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Genetic variability for yield contributing traits in bread wheat (*Triticum aestivum* L.) under timely sown irrigated condition

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Abstract

Bread wheat (*Triticum aestivum* L.) is among the most vital cereal crops, serving as a primary source of carbohydrates, proteins, and essential nutrients in human nutrition. The current research assessed the genetic variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance in bread wheat during the Rabi season of 2024 at the Agricultural Research Station, College of Agriculture, Dhule, Maharashtra. The aim was to better understand the genetic diversity among different bread wheat genotypes. The experiment was arranged in a Randomized Block Design with three replications, including thirty-six genotypes, and observations were recorded for nine quantitative traits. The analysis revealed significant variation among the genotypes for all characters studied. Notably, high estimates of GCV and PCV were showed for grain yield per plot, followed by the number of tillers per meter, spikelets per spike, and grains per spike. The PCV values exceeded than GCV for all traits, indicating environmental factors' influence on trait expression. Moreover, traits such as the number of tillers per meter and grain yield per plot showed high heritability coupled with substantial genetic advance as a percentage of the mean, suggesting the dominance of additive gene action and their suitability for selection. The combination of high heritability and genetic advance offers valuable insights into the effectiveness of selection in crop improvement efforts. These results can aid in identifying promising donor genotypes and developing high-yielding bread wheat varieties through future breeding programs.

Keywords: *Triticum aestivum*, genetic variability, heritability (h^2), genetic advance(GA), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV)

Introduction

Wheat (*Triticum aestivum* L.; $2n=42$) belongs to the genus *Triticum* in the Poaceae family and is one of the most crucial cereal crops cultivated worldwide. It serves as a staple food crop, playing a vital role in global food security by providing a significant portion of calories, carbohydrates, and proteins in human diets. India ranks second globally in wheat production, making a substantial contribution to the world's wheat supply. In the year 2024 – 25, wheat was cultivated across approximately 327.61 lakh hectares in India, yielding around 117.51 million tonnes with an average productivity of 3,587 kg per hectare (ICAR-IIWBR, 2025). Major wheat-producing states include Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, Rajasthan, and Bihar. In Maharashtra, wheat is an important Rabi crop, primarily grown under irrigated conditions. During 2024 – 25, wheat was cultivated on 11.89 lakh hectares in Maharashtra, producing 24.54 lakh tonnes with an average yield of 2,064 kg per hectare (Department of Agriculture, Government of Maharashtra, 2025). Enhancing wheat productivity through genetic improvement, developing superior genotypes, and adopting efficient crop management practices are essential for meeting future food requirements and strengthening food security at both national and state levels. The assessment of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), and genetic advance (GA) provides valuable insights into trait inheritance and the efficiency of selection. Therefore, evaluating genetic variability among bread wheat genotypes for grain yield and yield components is crucial for identifying superior genotypes and selecting desirable traits for developing improved varieties.

Materials and methods

The study utilized 36 bread wheat (*Triticum aestivum* L.) genotypes collected from the Agricultural Research Station, Nipahad. These genotypes were estimated during the Rabi season of 2024 at the Agricultural Research Station, College of Agriculture, Dhule, Maharashtra, under timely sown conditions. The experiment was arranged in a Randomized Block Design (RBD) with three replications. Each genotype was cultivated in a single row measuring 6.0 meters in length within the plot. Throughout the crop cycle, recommended agronomic practices were followed to ensure optimal growth and development. Data were collected for nine quantitative traits, including days to 50% flowering, days to maturity, plant height (cm), spike length (cm), number of spikelets per spike, number of grains per spike,

number of tillers per meter, thousand grain weight (g), and grain yield per plot (g). Observations for days to 50% flowering and days to maturity were recorded based on the entire plot, while for the other traits, measurements were taken from randomly selected competitive plants of each genotype. The collected data were analyzed statistically following standard procedures outlined by Fisher (1918)^[4] and Panse and Sukhatme (1995)^[10]. The genotypic and phenotypic coefficients of variation, which reflect the extent of genetic and phenotypic variability, respectively, were estimated according to Burton's (1952)^[1] formula. Heritability was calculated based on the method proposed by Burton and Devane (1953)^[2]. The genetic advance as a percentage of the mean was computed following the procedure described by Johnson *et al.* (1955)^[6].

Table 1: Analysis of variance for nine characters of bread wheat.

Sr. No	Characters	Mean sum of square		
		Replication	Genotype	Error
1	Days to 50 per cent flowering	12.861	22.295**	4.356
2	Days to maturity	19.509	39.355**	11.728
3	Plant height at maturity (cm)	61.583	134.552**	41.002
4	Spike Length(cm)	1.005	1.472**	0.481
5	No. of spikelets / spike	6.224	8.162**	2.5044
6	No. of grains / Spike	56.023	73.463**	22.539
7	No. of Tillers / m	317.444	977.245**	109.111
8	Test Weight (g)	2.385	15.383**	7.403
9	Grain Yield / plot (g)	48450.73	128652.00**	23242.02

*,** Exhibited significance at 5 % and 1% level, respectively.

Table- 2: Genetic variability parameters for yield and its contributing traits in bread wheat.

Sr. No.	Characters	Mean	Range		GCV (%)	PCV (%)	h ² (%)	GA	GA (%)
			Min.	Max.					
1	Days to 50 per cent flowering	61.16	56	65.7	3.99	5.25	57	3.83	6.26
2	Days to maturity	113.12	103	118	2.68	4.04	43	4.14	3.66
3	Plant height (cm)	90.88	75	106.3	6.14	9.34	43	7.56	8.31
4	Spike length (cm)	9.21	7.7	10.8	6.23	9.78	40	0.75	8.19
5	No. of spikelets/ spike	18.66	16.1	22.4	7.35	11.22	42	1.85	9.93
6	No. of grains / spike	56.00	48.3	67.2	7.35	11.22	42	5.56	9.93
7	No. of tillers / m	105.25	77.3	148	16.16	18.96	72	29.86	28.37
8	Test weight (g)	43.70	40.2	48.3	3.73	7.25	26	1.72	3.95
9	Grain yield /plot (g)	1042.15	685	1523	17.98	23.18	60	299.75	28.74

Result and Discussion

The variance analysis for the nine quantitative traits examined in this study is summarized in Table 1. The mean squares attributed to genotypes revealed highly significant differences across all traits, indicating substantial genetic diversity among the wheat genotypes. The estimates for range, overall mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance, heritability and genetic advance as a percentage of the mean are shown in Table 2. Generally, the PCV values were higher than the GCV values for all traits, suggesting environmental factors influence trait expression. The GCV ranged from 2.68% for days to maturity to 17.98% for grain yield per plot, with the highest GCV observed for grain yield per plot (17.98%), followed by the number of tillers per meter (16.16%), spikelets per spike (7.35%), grains per spike (7.35%), spike length (6.23%), and plant height (6.14%). Traits like days to maturity (2.68%), test weight (3.73%), and days to 50% flowering (3.99%) showed low GCV values. The highest PCV was recorded for grain yield per plot (23.18%), followed by the number of tillers per

meter (18.96%), spikelets per spike (11.22%), and grains per spike (11.22%). Traits such as days to maturity (4.04%), days to 50% flowering (5.25%), and test weight (7.25%) exhibited low PCV. High variability in both GCV and PCV was noted for grain yield per plot and tillers per meter, indicating considerable genetic diversity and potential for selection. Conversely, traits like days to maturity, days to 50% flowering, and test weight showed limited variability. Phenotypic expression reflects both genetic makeup and environmental influences. Heritability indicates the proportion of total phenotypic variation due to genetic differences among genotypes, providing an estimate of trait transmissibility. However, heritability alone does not fully predict the response to selection; it should be considered alongside genetic advance. In this study, heritability is ranged from 26% to 72%, with the highest for tiller number per meter (72%), followed by grain yield per plot (60%) and days to 50% flowering (57%). The lowest heritability was observed for test weight (26%). Similar results have been reported by researchers like Rajput and Singh (2023)^[12], Patil *et al.* (2024)^[11] and Kirana Kumara *et al.* (2024)^[7].

Genetic advance signifies the expected improvement in a trait through selection. In this study, genetic advance ranged from 0.75 to 299.75, with the highest for grain yield per plot (299.75), followed by tiller number per meter (29.86), and plant height (7.56). The lowest was for spike length (0.75) and test weight (1.72). The substantial genetic advance for grain yield and tiller number indicates significant genetic variability and potential for improvement via selection.

The highest genetic gain as a percentage of the mean was observed for grain yield per plot (28.74%), followed by tiller number per meter (28.37%). Traits such as days to maturity (3.66%) and test weight (3.95%) showed minimal genetic gain. High genetic gain percentages suggest effective selection for these traits. Traits like grain yield per plot and tillers per meter, which exhibited high heritability coupled with high genetic advance, imply that additive gene action predominates and can be targeted effectively through direct selection. Similar findings have been documented by Patil *et al.* (2024)^[11] and Kirana Kumara *et al.* (2024)^[7] in bread wheat.

Conclusion

The current study demonstrated considerable genetic diversity among bread wheat genotypes concerning yield and traits that contribute to yield. The values of GCV and PCV revealed that grain yield per plot and the number of tillers per meter showed greater variability, providing promising opportunities for effective selection. The small differences observed between PCV and GCV for most characters indicated that environmental factors had a limited impact on their expression. Traits such as grain yield per plot and tillers per meter exhibited high heritability along with substantial genetic advance as a percentage of the mean, suggesting that additive gene action plays a major role and that direct selection would be effective for genetic enhancement. Consequently, these traits should be considered key criteria for selecting superior bread wheat genotypes aimed at increasing yield potential in future breeding efforts.

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