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Analysis of genetic variability for morphological and physiological traits in bread wheat (*Triticum aestivum* L.)

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Abstract
The present investigation is carried out with 40 bread wheat (*Triticum aestivum* L.) genotypes in the experimental area of research farms, genetic and plant breeding section of Lovely Professional University, Jalandhar, Punjab during the rabi season of 2022-23 to assess the genetic parameters *viz*, genotypic, and phenotypic variance, genotypic and phenotypic coefficient of variance, heritability, and genetic advance as percent of mean. Fifteen different traits were recorded and recorded and assessed using Randomized Block Design. The analysis of variance unveiled notable variations among the assessed genotypes for each parameter considered. Environmental influence on the expression of the traits was minimal, as indicated by slight disparities between the genotypic and phenotypic coefficients of variation. Traits such as spike length, spike density, spike weight, and number of spikelets per spike displayed both a high degree of heritability and a substantial genetic advance as a percentage of the mean. This indicates that implementing straightforward selection methods would be successful in driving genetic enhancements for these traits.

Keywords: Variance, coefficient of variance, heritability, genetic advance as percent of mean

Introduction

Wheat, scientifically known as *Triticum* spp., holds immense significance as a major cereal crop globally, providing a staple food source for a substantial portion of the world's population. Belonging to the Poaceae family, wheat is cultivated across diverse agroecological zones worldwide (Mourad *et al*., 2019) [15]. Its nutritional value, versatility in food processing, and adaptability to various environmental conditions contribute to its prominence. *Triticum aestivum* L., commonly known as common wheat, falls within the Poaceae family, Triticeae tribe, Triticinea sub-tribe, and Triticum genus (Scheeren, 2011) [19]. Common wheat (2n = 42) is classified as an allohexaploid species (AABBDD) with three complete diploid genomes (Sears, 1952) [20]. Each genome originates from a different species: *Triticum urartu* represents the AA genome, *Aegilops speltoides* represents the BB genome, and *Aegilops tauschii* represents the DD genome (Brenchley *et al*., 2012) [3]. Due to its extensive cultivation, global production, importance as a staple food, and significant role in international food trade, wheat has earned the title of "king of cereals" (Sears, 1952) [20].

Historical evidence suggests that the earliest cultivation of wheat took place in Mesopotamia, situated along the Tigris and Euphrates rivers in the present-day region of Iraq (Tomasini & Ambrosi, 1998) [22]. Wheat is considered the first crop to be domesticated by humans, forming the foundation of diets in Asian, European, and African civilizations.

Having sufficient genetic variability is crucial in a crop improvement program. It is important to analyse the variability among traits and how a specific trait that contribute to crop yield. This analysis plays a significant role in designing a successful breeding program (Mary and Gopalan, 2006) [13]. The selection of parents is of utmost importance in a breeding program. To ensure effective selection, it is necessary to gather information about the nature and extent of variation within the population, the association of traits with yield and with each other, and the influence of the environment on the expression of these traits (Yagdi, 2009) [24]. Therefore, breeders need to assess variability using parameters such as phenotypic coefficient of variation, genotypic coefficient of variation. heritability, and genetic advance. These parameters provide valuable information about the availability of genetic variability for different traits in the germplasm.

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Consequently, studying the genetic variability of grain yield and its component traits among different varieties forms a solid foundation for selecting desirable genotypes that enhance yield and other agronomic characteristics.

Materials and Methods

In the plant Breeding section fields of Agriculture research farm of Lovely Professional University, located in phagwara, Punjab, India, we conducted an experiment during the Rabi season of 2022-23. The experiment involved the assessment of 40 different genotypes of bread wheat. Under irrigated conditions, the experiment followed a Randomized Block Design with three replications. Each genotype was cultivated in a plot consisting of four rows, each measuring 2.5 meters in length. The spacing between the rows was maintained at 22.5 centimetres, while the distance between individual plants within each row was kept at 10 centimetres. Irrigation was applied at specific stages, namely, crown root-initiation, late jointing, and milking. Throughout the experiment, standard agronomic practices were employed to ensure optimal crop growth and development.

Observations were documented for fifteen traits in each replication, including days to 50% heading, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, spike length, spike weight, spike density, number of spikelets per plant, number of grains per spike, biological yield per plant, grain yield per plant, harvest index, thousand-grain weight (Test weight), chlorophyll content. The collected data for each trait was subjected to statistical analysis by calculating the mean values across three replications. Separate analysis of variance (ANOVA) was conducted for all the traits, following the Randomized Block Design method. The analysis followed the methodology outlined by Panse and Sukhatme (1954) [16].

Phenotypic and genotypic variances

The determination of phenotypic ($\sigma 2p$) and genotypic variances ($\sigma 2g$) was carried out using the approach proposed by Panse and Sukhatme (1954) [68].

$$\sigma^2 g = \frac{MSS(treatments) - \sigma^2 e}{r}$$

$$\sigma^2 p = \sigma^2 g + \sigma^2 e \ [\text{ when G x E = 0}]$$

where,
$\sigma 2e$ = Environmental variance i.e., error variance = Error Mean sum of square (MSS) r = Number of replications.

Coefficient of variability

The assessment of variability present in grain yield and the traits contributing to yield was conducted following the method recommended by Burton and Devane.

Genotypic coefficient of variability (GCV)

$$(GCV) = \frac{\text{genotypic strandrad deviation}}{\text{general mean}} \times 100$$

$$= \frac{\sigma_g}{x} \times 100$$

Phenotypic coefficient of variability (PCV)

$$(PCV) = \frac{\text{phenotypic strandrad deviation}}{\text{general mean}} \times 100$$

$$= \frac{\sigma_p}{x} \times 100$$

The PCV and GCV value are ranked as low, moderate, and high (Shivasubramanian and Menon, 1973) [21] and are mentioned below.

Coefficient variation values	Level
0-10%	Low
10-20%	Moderate
20% and above	High

Heritability (Board Sense)

The broad-sense heritability, expressed as the ratio of genotypic variance to phenotypic variance, was calculated. The heritability was expressed as a percentage and estimated using the formula proposed by Johnson et al., (1955) [11]

$$h^2 (\text{broad sense}) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,
$\sigma 2g$ = Genotypic variance
$\sigma 2p$ = Phenotypic variance
$h2$ = Heritability (broad sense)
Hanson et al., (1956) [8] suggested the level and values pertaining to heritability (board sense)

Heritability values	Level
Below 40%	Low
40- 60%	Moderate
61 – 80%	High
Above 80%	Very high

Genetic advance percent of mean

The formula provided below was employed to calculate the genetic advances as a percentage of the mean value.

$$GA \ (\text{as percent of the mean}) = \frac{GA}{\bar{x}} \times 100$$

Where,
GA = Genetic Advance
$\bar{x}$ = mean of the trait
Johnson et al., (1955) [11] suggested the determination of expected genetic advance.

Genetic advance percent of mean values	Level
0-10%	Low
10-20%	Moderate
20% and above	High

Results and Discussion

Significant differences were found among the entries for all of the traits when analysing the variance. Previous studies by researchers have also reported considerable variability in various characteristics of wheat. The analysis of variance and the estimation of mean sum of squares indicated the presence

of significant variation across the entire set of traits among the genotypes studied. This suggests that there is sufficient variability in the evaluated materials, which can be effectively utilized in future breeding programs.

The analysis of variance revealed significant genetic variability among the studied materials for all the characters, as indicated by the significant mean sum of squares attributed to genotypes. Additionally, there was no significant variation for replication, suggesting that the influence of environmental error was minimal. The results of the analysis of variance for all the studied characters are presented in Table-1. Previous studies have also reported significant variations among the genotypes for various morphological and quality traits by Gauravrajsinh (2021) [23], Hassani *et al*., (2022) [9], Mangroliya and Sapovadiya, (2020) [12], Prasad *et al*., (2021) [18].

Table 1: Analysis of Variance

Traits		Mean sum of square [MSS]	
Replication (d.f = 2)		Treatment (d.f = 39)	Error (d.f = 78)
DTH	44.30	114.55**	23.39
DTM	64.75	130.47**	27.48
PH	46.70	158.53**	25.19
NTPP	0.73	1.26**	0.54
NPTPP	0.97	1.01**	0.35
SL	2.53	6.54**	0.34
SW	0.08	0.48**	0.11
SD	0.02	0.19**	0.009
NSPS	2.80	21.90**	0.90
NGPS	52.83	208.18**	33.44
BYP	34.23	29.10**	11.77
GYP	6.58	6.61**	2.13
HI	12.77	29.52**	6.57
TGW	13.23	15.12**	7.58
CC	15.73	24.15**	5.39

Table 2 displays the evaluated genotypic and phenotypic variances for all the traits examined. The highest estimates of variability (o2g and o2p) were observed for, number of grains per spike [NGPS] (58.24 and 69.39) followed by plant height [PH] (44.44 and 52.84), days to maturity [DTM] (34.33 and 43.49), days to 50% heading [DTH] (30.38 and 38.18)

respectively, in contrast, the remaining traits exhibited low estimates of variability (o2g and o2p) for harvest index (7.65 and 9.84)[HI] followed by number of spikelets per spike [NSPS] (7.00 and 7.30), chlorophyll content [CC] (6.25 and 8.05), biological yield per plant [BYP] (5.77 and 9.70), thousand grain weight [TGW] (2.51 and 5.04), spike length [SL] (2.06 and 2.18), grain yield per plant [GYP] (1.49 and 2.20), number tillers per plant [NTPP] (0.24 and 0.42), number of productive tillers per plant [NPTPP] (0.21 and 0.33), spike weight [SW] (0.12 and 0.16), spike density [SD] (0.061 and 0.064) respectively. In the analysis of all the studied traits, it was observed that the genotypic variances exhibited lower values when compared to the phenotypic variances. This difference suggests that non-genetic factors, such as the environment, likely played a significant role in influencing the expression of these traits. Similar findings were observed by Bayisa *et al*., (2020) [2], Gerema *et al*., (2020) [7].

Table 2 displays the estimated values for the coefficients of variation, both genotypic and phenotypic. The characters examined showed a wide range of PCV, ranging from 5.02 to 15.77. The number of grains per spike exhibited the highest PCV (15.77) followed by spike density (14.28), spike length (14.10), number of spikelets per spike (13.97), spike weight (12.76), grain yield per plant (11.83), plant height (9.23), biological yield per plant (9.20) etc. However, days to maturity revealed lowest phenotypic coefficient of variation (5.02). GCV varied from 4.34 to 14.45. The maximum GCV was recorded for number of grains per spike (14.45) followed by spike density (13.93), spike length (13.72), number of spikelets per spike (13.68), spike weight (11.17), grain yield per plant (9.74), plant height (8.46), biological yield per plant (7.10) etc. In contrast thousand grain yield revealed lowest genotypic coefficient of variation (4.34) followed by days to maturity (4.46). similar findings are observed by Mangroliya and Sapovadiya, (2020) [12], Prabha *et al*., (2022) [17], Barman *et al*., (2020) [1]. The results clearly suggested that selecting genotypes based on these characters would be feasible. Interestingly, there were minimal differences between the values of GCV and PCV, indicating a limited impact of the environment.

Table 2: Genetic parameters under study for all fifteen traits in bread wheat

Characters	Range	σ2g	σ2p	GCV	PCV	2 sense) %	GA as % of mean
DTH	85.3 – 110	30.38	38.18	5.626	6.30	79.57	10.33
DTM	117.6 – 144	34.33	43.49	4.46	5.02	78.93	8.17
PH	67.81 – 103.92	44.44	52.84	8.46	9.23	84.10	15.99
NTPP	6.93 – 9.86	0.24	0.42	6.07	8.02	57.44	9.48
NPTPP	6.2 – 8.66	0.21	0.33	6.33	7.88	64.68	10.49
SL	6.83- 13.4	2.06	2.18	13.72	14.10	94.72	27.51
SW	2.17 – 3.74	0.12	0.16	11.17	12.76	76.68	20.13
SD	1.33 – 2.61	0.061	0.064	13.93	14.28	95.86	28.02
NSPS	14.6-32.86	7.00	7.30	13.68	13.97	83.93	27.60
NGPS	32.93– 68.4	58.24	69.39	14.45	15.77	59.54	27.27
BYP	25.92-39.86	5.77	9.70	7.10	9.20	77.72	11.28
GYP	10.15-16.62	1.49	2.20	9.74	11.83	49.88	16.52
HI	32.68-43.21	7.65	9.84	7.38	8.37	77.65	13.41
TGW	32.66-42.33	2.51	5.04	4.34	6.15	95.31	6.32
CC	32.16-44.14	6.25	8.05	6.60	7.49	67.80	11.98

Broad – sense heritability and genetic advance as percentage of the mean were calculated foe all the traits under study. These are demonstrated in Table 2. Their performance was

adjudged based on Hanson *et al*., (1956) [8] and Johnson *et al*., (1955) [11] for heritability and genetic advance as percent of mean respectively. A perusal of broad sense heritability

showed that it was very high (> 80%) for traits namely spike density (95.86) followed by thousand grain yield (95.31), spike length (94.72), plant height (84.10), number of spikelets per spike (83.93) and high heritability (61-80%) were recorded for traits such as days to heading (79.57) followed by days to maturity (78.93), biological yield per plant (77.72), harvest index (77.65), spike weight (76.68), chlorophyll content (67.80) and number of productive tillers per plant (64.68). High (>20%) genetic advance as percent of the mean observed for spike density (28.02) followed by number of spikelets per spike (27.60), spike length (27.51), number of grains per spike (27.27), spike weight (20.13) and moderate genetic advance percent of mean is recorded by traits grain yield per plant (16.52) followed by plant height (15.99) harvest index (13.41) chlorophyll content (11.98), biological yield per plant (11.28), number of productive tillers per plant (10.49) and days to heading (10.33). In contrast to this number tillers per plant (9.48), days to maturity (8.17) and thousand grain weight (6.32) exhibited low genetic advance as percent of the mean. Similar findings were reported by Mangroliya and Sapovadiya, (2020) [12], Jaha et al., (2022) [10], Barman et al., (2020) [1]. The presence of both high genetic advance as percent of mean and high heritability suggests that the primary source of variation is attributed to additive gene effects. This indicates that if these specific traits are taken into account in a selection plan, a widely adaptable genotype can be developed to exploit the fixable genetic variance. The current study uncovered traits that exhibited high heritability in addition to high genetic advance as a percent of the mean, namely, spike length, spike density, spike weight and number of spikelets per spike. Similar findings were reported by Fouad, (2020) [6], Prabha et al., (2022) [17], Mehandi et al., (2022) [14]. Moderate heritability and high genetic advance as percent of mean was reported by number of grains per spike. Similar findings were reported by Barman et al., (2020) [1]. High heritability and low genetic advance as percent of mean was reported by days to maturity and thousand-grain weight respectively. Similar findings were reported by Prabha et al., (2022) [17], Prasad et al., (2021) [18], Mehandi et al., (2022) [14], Jaha et al., (2022) [1]. Moderate heritability couple with low genetic advance as percent of mean was reported by trait number of tillers per plant.

Conclusion
The analysis of variance revealed significant differences among the assessed genotypes for each parameter considered. Interestingly, it is noteworthy that environmental influence was minimal in the expression of all traits, as indicated by the slight disparities between genotypic and phenotypic coefficients of variation. High values of GCV and PCV were reported by traits such as number of grains per spike exhibited the highest followed by spike density, spike length, number of spikelets per spike, spike weight, grain yield per plant, plant height, biological yield per plant. The traits including spike length, spike density, spike weight and number of spikelets per spike exhibited both high heritability and high genetic advance as a percentage of the mean. This suggests that employing simple selection schemes would be effective in achieving genetic improvement for these specific traits. The traits such as days to maturity and thousand grain weight showed a high heritability and low genetic advance as percent of mean. Moderate heritability and low genetic advance as percent of mean is reported by number of tillers per plant thus

indicating involvement of both additive and non-additive gene actions in manifestation of this trait and to exploit heritability, we need to practice selections in later segregation generations of a hybridization programme.

Conflict of Interest
The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References
1. Barman M, Choudhary VK, Singh SK, Parveen R, Gowda AK. Correlation and path coefficient analysis in bread wheat (*Triticum aestivum* L.) genotypes for morpho-physiological traits along with grain Fe and Zn content. Current Journal of Applied Science and Technology. 2020;39(36):130-140.
2. Bayisa T, Tefera H, Letta T. Genetic variability, heritability and genetic advance among bread wheat genotypes at Southeastern Ethiopia. Agriculture, Forestry and Fisheries. 2020;9(4):128.
3. Brenchley R, Spannagl M, Pfeife RM, Barker GLA, D'Amore R, Allen AM, et al. Analysis of the bread wheat genome using whole-genome shotgun sequencing. Nature. 2012;491:705-710. https://doi.org/10.1038/nature11650
4. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agronomy journal. 1953;45(10):478-481.
5. Dewey DI, Lu KH. A Correlation and Path Coefficient Analysis of Components of Crested Wheatgrass Seed Production. Agronomy Journal. 1959;51:515-518.
6. Fouad H. Principal Component and Cluster Analyses to Estimate Genetic Diversity in Bread Wheat (*Triticum aestivum* L.) Genotypes. Journal of Plant Production. 2020;11(4):325-331.
7. Gerema G, Lule D, Lemessa F, Mekonnen T. Morphological characterization and genetic analysis in bread wheat germplasm: A combined study of heritability, genetic variance, genetic divergence and association of characters. Agricultural Science & Technology (1313-8820). 2020, 12(4).
8. Hanson WD, Robinson HF, Comstock RE. Biometrical studies of yield segregating population Korean lespandeza. Agron. J. 1956;48:268-272.
9. Hassani İ, Nimbal S, Singh V, Noori A. Genetic Variability Analysis and Correlation Studies of Bread Wheat (*Triticum aestivum* L.) Genotypes. Ekin Journal of Crop Breeding and Genetics. 2022;8(2):139-145.
10. Jaha SK, Dubey N, Avinashe HA. Genetic divergence and character association studies in bread wheat (*Triticum aestivum* L.) genotypes; c2022.
11. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implications in selection 1. Agronomy Journal. 1955;47(10):477-483.
12. Mangroliya UC, Sapovadiya MH. Estimation of genetic variability and diversity in bread wheat (*Triticum aestivum* L.) for yield and yield contributing traits. Journal of Pharmacognosy and Phytochemistry. 2020;9(5):784-789.
13. Mary SS, Gopalan A. Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. J. Applied

Sci. Res. 2006;2(10):805-808

14. Mehandi S, Rahman A, Prakash S, Yadav A, Mondal B, Praween N, *et al*. Harnessing the genetic variability and trait association of yield and yield-related traits in bread wheat (*Triticum aestivum* L.); c2022.

15. Mourad AM, Alomari DZ, Alqudah AM. Recent advances in wheat (*Triticum* spp.) breeding. In: Al-Khayri M, Jain SM, Johnson DV, editors. Advances in Plant Breeding Strategies: Cereals. New York (NY): Springer International Publishing. 2019;5:559-593.

16. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Statistical methods for agricultural workers; c1954.

17. Prabha AA, Avinashe H, Dubey N, Reddy JP, Reddy BT. Genetic studies on F3 population of bread wheat [*Triticum aestivum* L.] for yield and its components traits. Electronic Journal of Plant Breeding. 2022;13(2):369-376.

18. Prasad J, Dasora A, Chauhan D, Rizzardi DA, Bangarwa SK, Nesara K. Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes. Genetics and Molecular Research, 2021, 20(2).

19. Scheeren PL, Caierão E, Só e Silva M, Bonow S. Melhoramento de trigo no Brasil. In J. L. F. Pires, L. Vargas, & G. R. da Cunha (Eds.), Trigo no Brasil: Bases para a produção competitiva e sustentável. Passo Fundo: Embrapa Trigo; c2011. p. 427-451.

20. Sears ER. Homoeologous chromosomes in *Triticum aestivum*. Genetics. 1952;37:624.

21. Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agricultural Journal. 1973;60:1139.

22. Tomasini RGA, Ambrosi I. Aspectos econômicos da cultura de trigo. Caderno de Ciência & Tecnologia. 1998;15(2):59-84.

23. Vaghela Gauravrajsinh, Patel J, Rahevar Parthsinh, Muthuvel Gokulakrishnan. Assessment of genetic variability and character association for Morpho-Chemical traits in Bread Wheat (*Triticum aestivum* L.). Emergent Life Sciences Research. 2021;07:14-20. 10.31783/elsr.2021.711420.

24. Yagdi K, Sozen E. Heritability, variance components and correlations of yield and quality traits in durum wheat (*Triticum durum* Desf.). Pak. J Bot. 2009;41(2):753-759.