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APPRAISEMENT OF VARIABILITY PARAMETERS OF GRAIN YIELD, YIELD COMPONENTS AND PROTEIN CONTENT IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

The particulars of the current research comprised 20 propitious bread wheat lines which were devised in a randomized block design (RBD) with three replications at the experimental research farm of Suresh Gyan Vihar University, Jagatpura, Jaipur. An account of data on 8 quantitative/qualitative characters was ruled to different statistical and biometrical analysis. Analysis of variance imparted thoroughly significant differences in MSS values of genotypes for all the eight characters under study. The uttermost phenotypic coefficient of variation (PCV) was recorded by the number of effective tillers plant^{-1}, spike length (cm), number of grains spike^{-1}, yield kg plot^{1}, 1000 grain weight, and harvest index. The slightest PCV value was observed for plant height, protein content, and harvest index. The greatest possible degree of genotypic coefficient of variation (GCV) was procured by the number of effective tillers plant^{-1}, spike length, number of grains spike^{-1}, yield/plot (kg) and 1000 grain weight, whereas minimal GCV was acquired by plant height, protein content and harvest index. All the characters in the present study showed the highest heritability estimate. The maximum heritability was estimated by spike length, 1000 grain weight, number of effective tillers plant$^{-1,}$ and harvest index. The number of grains spike^{-1}, spike length, harvest index, and 1000 grain weight were quite encouraging since these characters exhibited high genetic advance as percent of mean and also they were accompanied with high heritability estimates.

Keywords: Genetic variability, PCV, GCV, heritability, genetic advance, wheat.

Introduction

Among the various breeding methods, the selection is the simplest and foremost method of crop improvement. Selection is the process which favours survival and further propagation of those crop plants with more desirable characteristics than others. The primary goal of selection is to identify and isolate desirable genotypes from the diverse population. The effectiveness of selection depends upon two factors viz., (i) extent of genetic variability present in the base population in which selection is practiced and (ii) heritability of the character accompanied by genetic advance. All these selection parameters help the breeder in making an effective selection for the improvement of certain desirable characters within and among the breeding population. Selection can not create variability but can act on heritable variability already existing in the population. Genetic variability pertains to the existence of variation among the crop plants of the specific population that consequences either due to dissimilarity in the genetic architecture of the individuals of a particular population or in the environment in which they are grown. The existence of variability in the base population is of paramount importance to a plant breeder for starting a judicious breeding programme. Therefore, the success of any breeding programme depends upon the knowledge of genetic variability and its components, as in crop plants it provides an opportunity for selecting desirable genotypes (Singh and Narayanam, 2015). Being a complex phenomenon, variability is measured by estimation of genetic parameters which includes the coefficient of variation, heritability, and genetic advance as percent of the mean (Nadarajan and Gunasekaran, 2008). The comparison of variability among all the characters would be possible only by working out their coefficient of variation. When the coefficient of variation is high, the sample is less consistent or more variable and when it is low, the sample is more consistent or less variable (Singh and Narayanam, 2015). Further, the coefficient of variation partitions the total variation into the genotypic, phenotypic and environmental coefficient of variations, determine the magnitude of these components involved in the expression of different characters. 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 the 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 adequate index of transmission of the characters from parents to their offspring need to be studied in order to determine the extent to which the observed variation is inherited. 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 promptly connected to heritability as it lends an indication about the typical genetic alterations on account of selection pertained to a particular trail. Therefore, heritability calculations escorted with genetic advances are better noteworthy than heritability alone in determining the absolute impact of selection on the characters of our interest. (Johnson *et al.,* 1955a and Shukla *et al.,* 2006). Therefore, an investigation was initiated to work out the extent of genetic variability, heritability and genetic advance among 20 promising wheat lines for yield, yield contributing components, and protein content.

Materials and Methods

A field experiment was carried out at the experimental research farm, School of Agriculture, Suresh Gyan Vihar University, Jagatpura, Jaipur. The experiment site is situated in 26.55° N latitude, 75.46° E longitude, and at an altitude of 431 m above sea level. A total of 20 promising bread wheat lines were rendered from wheat genetic stock of IARI, New Delhi and Durgapura Research Centre, Rajasthan (Table 1). The field trial (1x5 m) was laid on Randomized Block Design (RBD) with three replications. Each line was planted in a plot consisting of 4 rows with a 1x5m plot size and a plant geometry of 25x5 cm. A seed rate of 120kg ha^{-1} and fertilizer rate of 120:60:40 kg ha^{-1} NPK in the form of urea, DAP (di-ammonium phosphate), and MOP (Muriate of Potash) were applied. For data collection of different parameters, five randomly and competitive plants of each genotype from each replication were selected. The observation was recorded on eight characters viz. number of effective tillers $plant^{-1}$, spike length (cm), number of grains per spike, plant height (cm), harvest index (%), 1000 grain weight (gram), protein (%) and yield kg $plot^{-1}$. The data noted for the above pointed out components were averaged and verified statistically. The harvest index was calculated according to the following formula (Abrar *et al.,* 2011).

$$\text{Harvest Index} = \frac{\text{Economical yield}}{\text{Biological yield}} \times 100$$

Whereas grain protein content 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 following formula suggested by Burton and Devane (1953).

$$\text{PCV} = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100, \quad \text{GCV} = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

Heritability in a broad sense (h^2b) and genetic advance as percent of the mean was estimated according to the formula suggested by Comstock and Robinson (1952) and Johnson *et a*l. (1955a).

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

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

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

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

Genetic advance as percent of mean =

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

Results and Discussion

Analysis of variance

It is divulged from the Table-2 that mean sum of the square from the analysis of variance set down highly significant differences among the 20 wheat lines/genotypes for all the eight characters at 1% level of significance ($P<0.01$). This point out significant and passably high genetic variation between 20 wheat lines/genotypes for the characters studied in the present investigation viz., number of effective tillers $plant^{-1}$, spike length (cm), number of grains per spike, plant height (cm), harvest index (%), 1000 grain weight (gram), protein content (%) and yield kg $plot^{-1}$. These results are in conformity with the work reported by Pradeep *et al.* (2016), Kifle *et al.* (2016) and Berhanu *et al.* (2017). As the genotypes were genetically diverse, it could be the righteous possibility for a breeder to utilize them in future wheat improvement breeding programmes.

Variability Parameters

Data presented in Table-3 unveils that the extant of the phenotypic coefficient of variation (PCV) was found higher than the genotypic coefficient of variation (GCV) for all the characters under study, indicating that the environment had an important role in the expression of these characters and direct selection, therefore will not sufficiently be effective. Hence, it is desirable to go for indirect selection for the improvement of these attributes. The PCV and GCV values range from 9.81% and 6.89% for plant height to 20.66 % and 16.17 % for the number of effective tillers $plant^{-1}$. The GCV and PCV values were categorized as per Robinson *et al.* (1949), as low (less than 10 %), moderate (10-20 %), and high (more than 20%). Thus, accordingly, the highest PCV value was recorded by number of effective tillers $plant^{-1}$ (20.66 %) whereas its GCV value was moderate (16.17 %). Further, moderate GCV and PCV values were observed in spike length (13.22 and 18.19 %), number of grains per spike (11.34 and 14.56 %) and yield kg $plot^{-1}$(10.12 and 12.03 %) while 1000 grain weight (11.25 %), harvest index (11.23 %), and protein content (10.55 %) exhibited moderate values of PCV alone. Similar results of moderate PCV and GCV were also reported by Dhananjay *et al* (2012), Abrar *et al.* (2018), and Patil and Koujalagi (2018). This indicating that these characters are amenable for improvement because greater effectiveness of selection and improvement to be expected for these characters in future breeding programmes as the genetic variance is mostly due to additive gene expression.

Heritability

Heritability is the good index of the transmission of characters from parents to their offspring. A perusal of the data reflected in Table-2 indicates that heritability in the present study was estimated in a broad sense way i.e. ratio of the genotypic variance to the total or phenotypic variance. As suggested by Johnson *et al.* (1955a), heritability values are categorized as low (less than 30 %), moderate (30-60 %) and high (more than 60 %). Therefore, accordingly, all the eight characters studied under the present investigation recorded high heritability i.e. more than 60 %. Among the eight characters, the greatest estimate of heritability in a broad sense was noted by spike length (86.53 %) followed by 1000 grain weight (85.96 %), number of effective tillers $plant^{-1}$ (82.24 %), harvest index (81.98 %), number of grains $spike^{-1}$ (74.42 %), plant height (73.51 %), protein content (71.89 %) and yield kg $plant^{-1}$ (65.47 %). These results are in conformity with the findings Yadav *et al.* (2011), Abrar *et al.* (2018) and Pavan *et al.* (2018). High heritability for the above-cited traits indicates that the 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 traits with low heritability are more susceptible to environmental variation and selection of such traits will lead to misleading results.

Genetic advance

Genetic advance is the improvement in the mean genotypic value of the selected lines over the mean genotypic value of the parental population (original population before selection). Increased heritability values along with elevated genetic advance are generally more advantageous in signifying the improvement of traits under selection. According to Johnson *et al* (1955a)**,** 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 the mean. An appraisal from Table-3 indicates that the number of effective tillers plant^{-1} (53.32%), spike length (49.12%), harvest index (45.42%) and 1000 grain weight (45.02%) were quite encouraging since these characters exhibited high genetic advance as percent of mean and also they were accompanied with high heritability estimates. Thus, these traits are least influenced by the environment and might show the least genotype x environment interaction. Similar findings were also confirmed by Yadav *et al.* (2011), Abrar *et al* (2018) and Pavan *et al.* (2018). It suggested that there is an imperative need for portioning the overall variability with heritability and non-heritability component with the help of suitable heritable estimates and genetic advance.

Conclusion

The outcome of the present investigation illustrates the existence of reasonable genetic variability among the 20 promising wheat lines. The highest PCV value was observed by the number of effective tillers plant^{-1}, whereas the rest of the characters reflected moderate to low values of both PCV and GCV. Yield component traits viz., spike length, number of effective tillers plant^{-1}, harvest index, and 1000 grain weight were relatively acceptable since these attributes displayed great heritability measures along with high genetic advance as percent of the mean, indicating little or no influence of the environmental effect on the expression of such characters. Therefore, the selection for improvement of such characters will be more useful to get concurrent advancement of yield, yield contributing characters and protein content percentage in bread wheat.

Table 1 : List of 20 wheat varieties/genotypes with their pedigree and genetic characteristics

S.No	Name of varieties	Pedigree	Genetic characteristics
1	HD-2687	CPAN 2009/HD 2329	Tolerance to yellow and brown rust
2	HD- 2733	ATTILA/3/TUI/CARC//CHEM/CHOTO/4/ATTILA	Resistance to brown rust and tolerant to leaf blight
3	HD-2781	BOW /C 306 //C591/HW2004	Resistance to brown rust
4	HD-2824	PTO1/CNO79/PRL/GAA/3/HD195	Resistance to brown rust and tolerant to leaf blight
5	HD-2932	KAUZ/STAR//HD 2643	Resistance to brown rust and high zinc content
6	HD-2967	ALD/COC//URES/HD216 0M/HD2278	Wider adaptability and resistance to yellow and brown rust
7	PBW-343	ND/VG 7944//KAL/BB/3/YACO S/4/VEE# 5S	Double dwarf variety with profuse tillering and stiff straw
8	PBW-502	W 485 /PBW 343// RAJ 1482	Resistance to yellow rust, brown rust and karnal bunt
9	PBW-550	WH 594/RAJ 3858//W48	A high degree of resistance to yellow and brown
10	HUW-206	KAVKAZ/BUHO/KALYANSONA/BLUEBIRD	Resistant to all the three rusts
11	HUW-468	CPAN-1962 / TONI //LIRA'S'/ PRL'S	Tolerance to leaf blight
12	HUW-510	HD2788/HUW234//DL230-16	Resistance to brown and black rust, high-temperature terminal tolerance, fit to late sown condition
13	RAJ-1482	NAPO-TOB 'S'/8156/KAL-BB	Good for chapatti quality
14	RAJ-3765	HD 2402/VL639	Tolerance to terminal heat stress condition
15	LOK-1	S308/S331	Wider adaptability and good for chapatti quality
16	DBW-14	RAJ 3765/PBW 343	Tolerant to leaf blight
17	DBW-39	ATTILA/HUI	Resistance to black rust, brown rust and tolerant to leaf blight
18	K-0307	K 8321/UP2003	Tolerance to terminal heat stress condition
19	UP2554	SM4-HSN 24E/CPAN 209	Resistance to rust
20	UP2572	HD 2009/SKA //HD 2329	Resistance to yellow and brown r[ust

Table 2 : Analysis of variance for yield, yield components and protein content in wheat (*Triticum aestivum* L

Source of variation	Degree of freedom	No. of effective tiller plant^{-1}	Spike length (cm)	Number of grains per spike	Plant height (cm)	Harvest index (%)	1000 grain weight (g)	Protein content (%)	Yield/plot (kg)
Replication	2	3.7134	3.4561	17.421	131.421	10.213	13.164	0.952	1.867
Treatment	19	4.712**	6.667**	92.012**	242. 114**	28.089**	51.071**	0.722**	0.853**
Error	38	1.634	1.789	11.123	20.438	8.233	6.555	0.514	0.901

*Significant at 5% probability level; **Significant at 1% probability level

Table 3 : Mean, range, PCV, GCV, heritability and genetic advance as a percentage of the 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 effective tiller plant^{-1}	10.22	8.23-11.67	20.66	16.17	82.24	6.45	53.32
Spike length (cm)	9.12	7.22-12.41	18.19	13.22	86.53	4.48	49.12
No. of grains spike^{-1}	39.00	30.64-49.75	14.56	11.34	74.42	13.38	34.30
Plant height (cm)	88.41	85.65-96.41	9.81	6.89	73.51	18.56	20.99
Harvest index	36.52	33.19-41.33	11.23	8.33	81.98	16.59	45.42
1000 grain weight	38.91	37.21-43.57	11.25	9.57	85.96	17.52	45.02
Protein content (%)	10.72	9.77-11.71	10.55	8.22	71.89	2.23	20.80
Yield/plot (kg)	2.23	1.53-2.65	12.03	10.12	65.47	0.23	10.31

PCV= Phenotypic coefficient of variation, GCV=Genotypic coefficient of variation

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