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Assessment of genetic variability, heritability and genetic advance of yield, yield attributes and quality traits in bread wheat (*Triticum aestivum* L.)

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ABSTRACT

A field experiment was conducted at research farm of Sam Higginbottom Institute of Agriculture, Sciences and Technology, Allahabad, during rabi season 2013-14, using 15 wheat genotypes to assess the genetic variability, heritability and genetic advance of yield, yield attributes and quality of wheat. Data were recorded on 8 quantitative characters and subjected to different statistical and biometrical analysis. Analysis of variance revealed highly significant differences for MSS values of genotypes for all the eight characters under study. The maximum phenotypic coefficient of variation (PCV) was recorded for number of tillers per plant, spike length (cm), number of grains per spike, protein content, yield kg plot^{-1}, 1000 grain weight and harvest index, whereas lowest PCV value was observed for plant height. The maximum genotypic coefficient of variation (GCV) was obtained for number of tillers per plant, spike length, number of grains per spike and protein content. Lowest GCV was recorded for harvest index, plant height, 1000 grain weight and yield kg plot^{-1}. High heritability accompanied by high genetic advance as percentage of mean was observed for spike length, 1000 grain weight and protein content.

Key words: Genetic variability, GCV, PCV, heritability, genetic advance, wheat

INTRODUCTION

Bread or common wheat (*Triticum aestivum* L., 2n=6x=42) is the second most important cereal crop in the world after rice. It belongs to family *Poaceae* and is one of the first food grains domesticated by early man. In India, bread wheat is an important cereal crop which is used for making chapaties, bread, rolls and baby foods etc. It contributes almost 40% of the total food grain production every year in the country. India ranks second next to China, in global wheat production. Other wheat species viz., durum wheat (*Triticum durum*), club wheat (*Triticum compactum*) are also grown in a limited area for their some special significance in developing products for human consumption. *Triticum durum* is used for making pasta products such as macaroni, spaghetti, puffed breakfast cereals etc. *Triticum compactum* or club wheat is hexaploid and is used for making crackers, cookies, biscuits, doughnuts, pancakes, noodles and pizzas etc (Ajeet *et. al.*, 2017). The effectiveness of selection for any successful breeding programme depends upon the existence of genetic variability present in the base population (Vichitra et. al., 2017). It is proved that larger the variability greater is the scope of selection and improvement of character under study. Being a complex phenomenon, variability is measured by estimation of genetic parameters which includes coefficient of variation, heritability and genetic advance as percent of mean. The comparison of variability among all the characters would be possible only by working out their coefficient of variability. The magnitude of genetic and environmental effect involved in the expression of different characters is determined by the phenotypic and genotypic coefficient of variation. The genotypic coefficient of variation measures the range of variability available in crop plants, enables to compare the amount of variability present among different characters. While as phenotypic coefficient of variation measures the phenotypic expression of a character which is a result of interaction between the genotype and environment. Heritability, which is an index of transmissibility of the characters from parents to offspring need to be studied in order to determine the extent to which the observed variation is inherited (Priyanka *et al.*, 2017). The characters with high heritability values are of much importance to plant breeder than those which are less heritable and more susceptible to the environmental variation. Genetic advance is directly related with heritability as it gives an idea about the expected genetic changes on account of selection applied to a particular trait. Thus heritability estimates along with genetic advance are more meaningful than the heritability alone in predicting the ultimate effect of selection (Shukla *et al.*, 2006). Hence, an investigation was initiated to select a strategy for higher production of wheat with the objective to know the extent of genetic variability, heritability (broad sense) and genetic advance of yield and yield attributes to develop desirable wheat genotypes and to capture the maximum genetic variability.

MATERIALS AND METHODS

The material used for present investigation comprised of 15 wheat genotypes which were obtained from wheat genetic stock, Directorate of Research, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad. Table-1 reveals detailed information about 15 wheat genotypes used in the present study. The field experiment (1x5m) was laid down in randomized block design with four replications at Experimental Research Farm, Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad. Each plot consisted of 4 rows, 1x5m plot size with plant geometry of 25x5cm. All the recommended cultural practices were followed during the crop growth period. For data collection of different parameters, five randomly and competitive plants of each genotype from each replication were selected. The observations were recorded on eight quantitative characters viz. number of tillers per plant, spike length, number of grains per spike, plant height, harvest index, 1000 grain weight, protein content and yield kg plot^{-1}Grain protein was estimated by the method given by Lowry *et. al* (1951). The data recorded for the above mentioned parameters were averaged and analyzed statistically.

The genotypic and phenotypic coefficient of variation was calculated as per the formula suggested by Burton and Devane (1953).

Phenotypic coefficient of variation

$$\mathrm{PCV} = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100$$

Genotypic coefficient of variation GCV

$$= \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Where:

σ^2p=Phenotypic variation; σ^2g=Genotypic variation and *X*=Grand mean of the characters under study.

The GCV and PCV values were categorized as per Robinson *et al.,* (1949) into

i. Low (0-10%)
ii. Moderate (10-20%) and
iii. High (20% and above)

Heritability in broad sense (H^{2}b) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956)

Heritability in broad sense, H^{2}b (%) = $\frac{\sigma^2 g}{\sigma^2 p} \times 100$

Where, H^{2}b=Heritability in broad sense, σ2g=Genotypic variance and σ2p=Phenotypic variance. The heritability was categorized as low, moderate and high as given by Robinson *et al.,* (1949).

i. 0 – 30 %: Low
ii. 30 – 60%: Moderate
iii. 60% and above: High

The expected genetic advance (GA) for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al.,* (1955).

Genetic advance (GA) = h^{2}b.I or K x σp

Where, h^{2}b = Heritability in broad sense, I or K= Selection differential, the value of which is 1.76 at 10% and 2.063 at 5% level of selection intensity and σp = Phenotypic standard deviation.

Genetic advance as percent of mean was calculated using the formula given by Comstock and Robinson (1952)

Genetic advance as percent of mean =

$$\frac{(\text{Genetic advance} \times 100)}{\overline{X}} \text{ or } \frac{GA \times 100}{\overline{X}}$$

Where, GA=Genetic advance under selection and $\overline{X}$ = Grand or population mean of the trait

Genetic advance as percent mean was categorized as:

i. Low (0-10%)
ii. Moderate (10-20%) and
iii. High (≥20%) as given by Johnson *et al.* (1955)

RESULTS AND DISCUSSION

Analysis of variance of 15 wheat varieties was done separately for all the eight characters viz., number of tillers per plant, spike length, number of grains per spike, plant height, harvest index, 1000 grain weight, protein content and yield kg plot-1. It revealed (Table 1) that there were highly significant differences for MSS values of 15 genotypes for all the eight characters under study at 1% level of significance. This indicates relatively high magnitude of genetic variability among the genotypes for the characters studied in the present investigation. The comparison of variability among all the characters would be possible only by working out their coefficient of variability, as the unit of measurement of the character studied is not similar. The magnitude of genetic and environmental effects involved in expression of different characters is determined by phenotypic and genotypic coefficient of variation. The magnitude of phenotypic coefficient of variation (PCV) was found higher than the genotypic coefficient of variation (GCV) for all the characters under study. It was clear from the data (Table-2) that maximum phenotypic and genotypic coefficient of variability (PCV and GCV**)** was observed for number of tillers per plant (19.76, 14.47), spike length (17.39, 11.93) and number of grains per spike (13.77, 10.90). Our results are in conformity with, Sharma and Garg (2002), Kaul and Singh (2011) and Dhananjay *et al.,* (2012). This indicates that variability in respect to these attributes in the population might be due to additive part of the total genetic variability. It can be argued from the results that these traits are less influenced by environmental effect and selction for such traits will be more favourable. Therefore superior genotypes can be evolved through selction based on expression of these attributes.

Table.1: Analysis of variance for yield, yield components and protein content in wheat (*Triticum aestivum* L.)

Source of variation	Degree of freedom	Number of tillers per plant	Spike length (cm)	Number of grains per spike	Plant height (cm)	Harvest index (%)	1000 grain weight (g)	Protein content (%)	Yield/plot (kg)
Replication	3	3.993	3.275	16.351	144.458	9.770	12.591	0.862	0.004
Treatment	14	4.690**	7.386**	88.107**	222.149**	27.939**	50.281**	0.590**	0.0819**
Error	42	1.800	1.812	11.065	20.031	8.008	6.405	0.302	0.0089

Heritability specifies the proportion of the total variability that is due to genetic cause. It is a good index of the transmission of character from parent to offspring and helps in determining whether phenotypic difference observed among individuals are due to genetic or environmental factors. Genetic advance is directly related with the heritability as it gives an idea about the expected genetic change on account of selection applied to a particular trait. In the present investigation all the eight characters reported high heritability. It is revealed (Table 2) that high heritability estimate was recorded for spike length (84.43%), followed by protein content (83.76%), 1000 grain weight (80.04%), number of tillers per plant (79.95%), plant height (73.12%), number of grains per spike (71.41%), yield kg plot^{-1} (67.69%) and harvest index (61.37%). The results are in conformity with the findings of Pawar *et al.,* (2003), Gupta *et al.,* (2004), Saxena *et al.,* (2007) and Yadav *et al.,* (2011). High heritability for above traits indicates that proportion of phenotypic variance has been attributed to genotypic variances and therefore, reliable selection could be made for these traits on the basis of phenotypic expression. The characters with high heritability are more important to a plant breeder than those which are less heritable because such traits are more susceptible to environmental variation and selction of such traits will lead to misleading results.

Table 2: Mean, range, PCV, GCV, heritability and genetic advance as percentage of mean of 8 characters in wheat

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%) in broad sense	Genetic advance	Genetic advance as(%) of mean (Genetic Gain)
No. of tiller/spike	9.97	8.16-12.51	19.76	14.47	79.95	3.19	31.99
Spike length (cm)	10.85	9.12-13.25	17.39	11.93	84.43	4.39	40.46
No. of grains/Spike	41.00	33.68-50.63	13.77	10.90	73.12	11.28	27.50
Plant height (cm)	89.17	78.5-98.57	8.90	7.99	71.41	15.36	17.22
Harvest index	34.75	31.51-40.42	10.32	7.63	61.37	3.85	11.07
1000 grain weight	40.91	35.25-46.66	10.74	8.85	80.04	8.22	20.55
Protein content (%)	11.72	11.14-12.3	11.35	10.15	83.76	2.41	20.56
Yield/plot (kg)	2.00	1.73-2.25	11.23	9.32	67.69	0.51	25.43

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection. According to Johnson *et al* (1955)**,** a heritable estimate along with genetic advance as percent of mean is more meaningful than the heritability alone in predicting the ultimate effect of selection. Therefore, the heritable portion of variation could be determined with the help of estimates of heritability along with genetic advance as percent of mean. Spike length (40.46%), number of tillers per plant (31.99%), number of grains per spike (27.50%), yield kg plot^{-1} (20.56%), protein content (20.55%) and 1000 grain weight (17.22%) were quite encouraging since these characters exhibited high genetic advance as percent of mean and also they were accompanied with high heritability estimates. Similar findings were also confirmed by Yadav *et al.* (2003), Chandrashekhar *et al.* (2004) and Kaul and Singh (2011). These traits are least influenced by the environment and might show least genotype x environment interaction. It is suggested that there is imperative need of portioning the overall variability with heritability and non-heritability component with the help of suitable heritable estimates and genetic advance.

In conclusion, the present study identified the presence of adequate genetic variability among 15 tested genotypes. High phenotypic and genotypic coefficient of variability (PCV and GCV**)** was observed for number of tillers per plant, spike length and number of grains per spike. Spike length, number of tillers per plant, number of grains per spike, yield kg plot^{-1}, protein content and 1000 grain weight were quite encouraging since these characters exhibited high heritability estimates accompanied with high genetic advance. Selection for all the above traits would be more effective to bring about the simultaneous improvement of yield, yield component and protein content percentage in wheat.

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