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Genetic Variability and Character Association Analysis for Seed Yield and its Attributes in Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Author MKP has carried out the overall research and collected the data and performed analysis and interpretation of data as well as wrote the manuscript. Author AK has been involved in drafting the research program as well as the manuscript and revised critically for important intellectual content. Author VK has been involved in drafting the research program as well as the manuscript and revised critically for important intellectual content. Author VK also made substantial contributions to the conception of data and analysis and interpretation of data. Author ANB drafted and revised the manuscript critically for important intellectual content. Author ANB also made substantial contributions to the conception of data and analysis and interpretation of data. Author SK has made substantial contributions to the conception of data and analysis and interpretation of data. All authors read and approved the final manuscript.

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ABSTRACT

Introduction: The experiment was conducted in Research Farm, Rani Lakshmi Bai Central Agricultural University, Jhansi, during *Rabi* season 2019-2020 using augmented block design in five blocks. The objective was to assess the genetic variability and character association analysis of eighty-two wheat genotypes.

Methodology: Eighty-two genotypes including three checks (HI1544, DBW110, and GW322) observed its various quantitative traits for genetic variation, heritability, genetic advance, and character association. The observations were recorded on fifteen agro-morphological and physiological characters *viz*; days to 50 percent heading, days to maturity, canopy temperature (^{o}C), chlorophyll content, flag leaf width (cm), flag leaf length (cm), tillers per meter, peduncle length (cm), plant height (cm), spike length (cm), awn length (cm), 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%). Statistical analysis was carried out by R Programming and SAS version 9.2 statistical software.

Results: The genotypes IC443619, IC6165734, and IC624496 were having earlier days to maturity than the best check DBW110. HD3086, K0307, PBW343, RAJ3, 765, and MACS6478 have been found promising for grain yield per plant. The highest Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) were recorded for tillers per plant followed by awn length, peduncle length, flag leaf length, flag leaf width, plant height, and spike length. Heritability in broad sense wide ranged from 26.3 percent for canopy temperature to 95.63 percent for grain yield per plant. The grain yield per plant showed a positive and significant correlation with biological yield per plant, harvest index, and tillers per meter, whereas it showed a negative significant association with awn length.

Conclusion: The relationship between grain yield per plant and biological yield per plant, harvest index, and tillers per metre was positive and significant, indicating that an increase in these component characteristics will also boost economic grain yield per plant.

Keywords: Correlation; genetic advance; heritability; phenotypic and genotypic coefficient of variation.

1. INTRODUCTION

Wheat is commonly called the “King of Cereals” due to its prominent position in the international food grain trade and its high acreage, production, and productivity [1]. Wheat, the first domesticated food crop since 8000 years, is the stable food for various civilizations throughout the world. It originated from South-Western Asia and Central Asia and the Mediterranean and Ethiopian regions are centres of diversity for wheat and its related species [2]. There are 17 different species of wheat among which three species *viz.,* hexaploid bread wheat (*Triticum aestivum*), *Triticum durum* (tetraploid macaroni wheat) and tetraploid emmer wheat (*Triticum dicoccum*) are mostly cultivated and consumed throughout the world [3]. In the world, wheat occupies an area of 217 million hectares (Mha) with a total production of 765 million tonnes (Mt) and productivity of 3530 kg/ha (USDA, 2020). China has maximum productivity followed by India, Russia, and USA. In India area, production and productivity of wheat tremendously increased since the green revolution of 1967. During 2019-2020, 3rd estimation India occupies an area of 30.55 million ha with a total production of 107.17 million tonnes and productivity of 3508 kg/ha. Uttar Pradesh leads in an area of 9.35 Mha with a production of 32.09 Mt and a productivity of 3432 kg/ha in the country and Madhya Pradesh occupies the wheat area of 6.02 Mha with a production of 18.58 Mt and a productivity of 3083 kg/ha [4].

Wheat can be used to convert into innumerable products like chapatis, bread, cakes, biscuits, pasta, and many hot and ready-to-eat breakfast foods and is considered a nature’s unique gift to mankind [5]. Recent years have seen a plateau in wheat output, making it more challenging to enhance productivity and yield. Crop scientists and plant breeders have a bigger difficulty due to the limitations of biotic and abiotic stressors. In all areas of the Indian wheat belt, heat stress is a major abiotic stressor impacting crop and cereal output.

Improvement in any crop is possible through an effective breeding program which generally depends on the selection of suitable genotypes, the presence of variation within the population for different economic characteristics is required [6]. Therefore, the information on genetic diversity in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance, and genetic divergence is therefore of vital importance. The selection of desirable genotypes can be achieved through the proper characterization of available genotypes. Different authors, including Hayadar et al. [7]; Vaghela et al. [8] and Lamara et al. [9] have demonstrated the existence of variability, heritability, and genetic advancement in different yield-related parameters of bread wheat (2022). However, not much variability studies have been conducted for recent genotypes in the study area. The estimation of the correlation coefficient is of greater value to determine the nature and degree of relationship between different agro-morphological traits. Knowledge of this inter-relationship between the different characters is useful for breeders to improve selection performance. Sharma et al. [2]; Ahmed et al. [10]; Monpara and Kalariya [11]; Singh et al. [12], Sakhare and Ghawat [13]; Singh et al. [14] and Bayisa et al. [15] noted a stronger or weaker correlation between wheat yield and traits that contribute to wheat yield, and they hypothesised that wheat crop grain yield potential could be effectively increased by getting the most out of the characters that contribute to wheat yield and have the stronger correlation in the desired direction. Khanal et al. [16] found a positive correlation between grain yield with biomass yield, harvest index, thousand kernel weight, plant height and number of grains per spike. According to Khokhar et al. [17], days to maturity had a positive direct effect on grain yield. Positive direct effects of biological yield per plant on grain production were reported by Singh et al. [18].

With this background, the present investigation was undertaken to examine the genetic variability, heritability, genetic advance, and correlation with respect to various desirable characters in eighty-two genotypes of wheat. The acquired information will assist in recognizing promising lines for the hybridization programme to explore wheat varieties of high-yielding potential coupled with quality.

2. MATERIALS AND METHODS

2.1 Experimental Material, Area and Design

Eighty-two genotypes including three checks (HI1544, DBW110, and GW322) observed its various quantitative traits for genetic variation, heritability, genetic advance, and character association. This investigation was conducted at Research Farm, Rani Lakshmi Bai Central Agricultural University, Jhansi (Uttar Pradesh) during *Rabi*, 2019-2020 in Augmented Design in five blocks. Seeds of each genotype were sown in a unit plot size of 3 meters long with a spacing of 30 and 10 centimeters between rows and plants respectively, and a number of accessions in each block being sixteen. Standard agronomic practices were followed for an enhanced crop of wheat and competitive crop stand.

2.2 Data Collection

The observation was recorded on five randomly selected and representative plants from each genotype on fifteen agro-morphological and physiological characters *viz*; days to 50 percent heading, days to maturity, canopy temperature (^{o}C), chlorophyll content, flag leaf width (cm), flag leaf length (cm), tillers per meter, peduncle length (cm), plant height (cm), spike length (cm), awn length (cm), 1000-grain weight (g), grain yield per plant (g), biological yield per plant (g) and harvest index (%). The chlorophyll content was measured by SPAD-502 chlorophyll meter as well as canopy temperature was measured by using a handheld infrared thermometer.

2.3 Statistical Data Analysis

The analysis of variance for the quantitative character was carried out as per the standard statistical procedure for Augmented Randomized Complete Block Design (ARCBD) as given by Federer (1956) using the SAS version 9.2 statistical software.

2.3.1 Estimation of magnitude of variance component

The genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated by Burton and Dewane [19].

Various parameters of genetic variability were calculated by using the following formula

Genotypic variance (σ^2(g)) = $\frac{\text{MSST}-\text{MSSE}}{r}$

Phenotypic variance (σ^2(p)) = σ^2(g) + MSSE

Where,

σ^2(g) = Genotypic variance

σ^2(p) = Phenotypic variance
MSST = Mean sum of square of treatment (adjusted)
MSSE = Mean sum of square of error
r = No. of blocks

The test of significance was carried out using the 'F' table value of Fisher and Yates (1967).

The genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) for all the characters were calculated according to the formulae given by Burton and Dewane [19] are as follows.

Phenotypic coefficient of variation (PCV):

PCV (%)

$$= \frac{\sqrt{\text{Phenotypic variance (Vp)}}}{\text{General mean of population (GM)}} \times 100$$

Genotypic coefficient of variation (GCV):

GCV (%)

$$= \frac{\sqrt{\text{Genotypic variance (Vg)}}}{\text{General mean of population (GM)}} \times 100$$

2.3.2 Estimate of heritability and expected genetic advance

Heritability (H^2) in broad sense was computed for yield and yield related traits using the formula adopted from Allard [20] as follow:

$$H^2 = [\sigma^2(g) / \sigma^2(p)] \times 100$$

Where,

σ^2(g) = Genotypic variance

σ^2(p) = Phenotypic variance

The expected genetic advance resulting from selection of five percent superior individual were worked out by Burton and de Vane [19] and Johnson et al. [21]

Genetic advance = $H^2 \times \sqrt{\text{Vp}} \times K$

Where,

H^2 = Heritability in the broad sense
$\sqrt{\text{Vp}}$ = Phenotypic standard deviation
K = Selection differential (The value of K = 2.06)

$$\text{GAM} = \frac{\text{GA}}{\text{Gm}} \times 100$$

Where,

GAM = Genetic advance (as % of the mean)
GA = Genetic advance
Gm = General mean of population

2.3.3 Correlation analysis

Correlation coefficients were calculated at the genotypic and phenotypic levels using the formulae suggested by Falconer [22].

Coefficient of correlation between characters X and Y:

$$r_{xy} = \frac{\text{Cov}_{xy}}{\sqrt{\text{Var}_x \text{X} \, \text{Var}_y}}$$

Where,

r_{xy} = Correlation between characters X and Y
Cov_{xy} = Covariance between characters X and Y
Var_x Denotes variance between characters X. whereas, Var_y denotes variance between characters Y.

Statistical analysis was carried out by R Programming and SAS version 9.2 statistical software.

3. RESULTS AND DISCUSSION

The analysis of variance for different characters is presented in Table 1. Analysis of variance was performed for all fifteen quantitative traits under study and results revealed that significant genetic differences were observed among the wheat genotypes for fourteen characters *viz;* for tillers per meter, plant height, peduncle length, day to 50 percent heading, thousand-grain weight, biological weight per plant, harvest index, days to maturity, grain yield per plant, awn length, spike length, and flag leaf width at 1 percent level of significance, and chlorophyll content, flag leaf length, at 5 percent level of significance, and canopy temperature were nonsignificant at both 5 and 1 percent level. This result corroborates with the findings of Meles et al. [23], Bhanu et al. [24], Mishra et al. [3], and Tomar et al. [41].

Table 1. Analysis of variance (ANOVA) for fifteen quantitative traits in wheat

Source of variation	Blocks (adjusted)	Treatment (adjusted)	Check	Varieties	Check vs. Varieties	Error
Degree of freedom	4	81	2	78	1	8
Days to heading	10.66	41.76**	127.40**	42.42**	30.41*	3.56
Days to maturity	1.1	5.85**	10.86**	6.02**	4.76 ns	0.95
Chlorophyll Content	5.73	13.66*	2.94 ns	14.54**	8.71 ns	2.82
Canopy Temperature	5.55*	2.63 ns	2.37 ns	2.52 ns	0.13 ns	0.94
Flag leaf width	0.02	0.07**	0.03	0.08**	0.26**	0.01
Flag leaf length	4.78	12.29*	56.89**	16.88**	3.28**	2.97
Tillers / meter	478.27	798.44**	2078.87**	763.49*	604 ns	155.1
Peduncle length	0.84	45.63**	19.64**	52.91**	138.13**	2.04
Plant height	41.64**	171.69**	4.83	225.45**	292.35**	5.37
Spike length	0.84	2.10**	0.4 ns	2.33**	0.66 ns	0.23
Awn length	0.31	2.35**	1.70**	2.43**	0.01 ns	0.08
1000 grain Weight	1.58	23.41**	56.14**	22.36**	74.80**	4.22
Biological yield	0.32	21.36**	13.82**	23.91**	153.96**	0.81
Grain yield	0.003	4.62**	3.38**	4.74**	42.07**	0.04
Harvest index	0.45	6.32**	0.76	6.76**	16.20**	0.73

**Significant at 5 per cent level; **Significant at 1 per cent level; ns represents non-significant*

The estimates of range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), and genetic advance are presented in Table 2. The highest GCV was recorded for tillers per plant (11.19) followed by awn length (8.49), peduncle length (7.66), and the highest PCV was recorded for tillers per meter (16.63) followed awn length (9.29), peduncle length (8.51), flag leaf length (8.16). The magnitude of PCV estimates was higher than the GCV estimates for all fifteen quantitative characters, indicating that the substantial influence of environmental variations is present in the performance of genotypes. These findings were in agreement with those of Bhushan et al. [25], Rajput [26] and Dabi et al. [27]. Nukasani et al. [28] also reported high GCV and PCV for tillers per meter. The minimum value of GCV for days to maturity was consistent with the earlier findings of Bhanu et al. [24].

The range of heritability was observed from 26.30 percent for canopy temperature to 95.63 percent for grain yield per plant. Maximum values were observed for grain yield per plant (95.63 %), followed by plant height (86.10%), biological yield per plant (83.47%), awn length (83.45%), peduncle length (80.98 %), days to 50 percent heading (68.17%), spike length (61.00%) and harvest index (60.32%). The high estimate of heritability was also recorded by Abinasha et al. [29], Kumar et al. [30] and Rathwa et al. [31] for plant height, Nukasami et al. [28] for tillers per meter, 1000 grain weight, and plant height, Bhanu et al. [24]. Low value of heritability for canopy temperature, 1000 grain weight, flag leaf length and tillers per meter has been found among the genotypes. However, a high value of heritability for 1000 grain weight in wheat have been reported by Naveen et al. (2014), Rajput [26], Kyosev and Desheva [32] in a different set of genotypes of wheat.

The moderate value (10-20%) of genetic advance as a percent mean was reported for awn length (15.98%), followed by tillers per meter (15.53%), peduncle length (14.20%), biological yield per plant (13.01%), plant height (12.83%) and grain yield per plant (10.19%). High estimates of genetic advance as percent of mean were also observed by Rathwa et al. [31] for tillers per meter and number of grains yield per plant by Bhanu et al. [24].

High heritability coupled with high genetic advance percent of mean was observed for grain yield per plant. High heritability combined with moderate genetic advance percent of mean was exhibited by biological yield per plant, plant height, peduncle length, and spike length. Low heritability and the low genetic advance percent of mean were observed for canopy temperature, days to maturity, and chlorophyll content indicating slow progress through selection for these characters.

Table 2. Details of genetic variability parameters for all the quantitative traits of wheat

S. No.	Character	Coefficient of Variation		Heritability (bs) %	Genetic advance	(GAM)
		PCV	GCV			
1	Days to 50% heading	4	3.302	68.17	4.7	5.62
2	Days to maturity	1.06	0.756	50.8	1.45	1.11
3	Chlorophyll content	4.904	3.232	43.43	2	4.39
4	Canopy temperature (°C)	5.032	2.58	26.3	0.61	2.73
5	Flag leaf width (cm)	7.248	5.388	55.27	0.17	8.25
6	Flag leaf length (cm)	8.169	5.068	38.49	1.74	6.48
7	Tillers per meter	16.631	11.199	45.34	15.73	15.53
8	Peduncle length (cm)	8.513	7.661	80.98	5.47	14.2
9	Plant height (cm)	7.234	6.713	86.1	11.02	12.83
10	Spike length (cm)	6.978	5.45	61	0.98	8.77
11	Awn length (cm)	9.296	8.492	83.45	1.27	15.98
12	1000 grain weight (g)	6.838	4.648	46.2	2.73	6.51
13	Biological yield (g)	5.926	5.414	83.47	3.82	10.19
14	Grain yield (g)	6.606	6.46	95.63	1.93	13.01
15	Harvest index (%)	3.441	2.672	60.32	1.69	4.28

Table 3. Simple correlation analysis between fifteen characters in wheat

	DH	DM	CL	CT	FW	FL	TM	PL	PH	SL	AL	TGW	GYPP	BYPP
DM	0.213ns													
CC	-0.059ns	0.047ns												
CT	0.001ns	0.039ns	0.071ns											
FW	0.002ns	-0.015ns	0.119ns	-0.02ns										
FL	-0.300**	-0.074ns	-0.091	-0.06ns	0.255*									
TM	0.181ns	0.259*	-0.08ns	-0.118ns	-0.286**	-0.07ns								
PL	-0.306**	-0.026ns	-0.309**	0.012ns	-0.168ns	0.458**	0.051ns							
PH	-0.102ns	0.047ns	-0.290**	0.132ns	-0.304**	0.14ns	0.254*	0.758**						
SL	0.058ns	-0.095ns	0.07ns	0.298**	0.087ns	0.097ns	-0.280**	-0.057ns	-0.052ns					
AL	0.006ns	-0.125ns	-0.124ns	-0.046ns	0.172	0.093ns	-0.129	0.019ns	0.002ns	-0.06ns				
TGW	0.001ns	-0.328**	-0.15ns	0.011ns	0.239*	-0.031ns	-0.205ns	0.054ns	-0.009ns	0.226*	0.042ns			
GYPP	0.169ns	-0.03ns	-0.098ns	-0.0243*	-0.051ns	-0.04ns	0.348**	-0.067ns	0.085ns	-0.156ns	-0.214*	0.033ns		
BYPP	0.171ns	0.049ns	-0.142ns	-0.244*	-0.038ns	-0.067ns	0.360**	0.046ns	0.203ns	-0.111ns	-0.237*	0.048ns	0.890**	
HI	0.041ns	-0.17ns	0.069ns	-0.077ns	-0.028ns	0.025ns	0.081ns	-0.244*	-0.214*	-0.126ns	-0.042ns	-0.015ns	0.538**	0.097ns

DH-Days to 50% heading, DM-Days to maturity, CC-Chlorophyll content, CT-Canopy temperature, FW-Flaf leaf width, FL-Flag leaf length, TM- Tillers per meter, PL-Peduncle length, PH-Plant height, SL-Spike length, AL-Awn length, TGW-Thousand grain weight, GYPP-Grain yield per plant, BYPP- Biological yield per plant, HI-Harvest index.

**Significant at 5 per cent level; **Significant at 1 per cent level; ns represents non-significant*

Knowing correlation is important for selecting many characters at once using a simultaneous selection model, which makes the simple correlation a significant tool for this purpose [33]. Even if the goal is to choose based on a single characteristic, understanding correlation is crucial to preventing unfavourable associated changes in other characters. The character association analysis for different characters is presented in Table 3. Days to 50 percent heading showed non-significant association with days to maturity (0.213), tiller per meter (0.181), biological yield per plant (0.171), grain yield per plant (0.169), spike length (0.058), harvest index (0.041), awn length (0.006), flag leaf width (0.002), 1000 grain weight (0.001), and canopy temperature (0.001), while, this trait had shown a significant negative association with plant height (-0.102*). Days to maturity showed significantly high negative correlation with the thousand grain weight (-0.328**) suggesting that the early maturing genotypes in the present set can resist terminal heat stress, which is a key driver in yield decrease [24]. The number of tillers per meter exhibited a significant positive correlation with biological yield per plant (0.360**) followed by grain yield per plant (0.348**), days to maturity (0.259**), and plant height (0.254**). The Harvest index expressed a positive significant association with grain yield per plant (0.538**). Grain yield was positively correlated with different quantitative traits in the findings of Kumar et al. [34] and Kumari et al. [35] with biological yield, harvest index, and tillers per meter, Ayer et al. [36] and Rajput [26] with biological yield, harvest index and grains per spike and harvest index, Mecha et al. [37] with number of spikelets per spike, 1000 grain weight and biomass yield. Selection for these characters can directly be followed for immediate yield improvement of wheat crop [38-40].

4. CONCLUSION

A significant part of the nation's sustainable food security is played by wheat. As breeding tactics for high-yielding wheat cultivars, it is vital to analyse the variability and relationships between yield and yield-attributing characteristics. The study revealed that a wide range of variation was depicted for most of the characters *viz;* for tillers per meter, plant height, peduncle length, day to 50 percent heading, thousand-grain weight, biological weight per plant, harvest index, days to maturity, grain yield per plant, awn length, spike length, and flag leaf width. High PCV and GCV were exhibited for various characters such as tillers per plant, awn length and peduncle length. The narrow difference between PCV and GCV was recorded for the characters *viz.,* grain yield per plant, biological yield per plant, days to maturity, spike length, and chlorophyll content suggesting that expression of these characters is less influenced by the environmental factors and strong inherent association among these traits is present. High heritability estimates were exhibited by grain yield per plant, suggesting that these characters are least affected by environment and selection is effective due to the additive effect of genotypic. The moderately high value of genetic advance as percent of mean for awn length, tillers per meter, peduncle length, biological yield per plant, plant height, and grain yield per plant which revealed the additive gene action. Grain yield per plant possessed a positive and significant correlation with biological yield per plant, harvest index, and tillers per meter suggesting that an increase in these component traits simultaneously improves grain yield per plant. These genotypes will be further tested over time in multilocation studies or can be applied to upcoming hybridization projects.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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