__Original Research Article__

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

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, 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.) stands as one of the world's most crucial staple crops, serving as a primary source of nourishment for a significant portion of the global population. With an extensive global acreage of 221.41 million hectares, a production of 780.29 million metric tonnes, and a yield of 35.2 quintals per hectare, it ranks first in area and second in production among all food crops in 21–22. The aggregate wheat acreage in India during the 2020–21 growing season was 31.62 million acres, resulting in a production of 126.93 million metric tonnes and a yield of 3.44 metric tonnes per hectare [1]. Population growth in India is concerning, and the processes of urbanisation and industrialization pose future threats to food security. Over the next quarter century, there is a projected 60% increase in wheat demand in developing countries by 2050, while the global average wheat yield must rise from 2.6 to 3.5 t ha-1. [2]. To sustain an expanding population, wheat yield potential per unit area must be increased through the improvement of genotypes. A primary focus for plant breeders is the continuous enhancement of the most promising genotypes in order to augment their yield potential, either by directly improving them or by addressing other factors that indirectly contribute to high yield. Acquiring knowledge regarding the characteristics and extent of genetic variability is crucial to initiating a systematic breeding programme for crops. The increased likelihood of developing desired plant varieties is attributed to the significant genetic variability present in the base material [3]. In order to optimise breeding programmes and enhance productivity, it is imperative to thoroughly investigate the variability and genetic potential of genotypes. 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 passed from the parental generation to subsequent generations [4]. The utilisation of genotypic and phenotypic coefficients of variation is valuable in the identification and assessment of the extent of diversity that exists within germplasm [5]. The assessment of heritability is a valuable tool in the examination of genetic variations within a population that has undergone selective breeding [6]. The evaluation of broad-sense heritability reveals genetic defects that are influenced to a lesser extent by environmental factors, hence indicating the potential for effectively selecting a specific hybrid possessing the desired feature [7]. Nevertheless, when it comes to traits with a low degree of heredity, 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 evaluation of heritability aids breeders in identifying the necessary resources for efficiently enhancing desired traits and attaining optimal outcomes within limited time and resources [9]. The simultaneous evaluation of heritability and genetic advance is a more credible and useful approach compared to analysing them separately [10].

Understanding genetic parameters, such as heritability and genetic advance among selected traits, is crucial for predicting genetic progress in breeding programmes and formulating effective breeding strategies [11]. 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. MATERIAL 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), NDVI content, canopy temperature depression (°C), plant height (cm), peduncle length (cm), flag leaf area (cm2), 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.

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

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 [12]. 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. [13]. The calculation of the genetic advance as a percentage of the mean was performed using the formula suggested by Comstock and Robinson [14].

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 displays the mean sums of squares obtained from the analysis of variance (ANOVA) of the different characters studied. 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, and genetic progress among traits at the genotypic and phenotypic levels are displayed in Table 3.

Table 2. Analysis of variance (mean square) for 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
NDVI	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	NDVI	0.60	00.42-00.73	7.85	7.49	90.91	0.09	14.70

5	CTD	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

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. Grain filling duration, NDVI content, and grain weight were observed to have moderate estimations ranging from 5% to 10% in this study. Poonia et al. [15] and Kumar et al. [16] 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. [17]. 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 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, NDVI content, 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. Poonia et al. [15] observed significant genetic advance, expressed as a percentage of the mean, in tillers per metre and the number of grain yields per plant. Nath et al. [18] 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. [19] 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 (less than 60%), was observed for various traits including flag leaf area, grain yield, biological yield, carbon isotope discrimination (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. Jamil et al. [20] 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. [21] observed significant heritability and genetic advance for bread wheat grain weight. Nagar et al. [22] found a high heritability for traits including days to 50% flowering, plant height, and spike length.

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.

4. CONCLUSION

The 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**.**

REFERENCES

Certainly, here are your references with the formatting adjustments you requested:

1. USDA. Global market analysis circular series (World Agriculture Production 2023). Accessed on 9/5/2023.

2. Rosegrant MW, Agcaoili M. Global food demand, supply, and price prospects to 2010. IFPRI, Washington, D.C., USA, 2010.

3. Sabhrawal PS, Lodhi GP. Germplasm evaluation for different traits in wheat (*Triticum aestivum* L.). HAU J. Agri. Res. 1995; 25(4): 207-210.

4. Bello O, Ige S, Azeez M, Afolabi M, Abdulmaliq S, Mahamood J. Heritability and genetic advance for grain yield and its component characters in maize (*Zea Mays* L.). Int. J. Plant Res. 2012; 2(5): 138-145.

5. Datta S, Das L. Characterization and genetic variability analysis in Capsicum annuum L. germplasm. SAARC J. Agr.2013; 11(1): 91-103.

6. Falconer D. Introduction to Quantitative Genetics. 2nd edition. Longman group limited, Longman house, Harrow, England, 1981; 350.

7. Allard R. Principles of plant breeding. John Wiley and Sons, New York, 1960; 485.

8. Singh B. Principles of plant breeding. Kalyani Publisher, New Delhi, 1991; 250.

9. Smalley M, Daub J, Hallauers A. Estimation of heritability in maize by parent-offspring regression. Maydica.2004; 49(3): 221-229.

10. Nwangburuka C, Denton O. Inheritance of yield-related traits in maize under normal and drought conditions. Int. J. Agr. Res.2012; 7(7): 367-375.

11. Falconer D, Mackay F. Introduction to Quantitative Genetics, fourth ed. Longman, Burnt Mill, England, 1996, 464.

12. Burton GW, De Vane EW. Estimating heritability in tall fescue (*Festuca arundenacea*) from replicated clonal material. Agron. J. 1953; 45: 476-481.

13. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron J. 1955; 47: 314-318.

14. Johnson HW, Robinson HF, Comstock RE. Estimates of Genetic and Environmental Variability in Soybean. Agron. J. 1955; 47: 314-318.

15. Poonia M, Kumar A, Kumar V, Bhanu A, Kumar S. Genetic variability and character association analysis for seed yield and its attributes in wheat (*Triticum aestivum* L.). Int. J. Plant Soil Sci. 2023; 35(9): 123-131.

16. Kumar R, Kumar A, Singh J. Estimate of genetic parameters and correlation coefficient analysis for yield and its traits in bread wheat (*Triticum aestivum*L.). Int. J. Agric. Invention.2019; 4(02): 135-139.

17. Hossain S, Haque M. Genetic variability, correlation, and path coefficient analysis of morphological traits in some extinct local aman rice (*Oryza sativa* L). Rice Res.2016; Open Access. 4(1).https://doi.org/10.4172/2375-4338.1000158

18. Nath S, Das S, Basak D, Rout S, Hembram S, Roy S, et al. Exploring the genetic variability for yield attributing traits among the indigenous and exotic collection of wheat in cis-Himalayan region of West Bengal, India. Int. J. Plant Soil Sci. 2021;106-113. https://doi.org/10.9734/ijpss/2021/v33i2430758

19. Hossain M, Azad M, Alam M, Eaton T. Estimation of variability, heritability and genetic advance for phenological, physiological and yield-contributing attributes in wheat genotypes under heat stress condition. Am. J. Plant Sci. 2021;12(04), 586-602.https://doi.org/10.4236/ajps.2021.124039

20. Jamil A, Khan OUSS, Waqas M, Ullah Q, Ali S. Genetic variability, broad sense heritability and genetic advance studies in bread wheat (*Triticum aestivum* L.) germplasm. Pure Appl. Biol.2017; 6(2).https://doi.org/10.19045/bspab.2017.60055

21. Kumar V, Sharma P, Kumar H, Gupta V. Studies of variability and association of yield with some agromorphological characters in bread wheat (*Triticum aestivum* L.). Indian J. Agric. Res.2014; 48(6): 429.https://doi.org/10.5958/0976-058x.2014.01326.2

22. Nagar S, Kumar P, Vishwakarma S, Singh G, Tyagi B. Assessment of genetic variability and character association for grain yield and its component traits in bread wheat (*Triticum aestivum* L.). J. Appl. Nat. Sci. 2018;10(2): 797-804. https://doi.org/10.31018/jans.v10i2.1688