

## Genetic Variability, Heritability, and Genetic Advance Analysis for Yield and Yield Attributing Traits in Wheat (*Triticum aestivum* L.)

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**ABSTRACT:** Wheat (*Triticum aestivum* L.) is a vital cereal crop globally, providing sustenance to a significant portion of the world's population but in order to feed this growing population, it is necessary to improve genotypes to increase wheat production potential per unit area so, to overcome the barriers in high yield gain the investigation has been taken with 22 wheat genotypes for genetic variability, heritability, and genetic advance for yield and its component traits. Variability analysis revealed significant differences among the genotypes for traits such as plant height, number of grains per spike, test weight, single plant yield, days to maturity, days to heading, flag leaf length, number of tillers per plant, and spike length. High heritability was recorded for the test weight (99%) followed by plant height (97%), days to heading (96.3%), and single plant yield (85%) while low heritability was observed for the number of tillers per plant (39%) and numbers of grains per spike (65%). Additionally, heritability estimates indicated a high degree of heritability for most traits, suggesting the potential for genetic improvement. Notably, single plant yield and flag leaf length exhibited high genetic advance (GA), making them promising targets for wheat improvement. This study provides valuable insights for breeders and researchers working on enhancing wheat productivity to meet the growing demands of the Indian population.

**Keywords:** Wheat, genetic variability, heritability, genetic advance, yield.

### INTRODUCTION

As a staple diet for a significant proportion of the world's population, wheat is one of the most important cereal crops in the world. *Triticum aestivum* L., also known as wheat, is a type of crop that reproduces by self-pollination and is a member of the family Poaceae. It is classified as a segmental allohexaploid species, with  $2n = 6x = 42$  chromosomes. Wheat is native to Southwest Asia, where it was first domesticated (Filiz, 2012; Baenziger, 2016). It is referred to as the "King of Cereals" because of its large cultivated area, high production, and key role in global grain trade. The total area under wheat crop in India is about 31.82 million hectare with an annual production and productivity of 112.74 million metric tones and 35.43 quintals per hectare respectively (IIWBR, 2022). The biggest obstacle for Indian breeders is the country's growing population and in order to feed this growing population, it is necessary to improve genotypes to increase wheat production potential per unit area. By maximizing the genetic potential of the wheat genetic material, this might be achieved. Understanding the nature and extent of variation in a crop's accessible germplasm is typically necessary for genetic improvement. Thus, it is important to study various genetic parameters such as genetic variability, heritability and genetic advance. To

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facilitate breeding and the selection of desired genotypes, there must be genetic variability among the traits (Singh *et al.*, 2021). During breeding, the degree to which desired traits are transmissible to progenies can be evaluated using heritability (Falconer, 1996). A reliable estimate of the amount of genetic advance to be anticipated from a selection could be obtained by combining the genotypic coefficient of variation with heritability estimates. High heritability combined with high genetic advance would be a more effective tool in predicting the resultant effect in the selection of best genotypes for yield and its components (Bhanu *et al.*, 2018). Keeping in view, an effort has been made in the present study to evaluate a set of 22 wheat genotypes with an aim, to analyze the genetic variability, heritability, and genetic advance for yield and its component traits.

### MATERIAL AND METHODS

Experiment was conducted with total 22 wheat genotypes including release variety and advanced breeding lines were selected from the germplasm pool of wheat (Table 1). Wheat genotypes were grown in a randomized block design with three replications. The row-to-row distance was maintained at 22.5 cm and plant to plant distance at 10 cm. Recommended

package of practices and plant protection measures were followed for healthy crop growth during the season. Five randomly selected plants per line per replication were used for recording the observations viz., days to heading, days to maturity, plant height, spike length, flag leaf length, number of tillers per plant, number of grains per spike, test weight and single plant yield were recorded. The genetic parameters of variability, estimation of heritability and genetic advance were computed according to the method suggested by Johnson *et al.* (1955).

**Table 1: List of genotypes used in experiment.**

Sr. No.	Genotype	Sr. No.	Genotype
1.	DBW 88	12.	DBW 129
2.	DBW 173	13.	DBW 187
3.	HD 3171	14.	KRL 386
4.	HI 1612	15.	HUWL-1730
5.	K 1317	16.	HUWL-1727
6.	PBW 723	17.	HUWL-1726
7.	DBW 150	18.	HUWL-1725
8.	KBRL 82-2	19.	HUWL-1723
9.	AKAW 4899	20.	Extra Long panicle
10.	HUW-234	21.	Atilla
11.	HI 1609	22.	HD-3118

## RESULTS AND DISCUSSION

Results of analysis of variance revealed that the mean sum of squares of various characters viz. plant height, number of grains per spike, test weight, single plant

yield, days to maturity, days to heading, flag leaf length, number of tillers per plant, and spike length are highly significant thus indicating the presence of a sufficient amount of variability among the genotypes selected for the study (Table 2).

Table 3 and Fig. 1 showed that almost equal magnitude of GCV and PCV for the characters viz., plant height, 1000 grain weight, flag leaf length, spike length, days to heading and days to maturity indicating that environment plays a very minor role in the expression of above-mentioned traits. The number of tillers per plant, single plant yield and number of grains per spike were influenced by environmental effects as their respective environment coefficients of variation were recorded 10, 5.21 and 5.4 respectively. Hossain *et al.* (2021) reported less difference between GCV and PCV for these characters. Low estimates of GCV and PCV were observed for the days to heading, days to maturity, plant height, spike length, number of grains per spike, and test weight while, medium values were documented for single plant yield and flag leaf length. For the number of tillers per plant high and low values were recorded for PCV and GCV respectively, indicating a large amount of variation for this character among the genotypes was due to the environment only. Similar findings were also observed by for low value of GCV and PCV for days to heading, days to maturity, thousand-grain weights, and medium estimate of PCV and GCV for yield per plant Chaudhary *et al.* (2022); Sharma and Sood (2022) and Anzer *et al.* (2017).

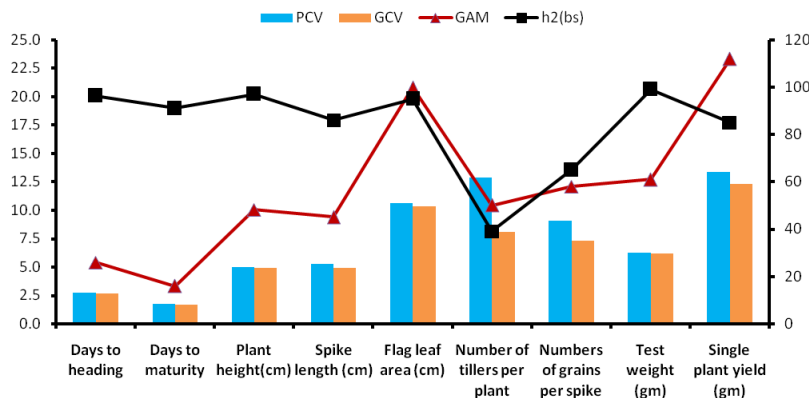
**Table 2: Analysis of variance (mean sum of squares) for yield and yield component characters in Wheat.**

Sources of variation	Days to heading (Days)	Days to maturity (Days)	Plant height (cm)	Spike Length (cm)	Flag leaf area (cm)	Number of tillers per plant	Numbers of Grains per Spike	Test weight (gm)	Single Plant Yield (gm)
Replication	0.345	0.583	1.355	0.180	0.266	1.776	17.109	0.218*	2.411
Genotype	12.538***	13.232***	50.08***	2.194***	10.473***	2.588**	45.453**	16.684***	14.178***
Residuals	0.156	0.422	0.441	0.108	0.178	0.878	7.011	0.065	0.801

(level of significance - \*\*\* = 0.001, \*\* = 0.01, \* = 0.05)

**Table 3: Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and yield components in Wheat.**

Character	Mean	Range		Coefficient of variation			Heritability (broad sense) h <sup>2</sup> (bs) %	Genetic advance as per cent of mean GAM
		Max.	Min.	GCV	PCV	ECV		
Days to heading	75.95	80.40	72.40	2.67	2.72	0.52	96	5.40
Days to maturity	123.23	129.2	118.6	1.67	1.75	0.52	91	3.29
Plant height (cm)	82.31	93.40	74.60	4.94	5.01	0.81	97	10.04
Spike Length (cm)	17.03	18.6	14.37	4.89	5.26	1.93	86	9.38
Flag leaf area (cm)	17.89	21.6	13.90	10.35	10.62	2.36	95	20.79
Number of tillers per plant	9.37	13.20	7.60	8.06	12.85	10.00	39	10.42
Numbers of Grains per Spike	49.06	60.40	39.80	7.30	9.07	5.40	65	12.08
Test Weight (gm)	37.97	41.68	33.46	6.20	6.24	0.67	99	12.70
Single Plant Yield (gm)	17.19	22.60	11.34	12.28	13.34	5.21	85	23.29



**Fig. 1.** Genetic variability parameters (GCV, PCV, heritability in broad sense  $\{h^2(bs)\}$ , and GA as % of the mean for nine morphological characters in wheat.

The heritability of a trait is dynamic in nature it changes with time, as genetic background and the environment can change and the interaction between these two factors can also change (Wray and Visscher 2008). Therefore, develop research to estimate the heritability of agronomic traits with different genotypes and in different growing environments is important. Here, heritability was categorized as low (0–30%); moderate (30–60%) and high (60% and above) (Robinson *et al.*, 1949). The heritability in a broad sense ranged from 39 to 99 per cent and maximum heritability was observed in test weight while minimum in the number of tillers per plant. A very high value of heritability was recorded in test weight followed by plant height, days to heading, flag leaf length and days to maturity similar value of the heritability was also observed for test weight by Thapa *et al.* (2019), for days to heading and maturity by Dabi *et al.* (2019), plant height by Sharma and Sood (2022); Chaudhary *et al.* (2022). The use of breeding will likely be successful in improving these traits or wheat genotype selections based on phenotype are effective. Low value of heritability was observed in number of tillers per plant which is similar to the findings of Dabi *et al.* (2019) and showing that major amount of variation is not genetic. These findings expressed that the selection alone can impact wheat improvement with respect to these characters. Present results were supported by the findings of Chaudhary *et al.* (2022); Arya *et al.* (2017). The range observed for genetic advance as percent of the mean (GAM) was from 3.29 to 23.29 and maximum GAM was recorded for the single plant yield followed by flag leaf length, test weight, number of grains per spike, number of tillers per plant, plant height, spike length, days to heading and days to maturity. Low value of GAM observed in days to heading (5.40), days to maturity (3.29) and spike length (9.3), a slightly different value than previously reported by Bayisa *et al.* (2020). A high estimate of GAM was observed in flag leaf length and single plant yield indicating that the additive genetic variance prevailed and findings matched with earlier findings of Chaudhary *et al.* (2022). Characters manifested high heritability with high genetic as percentage of mean were indicating predominance of additive gene action for these traits. The medium category of GAM was found in plant height, number of

tillers per plant, number of grains per spike and test weight, which is accordance with the results of Sharma and Sood (2022); Patidar *et al.* (2021); Santosh *et al.* (2019); Naik *et al.* (2015).

## CONCLUSIONS

The present study revealed a sufficient amount of variability for the studied traits among the genotypes. Low values of GCV and PCV were observed for yield attributing traits like number of grains per spike, test weight, plant height and spike length as high heritability were also observed for these traits, revealed that less genetic variation present in experimental genotypes with respect to above- mentioned characters. Single plant yield and flag leaf length exhibited a high value of GCV, PCV and high heritability coupled with high genetic advance as percent of the mean showed that presence of high variability indicates possibility of effective selection for the improvement of characters.

## FUTURE SCOPE

The promising genotypes identified in this study and can be exploited commercially as a parent for future hybridization programme for further enhancement of yield and yield attributing traits in context of crop improvement.

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**Conflict of Interest.** None.

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