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**Vinay Prakash Bagde**

Ph.D. Scholar, Department of  
Plant Breeding & Genetics,  
Jawaharlal Nehru Krishi  
Vishwavidyalaya, Jabalpur,  
Madhya Pradesh, India

**Dr. RS Shukla**

Principal Scientist, AICRP on  
Wheat, Department of Plant  
Breeding & Genetics, JNKVV,  
Jabalpur, Madhya Pradesh,  
India

**Shikha Upadhyay**

Ph.D. Scholar, Department of  
Plant Breeding & Genetics,  
Jawaharlal Nehru Krishi  
Vishwavidyalaya, Jabalpur,  
Madhya Pradesh, India

**Rahul Sonaniya**

Ph.D. Scholar, Department of  
Plant Breeding & Genetics,  
Jawaharlal Nehru Krishi  
Vishwavidyalaya, Jabalpur,  
Madhya Pradesh, India

## Trapping the genetic variability for yield and its components traits in wheat (*Triticum aestivum* L.)

**Vinay Prakash Bagde, Dr. RS Shukla, Shikha Upadhyay and Rahul Sonaniya**

### Abstract

The changing climate adversely affect the morphological characters of plant which, ultimate effect the identification of off types in seed production programme. This also leads to effect the genetic purity in seed production programme. To overcome this problem selection of progeny and its breeding depend upon the genetic variability in population. Fifteen varieties of wheat and their fifty four crosses were evaluated in randomized block design (RBD) with three replications for yield components and physiological traits during rabi 2021-22, to find out genetic variability, heritability and genetic advance percent of mean. Significant genetic differences were observed for all the quantitative characters studied, indicating considerable amount of variation among genotypes. Moderate genotypic and phenotypic coefficient of variation exhibited by numbers of tillers per plant, harvest index and flag leaf area value while, number of grains per spike, thousand grain weight and days to maturity showed low PCV and low GCV. All of the traits expressed high heritability except number of grains per spike and spike length. However, biological yield per plant and harvest index and grain yield per plant sowed high genetic advance, which, indicates that the heritability is most likely due to additive gene effect and selection may be effective for these traits. It is also observed that the performance of these characters is not under influence of environment. However, other characters might be effected by the change in climatic condition. Thus, in seed production programme at the time of rouging these characters must be considered to maintain the genetic purity of seed.

**Keywords:** Wheat, genotypic and phenotypic coefficient of variation, heritability, genetic advance

### Introduction

Abiotic stress factors such as heat, cold, drought, salinity, and nutrient stress have a huge impact on world agriculture, and it has been suggested that they reduce average yields by >50% for most major crop plants (Wang *et al.*, 2003) [13]. Wheat is also no exception to this. Among abiotic stresses heat stress is one of important abiotic stress which wheat faces today. Global climate models predict that rise in mean ambient temperature between 1.8 to 5.8 °C by the end of this century (Masson *et al.*, 2021) [7]. The changing climate adversely affect the morphological characters of plant which, ultimate effect the identification of off types in seed production programme. This also leads to affect the genetic purity in seed production programme. To overcome this problem selection of progeny and its breeding depend upon the genetic variability in population.

Wheat, the second most important staple food consumed by almost 35% of the world population and providing 20% of the total food calories. It occupies nearly about 32% of the total acreage under cereals crops in the world. There are three species of wheat namely, *Triticum aestivum* (Bread wheat), *Triticum durum* (Macaroni wheat) and *Triticum dicoccum* (Emmer or Khapli) grown on commercial basis in India. Of these species, *T. aestivum* continues to be the most important species accounting about 90-95% of total wheat area of the country and is grown in almost all the wheat growing states. *T. durum* is next in importance with approximately 5% of total wheat area and confined mostly to central and southern parts of India. The cultivation of *T. dicoccum* is confined largely to the southern region mainly Karnataka and southern Maharashtra.

Selection of progeny and its breeding depend upon the genetic variability in population. The extent of genetic variability has been considered as an important factor which is an essential pre-requisite for a successful hybridization aimed at producing high yielding progenies. The knowledge of heritability helps the plant breeder in predicting the behaviour of the succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection.

**Corresponding Author:**

**Vinay Prakash Bagde**

Ph.D. Scholar, Department of  
Plant Breeding & Genetics,  
Jawaharlal Nehru Krishi  
Vishwavidyalaya, Jabalpur,  
Madhya Pradesh, India

Higher estimates of heritability coupled with better genetic advance confirm the scope of selection in developing new genotypes with desirable characteristics. Hence, heritability estimates in this study would help to predict about the possible progress that can be attained by making the selection process effective. Moreover, genetic advance estimates give a clear picture of F1 generation to make selection effective. This study is aimed to estimate variability and genetic parameters for yield components and physiological characters. These values will help in making effective selection under variable environmental conditions for the improvement of characters under study.

### Material and Methods

The experimental material was comprised of fifty four F1 populations involving 15 selected genotypes as parents: GW-366, GW-273, GW-322, JW-1201, JW-1202, JW-1203, JW3336, JW-3288, JW3382, MP-4010, JW-3211. RAJ 3765, WH 730, DBW-14, and DBW-71. The experiment was carried out at Breeders Seed Production Unit, Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh (India) in the rabi season 2021-22.

The F1 Seeds and parents were grown in lines keeping plant to row to row distance at 20 cm and plant distance at 10 cm. All the crop protection measures were adopted on time. Data were collected for Days to 50% heading, Days to maturity, plant height, Number of tillers per plant, Number of spikelets per ear, Ear length (cm), Ear weight, Number of ears per plant, peduncle length, Number of grains per ear, 1000-grain weight, Biological yield per plant, Grain yield per plant, Harvest index. At maturity, five healthy and competitive

plants from the each F1 cross and each parent were taken at random and data were recorded and analyzed. The analysis of variances suggested by Burton (1952), heritability in broad sense ( $h^2_{bs}$ ) is suggested by Hanson *et al.*, (1950) and genetic advance (GA) was estimated by Johnson *et al.*, (1955). Mean sums of square were calculated as indicated in Table 1.

### Result and Discussion

#### Analysis of Variance (ANOVA)

To know the extent of variation for observed characters among the genotypes of wheat, analysis of variance was performed and presented in table 1. Results of analysis of variance indicated that the mean sums of squares due to genotypes were highly significant for all the traits under study, suggesting presence of sufficient variation among the genotypes for these traits. The mean sum of squares due to replication showed non-significant differences for all the traits under study indicating good homogeneity among replications. Maximum variability was observed for harvest index (293.59\*\*\*), while, minimum for flag leaf width (0.074\*\*\*). The magnitude of variability in decreasing order for other traits were as follows: biological yield per plant, plant height, flag leaf area, plant height, days to 50% harvesting, grain yield per plant, number of grains per spike, thousand grain weight, flag leaf length, days to maturity, number of spikelets per spike, number of tillers per plant and spike length. The variability among parental lines and F1s ranged from biological yield per plant to ear weight. This was in conformity with the findings of Ahmed *et al.*, (2015) [1], Singh *et al.*, (2015) [11], Naik *et al.*, (2015) [9], Tahmasebi *et al.*, (2013) [12], Hossain *et al.*, (2021) [3].

**Table 1:** Analysis of variance for yield and attributing trait

Mean sums of square								
S.V.	DF	DH 50%	PH	DM	FLL	FLW	FLA	NTPP
Replication	1	22.72	9.74	0.87	78.79	0.58	695.11	0.028
Treatment	68	68.37***	109.62***	17.07***	22.20***	0.074***	88.60***	3.41***
Error	68	1.87	3.70	2.97	1.68	0.009	9.62	0.61
Mean sums of square								
S.V.	DF	SL	SPS	NGPS	TGW	BYPP	HI	GYPP
Replication	1	0.34	0.67	2.22	0.035	2.37	40.84	1.67
Treatment	68	1.72***	4.79***	31.35***	29.56***	267.27***	293.59***	40.63***
Error	68	0.42	0.43	5.54	2.84	6.14	28.62	5.52

Where

DH 50% = Days to 50% heading, PH = Plant height, DM = Days to maturity, FLL= Flag leaf length, FLW = Flag leaf width, FLA= Flag leaf area, NTPP = No of tiller per plant, SL

= Spike length, SPS = Spikelets per spike, NGPS = No of grains per spike, TGW = Thousand grain weight, BYPP = Biological yield per plant, HI = Harvest index, GYPP = Grain yield per plant.

**Table 2:** Estimates of Genetic components

Characters	Range			GCV (%)	PCV (%)	H <sup>2</sup> (bs) %	GA as % of mean
	Mini.	Maxi.	Avg.				
DH 50	50.50	75.50	56.17	10.26	10.55	94.7	20.57
PH	66.10	106.67	90.08	8.07	8.35	93.5	16.08
DM	103.00	119.00	112.47	2.36	2.81	70.3	4.07
FLL	14.71	29.95	22.50	14.23	15.36	85.9	27.18
FLW	1.15	2.02	1.52	11.93	13.50	78.1	21.73
FLA	14.70	48.82	28.95	21.70	24.20	80.4	40.09
TPP	4.50	10.50	6.48	18.26	21.92	69.4	31.35
SL	7.73	11.25	9.25	8.71	11.20	60.5	13.96
SPS	13.66	20.59	16.70	8.84	9.68	83.5	16.65
NGPS	41.01	59.77	50.80	7.07	8.45	69.9	12.18
TGW	37.62	54.06	47.34	7.72	8.5	82.5	14.44
BYPP	18.60	72.26	30.50	34.47	38.34	95.5	75.43
HI	27.97	84.75	56.06	20.53	22.64	82.2	38.55
GYPP	8.74	32.12	16.32	25.67	29.43	76.1	46.13

Where

DH 50% = Days to 50% heading, PH = Plant height, DM = Days to maturity, FLL= Flag leaf length, FLW = Flag leaf width, FLA= Flag leaf area, NTPP = No of tiller per plant, SL = Spike length, SPS = Spikelets per spike, NGPS = No of grains per spike, TGW = Thousand grain weight, BYPP = Biological yield per plant, HI = Harvest index, GYPP = Grain yield per plant.

Degree of dispersion for the plant height ranged between 66.10 to 106.67 cm. with an average performance of 90.08 cm. Number of tillers per plant had an average performance of 6.48 with a range of 4.50 to 10.50. Number of spikelets per spike was recorded in the range of 13.66 to 20.59 with an average at 16.67. Spike length varied from 7.73 cm to 11.25 cm with a mean of 9.25 cm. Number of grains per spike showed a variation ranging from 41.01 to 59.77 with a mean value of 50.80. 1000 grain weight recorded a minimum value of 37.62 g and a maximum of 54.06 g with a mean value of 47.34 g. Range of variation observed for biological yield per plant was 18.60 g to 72.26 g with mean value of 30.50 g. Grain yield per plant recorded a minimum value of 8.74 g and a maximum of 32.12 g with a mean value of 16.32 g. Harvest index showed a variation ranging from 27.97% to 84.75% with a mean value of 56.06%.

#### Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV)

Phenotypic coefficients of variation estimates were higher than the genotypic coefficients of variation for all characters under study. Biological yield per plant recorded the high PCV (38.34) and GCV (34.47) followed by grain yield per plant (29.43, 25.67); whereas moderate PCV and GCV were recorded for number of tillers per plant (21.92, 18.26); flag leaf area (24.20, 21.70); and harvest index (22.64, 20.53). Rest all other traits showed low phenotypic and genotypic coefficient of variation. Similar findings were also reported by Kalimullah *et al.*, (2012) <sup>[4]</sup>, Kandel *et al.*, (2018) <sup>[5]</sup>, Mehendi *et al.*, (2022) <sup>[8]</sup>, Hossain *et al.*, (2021) <sup>[3]</sup>.

#### Heritability and Genetic advance as a % of mean

Heritability and genetic advance are important selection parameters. Heritability estimate along with genetic advance are normally more helpful in predicting the gain under selection than heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance. Genetic advance can be estimated both from parental as well as segregating populations. Estimates of genetic advance help in understanding the types of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action. It also helps in deciding a breeding procedure for the genetic improvement of various polygenic traits by determining the gene action. Results showed that all the characters expressed high estimates of heritability except number of tillers per plant (69.40%), spike length (60.50%) and number of grains per spike (69.90%). It indicates that the heritability is most likely due to additive gene effect and selection may be effective. The high genetic advance as percentage of mean was showed by flag leaf area (40.09%), biological yield per plant (75.43%), harvest index (38.55%), and grain yield per plant (46.13%). However, moderate genetic advance was recorded for number of tillers per plant

(31.35%), and flag leaf length (40.09%). In this study high heritability with high genetic advance was observed for biological yield per plant, harvest index and grain yield per plant and high heritability with moderate genetic advance was also observed for flag leaf length indicated predominance of additive gene action for controlling these characters. Thus, simple selection can be practiced to improve these characters. This was in consonance with the findings of Roy *et al.*, (2021) <sup>[10]</sup>, Yadav *et al.*, (2021) <sup>[14]</sup> and Dave *et al.*, (2021) <sup>[2]</sup>, Laghari *et al.*, (2021) <sup>[6]</sup>.

#### Conclusion

It is concluded from these study that characters like harvest index and days to 50% heading are not under influence of environment. However, other characters might be affected by the change in climatic condition. Thus, in seed production programme at the time of rouging these characters must be considered to maintain the genetic purity of seed.

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#### Conflict of interest: None

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