K-9162, K-1508 of cluster I are less important for grain yield improvement through bolder seed size. Cluster II had minimum value for plant height, which is desirable therefore the strain of genotype K-9533, K-8027, DBW-14, PBW-13, LOK-1, K-1412, K-1507 may be used for development of dwarf plant type. Cluster III exhibited lowest mean value for days to maturity; therefore the strain K-1317, K-68, K-1405, K-1501, K-1513, HI-1563 and DBW-107 may be used for improvement of respective trait through hybridization programme. Clusters IV exhibited lowest mean value for reproductive tiller per plant length of spike, spikelets per spike and grain yield per plant, therefore the strain K-0402, K-7903, K-1402, K-9851 showed poor performance, so these genotypes are not useful for breeding programme. Cluster V exhibited highest mean value for days to maturity and lowest value for grains/ spike, therefore the strain K-9107, PBW-41, PBW-502, K-0307, K-1416, K-424, PBW-38, K-8423, NW-1012, HI-8699, K-9644, K-8962 may be used for development of late maturing variety. Cluster VI having highest mean value for length of spike, grains/ spike and grain yield/plant, therefore the strain K-1504, PBW-343, PBW-550 and K-1512 may be used for enhancement of economic yield. Cluster VII having highest mean value for plant height, spikelets/spike and test weight, therefore the strain K-9006 and K-9465 may be used for the improvement of respective traits through hybridization programme.

Cluster VIII having highest mean value for reproductive tillers/plant so the strain K-65, MACS-6348, K-1503, UP-2525, PBW-396, UP-2529, K-1006 may be used for breeding programme. Kumar *et al.* (2015)^[8] also observed significant differences for character among the genotypes in respect to all traits under all environments. Fifty genotypes were grouped into 10 diverse clusters under different environment. Most of the genotypes (9) were grouped in cluster I and 7 genotypes in cluster I and II under normal and stress conditions. Maximum divergence was observed in cluster II and IX under normal conditions cluster VI and VIII under stress conditions. Mehari *et al.* (2015)^[10] also reported that the presence of genetic divergence is an important entry point for selection and hybridization. The inter-cluster distance of the twenty wheat

genotypes ranges from 0.57536 in cluster one to 212.02335 in cluster four. The maximum inter-cluster distance was between cluster two and cluster four which was 212.0233. Khare *et al.* (2015) [9] studied wheat genotypes and grouped into six different clusters by using Mahalanobis D² analysis. Cluster V had maximum number of (12) genotypes while, cluster I had only one genotypes. Genetic divergences in 24 spring wheat genotypes were also estimated by Rahman *et al.* (2015) [11] using Mahalanobis D²-statistics and principal component analysis. The genotypes under study were grouped into three clusters. Cluster III had the maximum (12) and cluster II had the minimum (3) number of genotypes. The intra cluster value

was maximum in cluster III and minimum in cluster II. Similar results were also reported by Singh and Salgotra (2014) [12], Khan *et al.* (2012) [15], Singh and Jaiswal (2010) [13] and Mittal *et al.* (2008) [14].

Contribution of individual character towards total divergence was worked out and presented in Table-4. Test weight showed maximum contribution (61.88 %) followed by plant height (15.35%), grains/spike (6.37%), reproductive tillers/plant (4.57%), length of spike (4.33%), grain yield/plant (4.33%), spikelets/spike (2.69%) and days to maturity (0.49%) respectively in decreasing order. Similar result was also reported by Khare *et al.* (2015) [9].

Table 1: Grouping of fifty strains of wheat

Cluster No.	Strains /varieties	No. strains per cluster
I	K-906,K-9423,DBW-41,DBW-2594,K-9351,K-9162,K-1508	7
II	K-9533,K-8027,DBW-14,PBW-13,LOK-1,K-1412,K-1507	7
III	K-1317,K-68,K-1405,K-1501,K-1513,HI-1563,DBW-107	7
IV	K-0402,K-7903,K-1402,K-9851	4
V	K-9107,PBW-41,PBW-502,K-0307,K-1416,K-424,PBW-38,K-8423,NW-1012,HI-8699,K-9644,K-8962	12
VI	K-1504,PBW-343,PBW-550,K-1512	4
VII	K-9006,K-9465	2
VIII	K-65,MACS-6348,K-1503,UP-2525,PBW-396,UP-2529, K-1006	7

Table 2: Intra and inter cluster distance (D²) values

Cluster	I	II	III	IV	V	VI	VII	VIII
I	150.59	484.76	375.92	354.79	1022.78	1082.76	1755.86	976.05
II		94.51	165.47	262.91	220.31	284.69	654.01	315.92
III			111.14	291.71	338.79	392.12	694.45	305.13
IV				175.36	528.12	617.80	1144.22	654.02
V					107.46	229.82	365.75	262.18
VI						156.82	318.09	290.10
VII							120.89	272.00
VIII								187.12

Table 3: Cluster means for eight characters in wheat

Cluster	Plant height(cm)	Reproductive tillers per plant	Length of spike	Spikelets/spike	Days to maturity	Grains/spike	Test weight(gm)	Grain yield/plant(gm)
I	73.04	7.97	9.54	17.59	119.76	41.57	32.34*	11.09
II	72.60*	7.77	10.03	18.03	118.09	40.94	36.54	11.12
III	81.73	8.06	9.80	18.46	117.52*	41.53	35.49	12.72
IV	76.07	6.53*	8.05*	15.76*	120.00	45.26	34.95	9.70*
V	74.35	7.57	8.57	17.49	120.41**	39.65*	38.86	11.65
VI	80.70	7.78	11.91**	18.25	119.83	46.08**	38.60	13.40**
VII	93.59**	8.73	9.66	19.36**	119.33	42.46	40.40**	13.23
VIII	86.01	9.12**	9.04	18.48	119.28	40.73	38.02	13.04

**Maximum mean value, * Minimum mean value

Table 4: Contribution of each character towards divergence

S. No.	Plant height(cm)	Productive tillers/plant	Length of spike	Spikelets/spike	Days to maturity	Grains/spike	Test weight	Grain yield/plant
Number of time appearing 1 st rank	188.00	56.00	53.00	32.00	6.00	78.00	758.00	54.00
Percent contribution (%)	15.35	4.57	4.33	2.69	0.49	6.37	61.88	4.33

Conclusion

On the basis of studies made on genetic divergence, the genotypes, K-906, K-9423, DBW-41, DBW-2594, K-9351, K-9162, K-1508 of cluster I was found to be more divergent to the genotypes, K-9006, K-9465 of cluster VII. So cross between the genotypes of cluster I and that of cluster VII will give fruitful result.

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