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Genetic variability, heritability, and genetic advance analysis in bread wheat (*Triticum aestivum* L.)

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Abstract

Wheat is an essential crop which is cultivated across the globe, and consumed by a substantial proportion of the human population. There is huge need to increase the yield and productivity of the wheat for feeding the exponentially expanding human population. So the recent research was aimed to analyse the genetic variability, broad sense heritability, and genetic advance on yield and its associated traits. It was carried out on 100 different wheat genotypes which included 4 checks, in the experimental fields of Lovely Professional University in an augmented design. ANOVA demonstrated a significant difference among the studied genotypes for the traits under investigation. High genotypic and phenotypic coefficients of variation were noticed in the traits number of productive tillers per plant, and plot yield per genotype, while moderate GCV coupled with PCV were noticed for traits thousand grain weight, grain yield per plant, biological yield per plant, and harvest index. Heritability was higher for all traits, while higher heritability along with higher genetic advance over percent mean was found for traits *viz.*, number of productive tillers per plant, thousand grain weight, plot yield per genotype, grain yield per plant, biological yield per plant and harvest index. So the traits number of productive tillers per plant, thousand grain weight, plot yield/genotype, grain yield/plant, biological yield/plant and harvest index can be chosen in breeding programs as they can be inherited into the off springs easily.

Keywords: GCV, genetic variability, genetic advance, heritability, PCV

Introduction

Wheat (*Triticum aestivum* L.) is an essential crop exhibiting segmental allohexaploidy (2n = 6x = 42) originated from Southwestern Asia (Bharath *et al.*, 2023) [5], and placed in the family poaceae, exhibits autogamy. Wheat is cultivated all over the globe in a variety of environments and occupies one sixth of the total arable land of world. Wheat being the largest cereal crop in terms of production and area of cultivation is known as "King of cereal crops." (Bhanu *et al.*, 2018) [4]. Wheat being consumed by almost 40% of the world population supplies one fifth of the total calories and proteins required by humans in their diets (Bhutto *et al.*, 2016) [6]. Wheat grain is composed of starch (60-68%), fat (1.5-2.0%), cellulose (2.0-2.5%), protein (6-21%), minerals (1.8%), and vitamins. It is unique from other cereal grains because of gluten which makes its dough to rise by forming gas cells and this makes the bakers to produce delicious breads. (Malav *et al.*, 2017) [24].

The total area under wheat during 2021-22 was 222.12 mha with production of 777.7 mt with the average yield as 3.51 metric tons/ha (USDA, 2023) [32]. Wheat production in India was 107.74 million tonnes during 2021-22 (PIB India, 2023). Among all the wheat producing countries in the world, India stands second in both production and consumption of wheat next to China by contributing 14% to the total wheat production of the world (FAO, 2022). It is being estimated that 800.9 mt of wheat will be produced in the world during 2022-23 (FAO, 2023) [12]. There is an estimation that 112.18 million tonnes of wheat will be produced during 2022-23 in India (PIB India, 2023).

The primary goal for any plant breeder is to create varieties with high production potentials and good quality. The awareness on genetic variability of yield and its attributed traits assists in boosting the yields and also in drafting a productive breeding programme (Singh *et al.*, 2018) [31]. An estimate stated that wheat production requires an increment by 60% to meet the demands of exponentially expanding population. (Akbarzai *et al.*, 2023) [1]. Noting these points the current study was formulated to assess the variability, broad sense heritability, and genetic advance of several yield influencing traits along with yield.

Materials and Methods

The current research was carried out during *rabi* season within the time frame of November 2022 to April 2023 under irrigated conditions in the experimental plots of Lovely Professional University. The topography and fertility of the research area were remarkably uniform. The average temperatures at the research location ranged from 15 ºC to 36 ºC. There were few rainfall days in the time span of research.

The research was carried out on 96 entries and 4 check varieties. These entries were grown in an augmented design with an area of 285 m^2 which had length and breadth of the plot as 19 m and 15 m, respectively. The entire area was divided into 6 blocks, where each block consisted of 16 entries and 4 checks were randomly grown between the entries. Each treatment was grown in 2 rows with 2 meters length, and a spacing of 22.5 cm was given between each row. Plant-to-plant spacing was 10 cm within each row. A gap of 45 cm was given between each entry within the block. A space of 1 m was provided between the blocks for accessing all the entries and to make the data collection easier. All the recommended agronomic practices required for wheat cultivation were paid attention during the research trial.

Observations were taken for yield and various yield influencing traits. Data on spike length (SL), plant height (PH), number of productive tillers per plant (NPT), chlorophyll content (CC), biological yield/plant (BYP), grain yield/plant (GYP), and harvest index (HI) were taken on plant basis of 5 plants. For the traits days to 50% flowering (DFF), days to maturity (DM), thousand grain weight (TGW), and plot yield/genotype (PYG) observations were taken on plot basis.

The means of all treatments for various characters studied were computed for analysis of variance (ANOVA) on a model proposed by Federer (1992) [11]. Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were assessed using the formula proposed by Burton (1952) [8]. Broad sense heritability (h^2 (bs)) was calculated by the formula developed by Hanson *et al.* (1956) and the genetic advance over percent mean (GAM) was worked out utilizing the equation designed by Johnson *et al.* (1955) [16].

Results and Discussion

ANOVA: The outcomes from ANOVA, which were presented in Table 1 unveiled that treatments were significant for every trait evaluated. It implied that there was good amount of genetic variation present among the treatments for all the traits analysed. Similar outcomes were found by Barman *et al.* (2020) [2], Bedada *et al.* (2022) [3], and Meherbabu *et al.* (2023) [25].

Variability parameters

The results for minimum, maximum, mean, CV, GCV, PCV, h^2 (bs), GA, and GAM are placed in the Table 2.

Genotypic and phenotypic coefficients of variation

The results decoded that GCV was little lower than PCV for every trait analysed. It specified, there was little impact of environment in expressing the phenotypes. It implies, selection based on phenotype can be worthy in improving these traits. High GCV, and PCV were noted for the traits NPT (20.98 and 22.71), and PYG (20.05 and 21.16). Similar outcomes were seen by Bedada *et al.* (2022) [3], and Kumar *et al.* (2017) [18] for NPT. Bhuwal and Kumar (2021) [7], and Shahi *et al.* (2018) [28] had similar matches for PYG. So it is clear that these traits have high genetic variability and provide good chance for improving them through selection. Moderate GCV, and PCV were detected for TGW (11.95 and 12.92), GYP (14.86 and 16.35), BYP (13.33 and 14.75), and HI (10.12 and 10.31). Similar outcomes were seen by and Kumari and Shukla (2022) [23] for TGW. Kumar *et al.* (2022) [19], Vaghela *et al.* (2021) [33] had similar results for GYP. Similarity in results for BYP were noticed by Kumar *et al.* (2019) [22], and Reddy *et al.* (2020) [27]. Similar kind of results for HI were observed by Phougat *et al.* (2017) [26], and Shahi *et al.* (2018) [28]. These traits with moderate GCV and PCV also have good opportunity for selection and refinement. Figure 1 represents the bar graph with GCV and PCV for various traits studied.

Heritability and genetic advance over percent mean

Heritability was high for almost all characters analysed, while higher heritability along with higher genetic advance over percent mean was noticed in traits NPT (89.59 and 40.97), TGW (85.59 and 22.81), PYG (93.68 and 34.94), GYP (82.66 and 27.87), BYP (81.68 and 24.85), and HI (96.33 and 20.48). Similarity in outcomes were found by Sharma *et al.* (2018) [29], and Vaghela *et al.* (2021) [33] for NPT. The results for TGW were similar with those of Singh *et al.* (2018) [31], and Chaudhary *et al.* (2022) [3]. Relatable results for PYG were found by Bedada *et al.* (2022) [3], and Hassani *et al.* (2022) [15]. Relevant results were found by Krishna *et al.* (2022) [17], and Sharma *et al.* (2023) [30] for GYP. Similar kind of results for BYP were found by Kumar *et al.* (2020) [20], and Krishna *et al.* (2022) [17]. HI results were relevant with that of Phougat *et al.* (2017) [26], and Singh *et al.* (2018) [31]. High h^2 (bs) coupled with moderate GAM was spotted for the traits PH (92.00 and 17.68), SL (79.01 and 17.81), and CC (83.22 and 14.6). Similar results for PH were seen by Kumar *et al.* (2019) [22], and Krishna *et al.* (2022) [17]. Relevant results for SL were seen by Shahi *et al.* (2018) [28], and Bedada *et al.* (2022) [3]. CC results were comparable with those of Elahi *et al.* (2020) [10], and Kumari and Shukla (2022) [23]. All these traits having higher h^2 (bs) accompanied with higher or moderate GAM indicated presence of additive gene action and their selection will be highly beneficial. Figure 2 represents the bar graph with h^2 and GAM for various traits studied.

Table 1: ANOVA for yield and its attributing traits

Source	Treatment (Ignoring Blocks)	Treatment (Check)	Treatment (Test vs Check)	Treatment (Test)	Block (Eliminating Treatments)	Residuals
Degrees of Freedom	99	3	1	95	5	15
Days to 50% Flowering	12.26**	81.94**	8.53**	10.1**	1.77	0.88
Days to Maturity	41.26**	37**	2163.25**	19.06**	0.6	0.93
Plant Height	89.77**	108.42**	99.13**	89.08**	9.95	7.13
Spike Length	1.72**	2.94**	13.48**	1.55**	0.17	0.33
Number of Productive Tillers	7.5**	7.12**	155.38**	5.95**	0.79	0.62
Chlorophyll Content	11.55**	28.3**	174.93**	9.31**	3.67	1.56
Thousand Grain Weight	30.89**	117.07**	13.95	28.35**	2.41	4.08
Plot Yield per Genotype	0.01**	0.04**	0.4**	0.01**	0.000047	0.0001
Grain Yield per Plant	15.62**	27.88**	540.81**	9.7**	1.66	1.68
Biological Yield per Plant	69.15**	152.38**	246.68**	64.66**	9.95	11.85
Harvest Index	21.54**	0.23	883.95**	13.13**	1.77*	0.48

* - $p \leq 0.05$ and ** - $p \leq 0.01$

Table 2: Various parameters for yield and its attributing traits

Traits	Range		Mean	CV	GCV	PCV	h^2	GA	GAM
	Minimum	Maximum							
Days to 50% Flowering	90.33	106.83	95.44	3.98	5.18	5.33	91.31	5.99	6.27
Days to Maturity	117.25	139.5	126.81	3.75	4.36	4.44	89.1	8.57	6.75
Plant Height	78.01	141.71	101.3	5.63	8.94	9.32	92	17.91	17.68
Spike Length	8.49	13.88	11.41	6.95	9.71	10.93	79.01	2.03	17.81
Number of Productive Tillers	5.74	17.94	11.01	7.87	20.98	22.17	89.59	4.51	40.97
Chlorophyll Content	28.71	43.78	35.88	6.44	7.76	8.5	83.22	5.24	14.6
Thousand Grain Weight	32.55	58.95	41.21	7.89	11.95	12.92	85.59	9.4	22.81
Plot Yield per Genotype	0.4	0.75	0.52	1.89	20.05	21.16	93.68	0.18	34.94
Grain Yield per Plant	14.4	30.62	19.05	8.52	14.86	16.35	82.66	5.31	27.87
Biological Yield per Plant	36.79	74.22	54.53	6.25	13.33	14.75	81.68	13.55	24.85
Harvest Index	28.36	42.35	35.16	3.92	10.12	10.31	96.33	7.2	20.48

CV: Coefficient of Variation; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; h^2: Broad Sense Heritability; GA: Genetic Advance; GAM: Genetic Advance over percent Mean

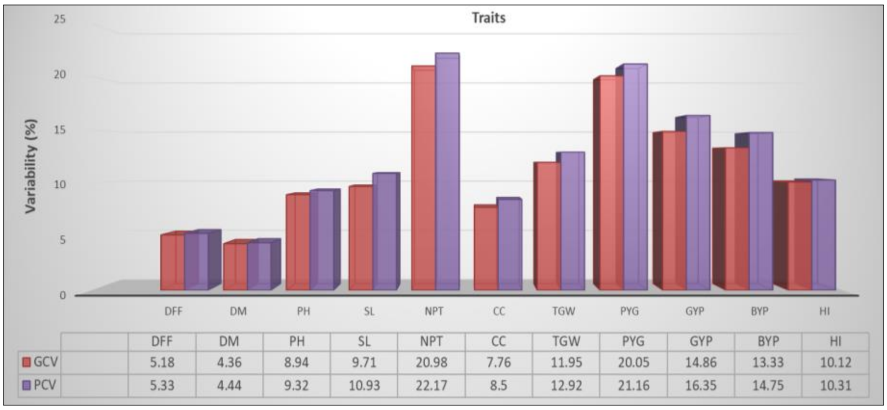

Fig 1: Bar chart representing GCV and PCV for various characters

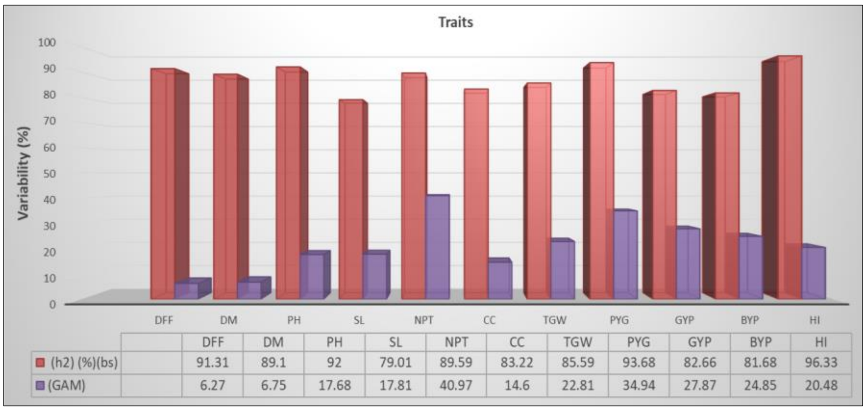

Fig 2: Bar chart representing h^2 (bs), and GAM for various characters

Conclusion

The current study unveiled the presence of variation between the entries for various traits analysed. Number of productive tillers per plant, thousand grain weight, plot yield/genotype, grain yield/plant, biological yield/plant, and harvest index can be considered for selection and improvement in further breeding programs.

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.

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