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Study of Genetic Variability for yield and yield contributing characters in Bread Wheat (*Triticum aestivum* L.)

SHIVANI KHATRI*, RAKESH SINGH NEGI and SHIVANI NAUTIYAL

Department of Seed Science and Technology, Baba Farid Institute of Technology Suddhowala, Dehradun affiliated from Hemvati Nandan Bahuguna Garhwal University Srinagar (Uttarakhand)

**Corresponding author's email id: shivanikhatriddn@gmail.com*

ABSTRACT: Twenty-one genotypes of wheat were evaluated for the genetic variability so the genotypes can be categorized based on their variability for hybridization programme. The analysis was carried out in Rabi season 2021-22 at Agricultural field block of Baba Farid Institute of Technology, Dehradun, in randomized block design (RBD) with 3 replications. The pre-harvest (plant height, spike length, number of tillers, days to 50% maturity and days to maturity) and post harvest (No. of seeds per spike, biological yield, economic yield, harvest index and 1000 seeds weight) parameters recorded on plant morphological traits and grain yield. On analysis of variance for the above studied parameters, it indicated wide variability among the twenty-one genotypes of wheat and shows that through crop improvement methods considerable amount of improvement can be achieved. The GCV and PCV shows highest variability in the following characters harvest index, biological yield per plot, test weight, economic yield per plot number of tillers respectively. These traits in wheat had showed high variance that can be preferred for further improvement. Economic yield per plot the essential yield attributes has positive significant correlation with harvest index and possessed positive non-significant correlation with number of seed per spike, biological yield per plot, test weight while it has negative significant correlation with days to 50% maturity. It has negative non-significant correlation with plant height, number of tillers. This represent that the twenty-one genotypes taken have substantial variation for different traits evaluated and significant association with yield that can be considered in breeding programme for increasing yield.

Key words: Analysis of variance, correlation, genotypic variance, GCV, phenotypic variance, PCV, randomised block design.

South-western Asia is the center of origin for bread wheat (*Triticum aestivum* L.) which is a self-pollinated crop. It is regarded as the second most significant cereal crop in India after rice. It has been referred to as the “King of Cereals” due to its enormous acreage, great output and major position in the global food grain market. There are 17 different species in the “*Triticum*” genus that belongs to family poaceae (graminae). *Triticum* species in their natural habitat can be found in abundance in northern Israel, Lebanon, Syria, eastern Turkey and Iraq. The Central Asian, Ethiopian and Mediterranean regions are the significant centers of diversity for the genus *Triticum* and its allied species (Perrino and Porcedu, 1990, Kundu and Nagarajan, 1996). Hindukush region is the epicenter of hexaploid wheat species diversity (Kundu and Nagarajan, 1996). *Triticum aestivum* L. (hexaploid), *Triticum durum* (tetraploid) and *Triticum dicoccum* (diploid) often known as bread wheat, macaroni wheat and emmer wheat respectively are the three principal

species of genus *Triticum*. Bread wheat is the most important species covering 95% of the cultivated area worldwide followed by durum wheat with second most popular wheat accounting roughly 4% of total area whereas emmer wheat accounts less than 1%.

India is the world's second largest producer of wheat in terms of area and production, behind China. About 30% of the world's total production of food grains comes from India. It is grown in 217 million hectares worldwide, producing approximately 774.55 million tones and on 30.56 million hectares in India, producing 109.24 million tones (statistica, 2021). The crop grows best in temperate climate though it may be grown in sub-tropical and tropical zones. It needs cool growth season, it can only be grown during the winter in warmer climates. The primary wheat growing states in India include Uttar Pradesh, Punjab, Haryana, Rajasthan, Bihar, Madhya Pradesh, Gujarat, Maharashtra and Karnataka. Wheat is self-

pollinated in most cases, with cross pollination occurs in a range of 0.5 to 1%. International wheat breeding is done by CIMMYT in Mexico with the successful use of Norin 10 wheat germplasm to introduce dwarfing into modern wheat cultivars to increase production potential and tolerance or resistance to various biotic and abiotic challenges. Yield is polygenically controlled composite character as a result effective selection of yield is a difficult task thus the study of correlation is a must for any breeding programme that aims to change plant framework. The efficiency of selection can be improved by understanding the relationship between yield and its components characters as well as among the component characters themselves. This helps in study of traits to assist the selection of genotypes that can be used in future to enhance varieties for higher yield and quality.

MATERIALS AND METHODS

The present experiment was conducted to evaluate twenty-one wheat varieties. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experiment field was done according to Randomized Block Design (RBD) with three replications. Each plot was consisted of two row of 2.5m length with spacing of 5 cm within the rows and 25cm between the rows. The recommended cultural practices were being followed to raise a good normal crop. The observations were recorded on five randomly selected plants from each plot except days to fifty

percent flowering and days to maturity where data will be recorded on plot basis. Appropriate cultivation practices were done for the experiment. Observations were recorded for both pre- harvest variables such as plant height (cm), spike length (cm), number of tillers, days to 50% maturity and days to maturity followed by post-harvest variables such as number of seeds per spike, biological yield per plot, economic yield per plot, harvest index and test weight. The data collected in respect to ten characters on 21 genotypes by taking mean values of selected plants in each plot and subjected to analysis of variance ANNOVA, coefficients of variation and estimation of correlation coefficients.

RESULTS AND DISCUSSION

The analysis of variance for various traits is represented in Table 1. All the characters studied were significantly diverse among the genotypes, revealing a vast range of variation in twenty-one genotypes of bread wheat. For each of the ten characters tested, the analysis of variance indicated wide variability among the genotypes. This information suggests that considerable amount of variation persists for all the characters and considerable improvement can be achieved by selection for these characters. The traits harvest index, biological yield per plot, test weight, economic yield per plot and number of tillers had highest genotypic coefficient of variance and phenotypic coefficient of variance. The values of genotypic variance, phenotypic variance, GCV and

Table 1: Annova summary (MSS) for various traits among 21 genotypes of wheat

Sl. No.	Source Degrees of freedom	Replication 2	Treatment 20	Error 40
1	Plant height (cm)	1.5530	89.849**	6.799
2	Spike length (cm)	0.0210	2.196**	0.043
3	Number of tillers	0.0090	3.816**	0.026
4	Days to fifty percent maturity	5.730	55.554**	5.563
5	Days to maturity	7.0480	73.838**	10.064
6	Number of seeds per spike	0.9420	88.593**	0.618
7	Biological yield per plot	00	0.508**	0.002
8	Economic Yield Per Plot	00	0.046**	0
9	Harvest Index (%)	0.0290	321.823**	1.712
10	Test weight (g)	0.9180	165.668**	1.058

MSS: Mean sum of squares, * Significant at 5%,** Significance at 1%

Table 2: Range, mean, Sem (\pm), Phenotypic and genotypic variance, PCV, GCV of various traits among 21 genotype

Characters	Range		Grand mean	SEm (\pm)	Genotypic Variance	Phenotypic variance	GCV	PCV
	Min.	Max.						
Plant Height(cm)	71.77	95.19	83.82	1.51	27.68	34.48	6.28	7.01
Spike length(cm)	7.87	10.96	9.99	0.12	0.72	0.76	8.48	8.73
No. of tillers	3.38	7.52	5.50	0.09	1.26	1.29	20.44	20.64
Days to 50% maturity	104.67	119	112.40	1.36	16.66	22.23	3.63	4.2
Days to maturity	107	122	116.57	1.83	21.26	31.32	3.96	4.8
No. of seeds per spike	18.02	37.70	30.23	0.45	29.33	29.94	17.91	18.1
Biological yield per plot (kg)	1.11	2.68	1.57	0.02	0.17	0.17	26.09	26.23
Economic yield per plot (kg)	0.30	0.76	0.58	0.01	0.02	0.02	21.2	21.37
Harvest Index (%)	20.51	52.23	38.50	0.76	106.7	108.42	26.83	27.04
Test weight (g)	26.28	49.70	34.15	0.59	54.87	55.93	21.69	21.9

Table 3: Phenotypic correlation

	Phenotypical Correlation Matrix									
	Plant height (cm)	Spike length (cm)	Number of tillers	Days to fifty percent maturity	Days to maturity	Number of seeds per spike	Biological yield per plot	Harvest Index (%)	Test weight (g)	Economic Yield Per Plot
Plant height (cm)	1.0000	0.354*	0.450**	-0.0796	-0.1661	0.0467	0.432**	-0.399*	-0.1069	-0.1542
Spike length (cm)		1.0000	0.2403	0.411**	-0.1551	-0.0893	0.2029	-0.0961	0.285*	-0.0056
Number of tillers			1.0000	0.0603	-0.0667	-0.1742	0.1542	-0.1008	0.1081	-0.0370
Days to fifty percent maturity				1.0000	0.0408	-0.2170	-0.2169	-0.1067	0.1519	-0.311*
Days to maturity					1.0000	-0.252*	0.1229	-0.0932	0.1306	-0.0027
Number of seeds per spike						1.0000	0.1791	0.0370	-0.452**	0.1632
Biological yield per plot							1.0000	-0.615**	-0.330*	0.1017
Harvest Index (%)								1.0000	0.289*	0.703**
Test weight (g)									1.0000	0.0670
Economic Yield Per Plot										1.0000

Table 4: Genotypic Correlation

	Genotypical Correlation Matrix									
	Plant height (cm)	Spike length (cm)	Number of tillers	Days to fifty percent maturity	Days to maturity	Number of seeds per spike	Biological yield per plot	Harvest Index (%)	Test weight (g)	Economic Yield Per Plot
Plant height (cm)	1.0000	0.411**	0.501**	-0.0587	-0.1589	0.0392	0.479**	-0.442**	-0.1170	-0.1689
Spike length (cm)		1.0000	0.2350	0.523**	-0.2236	-0.0889	0.2159	-0.1018	0.304*	-0.0055
Number of tillers			1.0000	0.0796	-0.0882	-0.1799	0.1571	-0.1025	0.1106	-0.0382
Days to fifty percent maturity				1.0000	0.0321	-0.263*	-0.2463	-0.1363	0.1656	-0.371*
Days to maturity					1.0000	-0.259*	0.1670	-0.1277	0.1443	-0.0049
Number of seeds per spike						1.0000	0.1792	0.0369	-0.457**	0.1641
Biological yield per plot							1.0000	-0.616**	-0.338*	0.1040
Harvest Index (%)								1.0000	0.298*	0.701**
Test weight (g)									1.0000	0.0730
Economic Yield Per Plot										1.0000

PCV are summarized in Table 2. The table suggests that the PCV is little bit higher than GCV of their respective characters. Except for Harvest index other characters shows similar trends suggesting that the characters have a good scope of selection. The maximum GCV is showed by harvest index followed by biological yield per plot.

Correlation analysis provides information on the nature and magnitude of association of different components with grain yield. It also helps us to understand the nature inter-relationship among the components traits themselves. Ultimately, this kind of analysis could help the breeder to design his selection to improve grain yield. Economic yield per

plot had positive significant correlation with harvest index. It also possessed positive non-significant correlation with number of seeds per spike, biological yield per plot and test weight. It had negative significant correlation with days to fifty percent maturity. It had negative non-significant correlation with plant height and number of tillers at both phenotypic and genotypic level suggesting that only positively correlated traits should be considered for increasing yield and much attention should be paid towards negatively correlated traits for avoiding objectionable results. Genotypic and phenotypic correlation is summarized in Table 3 and 4.

CONCLUSION

The analysis of variance revealed that the genotypes differ significantly for all the ten characters indicating the existence of significant amount of variability among the studied genotypes. The traits such as harvest index, biological yield per plot, test weight and economic yield per plot had the highest GCV and PCV. These traits can be preferred for further improvement. Economic yield per plot shows positive significant correlation with harvest index and have negative significant with days to 50% maturity at both genotypical and phenotypical level. This investigation has showed that an ample amount of variability among the wheat genotypes can be exploited that in turn lead to better identification of genes for further increase of yield.

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