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Estimation of variability, heritability and genetic advance for yield and quality characters in bread wheat (*Triticum aestivum* L.)

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Abstract

Fifty genotypes of Bread Wheat (*Triticum aestivum* L.) were evaluated against four check varieties *viz.*, DBW 187, DBW 222, GW 322, and WB 02 for fourteen different yield and quality characters to study the genetic variability, heritability and genetic advance in Augmented Block Design during Rabi 2021-2022 at crop research farm, BAU, Kanke, Ranchi. The results revealed that highest grain yield per plant attained by GW 2021-1022 (9.45g) followed by QLD 125 (8.79g) and PBS 03 (7.91g). As far as quality parameters is concerned, the maximum protein, iron and zinc content was recorded in BNSR 8 (14.52%), INDB 2119 (53.87 ppm) and PBS 01 (53.79 ppm) respectively. High genotypic and phenotypic co-efficient of variation (GCV & PCV) was recorded for Zinc content and sedimentation value. High range of heritability coupled with high genetic advance was observed for the characters *viz.*, number of grains per spike, spike length, biological yield per plant, sedimentation value, iron content and zinc content.

Keywords: Bread wheat, variability, heritability and genetic advance

Introduction

Bread wheat (*Triticum aestivum* L.) is an annual allohexaploid *Rabi* crop with somatic chromosome no. 2n=42 of the family Poaceae (Gramineae). India is the second largest producer after China. Its production is estimated at 112.18 million tones as per 2^{nd} advance estimates for the year 2022-23 which is 4.44 million tones higher from the last year (*pib.gov.in*). Besides the carbohydrate and protein content in the bread wheat, other nutritional component like zinc and iron content is also very important, which needs to be improved by different methodology of crop improvement. Genetic variability plays an important role to achieve desired objective by exploring diverse genotypes. More diverse the genotype, greater will be the chance of exploitation, to generate productive recombinants and high variability. The estimation of heritability in broad sense provides information about transmission of characters from one generation to another for a specific character. High heritability coupled with high genetic advance value offers a most suitable criterion for selection towards desired objective.

Materials and Methods

A field experiment was laid out at crop research farm, BAU, Kanke, Ranchi during *Rabi*-2021, which is located at an average elevation of 611 meter above mean sea level with 85°18'48.3"East longitude and 23°25'47.3"North latitude. Fifty wheat genotypes were evaluated against four nutritionally rich check varieties *viz.*, DBW 187, DBW 222, GW 322, and WB 02. The experimental materials were accommodated in five blocks in Augmented Block Design where the checks were replicated in each block. Each genotype was sown in six rows of 4m length at 20cm apart. All the agronomic practices and plant protection measures were applied for proper plant growth.

Observations for ten quantitative characters were recorded on five randomly selected plants of each genotype in each block. The characters recorded were, days to 50 per cent flowering, days to 50 per cent maturity, plant height (cm), spike length (cm), number of effective tiller per plant, number of grains per spike, 1000-grains weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%). In addition, four quality parameters namely, protein content (%), grain zinc content (ppm), grain iron content (ppm) and sedimentation value (ml) were also estimated in the laboratory.

Results and Discussion

The analysis of variance consisting mean sum of square value against different source of variation for fourteen characters has been presented in Table-1. The data revealed that treatments highly significant for almost all the characters studied except number of effective tillers per plant, thereby suggesting the presence of considerable amount of variability among the fifty-four wheat genotypes. The results are in accordance with Thapa *et al.*, (2019) ^[6] who reported highly significant mean squares due to treatments for all the traits studied.

The estimates of population mean and range values are presented in Table-2. The data revealed that the maximum range of variability was for plant height, number of grains per spike, sedimentation value. A wide range of variation was recorded for different characters while comparison of the general means of germplasm using least significant differences, indicates the existence of high degree of variability for all the characters in the indigenous genotypes of wheat.

Table 1: Analysis of variance (ANOVA) for fourteen characters in Bread Wheat.

		MEAN SQUARES													
sov	DF	50% Flowering days	50% Maturity days	Effective tiller	Grains per spike	Plant Height (cm)	Spike length (cm)	1000 grains weight (g)	Grain yield (g/plant)	Biological yield (g/plant)	Harvest index (%)	Protein content (%)	Sediment action value (ml)	Iron content (ppm)	Zinc content (ppm)
Blocks	4	1.41	22.27**	0.27	40.72**	73.79**	0.38	7.19**	2.58**	7.14**	66.58**	2.26*	74.80**	14.93**	26.73**
Treat	53	27.47**	42.31**	0.21	58.22**	38.00**	1.07**	13.90**	1.90**	4.26**	49.16**	1.47*	62.16**	33.48**	55.94**
Entries	49	28.18**	33.64**	0.22	50.20**	44.81**	1.07**	12.38**	1.63**	4.73**	41.12**	1.27*	51.22**	22.85**	37.40**
Check	3	22.58**	209.80**	0.07	153.32**	26.96*	1.61**	36.04**	5.10**	3.91*	188.19**	5.15**	215.49**	95.12**	89.74**
Check Vs entries	1	7.67	-35.62	0.18	166.25**	-262.58	-0.45	21.86**	5.47**	-17.83	26.11	0.04	138.00**	369.38**	863.26**
Error	12	2.29	2.88	0.16	2.54	5.52	0.17	1.22	0.45	0.91	9.87	0.44	9.13	0.18	0.08

*significant at 5%, **significant at 1%

Table 2: Estimation of phenotypic variability for fourteen characters in bread wheat.

Characters	Ra	inge	Denulation Maan		
Cnaracters	Lowest	Highest	Population Mean		
50% flowering days	72	90	81.84		
50% maturity days	116	136	127.59		
Effective tiller per plant	1.92	4.27	3.03		
Grains per spike	28.81	63.36	49.587		
Plant Height (cm)	80.26	119.26	94.17		
Spike length (cm)	5.77	10.52	8.771		
1000-grains weight (g)	40.64	59.8	46.38		
Grain yield (g/plant)	3.09	9.45	6.5		
Biological yield (g/plant)	10.57	21.05	16.27		
Harvest index (%)	21.59	57.33	39.89		
Protein content (%)	8.97	14.52	11.3		
Sedimentation value (ml)	25.63	58.95	37.88		
Iron content (ppm)	34.24	53.87	38.83		
Zinc content (ppm)	25.99	53.79	33.15		

Genetic variability is the tendency of individuals in a population, to vary from one another. Statistically, the total variability is expressed in terms of phenotypic coefficient of variation (PCV) whereas genotypic variability is expressed in terms of genotypic coefficient of variation (GCV). The estimation of genotypic and phenotypic coefficient of variation together with heritability and genetic advance are presented in the Table-3.

The estimates of phenotypic coefficient of variation were high for the traits such as, grain yield per plant, sedimentation value and zinc content, while the estimates of genotypic coefficient of variation were high for the characters, sedimentation value and zinc content. This indicated greater scope of obtaining high selection response for these traits owing to presence of high genetic variability. Similar results were also revealed by Yadav *et al.*, (2021)^[7] while investigating seventy-six bread wheat genotypes and observed high estimates of GCV and PCV were recorded for grain yield per plant, biological yield per plant and sedimentation value.

Among all the studied characters, quality parameters namely, protein content and iron content, and the yield attributes *viz.*, effective tillers per plant, number of grains per spike, spike length, biological yield per plant, and harvest index recorded moderate PCV whereas iron content and the yield attributes effective tillers per plant, number of grains per spike, spike length, grain yield per plant, biological yield per plant, and harvest index recorded moderate GCV indicating the scope for improvement of these traits. Kumar & Kumar (2021)^[3] observed high

International Journal of Advanced Biochemistry Research

estimates of GCV and PCV were observed for the characters, awn length, plant height and grain yield per plant. Hassani *et al.*, (2022) ^[1] recorded higher values of GCV and PCV for grain yield followed by thousands grains weight.

 Table 3: Genetic estimation for fourteen characters in bread wheat.

Characters	PCV (%)	GCV	h ² (%)	GA	GA as % of mean
50% flowering days	6.91	6.65	92.83	10.81	13.21
50% maturity days	5.50	5.34	94.15	13.62	10.68
Effective tiller	15.39	7.61	24.49	0.24	7.76
Grains per spike	16.64	16.33	96.27	16.37	33.01
Plant Height (cm)	7.03	6.57	87.40	11.91	12.65
Spike length (cm)	12.63	11.75	86.46	1.97	22.50
1000-grains wt.(g)	8.67	8.33	92.47	7.66	16.51
Grain yield (g/plant)	22.05	17.62	63.82	1.87	28.99
Biological yield (g/plant)	13.54	12.21	81.32	3.69	22.68
Harvest index (%)	17.88	13.94	60.79	8.86	22.39
Protein content (%)	11.37	9.75	73.55	1.95	17.23
Sedimentation value (ml)	22.33	20.86	87.24	15.21	40.14
Iron content (ppm)	16.17	16.13	99.55	12.87	33.15
Zinc content (ppm)	24.48	24.47	99.87	16.70	50.37

High PCV or GCV did not provide a clear picture of the extent of genetic gain to be achieved from selection, for the phenotypic traits unless the heritable fraction of the trait was known (Kumar *et al.*, 2017)^[2]. Broad sense heritability gives an idea about portion of observed variability attributable to genetic differences. Hence, heritability indicates effectiveness of selection for phenotypic performance. The estimates of heritability, genetic advance and genetic advance as percent of mean for fourteen characters have been presented in Table-3.

In the present study, high heritability coupled with high genetic advance as per cent of mean were recorded for quality trait like sedimentation value, iron content, zinc content and yield attribute like grains per spike, biological yield per plant, spike length. This indicates that there was low environmental influence on the expression of these characters and hence, selection is rewarded. Similarly, high heritability and genetic advance as per cent of mean for the traits zinc content, iron content, 1000-grain weight, grain yield per plant, days to maturity, grain weight per spike, days to 50% flowering and biological yield, was reported by earlier scientist Kumari *et al.*, (2020)^[4] in bread wheat genotypes.

High heritability coupled with moderate genetic advance as per cent of mean observed for quality parameter like sedimentation value, phenological traits like 50% flowering days, 50% maturity days and yield attributes like 1000-grain weight, plant height. Singh *et al.*, (2022) ^[5] reported high estimates of heritability together with high estimates of genetic advance in percent over mean for biological yield per plant, flag leaf area, and peduncle length while was found for flag leaf area, biological yield and number of productive tillers.

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