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Assessment of Genetic Variability for Morpho-physiological and Yield Traits in Bread Wheat (*Triticum aestivum* L.)

Babita Bhatt [a*], Swati [a], Jai Prakash Jaiswal [a], Rubina Khan [b], Sivendra Joshi [a] and Divya Chaudhary [a]

[a] Department of Genetics and Plant Breeding, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar-263145, Uttarakhand, India.
[b] Department of Genetics and Plant Breeding, Sri Karan Narendra College of Agriculture, Sri Karan Narendra Agriculture University, Jobner-303328, Jaipur, Rajasthan, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

In order to estimate genetic variability parameters for seventeen traits of wheat, 28 F1s were obtained by crossing 8 parents in 8×8 diallel fashion, excluding reciprocals and evaluation trial was laid down in randomised complete block design at Pantnagar, Uttarakhand. Analysis of variance revealed that highly significant differences between genotypes exist for all seventeen characters. Eleven out of seventeen characters were observed to exhibit elevated values for both the PCV and GCV. The observed phenotypic coefficient of variation (PCV) values was determined to be greater than the genotypic coefficient of variation (GCV) values, indicating that the expression of traits is comparatively less influenced by environmental factors. A significant degree of heritability, along with a notable genetic advance, was observed for various traits, including flag leaf area, followed by grain yield, biological yield, canopy temperature depression (CTD), harvest index, tillers per plant, peduncle length, grains per spike, awn length, plant height, grain filling duration, spikelet per spike,

*Corresponding author: E-mail: babita44379@gmail.com;

spike length, and normalised difference vegetation index (NDVI) content. This study has thus identified significant genetic variability in wheat traits, highlighted traits with high heritability and genetic advance, and suggested that these traits could be targeted for improvement in wheat breeding programs.

Keywords: Genetic variability; diallel; PCV; GCV; heritability; genetic advance; wheat.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important staple crops in the world, providing a major section of the world's population with their primary source of nutrition. It is the most productive food crop in the world in terms of production and area, with 221.41 million hectares worldwide, yielding 35.2 quintals per hectare, and producing 780.29 million metric tonnes in 21–22. In the 2020–21 growing season, 31.62 million acres of wheat were planted in India. The obtained yield was 3.44 metric tonnes per hectare, resulting in a total production of 126.93 million metric tonnes [1]. Food security may be threatened in the future by the urbanisation and industrialization processes, as well as India's alarming population increase. The average global wheat yield has to increase from 2.6 to 3.5 t ha-1 during the next 25 years, since the demand for wheat is expected to rise by 60% in developing nations by 2050 [2]. Increased wheat yield potential per unit area requires improved p1genotypes in order to support a growing population. The ongoing improvement of the most promising genotypes in order to increase their yield potential, either through direct improvement or by addressing other aspects that indirectly contribute to high yield, is a primary priority for plant breeders. The first step in launching a systematic crop breeding strategy is gaining an understanding of the traits and degree of genetic variability.

Genetic variability in plant breeding refers to the presence of genetic differences within a plant species that can be utilized to develop new and improved plant varieties. Genetic variability among breeding materials is of primary importance in the achievement of good crop production [3]. The level of success achieved in crop production is influenced by both the quantity and quality of genetic variation within the crop. This variation is transmitted to succeeding generations from the parental generation [4]. The application of genotypic and phenotypic coefficients of variation is beneficial for determining and evaluating the degree of diversity present in germplasm [5]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are measures of the amount of variation in a trait within a population. The phenotypic coefficient of variation measures the amount of variation in a trait that is due to both genetic and environmental factors, while the genotypic coefficient of variation measures the amount of variation in a trait that is due to genetic factors alone. These measures are used to estimate the heritability of a trait, which is the proportion of the total variation in a trait that is due to genetic factors. The evaluation of heritability serves as a valuable tool when investigating genetic variations that have developed within a selectively bred population [6]. A general look at heritability shows that environmental factors don't have a big effect on genetic defects. This means that it might be possible to quickly choose a hybrid with the trait that is desired [7]. Nevertheless, when it comes to traits with a low heritability, the process of selection might prove to be very challenging or even practically unattainable. This is mostly due to the influence of the environment, which has the ability to mask or diminish the impacts of genotypic factors [8]. The assessment of heritability assists breeders in determining the essential resources required to effectively improve desired traits and achieve optimal results with restricted time and resources [9]. Comparing heritability and genetic advance simultaneously is a more reliable and practical methodology [10]. Genetic advance is a crucial parameter in plant breeding that helps breeders select superior varieties from segregating populations. It is a measure of the degree of gain in a character obtained under a particular selection pressure and is a useful indicator of the effective and efficient selection progress that can be expected as a result of exercising selection on the base population. Comprehending genetic parameters, including heritability and genetic advance among selected traits, is of the utmost importance in order to predict genetic progress in breeding programmes and devise effective breeding approaches [11]. Various morphophysiological and yield-related traits, ranging from growth and development to yield and quality, play a fundamental role in determining the productivity and adaptability of wheat varieties. Days to 75 percent heading refers to the number of days it takes for the wheat plants to reach the stage of 75 percent heading. It is a critical indicator of the crop's growth progress and helps in timing various agricultural practices. Ameen [12] found that selection for early heading dates resulted in significant genetic gains but also observed negative correlations between heading dates and grain yield. Days to Maturity denotes the duration from planting to the time when wheat is ready for harvest. Different wheat varieties have varying maturity periods, and this trait is essential for crop planning and management. The consideration of maturity categorization holds significant importance in the selection of a wheat variety. In a particular year, it is usually observed that abiotic stress factors, such as freezing temperatures, drought, or heat, do not uniformly impact maturity classes. To mitigate the impact of abiotic stress, growers have the option to allocate their crop area among several kinds that exhibit early, medium, and late maturation. This strategic approach enables them to minimise the overall risk associated with abiotic stress factors**.** Grain Filling Duration represents the period in days during which the wheat grains are filled and matured. It directly influences the final grain yield, as a longer grain-filling duration can lead to larger and more abundant grains. Longer grain-filling duration can lead to larger and more abundant grains in spring wheat, as studied by Tiwari, V. K. [13], and also in bread wheat, as suggested by Monpara, B. A. [14]. Normalized Difference Vegetation Index (NDVI) content is a remote sensing measure that assesses the health and vigour of crops. In wheat, it is used to monitor plant growth and detect stress conditions such as disease, nutrient deficiency, or water stress. Alemayehu et al. [15] found that the use of NDVI would help in complementing the identification of drought-tolerant genotypes in durum wheat. Monitoring Canopy temperature depression (°C) is crucial for evaluating the heat and drought stress tolerance of wheat varieties. A lower canopy temperature depression often indicates better resistance to heat stress. Canopy temperature depression has been used as a selection criterion for tolerance to drought and high temperature stress in wheat breeding. The plant height of wheat is a significant trait. Shorter, semi-dwarf varieties are often preferred as they are less prone to lodging and allocate more energy into grain production. The length of the peduncle, the stem that supports the wheat head, can influence the plant's ability to hold grains upright. Shorter peduncles are advantageous for reducing the risk of lodging. The exposed peduncle is a photosynthetically active organ that produces photosynthates and thereby makes a crucial contribution to grain growth, particularly during the late stages of grain filling [16]. The flag leaf is the top leaf on a wheat plant and is crucial for photosynthesis. A larger flag leaf area is associated with increased photosynthetic activity and higher grain yield. A larger flag leaf area is associated with increased photosynthetic activity and a higher grain yield [17]. The tillering capacity of a wheat plant, or the ability to produce additional shoots, is important for determining the number of grain-bearing spikes per plant and, ultimately, grain yield.

The length of the wheat spike, where grains are produced, directly impacts the number of spikelets and grains per spike and, consequently, grain yield. Awns are bristle-like structures on wheat spikes. Their length can affect the plant's ability to capture sunlight, water, and nutrients, influencing overall growth and yield. The number of spikelets on a single spike is a key determinant of the potential grain yield of a wheat plant. Grain per spike is the actual number of grains produced on each spike, which is a crucial factor in determining grain yield. The weight of a thousand grains is a measure of grain size and is associated with grain quality and yield. Thousand grain weight and weight of grain per spike exhibited a positive and strong association with grain yield [18]. Biological yield refers to the total biomass, or above-ground plant material, produced by a wheat crop. It contributes to the overall potential for grain production. Grain yield is the ultimate measure of a wheat crop's success in terms of producing edible grains for consumption or processing. The harvest index represents the proportion of total biological yield that is allocated to the grain. A high harvest index indicates efficient resource allocation and increased grain yield [19]. The harvest index is a critical factor for grain yield across diverse wheat cultivars under terminal high temperatures and water shortages in Mediterranean areas [20]. Thus, a thorough understanding of these morphophysiological and yield-related traits is essential for wheat breeders and farmers to develop high-yielding and resilient wheat varieties that can thrive under various environmental conditions and meet global food demand. By optimising these traits, wheat cultivation can be more sustainable and productive.

Considering the relevance of genetic parameters, the current study analyses the genetic variability, heritability, and genetic advance across a set of 38 wheat genotypes in field settings with the objective of identifying the crucial morpho-physiological and yield-contributing traits in bread wheat.

2. MATERIALS AND METHODS

2.1 Experimental Material and Site

The field experiment for this study was carried out at the Norman E. Bourlaug Crop Research Centre, Pantnagar, Uttarakhand. The experimental material for the present investigation consisted of 38 genotypes, including 8 parental lines, their 28 F1 crosses, and two released varieties, viz., HD2967 and UP2903, as checks. Crosses were developed by crossing eight parental lines in a diallel fashion during Rabi, 2020–21. The diallel mating design is a methodical approach in which a predetermined set of parents are crossed to generate F1 offspring. An evaluation trial of all 38 genotypes was laid out in a randomised block design (RBD) with three replications during Rabi 2021–22. Each plot consisted of 2 rows of 1 m in length with a row-to-row and plant-to-plant distance of 20 cm and 10 cm, respectively. Observations were recorded on five randomly selected plants from each plot for seventeen morpho-physiological and yield contributing characters, viz. days to 75 percent heading, days to maturity, grain filling duration (days), normalised difference vegetation index (NDVI) content, canopy temperature depression (°C), plant height (cm), peduncle length (cm), flag leaf area (cm^2), number of tillers per plant, spike length (cm), awn length (cm), spikelets per spike, grain per spike, thousand grain weight (g), biological yield (g/plot), grain yield (g/plot) and harvest index. All the recommended cultural packages and practices were adopted to raise the crop. The details of genotypes with checks undertaken for study are presented in Table 1.

2.2 Statistical Analysis

Analysis of variance was first performed for the data in a Randomised Complete Block Design. The mean is calculated by dividing the sum of all observations within a sample by the total number of observations. The range is determined by subtracting the lowest value from the highest value for each character. The genotypic and phenotypic coefficients of variation were calculated using the formula proposed by Burton and De Vane [21]. The estimation of heritability in broad sense and the expected genetic advance (GA) for various characteristics under selection were done using the formula proposed by Johnson et al. [22]. The calculation of the genetic advance as a percentage of the mean was performed using the formula suggested by Comstock and Robinson [23].

Table 1. Details of genotypes and checks undertaken for study

S. No.	Genotypes
	Parents
1	PBW660
2	WH1080
3	UP2572
4	VL967
5	VL829
6	C306
7	UP262
8	WH1142
	F1 crosses
1	PBW660×WH1080
2	PBW660×UP2572
3	PBW660×VL967
4	PBW660×VL829
5	PBW660×C306
6	PBW660×UP262
7	PBW660×WH1142
8	WH1080×UP2572
9	WH1080×VL967
10	WH1080×VL829
11	WH1080×C306
12	WH1080×UP262
13	WH1080×UP1142
14	UP2572×VL967
15	UP2572×VL829
16	UP2572×C306
17	UP2572×UP262
18	UP2572×WH1142
19	VL967×VL829
20	VL967×C306
21	VL967×UP262
22	VL967×WH1142
23	VL829×C306
24	VL829×UP262
25	VL829×WH1142
26	C306×UP262
27	C306×WH1142
28	UP262×WH1142
	Checks
1	HD2967
2	UP2903

3. RESULTS AND DISCUSSION

The analysis of variance revealed statistically significant differences across all seventeen variables, indicating the presence of significant genetic variability among the various genotypes. Table 2 shows the mean sums of squares obtained from the analysis of variance (ANOVA) of morpho-physiological and yield contributing characters in 38 bread wheat genotypes. The extensive range of variability offers enhanced opportunities for the selection and utilisation of significant morphological, physiological, and yield-related features in the field of wheat breeding. The genetic data acquired from the examination of genetic variability, heritability in a broad sense (h^2 $_{bs}$), and genetic advance (GA), as well as Genetic advance as a percentage over the mean (GAM) among traits at genotypic and phenotypic levels, is displayed in Table 3.

3.1 Coefficient of Variation

The character exhibiting a high genotypic coefficient of variation value demonstrates a greater potential for enhancement through the process of selection. The determination of the impact of the environment on individual traits can be achieved by assessing the difference between the phenotypic coefficient of variation and the genotypic coefficient of variation. Table 3 illustrates that the phenotypic coefficient of variation (>10%) and genotypic coefficient of variation were found to be high for eleven out of seventeen traits. These traits include canopy temperature depression, plant height, peduncle length, flag leaf area, tillers per plant, spike length, awn length, spikelets per spike, grains per spike, biological yield, grain yield, and harvest index. The higher magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for grain yield, biological yield, productive tillers per plant and plant height so obtained were found to be consistent with the results of Bhushan et al. [24]. In the present study grain filling duration, normalised difference vegetation index (NDVI) content, and thousand grain weight were observed to have moderate estimations ranging from 5 % to 10 %. Poonia et al. [25] and Kumar et al. [26] both reported comparable results indicating increased PCV and GCV values. The remaining characteristics exhibited moderate to low phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), which is consistent with the results reported by Hossain et al. [27]. The phenotypic coefficient of variation had a greater magnitude compared to the genotypic coefficient of variation in relation to the traits, indicating a greater degree of interaction between the genotypes and the environment.

3.2 Heritability and Genetic Advance

Heritability, in a broad sense, provides an estimation of the extent to which environmental factors contribute to the phenotypic expression of a character. The concept of broad-sense heritability might be seen as the maximum extent

Table 2. Mean sums of squares obtained from the analysis of variance of morpho-physiological and yield contributing characters in 38 bread wheat genotypes

Characters	Replication	Genotypes	Error
df	2	37	74
Days to Heading	3.868	19.994***	1.247
Days to Maturity	4.167	69.872***	1.383
Grain Filling Duration	3.746	40.498***	1.349
Normalised Difference Vegetation Index	0.000	0.006***	0.000
Canopy Temperature Depression	0.029	4.253***	0.182
Plant Height	5.629	219.858***	13.746
Peduncle Length	0.694	82.267***	3.466
Flag Leaf Area	0.802	177.704***	3.608
Tillers	0.033	13.258***	0.461
Spike Length	0.796	3.939***	0.321
Awn Length	0.111	3.310***	0.228
Spikelets Per Spike	1.719	12.9715***	1.481
Grain Per Spike	0.011	142.642***	0.570
Thousand Grain Weight	8.400	37.984***	7.323
Biological Yield	2.990	1289.330***	27.390
Grain Yield	3.159	209.162***	4.318
Harvest Index	28.673	195.506***	23.256

*Significance levels -** P < 0.05; * ** P < 0.001, df -degree of freedom*

Table 3. Estimates of variability parameters for seventeen characters in bread wheat

S. No.	Characters	Grand Mean	Range	Coefficient of variation %		h^2_{bs} (%)	GA	GAM (%)
				PCV	GCV			
1	Days to heading	85.58	79.00-92.00	3.20	2.92	83.37	4.70	5.49
2	Days to maturity	124.423	115.00-134.00	3.95	3.84	94.29	9.56	7.68
3	Grain filling duration	38.80	29.00-48.00	9.78	9.31	90.63	7.08	18.26
4	Normalized Difference Vegetation Index	0.60	00.42-00.73	7.85	7.49	90.91	0.09	14.70
5	Canopy Temperature Depression	4.77	2.20-9.00	26.00	24.41	88.16	2.25	47.22
6	Plant height	78.92	60.67-117.00	11.51	10.50	83.33	15.59	19.75
7	Peduncle length	32.00	21.37-49.33	17.04	16.01	88.34	9.92	31.01
8	Flag leaf area	17.90	6.31-54.12	43.87	42.57	94.15	15.23	85.08
9	Tillers per plant	12.20	7.00-19.81	17.83	16.93	90.25	4.04	33.14
10	Spike length	11.32	7.97-14.00	10.92	9.71	79.01	2.01	17.77
11	Awn length	6.62	4.00-10.17	16.92	15.31	81.84	1.89	28.53
12	Spikelet per spike	19.04	13.00-23.67	12.11	10.28	72.11	3.42	17.99
13	Grains per spike	47.68	30.33-64.67	14.52	14.43	98.81	14.09	29.56
14	Thousand grain weight	47.67	34.50-59.10	8.79	6.71	58.26	5.03	10.54
15	Biological yield	53.35	31.25-156.25	39.67	38.44	93.89	40.94	76.73
16	Grain yield	20.35	7.68-62.00	41.87	40.61	94.05	16.51	81.13
17	Harvest index	38.61	19.25-62.27	23.26	19.63	71.17	13.17	34.11

to which a trait can be transmitted. In present study the heritability estimates for several morphophysiological and yield-contributing traits were found to range from 58.26% to 98.81%. A high level of heritability suggests that the selection process for these traits would likely be effective, as it would be less susceptible to the influence of external factors. The current investigation revealed a significant genetic advance, expressed as a percentage of the mean, exceeding 10%, for various traits including grain filling duration, normalised difference vegetation index (NDVI) content, canopy temperature depression (CTD), plant height, peduncle length, flag leaf area, tillers per plant, spike length, awn length, spikelet per spike, grains per spike, thousand grain weight, biological yield, grain yield, and harvest index. Genetic advance offers a distinct advantage over heritability as a guiding principle for plant breeders in selection programmes aimed at improving a specific trait through successive rounds of selection in segregating generations. In general, it is widely accepted that if a character is subject to non-additive gene action, it is likely to exhibit high heritability but low genetic advance. Conversely, if a character is influenced by additive gene action, both heritability and genetic advance are expected to be high.

Poonia et al. [25] observed significant genetic advance, expressed as a percentage of the mean, for tillers per metre and the number of grain yields per plant. Nath et al. [28] noticed a significant genetic advance as a percentage of the mean for yield-attributing traits in their study on wheat conducted in the Cis-Himalayan region of West Bengal. In addition, Hossain et al. [29] conducted a study on wheat genotypes subjected to heat stress conditions, which revealed a significant genetic advance in many phenological, physiological, and yield-contributing characteristics.

Significant genetic advance, coupled with a high degree of heritability (more than 60%), was observed for various traits including flag leaf area, grain yield, biological yield, canopy temperature depression (CTD), harvest index, tillers per plant, peduncle length, grains per spike, awn length, plant height, grain filling duration, spikelet per spike, spike length, and normalised difference vegetation index (NDVI) content. These findings suggest the involvement of both additive and additive x additive gene effects in the expression of these traits. Furthermore, it can be inferred that the enhancement of these characteristics would be facilitated by the use of selection schemes that specifically target the utilisation of additive genetic variance. High heritability coupled with high genetic advance as percent of means for plant height, harvest index, biological yield and grain yield were recorded is in accordance with the findings of Bhushan et al. [24] that indicated predominance of additive gene action in the inheritance of these traits. Jamil et al. [30] found that bread wheat germplasm has a high expected genetic advance and high heritability, suggesting additive gene effects and early selection for these traits. Kumar et al. [31] observed significant heritability and genetic advance for bread wheat grain weight. Nagar et al. [32] also found a high heritability for spike length. Patil et al. [33] observed high heritability coupled with high genetic advance for harvest-index as obtained in the present study thus suggesting that harvest index show additive gene action in its expression.

4. CONCLUSION

This study explores the genetic variability of seventeen important traits in wheat, revealing significant differences among genotypes. The analysis of variance reveals a rich pool of genetic diversity available for further exploration in wheat breeding programs. Flag leaf area, grain yield, and biological yield are identified as traits with the highest potential for genetic improvement. The phenotypic coefficient of variation (PCV) values is higher than the genotypic coefficient of variation (GCV), indicating that environmental factors have a smaller influence on the expression of these traits. These traits, such as flag leaf area and grain yield, hold significant promise for targeted improvement in wheat breeding programs due to their high heritability and genetic advance. This study provides a roadmap for breeders and researchers to identify specific traits that are genetically controlled, heritable, and offer potential for meaningful genetic improvement**.**

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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