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**Prachi Pal**  
Faculty of Agriculture Sciences  
and Allied Industries, Rama  
University, Kanpur, Uttar  
Pradesh, India

**Aneeta Yadav**  
Faculty of Agriculture Sciences  
and Allied Industries, Rama  
University, Kanpur, Uttar  
Pradesh, India

**Syed Mohd Quatadah**  
Faculty of Agriculture Sciences  
and Allied Industries, Rama  
University, Kanpur, Uttar  
Pradesh, India

**Koushik Saha**  
Faculty of Agriculture Sciences  
and Allied Industries, Rama  
University, Kanpur, Uttar  
Pradesh, India

**Corresponding Author:**  
**Prachi Pal**  
Faculty of Agriculture Sciences  
and Allied Industries, Rama  
University, Kanpur, Uttar  
Pradesh, India

## Assessment of genetic variability and heritability for yield and its attributing traits in wheat (*Triticum aestivum* L.)

Prachi Pal, Aneeta Yadav, Syed Mohd Quatadah and Koushik Saha

### Abstract

An experiment has been conducted at the Agricultural Research Field of Department of Genetics and Plant Breeding, Rama University, Kanpur to understand the pattern of genetic variability and heritability through the investigation of 27 wheat genotypes including checks. The trial has been conducted in randomized block design in three replication and the observations have been noted on the eleven metric traits viz., days to 50% flowering, days to maturity, flag leaf area (cm<sup>2</sup>), number of tillers per plant, plant height (cm), spike length (cm), number of spikelets per spike, grain yield per plant (g), biological yield per plant (g), 1000-grains weight (g) and harvest index (%). The analysis of variance showed a significant mean sum of squares due to all traits under study. High estimates of heritability were observed for all of the traits viz., grain yield per plant (94.90%) followed by 1000-grains weight (94.03%) and harvest index (93.85%), whereas, high estimates of genetic advance (>20%) in percent over mean was recorded for the traits grain yield per plant (24.76%) followed by spike length (22.22%), 1000-grains weight (21.88%). High heritability accompanied with high genetic advance for the traits showed additive gene action and the selection for such traits would be rewarding.

**Keywords:** Wheat, *Triticum aestivum*, genetic variability, heritability, genetic advance

### Introduction

The wheat is a hexaploid (allohexaploid) species ( $2n = 6x = 42$ ) having AABBDD with A, B and D genome. The species of bread wheat may be divided into diploid, tetraploid and hexaploid species with chromosome numbers  $2n=14=AA$ ,  $2n=14=BB$ ,  $2n=28=AABB$  and  $2n=42=AABBDD$  respectively with basic chromosome numbers ( $x$ ) = 7 (Sleper and Poehlman, 2006) [11]. However, DNA studies revealed that *Triticum urartu* is diploid and has used as donor of A genome instead of *Triticum monococcum* (Dvorak *et al.*, 1993) [1] and *Aegilops speltoides* which is a wild diploid; has used as a possible donor of B genome. Wheat, a self-pollinating annual plant in the true grass family Gramineae (Poaceae) and genus *Triticum*, is the world's most famous energy rich cereal crop. It has been described as the "King of the cereals" because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. It is currently grown on approximately 225 mha Area globally, with an average productivity of 3 t/ha. It exhibits considerable variation between different agroecological zones (Singh *et al.*, 2008) [10]. It supplies about 25% of protein and 20% of the calories consumed by human beings in the daily diet. According to FAOSTAT, India is the second largest wheat producer in the world after China. Total food grain production is estimated to rice 2.66% to a new record- 305.43 MT for-2020-21 crop year higher than 291.9 MT last year. In addition, India is set to harvest a record wheat production of 108.75 MT in the 2020-21 crop year on the back of food grain according to latest government of India. Wheat production is rising year on year and the previous record of 107.86 MT was achieved during the 2019-20 crop years (Source: [www.livemint.com](http://www.livemint.com) May, 2021) [12].

Genetic diversity is a natural phenomenon, and for any crop species to effectively utilize it, systematic collection, appraisal, and classification based on economic characteristics are required. The necessary level of genetic diversity for effective use of direct and indirect selection. Understanding the genetic architecture of various traits and the direct and indirect selection criteria aids in developing breeding plans that maximize genetic variety for plant improvement.

Keeping the above facts in view the present investigation has been carried out to understand the pattern of genetic variability present among available germplasms.

## Materials and Methods

### Experimental site and weather

Kanpur is situated in central part of Uttar Pradesh at an elevation of 126.49 meters from mean sea level in the Gangetic plain and lies between latitude and longitude 26°33'0'' north and 80°13'28'' east respectively. This tract enjoys a subtropical climate with occasional showers in winter. The meteorological data during the crop period as recorded in the meteorological laboratory of the Rama University Mandhana Kanpur U.P. are presented below in table and represented by the summers are hot and dry, May and June are the hottest months. December and January constitute the cooler months of the year. The maximum temperature goes up to 34.4 °C during summer and the minimum goes as low as 4.6 °C during winter. The seasonal rainfall of about 629.5 mm was received mostly from II<sup>nd</sup> Fortnight of June or first Fortnight of July to mid-October with a few showers in winter season.

### Experimental materials and methods

The experimental material for the present investigation comprised of 25 wheat genotypes including two checks *viz.*, HD 2733 and PBW 502, from germplasm materials available in "The Department of Genetics and Plant Breeding, Rama University, Mandhana, Kanpur. The experiment was sown in randomized block design with three replications at the experimental field. Each plot consists of two rows of 2.5 m spacing of 5cm plant to plant within the row and 20 cm between the rows. Fertilizer was applied at the rate of 120 kg N, 60 kg P, and 40 kg K. These accessions were raised and followed recommended packages and practices during the *Rabi* season, 2022-23 to grow a healthy crop.

### Observations recorded

The observation on 11 quantitative characters *viz.*, days to 50% flowering, days to maturity, flag leaf area (cm<sup>2</sup>), number of tillers per plant, plant height (cm), spike length (cm), number of spikelets per spike, grain yield per plant (g), biological yield per plant (g), 1000-grains weight (g) and harvest index (%), were recorded to estimate genetic variability, heritability, and genetic advance.

### Statistical analyses

The experimental data collected the respect of 11 characters on 25 wheat genotypes and 2 checks were compiled by taking the mean values of selected plants in each plot and subjected to the following statistical analyses: Analysis of variance (Panse and Shukhatme, 1988) [8], Estimation of Heritability and Genetic advance as percent of mean (Johnson *et al.*, 1955) [4].

## Results and Discussion

### Analysis of variance

The mean sum of squares, based on ANOVA of 27 wheat genotypes including two checks for 11 characters revealed that the mean sum of squares due to treatment was highly significant for all of the traits at a given level of probability as shown in table 1.

**Table 1:** ANOVA for 11 traits of wheat germplasm for randomized block design

Source of variation	Replications	Treatments	Error
df	2	26	52
Days to 50% Flowering	3.01	11.81**	0.83
Days to maturity	3.07	16.84**	1.64
Plant Height (cm)	0.71	121.01**	9.03
Number of tillers per plant	0.069	0.848**	0.042
Spike length (cm)	0.072	3.558**	0.117
Number of spikelets per spike	0.133	2.000**	0.41
Flag leaf area (cm <sup>2</sup> )	0.3	29.54**	0.8
1000 grains weight (g)	0.49	37.54**	0.78
Biological yield per plant (g)	0.17	9.71**	0.24
Harvest index (%)	0.05	87.22**	1.86
Grain yield per plant (g)	0.1	3.031**	0.053

\*,\*\* Significant at 5% and 1% level of probability respectively.

### Heritability

The estimates of broad sense heritability (H<sup>2</sup>bs) and genetic advance in percent over mean (GA) for different characters are given in Table 2.

Heritability and genetic advance are important selection parameters. Heritability estimate along with genetic advances are normally more helpful in predicting the gain under selection than heritability estimates alone. The estimate of heritability can be utilized for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of best individual. Hence, estimate of heritability is an essential pre-requisite for the formation of an effective selection method for genetic improvement. High estimates of heritability (>60%) were observed for all of the traits *viz.*, grain yield per plant (94.90%) followed by 1000-grains weight (94.03%), harvest index (93.85%), biological yield per plant (92.96%), flag leaf area (92.33%), spike length (90.71%), number of tillers per plant (86.62%), days to 50% flowering (81.55%), plant height (80.52%) and days to maturity (75.51%) except number of spikelets per spike (56.36%) which possessed moderate heritability, indicating that a plant breeder can concentrate on these traits to exploit effective selection for genetic improvement. None of the traits under investigation had low estimates of heritability. Previously, similar results for various traits were also noted by Gautam *et al.* (2017) [3], Gaur, (2019) [2], Sahu *et al.* (2019) [9], Tarkeshwar *et al.* (2019) [13], Kumar *et al.* (2020) [6] and Kumar *et al.* (2022) [5].

### Genetic Advance

Genetic advance is the improvement in the mean genotypic value of selected individuals over the parental population. High heritability accompanied by high genetic advance indicates that the heritability is due to additive genetic effect and selection may be effective, while high heritability coupled with low genetic advance indicates the predominance of non-additive gene action, while low heritability is exhibited due to the influence of environmental interactions rather than genotypic selection for such characters may not be rewarding. High estimates of genetic advance (>20%) in percent over mean were recorded for the traits grain yield per plant (24.76%) followed by spike length (22.22%), 1000-grains weight (21.88%), harvest index (21.79%) and biological yield per plant (21.26%). While, moderate (10-20%) genetic advances in percent over mean were found for flag leaf area

(19.85%), number of tillers per plant (16.91%) and plant height (12.99%). Further, low levels (<10%) of genetic advance were observed for number of spikelets per spike (6.64%), days to 50% flowering (4.30%) and days to maturity (3.24%). Earlier, similar results for various traits were also noted by Tarkeshwar *et al.* (2019) [13], Kumar *et al.* (2020) [6], Kumar *et al.* (2022) [5].

### Coefficient of variation

Highest values of the phenotypic coefficient of variation (PCV) along with the genotypic coefficient of variation were estimated for grain yield per plant followed by spike length,

1000-grains weight, harvest index, and biological yield per plant respectively as shown in Table 2. The high variance due to genotype as well as phenotype has been observed for some traits like plant height, harvest index, 1000-grains weight and flag leaf area. The highest contribution towards variability was made by days to 50% flowering, days to maturity, plant height, and number of spikelets per spike. Mishra *et al.* (2016) [7] and Gautam *et al.* (2017) [3] also found parallel results for most of the traits. The traits days to maturity (13.01%) followed by days to 50% flowering (12.36%), plant height (12.01), and number of spikelets per spike contributed most towards variability.

**Table 2:** Estimates of PCV, GCV, heritability, and genetic advance in 25 germplasm lines of Wheat

Genotypes	Range			Variance		Heritability (%)	Genetic Advance		Coefficient of variation		% contribution
	Min	Max	Mean	var (g)	var (p)		GA	GA% mean	GCV (%)	PCV (%)	
Days to 50% Flowering	78.88	85.96	82.73	3.66	4.49	81.55	3.56	4.30	2.31	2.56	12.36
Days to maturity	119.06	127.61	124.35	5.07	6.71	75.51	4.03	3.24	1.81	2.08	13.01
Plant Height (cm)	66.78	102.13	86.97	37.33	46.36	80.52	11.29	12.99	7.02	7.83	12.31
Number of tillers per plant	4.57	6.89	5.88	0.27	0.31	86.62	0.99	16.91	8.82	9.48	9.69
Spike length (cm)	8.13	12.59	9.45	1.15	1.26	90.71	2.10	22.22	11.33	11.89	6.66
Number of spikelets/spike	15.52	18.27	16.97	0.53	0.94	56.36	1.13	6.64	4.29	5.72	10.94
Flag leaf area (cm <sup>2</sup> )	24.85	37.87	30.87	9.58	10.38	92.33	6.13	19.85	10.03	10.44	6.76
1000 grains weight (g)	26.25	40.32	31.96	12.25	13.03	94.03	6.99	21.88	10.95	11.30	9.11
Biological yield/plant (g)	12.33	19.37	16.59	3.16	3.39	92.96	3.53	21.26	10.71	11.10	6.93
Harvest index (%)	37.74	58.84	48.86	28.45	30.31	93.85	10.64	21.79	10.92	11.27	7.76
Grain yield per plant (g)	5.79	10.07	8.07	0.99	1.05	94.90	2.00	24.76	12.34	12.67	4.48

### Conclusion

High heritability accompanied by high genetic advance indicated that the heritability is due to additive genetic effect and selection may be effective while high heritability coupled with low genetic advance indicates predominance of non-additive gene action while low heritability is exhibited due to influence of environmental interaction rather than genotypic selection for such characters may not be rewarding. The high magnitude of heritability coupled with high genetic advance in percent of mean was observed for grain yield per plant followed by spike length, 1000-grains weight, harvest index, and biological yield per plant; which indicated that good response to selection is likely to be observed for these characters. The existence of high character heritability with moderate genetic advance for flag leaf area, number of tillers per plant, and plant height indicate that these characters may also provide good response to selection owing to their moderate transmissibility and variability.

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