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Estimation of genetic variability in wheat (*Triticumaestivum* L.)

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Abstract

The present investigation was carried out with the objective to estimate genetic variability involving 65 genotypes (fifteen parents and fifty F₁s crosses) grown in a randomized block design with three replications at crop research farm Nawabganj. The analysis of variance revealed the significant differences among the treatments for seven characters out of eight characters indicating considerable variability among the genotypes for days to flowering (75%), plant height (cm), number of productive tillers/plant, flag leaf area (cm)², spike length (cm), number of spikelets/spike and grain yield/plant (gm). Variability also reflected based on mean, range, phenotypic coefficient of variation and genotypic coefficient of variation therefore selection of the parents under study based on morphological differences for different characters was validated through ANOVA and other parameters. The range varied from days to maturity (112.00-120.33) for parents and days to maturity (112.00 to 119.66) for F₁ and maximum phenotypic coefficient of variation (PCV) of traits days to maturity (112.00 to 119.66) for parents were generally higher than genotypic coefficients of variance (GCV) 36.72 (Grain yield/plant) indicating the presence of enough genetic variability in the material under study.

Keywords: Estimation, variability, *Triticumaestivum* L.

Introduction

Wheat (Allohexaploid 2n=6x=42, AABBDD) belongs to genus *triticum* and family poaceae (old name Gramineae) having haploid genome size of 16GB. Wheat is one of the most important cereal crops grown in different environments due to its versatile nature over the world. At global level, it was cultivated over 214.79 million ha and production 735.18 million with an average productivity 34.22 quintals per hectare (FAOSTAT, 2018) [5]. In India, Wheat has second rank after paddy both in area and production, occupying 29.14 million ha acreage area with production of 102.19 million tones and the productivity of 35.07 quintals per hectare (IIWBR, 2018-19). Wheat is providing global food security and providing well nutrition for human beings and it is considered as a staple food over worldwide. It has good nutrition value such as protein content 10-12%. Human have limited resources such as land. So meet the challenge of limited resources, it is a difficult task that breeder will enhance the production in limited areas. Therefore, breeders search that genotype that has genetic variability.

The main aim of plant breeder is, to enhance the crop productivity. Genetic variability is a primary need for plant breeders. If a population have variability, it can be directly utilized for crop improvement, if it is not available in crop then it will be created by the several methods such as mutation, crossing over and by the recombination. First choice of any plant breeder is to exploit the variability for crop improvement programme. Exploitation of genetic variability for enhancement of yield in crop need to know the component of genetic variation. Genetic parameters are used to assess the genetic variation in wheat crop.

The nature and magnitude of genetic parameters of component of variation is obtained from analysis of variance that described by the Singh and Chaudhary (1985) [10] and Falconer (1989) [4]. Genetic variability is the result of genetic variation that occurred in different individual in a population. Genetic variability, which is due to the genetic differences among individuals within a population, is the main aim of plant breeding programs, because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Sharma, 1998) [9].

Genetic variability among traits is important for breeding and in selecting desirable types. As the breeders are interested in selection of superior lines based on phenotypic performance. The development of high yielding wheat cultivars is the main objective of any wheat breeding programmes in the world as well as in India. Improvement in crop depend upon the magnitude of genetic variability in economic characters therefore, the evaluation and utilization of genetic variability in desired direction becomes extremely important in any field improvement programme. In this regard, it is necessary to survey the available useful variability and nature of association among the various plant characters in the basic material. Yield is quantitative character and is governed by many genes having smaller effects i.e., polygenes. Thus, we can say that the yield is the final product of yield components. These components may affect the yield directly or indirectly. Therefore, yield can be maximized by improving the yield components provided there is no unfavourable association.

Material and methods

The investigating material consisting of 65 genotypes (fifteen parents, fifty F₁s crosses) was sown in a randomized block design with three replications at crop research farm Nawabganj of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. Each parent and F₁ was planted in single row, of 3 meter long plot and 22.5 cm apart and 10 cm Plant to plant distance was maintained. All the recommended cultural practices were applied to raise good crop. The random sample has been taken to evaluate the genetic variability for eight quantitative traits viz., days to

flowering (75%), plant height (cm), days to maturity, number of productive tillers per plant, flag leaf area (cm)², spike length (cm), number of spikelets per spike and grain yield per plant (cm). Standard statistical procedures were followed for estimating the analysis of variance and genetic constants i.e. phenotypic and genotypic coefficients of variation.

Result and Discussion

Analysis of variance revealed highly significant differences among the genotypes for all eight characters such as days to flowering (75%), plant height (cm), days to maturity, number of productive tillers per plant, flag leaf area, spike length, number of spikelets per spike and grain yield per plant. The result overwhelmed that experimental material have high variability for characters studied. The magnitude of variance for any trait in the population is of great importance to a plant breeder for starting a breeding programme. All results have been given below.

The significant differences have been observed among treatments, parents, parents (lines), parents (testers), parents (Lines Vs Testers) and parents Vs crosses for all the characters except days to maturity and days to flowering (75%), phenol color reaction in Parents (testers), days to flowering (75%), number of spikelets/spike, biological yield/plant (gm), seed hardness, phenol color reaction in parents (lines Vs testers), flag leaf area (cm)² in parents Vs crosses (Table-1). The same result is indicated by Cheema *et al.*, (2006) [3], Desheva and Kyosev (2015) [8], Ghaffar *et al.*, (2018) [6].

Table 1: ANOVA of Parents+F₁s for 08 characters in line × tester cross analysis of wheat (*Triticum aestivum* L.) mean sum of square.

Source of variation	d.f.	Days to flowering (75%)	Plant height (cm)	Days to maturity	Number of productive tillers/ Plants	Flag leaf area (cm) ²	Spike length (cm)	Number of spikelets/ Spike	Grain yield/Plant (gm)
Replication	2	1.91	0.08	23.52	0.04	3.71**	0.1	0.27	0.31*
Treatments	64	26.69**	83.54**	63.01	11.75**	15.54**	4.02**	4.21**	122.67**
Parents	14	66.02**	194.04**	16.16	2.14**	27.69**	2.41**	3.75**	20.85**
Parents (Line)	9	93.91**	201.91**	14.37	2.42**	35.41**	1.38**	4.41**	13.26**
Parents (Testers)	4	16.93	38.23**	14.56	1.71**	15.45**	2.95**	3.15**	41.79**
Parents (L vs. T)	1	11.37	746.49**	38.67	1.39**	7.18**	9.60**	0.27	5.37**
Parents vs. Crosses	1	85.44**	33.79**	3.44	423.82**	0.35	110.33**	132.01**	4881.76**
Error	128	12.32	0.57	55.18	0.07	0.29	0.08	0.15	0.07

In the present investigation, in general, the mean, range performance and genotypic coefficient of variation and phenotypic coefficient of variation of the parents and F₁s for all eight characters are presented in Table no. 02. The variation within parents and F₁s was found to be significant for all the characters but its magnitude varied from character to character. A wide range of variability was recorded within parents for days to maturity (112.00-120.33) followed by days to flowering (82.33-89.33), plant height (74.66-104.2), number of spikelet's per spike (17.86-22.26), flag leaf area (17.21-26.36), spike length (8.53-11.86), grain yield per plant (4.53-13.66) and number of productive tillers (3.6-6.13). In F₁ the maximum variation was observed for days to maturity (112-119.66) followed by days to flowering (82.66-91.33), plant height (81.53-101), number of spikelets per spike (19.6-23.8), flag leaf area (17.75-25.95), grain yield per plant (12.53-31.6), spike length (9.4-12.6) and number of productive tillers per plant (5.46-12.46).

In the present investigation, in general, estimates of

phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the little influence of environment on the expression of these characters. A wide range of phenotypic coefficient of variation (PCV) was observed for all the traits in Parents+F₁ generation ranged from 4.81 (Days to flowering) to 36.76 (Grain yield/plant), higher magnitude of PCV was recorded 36.76 (Grain yield/plant) followed by 27.38 (Number of productive tillers/plant), 10.67 (Spike length), 10.53 (Flag leaf area), 6.54 (Days to maturity), 5.81 (Plant height), 5.59 (Number of spikelets/spike), 4.81 (Days to flowering). Genotypic coefficients of variation (GCV) ranged from 1.38 (Days to maturity) to 36.72 (Grain yield/plant), higher magnitude of GCV was recorded 36.72 (Grain yield/plant) followed by 27.13 (Number of productive tillers/plant), 10.35 (Spike length), 10.23 (Flag leaf area), 5.75 (Plant height), 5.29 (Number of spikelets/spike), 2.54 (Days to flowering) and 1.38 (Days to maturity). The same result is indicated by Bhusan *et al.*, 2013, Arya *et al.*, 2017 [1].

Table 2: Mean, range of parents+F₁s, genotypic coefficients of variation and phenotypic coefficient of variation for 15 characters derived from line × tester crosses in wheat (*Triticumaestivum* L.).

Character	General Mean	Range of variation		Coefficient of variation	
		Parents	F ₁	GCV	PCV
Days to flowering (75%)	85.96	82.33 to 89.33	82.66 to 91.33	2.54	4.81
Plant height (cm)	91.43	74.66 to 104.20	81.53 to 101.00	5.75	5.81
Days to maturity	116.18	112.00 to 120.33	112.00 to 119.66	1.38	6.54
Number of productive tillers/plant	7.27	3.60 to 6.13	5.46 to 12.46	27.13	27.38
Flag leaf area (cm) ²	22.03	17.21 to 26.36	17.75 to 25.95	10.23	10.53
Spike length (cm)	11.07	8.53 to 11.86	9.40 to 12.60	10.35	10.67
Number of spikelets/spike	21.97	17.86 to 22.26	19.60 to 23.80	5.29	5.59
Grain yield/plant	17.41	4.53 to 13.66	12.53 to 31.60	36.72	36.76

Conclusion

In the present investigation, estimate of the analysis of variance, phenotypic and genotypic coefficient of variation for eight characters in parents and F₁s reveals sufficient variability for each of traits and thus, ample scope for genetic improvement of these traits through selection. The estimate of phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the little influence of environment on the expression of these characters.

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