



Research Article

GENETIC VARIABILITY, HERITABILITY, AND GENETIC ADVANCE FOR YIELD AND ITS COMPONENTS IN WHEAT (*Triticum aestivum* L.)

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Abstract: This study, to determine the genetic variability, heritability, genetic advance for yield, and its component traits in 86 wheat genotypes. The result showed significant differences in respect of yield and yield contributing traits. In general, the magnitude of PCV was higher than GCV for all the traits. The high estimation of PCV (>20%) was not detected. Moderate estimation (10-20%) of phenotypic coefficient of variance recorded only to the tiller per plant (12.27). The high estimate of heritability in a broad sense (>75%) was recorded for plant height (0.978), spike length (0.782), and peduncle length (0.773). Tiller per plant (12.654), Peduncle length (12.386), and Spike length (12.368) showed a moderate estimate of the genetic advance percent of the mean (10-20%) while tiller per plant (7.074) show 5% of the genetic advance. It indicates that these traits were governed by the additive genetic effect which is the fixable type and consequently, desirable selection will reward improvement for those traits.

Keywords: Wheat, Variability, PCV, GCV, Heritability & Genetic advance

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Introduction

Wheat (*Triticum aestivum* L.) is a cereal crop that is a worldwide staple food [1]. Wheat is a very popular and highly demandable cereal crop in the world. It provides 20 percent of food resources in the world. Wheat is one of the cereal crops, highly grown all over the world and it has 1st rank in world crop production. There are many types of wheat. These are Emmer wheat (*Triticum dicoccum*), Macaroni wheat (*Triticum durum*), Common bread wheat (*Triticum vulgare*), and Indian dwarf wheat (*Triticum spherococcum*) and last one is Bread Wheat (*Triticum aestivum*).

Grain yield is a complicated feature in wheat that is influenced by its constituent traits. It is necessary to investigate the nature of genetic variability for yield-related attributes and quality features in wheat to genetically manipulate grain production, quality, and other characteristics. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) assists in genotype selection, and heritability combined with genetic progress would be a more beneficial tool in forecasting the consequent effect for genotype selection.

Heritability estimates provide information about the traits that are transmitted from parents to their offspring and it has a crucial role in selection criteria to improve grain yield. It provides information on genetic variation and can be used to forecast how individuals will respond to selection in future generations. The type of gene action affects heritability [2]. Breeding for improved grain yields requires a better understanding of the genetic control of critical features in bread wheat.

The occurrence of genetic variability in breeding materials is critical for increasing the gene pool and, as a result, for plant breeding program success. Heritability is a measurement of how well characteristics are transferred from parents to their offspring, and it's extensively applied in breeding programs [3]. Considering heritability provides information on the degree of genetic control over a trait's expression as well as the phenotypic reliability of forecasting its breeding value. Another key statistic is the genetic advance, which is used to predict the expected response to selection [4].

The most successful condition for selection is high genetic advance combined with high heritability [5], which implies the existence of additive genes in trait inheritance.

In wheat, phenotypic and genotypic coefficients of variation, heritability, and genetic advance have all been used to assess the extent of diversity in breeding material, define acceptable selection processes, and anticipate breeding progress in improving critical traits.

The present study was carried out to evaluate the variability, heritability, and genetic advance for some grain yield traits in a set of wheat genotypes and breeding lines and to provide necessary genetic information for the improvement of grain quality in a wheat breeding program.

Material and Methods

The present investigation was carried out at the main experimental station of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (UP) in *Rabi*, 2019-21. The experimental materials of the study comprised 86 treatments of wheat. These materials included 60 F₁'s, 23 parental lines (20 recipients + 3 doner), and three check varieties. 20 lines were crossed with 3 testers following line x tester mating design during *rabi* season 2019-20. Geographically, the experimental site is located between latitudes 24°47' to 26°56' N, longitudes 82°12' and 83°98' E and at an altitude of 113 m above sea level, this area is located in the sub-tropical climate zone. The area is subtropical (Indo-Gangetic plain).

Observations were recorded on 5 randomly selected plants in each replication for plant height, tillers per plant, flag leaf area (cm²), spike length (cm), peduncle length (cm), number of grains per spike, test weight (g), biological yield/ plant (g), harvest index (%) and grain yield per plant (g) except days to 50% flowering and days to maturity on a plot basis.

Statistical analysis

The analysis of variance for the Randomized Block Design of the experiment was carried out Panse and Sukhatme (1967) [6]. The fixed-effect model is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of i^{th} entry in the j^{th} replication

μ = General mean

t_i = Effect of the i^{th} entry ($i = 1, 2, \dots, v.$)

b_j = Effect of the j^{th} replicate ($j = 1, 2, \dots, r.$)

e_{ij} = Environmental effect

The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), and environmental coefficient of variability (ECV) were computed following Burton and de Vane (1953) [7].

$$GCV = (\text{Genotypic standard deviation})/\text{Mean} \times 100 \text{ Or } (\sigma_g/\bar{x}) \times 100$$

$$PCV = (\text{Phenotypic standard deviation})/\text{Mean} \times 100 \text{ Or } (\sigma_p/\bar{x}) \times 100$$

Heritability in a broad sense (h^2_{bs}) was calculated according to the formula suggested by Hanson *et al.* (1963) [8].

$$H^2_{bs} = (\sigma^2_g)/(\sigma^2_p) \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The genetic advance was estimated by using the formula given by Johnson *et al.* (1955) [5].

$$\text{Genetic advance (Ga)} = h^2_{bs} \times K \times \sigma_{ph}$$

Genetic advance in per cent of mean for the character

$$GA (\%) = ((h^2_{bs} \times K \times \sigma_{ph})/\bar{x}) \times 100$$

Where,

K = Selection differential at 5 per cent selection intensity ($K = 2.06$)

h^2_b = Heritability coefficient (Broad sense)

σ_p = Phenotypic standard deviation.

\bar{x} = Mean value of the character

Result and Discussion

Analysis of variance

In [Table-1], The analysis of variance indicated highly significant differences in all of the characters studied between genotypes. The mean sum of squares due to treatments was highly significant for days of 50% flowering, day to maturity, plant height, tiller per plant, flag leaf area, spike length, peduncle length, number of seeds per spike, test weight, biological yield, and harvest index while grain yield per plant (1.285) exhibited non-significant. The mean sum of squares due to replications were found significant for spike length (1.265) and peduncle length (6.668) rest of all the characters exhibited non-significant.

Table-1 Analysis of variance for 12 characters in wheat

Characters	Source of Variation			
	Df	Replication	Treatments	Error
	2	82	164	
Days to 50% flowering	0.229	4.058**	1.522	
Days to maturity	3.040	5.860**	2.308	
Plant height (cm)	0.003	59.991**	0.429	
Tiller per plant	0.807	1.278**	0.297	
Flag leaf area (cm)	0.488	0.993**	0.338	
Spike length (cm)	1.265*	4.615**	0.379	
Peduncle length (cm)	6.668**	9.779**	0.906	
Numbers of Seed per spike	7.281	16.743**	8.090	
Test Weight (g)	4.635	4.467**	2.364	
Biological yield per plant	0.035	5.331**	0.834	
Harvest index (%)	15.609	25.641**	11.671	
Grain Yield Per Plant	0.517	1.285	0.267	

Estimates of genetic parameter

In [Table-2], the Range and mean performance for 12 characters of all the treatments have been presented.

Phenotypic and genotypic coefficient of variation

In general, the magnitude of the phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all the observation traits. The high estimation of PCV and GCV (>20%) were not detected. That cannot be used for these features and is not suggested possible improvement through direct selection. Moderate estimation (10-20%) of phenotypic and genotypic coefficient of variance recorded only to the tiller per plant (12.27), This suggested that through selection processes, there is a lot to improve in this attribute in the desired direction. The low estimates of PCV and GCV were observed for harvest index (%), peduncle length (cm), spike length (cm), number of seeds per plant, and grain yield per plant suggesting that genetic factors play a significant impact on the manifestation of these characteristics.

Heritability and Genetic advance as a % of the mean

Estimates of heritability combined with genetic advances were more useful than heritability alone in estimating the resultant gain under best-individual selection. In the present investigation, the high estimate of heritability in a broad sense (>75%) was recorded for plant height (97.8%), spike length (78.2%), and peduncle length (77.3%), a high value of heritability shows that unless the character is least influenced by environmental effects, selection for such a feature may not be useful, because heritability is the estimate of both fixable and non-fixable variances. Moderate heritability (<70%) was reported in biological yield per plant (63.9%), grain yield per plant (55.8%), and tiller per plant (50.1%). Low estimation of heritability was observed in flag leaf area (38.8%), day of 50% flowering (36.4%), and days of maturity (35.8%), that traits are highly influenced by environmental effect and genetic improvement through selection will be difficult. A similar result was found by [9,10].

Moderate estimates of Genetic Advance as a % over a mean (10-15%) were observed in tiller per plant (12.65%), followed by spike length (12.36%) and peduncle length (12.38%), and the lowest value was observed in plant height (9.55%) followed by grain yield per plant (7.05%) and harvest index (5.76%) the lowest value suggestion utilization heterosis breeding for improvement of this characters as it is governed by non-additive genes. A similar result was found by [11-14].

As a result, the high heritability, as well as higher estimates of genetic advance over the percentage of mean, will be rewarding because it is most likely driven by additive genes and selection will be effective. Even though high estimates of heritability and medium genetic advance over a percentage of mean were observed for spike length and peduncle length, and high heritability to low genetic advance was observed for plant height, grain yield per plant, and biological yield per plant, selection will be ineffective because the trait is highly influenced by the environment.

Conclusion

The moderate estimation of phenotypic and genotypic coefficients of variance was reported only to the tiller per plant in this experiment. This indicated that there is a lot to enhance in this attribute in the desired direction through selecting processes. Harvest index (%), peduncle length (cm), spike length (cm), number of seeds per plant, and grain yield per plant all had low PCV and GCV estimations, indicating that genetic variables play a significant role in the expression of these traits. Even though spike length and peduncle length had high estimated heritability and middling genetic progress over a percentage of mean, Plant height, grain yield per plant, and biological yield per plant all have a high heritability to low genetic advance, hence selection will be ineffectual because the trait is significantly influenced by the environment.

Application of research: Study was extremely beneficial to breeders in terms of increasing yield per se performance.

Research Category: Genetics and Plant Breeding

Abbreviations: PCV: phenotypic coefficient of variation

GCV: genotypic coefficient of variation, F1: first failure generation

Table-2 Estimate of range, coefficient of variation (PCV and GCV), heritability, genetic advance, and genetic advance in percent of the mean for 12 characters in wheat

Traits	Parents Range	Crosses Range	General Mean	GCV	PCV	H ² (Broad Sense)	Genetic advance 5%	Genetic Advance as% of Mean 5%
Days to 50% flowering	79.00-83.00	78.33-83.00	80.841	1.146	1.898	0.364	1.152	1.425
Days to maturity	119.33-125.67	119.67-126.00	123.43	0.914	1.528	0.358	1.390	1.126
Plant height (cm)	91.47-99.44	83.88-100.18	94.469	4.691	4.744	0.978	9.028	9.556
Tiller per plant	5.43-7.67	4.93-7.57	6.409	8.682	12.27	0.501	0.811	12.654
Flag leaf area (cm)	19.65-21.68	19.16-21.66	20.441	2.275	3.651	0.388	0.597	2.921
Spike length (cm)	15.6-17.07	15.76-22.24	17.162	6.791	7.681	0.782	2.123	12.368
Peduncle length (cm)	24.63-28.50	20.32-28.38	25.362	6.839	7.779	0.773	3.141	12.386
Numbers of Seed per spike	45.67-55.33	45.33-57.00	50.86	3.311	6.486	0.261	1.771	3.482
Test Weight(g)	36.14-40.98	37.85-44.14	39.96	2.084	4.327	0.232	0.826	2.068
Biological yield per plant	26.73-30.55	28.49-32.68	30.384	4.02	5.027	0.639	2.012	6.621
Harvest index(%)	37.61-45.98	28.23-46.30	40.948	5.219	9.731	0.288	2.361	5.767
Grain Yield Per Plant	11.29-13.38	11.02-13.61	12.464	4.598	6.157	0.558	0.882	7.074

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Cultivar / Variety / Breed name: Wheat (*Triticum aestivum* L.)

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