

Research Article

Genetic Variability, Heritability and Genetic Advance for Yield and Yield Associated Traits in Bread Wheat (*Triticum Aestivum* L.)

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Received: January 12, 2023; **Accepted:** February 24, 2023; **Published:** March 03, 2023**Abstract**

The experiment carried out during Rabi 2018-2019, ten genotypes and 45 F₁s of bread wheat were assessed for yield and yield associated traits in a Randomized Block Design (RBD) with three replications to determine genetic variability, heritability, and genetic advance percent of mean. The value of GCV ranged from 1.37 (days to maturity) to 19.87 (grain yield per plant) and PCV ranged from 1.59 (days to maturity) to 19.86 (grain yield per plant). The value of GCV and PCV as observed for grain yield per plant, productive tillers per plant, biological yield per plant and flag leaf area are (19.78,19.86), (13.11,14.07), (13.87,13.91) and (12.32,12.46) respectively. The traits like days to heading, plant height, flag leaf area and grains per spike shows high narrow sense heritability which has a great scope of genetic improvement through selection method whereas as flag leaf area and grains per spike shows high narrow sense heritability along with high genetic advance which are mainly governed by additive gene effects.

Keyword: GCV; Genetic advance; Narrow sense heritability; PCV; Wheat

Introduction

Wheat (*Triticum aestivum* L.) is one of the world's most significant and extensively grown crops, primarily for human consumption and as a major source of animal feed straw especially in India. Hexaploid wheat (*Triticum aestivum* L.) 2n = 42, AABBDD) is about 1.7 x 10¹⁰ bp, which is about 100 times that. The genome of Arabidopsis is 40 times that of rice and about 6 times that of corn. Wheat is the most widely cultivated cereal in the world 224.49 million hectares with production 792.40 million tons in 2020-21 year and in India wheat production 108.75 million tonnes with an average national productivity of 3424 kg/ha during 2020-21 [3]. India is already self-sufficient in fulfilling its population's wheat grain consumption, but a significant increase in wheat production will be necessary to ensure food security for our country's ever-growing population. By 2020, India's population is expected to be approximately 1.3 billion people [19]. As a result, increasing wheat production is one of the options for meeting the country's internal demand. Since the green revolution, continuous increases in wheat pro-

ductivity have been attributed to genetic improvements in yield as well as improved agronomic practices [4]. The fundamental goal of genetic improvement in any crop generates the information regarding connections, genetic variability and methods involved in inheritance of the genetic factors. The genotypic and phenotypic coefficients of variation are useful in gaining a clear picture of the material's existing variability. Many studies have found genetic differences in wheat genotypes for several yield associated traits [14]. Heritability as accompanied by high genetic advance would be a more beneficial tool for predicting the ensuing effect in genotype selection for yield and yield associated traits. Ibrahim [1]. The greater the chances of heterotic responses in F₁ and a broad spectrum of variability on segregation, the more diverse parents within all fitness constraints [2]. As a result, the current study was carried out with the goal of determining the genetic variability of different wheat genotypes based on their agro-morphological characteristics.

Materials and Methods

The ten genotypes namely HD2967, UP 2748, WH 1105, UP 2565, UP 2572, UP 2628, UP 2526, HD 3059, WH 1021, and HD 3086, were collected from the department of genetics and plant breeding, G. B. Pant University of agricultural technology, Pantnagar (U.K.). The above breeding materials were collected on the basis of their difference in origin, adaptability and morphology. All these parents have genetic variability in terms of yield level and different desirable yield components. In this study, all possible single crosses were made during the year 2017-18 via 10 x 10 half diallel mating design. In the year 2018-2019, ten parental lines and forty five crosses were evaluated in a Randomized Block Design (RBD) with three replications at Crop research farm, Janta Vedic College, Baraut Baghpat (UP). In every replication, the experimental material was sowed in three rows with parents and F_1 s. Every row was 2 m long with a 25 cm inter-row gap and a 10 cm intra-row distance. To raise a good crop and for optimum material expression, all of the prescribed agronomic measures were followed. The data was obtained on randomly collected five plants on the basis of following traits i.e. days to heading, days to maturity, Plant height (cm), productive tillers per plant, flag leaf area (cm), spike length (cm), grains per spike, 1000-grain weight, biological yield per plant, harvest index and grain yield per plant. The statistical analyses are as follow:

- The genotypic and phenotypic coefficient of variance was calculated according to Burton's methods of calculation (1952) and was classified according to Sivasubramanian and Madhavamenon, 1973 i.e. Low (<10%), medium (10-25%), and high (>25%).

- Heritability in narrow sense was calculated according to the method suggested by Crumpacker and Allard [7], which is based on the component analysis and the estimates of heritability in narrow sense were categorized according to Robinson (1965) i.e. High (>30%), moderate (10-30%) and low (<10%).

- The range of genetic advance as mean percent is classified as suggested by Johnson et al., 1955a. i.e. High (>20%), Moderate (10-20%) and Low (<10%).

Results and Discussion

Significant differences between genotypes were observed for all the traits examined, indicating considerable variability

among them. Estimating the genetic diversity parameters of all characters. A future breeding program might be able to capitalize on the significant genetic variability in the material. The phenotypic coefficient of variation component slightly differ from the genotypic coefficient of variation component in terms of value, the phenotypic coefficient of variation component, indicating that the existent variability was due to the combination of the genotypes' inherent character and the influence of environmental factors. The Genotypic Coefficient of Variation (GCV) ranged from 1.37 to 19.87 for (days to maturity) to (grain yield per plant). The current study revealed that none of the traits was found higher at Genotypic Coefficient Variance (GCV) level. Moderate genotypic coefficient variation observed for grain yield per plant (19.78), biological yield per plant (13.87), productive tiller per plant (13.11), flag leaf area (12.32) and grains per spike (10.72) whereas the rest of the traits shows lower GCV value for harvest index (9.84), spike length (7.17), 1000 grain weight (5.94), plant height (4.58), days to heading (2.19) and days to maturity (1.37). The Phenotypic Coefficient of Variation (PCV) ranged from 1.59 (days to maturity) to 19.86 (grain yield per plant) (Table 1). None of the traits shows higher at Phenotypic Coefficient Variance (PCV) levels. Moderate PCV were observed for grain yield per plant (19.86), productive tiller per plant (14.07), biological yield per plant (13.91), flag leaf area (12.46), and grains per spike (10.82) whereas, the lower value of PCV was observed for harvest index (10.11), spike length (7.37), 1000-grain weight (5.98), plant height (4.61), days to heading (2.34) and days to maturity (1.59).

The genotypic and phenotypic coefficients of variation, indicates lots of genetic variability in the evaluated traits. This means that selecting these characters can be very fruitful because the effectiveness of selection is dependent upon the variability in the germplasm. The current findings are backed [3,8,9,10,13,14,16,22,23]. The attributes with lower variability showed that increase in gene flow and fixing favourable alleles by intercrossing F_2 generation followed by recurrent selection is required to improve the base population. The above findings are backed [14,15,19]. Heritability is a helpful quantitative parameter that evaluates how genetics and environment interact to determine a trait's manifestation. High heritability narrow sense were observed days to heading (51.4), plant height (cm) (50.2), flag leaf area (38.1), grains per spike (35.4) whereas, moderate narrow-sense heritability were observed for productive

Table 1: Estimation of mean, range, coefficient of variance (GCV & PCV), narrow sense heritability and genetic advance for yield and yield associated traits in wheat (*Triticum aestivum* L.).

Characters	Mean	Range	GCV	PCV	Narrow sense Heritability	Genetic Advancement 5%	Gen. Adv as % of Mean 5%
Days to heading	84.95	79.67 - 88.67	2.19	2.34	51.4	3.59	4.23
Days to maturity	123.02	119.33 - 128.33	1.37	1.59	16.4	3.01	2.45
Plant height(cm)	90.70	84.33 - 100.57	4.58	4.61	50.2	8.50	9.37
Productive tillers/ plants	6.99	4.47 - 9.10	13.11	14.07	25.2	1.76	25.16
Flag leaf Area (cm)	27.52	21.29 - 36.41	12.32	12.46	38.1	6.91	25.10
Spike length (cm)	11.58	10.45 - 13.07	7.17	7.37	17.8	1.67	14.38
Grains per spike	48.10	39.01 - 60.11	10.72	10.82	35.4	10.53	21.90
1000-grain weight	40.17	34.83 - 44.33	5.94	5.98	21.4	4.89	12.18
Biological yield/ Plant	52.07	34.32 - 70.17	13.87	13.91	13.7	15.00	28.47
Harvest Index	41.74	34.13 - 49.94	9.84	10.11	18	8.24	19.74
Grain yield/ Plants	22.21	14.7 - 32.51	19.78	19.86	21.4	9.02	40.59

tillers per plant (25.2), grain yield per plant (21.4), 1000-grain weight (21.4), harvest index (18), spike length (17.8), days to maturity (16.4), and biological yield per plant (13.7). Expected genetic advance evaluates the level of a trait's stability under selection pressure and reflects the expected genetic progress for that trait during selection cycles. High genetic advance mean percent were observed in grain yield per plant (40.59), biological yield per plant (28.47), productive for tillers per plant (25.16), flag leaf area (25.10), grains per spike (21.90). Moderate genetic advance mean percent were observed in 1000-grain weight (12.18), spike length (14.38), and harvest index (19.74). The lower genetic advance mean percent was observed in only three traits namely plant height (9.37), days to maturity (2.45) and days to heading (4.23). Heritability coupled with genetic advance is usually more authentic than alone heritability assessment [12]. Where flag leaf area and grains per spike traits revealed high heritability along with high genetic advance this means these traits are mainly governed by additive gene effects. Consequently, selection would be effective for the improvement of these traits. Similar finding were also reported [8,10,19]. Days to heading and plant height revealing high heritability coupled with low genetic advance shows the predominance of heritable but non-additive gene effects. These traits show great environmental effect in the expression. As a result, selection would be ineffective for the improvement of these traits. Similar findings were also reported earlier [10,11,18]. High genotypic coefficient of variation combined with high heritability and genetic advance provides greater information than other criteria alone [1]. In present study grain yield per plant, biological yield per plant, flag leaf area showed high heritability along with high genetic advance and genotypic coefficient variance. These are the most significant quantitative traits to consider for optimal wheat selection.

References

- Akanda, MAL, Alam MS, Uddin MM. Genetic variability, correlation, and path analysis in maize (*Zea mays* L) in breads. *Bangladesh J. Plant Breed Genet.* 1997; 10: 57-61.
- Anand IJ, Murty BR. Genetic divergence and hybrid performance in linseed. *Indian J Genet Plant Breed.* 1968; 28: 178-185.
- Anonymous. Progress report of AICRP on wheat and barely 2020-21. *Social sciences.* 2021.
- Arya VK, Kumar P, Singh J, Kumar L, Sharma AK. Genetic analysis of some yield and quality traits in bread wheat (*Triticum aestivum* L.). *Wheat and Barley Research.* 2018; 10: 25-32.
- Burton GW. Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.* 1952; 1: 277 - 283.
- Burton GW, Devane EH. Estimating the heritability in tall fescue (*Festuca arundinacea*) from replicated Clonal material. *Agronomy J.* 1953; 45: 478- 481.
- Crumpacker DW, Allard RW. A diallel cross analysis of heading date in wheat. *Hilgardia.* 1962; 32: 275-318.
- Deoraj MG, Dahat DV, Rajput HJ, Wakale MB. Studies on Variability in Wheat (*Triticum aestivum* Linn.). *International research journal of multidisciplinary studies.* 2016; 2: 1-4.
- Harshwardhan, Kumar A, Kumar A, Prasad B. Study of variance, heritability and genetic advance for various yield contributing and quality traits in spring wheat (*Triticum aestivum* L.). *Journal of Applied and Natural Science.* 2016; 8: 1811-1814.
- Ibrahim AU, Yadav B, Raj A, Magashi AI. Heterosis studies in durum wheat (*Triticum durum* L.). *Journal of Genetics, Genomics & Plant Breeding.* 2020; 4: 2-8.
- Jaiswal A, Singh L, Singh M, Singh SV, Kumar S, et al. Analysis of correlation and path coefficient for yield and yield related traits in wheat genotypes. *The Pharma Innovation Journal.* 2022; 11: 294-298.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soy bean. *Agronomy J.* 1955; 47: 14-18.
- Joshi A, Kumar A, Budhlakoti V, Bhatt N, Tabassum. Estimation of genetic variability parameters for yield and its components in bread wheat (*Triticum aestivum* L. em. Thell) genotypes. *Journal of Pharmacognosy and Photochemistry.* 2018; SP5: 87-90.
- Kumar A. Genetic variability, heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *Research in Environment and Life Sciences.* 2016; 9: 317-319.
- Kumar D, Kerkhi SA. Genetic variability, heritability and genetic advance for yield component and quality traits in spring wheat (*Triticum aestivum* L.). *The Bioscan (the int. quarterly journal of life science).* 2020; 10: 2125-2129.
- Kumar D, Srivastava R.K., Yadav, P.K., Kumar, A. & Yadav, R.S. (2017). Studies on Variability, Heritability and Genetic Advance in Some Quantitative Characters in Bread Wheat (*Triticum aestivum* L.). *Int J Curr Microbiol App Sci.* 2017; 6: 873-877.
- Kumar S, Tyagi BS, Kumar A, Kumar P, Kumar J, et al. Study of genetic variability and character association for yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *Res Environ Life Sci.* 2016; 9: 882-886.
- Meena HS, Kumar D, Prasad R. Genetic variability and character association in bread wheat (*Triticum aestivum*). *Indian J Agric Sci.* 2014; 84: 487-91.
- Nagar SS, Kumar P, Vishwakarma SR, Singh G, Tyagi BS. Assessment of genetic variability and character association for grain yield and its component traits in bread wheat (*Triticum aestivum* L.). *Journal of Applied and Natural Science.* 2018; 10: 797-804.
- Saini PK, Kumar S, Singh SV. Heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *International Journal of Chemical Studies.* 2019; 7: 3078-3081.
- Saini PK, Kumar S, Singh SV. Heritability and genetic advance for yield and its contributing traits in bread wheat (*Triticum aestivum* L.). *International Journal of Chemical Studies.* 2019; 7: 3078-3081.
- Singh M, Devi EL, Aglawe S, Kousar N, Behera C. Estimation of heterosis in different crosses of bread wheat (*Triticum aestivum* L.). *The Bioscan.* 2013; 8: 1393-1401.
- Yadav AK, Maan RK, Kumar S, Kumar P. Variability, heritability and genetic advance for quantitative characters in hexaploid wheat (*Triticum aestivum* L.). *Electronic Journal of Plant Breeding.* 2011; 2: 405-408.