EVALUATION OF GENETIC POTENTIAL AND HERITABILITY ESTIMATES IN WHEAT GENOTYPES

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Abstract

Wheat (*Triticum aestivum* L.) is one of the three most consumed crops after rice and maize. Boosting wheat yield is necessitated by the rising food demand owing to the growing global human population. Thus, screening existing wheat germplasm for high-yield potential is pivotal to breeding programs to develop high-yielding and climate-smart wheat varieties. This study aimed to screen wheat genotypes for genetic potential and heritability of yield-contributing traits in agro-climatic conditions of Dera Ismail Khan. The research work comprised twenty-five wheat genotypes and two local checks to carry out genetic variability, heritability & correlation studies in yield contributing traits as selection criteria for high-yielding wheat genotypes at Gomal University Dera Ismail Khan. Analysis of variance revealed significant differences among the twenty-seven wheat genotypes for all the traits under study at a 1% level of significance. High genotypic co-efficient of variiqnce (GCV) and phenotypic co-efficient of variance (PCV) values were recorded for No. of tiller per plant, spike length, spikelet per spike and No. of grains per plant owing to the predominance of additive gene action. High broad sense heritability combined with high genetic advance as percent of mean was obtained for the number of tillers per plant, number of spikelets per spike and grain yield per plant for G4 and G26 genotypes recommended for improvement in breeding material via the breeding procedure, while genotypes such as G2, G4, G18, G21, G23, & G24 possess a highly diverse genetic background and are useful for future breeding programs.

Keywords: Heritability, Genetic advance, Genetic variability, Yield components

Introduction

Wheat (*Triticum aestivum* L.) is an anuual, self pollinating cereal crop and primary food source and stable food for the majority of global human population. The dependency of the global human polulation on wheat makes it a vital cereal crop for food and nutritional security (Zewdu *et al.*, 2024). It covers more than 200 millions of area under wheat cultivation, thus making an important trade commodity for global trade (Iqbal *et al.*, 2022). The pre-requisite of any wheat breeding program is to screen the available wheat germplasm for different yield related attributes, determine genetic diversity, sort out best yield performing lines, and assess their genetic advance and heritability. Such best performing lines and desired traits with high heritability are the base of successful wheat breeding program aimed at developing best yield producing cultivars. Genetic diversity plays the impartant role in generating new effective plant species under different environments (Mary and Gopalan, 2006).

Bread wheat consumption is at high level in Pakistan, grain yield being highly impacted by climate and enivronment is genetically controlled character, Hence improvement can be achieved by using developed and better genotypes in droughts and diverse climatic conditions (Inamullah *et al.*, 2006). In 2022-23, wheat were cultivated on 9,043 thousand hectares against last year's area of 8,977 thousand hectares recorded increase of 0.7 percent. Grain yield is the most complicated trait of plant is highly impact by the genetic factors and environmental alterations thus limiting the free selection criteria for yield, ascribed traits & breeding programmes & emphasizing the crucial need for dependence over the expertise of & inter-relationship of grain yield with different morphological traits (Ullah *et al.*, 2011).

Genetic diversity contribute in two ways; diversity in plants & second in germplasm pool the quantity of original parents that are to be used for refinement (Joshi *et al.*, 2004). Every breeding program and its success is dependant on the available diversity & variability of the germplasm under use. More variability means more chance of improvement in crop plants. Diveristy in wheat is classified on several levels acting as wheat genetic resources. The close relatives of domesticated wheats represent an ideal gene pool for the use of breeders. The genera *Aegilops* and *Triticum* are known as the main gene pool of domesticated wheat, including numerous species with different and interesting genomic constitutions. According to the literature, each wild relative harbors useful alleles which can induce resistance to various environmental stresses. Furthermore, progress in genetic and biotechnology sciences has provided accurate information regarding the phylogenetic relationships among species, which consequently opened avenues to reconsider the potential of each wild relative and to provide a context for how we can employ them in future breeding programs (Pour-Aboughadareh *et al.*, 2021). This study was aimed to screen wheat genotypes for genetic variability, genetic potential and heritability of yield contributing traits in agro-climatic conditions of Dera Ismail Khan.

Materials and Methods

The research experiment was conducted at the Plant Breeding and Genetics department of the Faculty of Agriculture at Gomal University Dera Ismail Khan during the 2019–2020 academic year.

Seeds were sown in the month of November, during the Rabi season. The studied germplasm was kindly provided by the Arid zone research center (AZRC) Dera   Ismail   Khan.

Data was taken on five randomly selected plants. The selection of plant material was based on variations in morpho-physiological traits and adaptability.

The field was prepared by two to three deep ploughings and one rotavator operation.

In accordance with Randomized Complete Block Design (RCBD), the experimental plot was created. In order to plant seeds in rows, the spacing between rows was maintained at 30 cm. Before and after wheat genotypes were sown in experimental plots, recommended dosages of phosphorus and nitrogen were administered. Data were taken on different traits, such as grains, spike length, spikelet per spike, and tiller per plant from five randomly selected plants in each line. All of the aforementioned characteristics' data were collected, and using Singh and Chaudhary's statistical model (1985), the analysis of variance approach was used to test the null hypothesis that there were no differences between the different genotypes.The phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were calculated using the mean in genetic analysis, following Singh and Chaudhary's (1985) methodology.

Statistical Analysis

The Singh and Chaudhary (1985) statistical model was used to analyze the collected data using the analysis of variance approach. The Falconer (1989) formula was used to determine the broad sense heritability (H2BS), and Singh and Chaudhary's (1985) method of calculating the phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) using mean was used for genetic analysis. Genetic Advance was computed using Singh & Chaudhary (1979) & Allard (1960). According to Kwon and Tourie (1964), the phenotypic and genotypic correlation between parameters was computed.

Heritability

The Falconer (1989) formula was used to compute broad sense heritability (h2BS).

$$h^2_{BS} = GV/PV$$

Phenotypic and genotypic coefficient of variation

The mean was used for genetic studies in order to calculate PCV and GCV in accordance with Singh and Chaudhury (1985).

Genetic advance

Following Singh and Chaudhary (1985) and Allard (1960), genetic advancement was achieved.

$$\text{Genetic advance (as percent of mean)} = k \times h \times \frac{\sqrt{Phenotypic\ variance}}{Mean\ value\ of\ treat} \times 100$$

GA as % of mean (GAM) = (GA/Mean Value)*100

Results

Analysis of Variance. The mean square of all the traits studied showed the presence of significant differences ($P < 0.05$) among the tested accessions is suggests that the studied breeding materials have an adequate genetic variation for all of the traits. This indicates that crop improvements through selection are possible.

Number of Tillers per plant. According to the mean data for number of tillers plant-1, the range of variation was 7.60-13.47 with a grand mean value of 10.817. The mean value for check variety G26 was 14.57, whereas G27 was 11.6.The genotype G22 had the greatest value for Number of tillers plant-1 (13.467A), followed by genotypes G4 (13.400A) and G9 (13.333A), while genotype G6 (7.600I) had the lowest mean value.

Spike Lenght. According to the mean data for spike length, the range of variation was 0.43-1.21 with a grand mean value of 10.894. The mean value for check variety G26 was 12.47, whereas G27 was 14.28.

Genotype G16 had the longest spike length value (14.223A), followed by genotypes G21 (14.053AB) and G19 (12.767ABC), while genotype G12 (7.667I) had the lowest mean value.

Number of Grain per Spike. According to the mean data for the number of grains spike-1, the range of variation was 27.67-59, with a grand mean value of 45.347. The mean value for check variety G26 was 47.33, whereas for G27 it was 57.00. The genotype G12 had the greatest value for the number of grains spike-1 (59.000A), followed by genotypes G22 (59.000A) and G20 (58.333A), while genotype G8 (27.667L) had the lowest mean value.

Number of spikelets per Spike. According to the mean data for the number of spikelet spike-1, the range of variance was 19-25.33, with the grand mean value at 22.227. The mean value for check variety G26 was 26.33, while for G27 was 24. The genotype G4 had the greatest value for number of spikelet spike-1 (25.333A), followed by genotypes G20 (25.000AB) and G3 (24.333ABC), while genotype G18 (19.000E) had the lowest mean value.

Spike density. According to the mean data for spike density, the range of variation was 0.43-1.21, with a grand mean value of 1.3660. The mean value for check variety G26 was 1.28, whereas for G27 it was 1.52. The genotype G16 had the highest spike density (1.7733A), followed by genotypes G20 (1.7400A) and G1 (1.6333AB), while genotype G13 (0.7367F) had the lowest mean value.

Grain yield plant^{-1} . According to the mean data for grain yield plant-1, the range of variation was 16.33-34, with a grand mean value of 22.813. The mean value for check variety G26 was 31, whereas G27 was 30.33. G4 had the greatest value for grain yield plant-1 (34.000A), followed by genotypes G23 (33.667A) and G24

(32.000A), in that order, while genotype G7 (16.333H) had the lowest mean value.

1000-grains weight. According to the ANOVA table pursuant to mean data for 1000-grains weight the range of this variation was 19-77.33 & the grand mean value stood at 35.267. Mean value for check variety G26 was 43 & for G27 was 40.67. The genotype G4 exhibited highest value for 1000-grains weight (77.333A) followed by genotypes G2 (51.000B) & G25 (48.000C) sequentially whereas genotype G20 (19.000N) stood at lowest mean value. The values of GV & PV were 155.26 & 158.34 sequentially. The value of GCV & PCV of 1000- grains weight stood at 2.66 & 2.68 sequentially. Heritability approximation was 98.05 along with genetic advance at 25.42 & Genetic gain or Genetic advance as percent of mean at 72.07.

Genotypic and Phenotypic Coefficients of Variation.

According to Burton and Devane, GCV and PCV are classified as high (>20%), medium (10–20%), and low (<10%). In the present study, GCV ranged from 5.35 for No of spikelete per spike to 19.90 for No of grains per spike. PCV ranged from 11.61 for No of spikelete per spike to 27.46 for spike density.

Estimation of Heritability in the Broad Sense and Genetic Advance

The estimated heritability was studied for all traits (Table 3) heritability values ranged from 40.186 for the grain-filling period to 87.042% for the number of seeds per spike. Robinson et al. classified heritability values as low (0–30%), moderate (30–60%), and high (60 and above). High heritability was observed for number of grains per spike (93.28), grain yield (75.90), spike length (66.33) which indicates that environment had a low influence on the expression of the traits suggesting direct selection for improvement. Tillers per plant (54.80) and

spike density (30.13) showed moderate heritability values. Low heritability values was observed in spikeletes per spike (21.27). which indicates that environment had high impact on these traits and can not recommended for further selection.

Discussion

The present investigation was carried out to evaluate the genetic variability and heritability for yield and yield-related traits in wheat genotypes. The analysis of variance (ANOVA) revealed significant differences among the genotypes for all the studied traits, indicating the presence of genetic variability. The high heritability estimates for most of the traits suggest that the phenotypic variation observed was largely due to genetic factors.

Number of Tillers per Plant The significant variation in the number of tillers per plant among the genotypes indicates the presence of genetic diversity for this trait. Genotypes G22, G4, and G9 exhibited the highest number of tillers, suggesting their potential for higher yield. These results are in accordance with the reported results of Fikre *et al.,* (2015); Bhushan *et al.,* (2013); Deepak *et al.,* (2017) & Jamil *et al.,* (2017).

Spike Length The variation in spike length among the genotypes was also significant. Genotype G16 had the longest spike length, followed by G21 and G19. These genotypes could be potential sources of genes for increasing spike length. These results are in accordance with the results of Fikre *et al.,* (2015) & Bhushan *et al.,* (2013).

Number of Grains per Spike The number of grains per spike is a major determinant of yield. Significant variation was observed among the genotypes for this trait. Genotype G12 had the highest number of grains per spike, followed by G22 and G20. These genotypes could be valuable sources of genes for increasing grain number. Results are in accordant to the reported

results of Bhushan *et al.,* (2013); Deepak *et al.,* (2017) & Jamil *et al.,* (2017).

Number of Spikelets per Spike The number of spikelets per spike is another important yield component. Significant variation was observed among the genotypes for this trait. Genotype G4 had the highest number of spikelets per spike, followed by G20 and G3. These genotypes could be potential sources of genes for increasing spikelet number.

Spike Density Spike density is a crucial factor affecting yield. Significant variation was observed among the genotypes for this trait. Genotype G16 had the highest spike density, followed by G20 and G1. These genotypes could be valuable sources of genes for increasing spike density. Alike findings were also described by Kalimullah *et al.,* (2012) & Kumar *et al.,* (2017).

1000-Grain Weight 1000-grain weight is another important yield component. Significant variation was observed among the genotypes for this trait. Genotype G4 had the highest 1000-grain weight, followed by G2 and G25. These genotypes could be valuable sources of genes for increasing 1000-grain weight. Similar results were reported by Fikre *et al.,* (2015); Deepak *et al.,* (2017) & Jamil *et al.,* (2017).

Grain Yield per Plant Grain yield per plant is the ultimate trait of interest in wheat breeding. Significant variation was observed among the genotypes for this trait. Genotype G4 had the highest grain yield per plant, followed by G23 and G24. These genotypes could be potential high-yielding varieties. Alike with the described results of Fikre *et al.,* (2015); Bhushan *et al.,* (2013); Deepak *et al.,* (2017) & Jamil *et al.,* (2017). Such sort of results can better be used as improvement tools in breeding programmes.

Heritability of wheat yield attributes
Heritability estimates provide valuable insights into the genetic basis of traits and

their potential for improvement through selective breeding. In this study, heritability values ranged widely across the evaluated traits, indicating varying degrees of genetic control. Traits with high heritability, such as number of grains per spike, grain yield, and spike length, exhibited a strong genetic component. This suggests that genetic factors play a major role in determining the expression of these traits. Consequently, direct selection for these traits is likely to be effective in improving crop performance. Traits with moderate heritability, such as tillers per plant and spike density, showed a moderate genetic influence. While genetic factors contribute to the variation in these traits, environmental factors also play a significant role. Therefore, a combined approach of genetic selection and appropriate environmental management may be necessary to optimize these traits. Traits with low heritability, such as spikelets per spike, were strongly influenced by environmental factors. This implies that genetic selection alone may not be sufficient to improve these traits. To enhance the performance of these traits, it is crucial to focus on optimizing environmental conditions and adopting appropriate agronomic practices. In support of the present study, Alemu *et al.* 2017, Dabi et al., 2017, Din et al., 2018, Balkan et al., 2018, Bagisa et al., 2020, Gerema et al., 2020, Hossain et al., 2021 and Ullah *et al.,* 2021 reported high heritability for spike length, grain yield and number of grains per spike. In accordance with our findings, Zewda et al., 2024 and Dabi et al., reported moderate values of heritability for tillers per plant. In contrast, Ullah et al. 2021 and Din et al.,2018 reported high heritability values for tillers per plant and spikelets per spike. The high heritability estimates for most of the traits indicate that

selection for these traits would be effective in improving wheat yield. The identification of high-yielding genotypes with desirable agronomic traits can be useful for wheat breeding programs. Further studies are needed to validate these findings and to develop high-yielding wheat varieties.

Conflicts Of Interest
The authors declare no conflicts of interest.

Authors Contribution
Sundas Batool and Aiman Sana conceived the idea, designed the study, conducted the field trial, collected the and analyzed the data and drafted the manuscript. Muhammad Shoaib, Arsalan Khan and Muhammad Yousaf Shah Hashmi helped in data collection. Nasr Ullah Khan helped in provided critical evaluation of the manuscript and constructive feedback in this project.

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List of tables
Table 1. Experimental site analysis.

Site	Altitude	Latitude	Longitude	Annual rainfall (mm)	Average annual temperature (°C)
Dera Ismail Khan	195.00m/639.76ft	31° 48' 59.99" N	70° 54' 59.99" E	268.8 mm (10.6 in)	24.2

Table 2. The listed of bread wheat genotypes to be studied.

Entry	Name	Representation	Entry	Name	Representation
1	MILLAT 2011/KVZ/PPR47.89C//3*PBW65/2*PASTOR	G1	15	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/NARC 2011	G15
2	PUNJAB2011/KVZ/PPR47.89C//TACUPETOF2001*2/BRAMBLING/3/2*TACUPETOF2001*2/BRAMBLING//WAFAQ 2001	G2	16	KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/W15.92/4/PASTOR//HXL7573/2*BA3/WBLL1	G16
3	2011/MUNIA/CHTO/3/PFAU/BOW//VEE#9/4/CHEN/AEGILOPSSQUARROSA(TAUS)//BCN/5/BABAX/LR42//BABAX	G3	17	GALAXY/MILLAT 2011	G17
4	AARI-11/GS/TH.SC//3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHI	G4	18	GALAXY/MILLAT 2011	G18
5	MILLAT 2011/NARC 2009	G5	19	PIRSABAK 2005/NARC 2011	G19
6	BHAKKAR/SOKOLL/3/PASTOR//HXL7573/2*BAU	G6	20	PAKISTAN 2013/NARC 2009	G20
7	INQLAB 91/DHARABI 2011	G7	21	PAKISTAN 2013/NARC 2009	G21
8	MH 97/SOKOLL/3/PASTOR//HXL7573/2*BAU	G8	22	SAHAR 2006/KACHU//WBLL1*2/BRAMBLING	G22
9	PBW343*2/KUKUNA/3/PGO/SERI//BRI//BAV92/NARC2011	G9	23	CMH76A.912/CMH76A.769/PAKISTAN 13	G23
10	PBW343*2/KUKUNA/3PGO/SERI//BAV92/NARC2009	G10	24	ATTILA-7/PAKISTAN 13	G24
11	KRICHAUFF/2*PASTOR/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	G11	25	CS/TH.SC//3*PVN/3/MIRLO/BUC/4/MILAN/5/TILHI/SOKOLL/3/PASTOR//HXL7573/2*BAU	G25
12	SOKOLL/3/PASTOR//HXL7573/2*BAU/PAKISTAN13	G12	26	LOCAL CHECK(BORLAUG-16)	CHECK 1

13	SOKOLL/3/PASTOR//HXL7873/2*BAU/W15.92/4/PA STOR//HXL7573/2*BAU/3/WBLL1	G13	27	LOCAL CHECK(PIRSABAK)(PS-15)	CHECK 2
14	SAHAR 2006/NARC 2009	G14			

Table 3. GV, PV, GCV, PCV, h^2_{BS} & genetic advance of various quantitative traits of twenty-five wheat genotypes.

Parameters	Vp	Vg	PCV	GCV	$h^2_{(BS)}$	GA	GG
Grain yield plant^{-1}	24.77	18.80	7.98	6.95	75.90	7.78	34.11
No of grains spike^{-1}	87.29	81.42	3.74	3.61	93.28	17.95	39.59
No of spikelets spike^{-1}	6.66	1.42	27.19	12.54	21.27	1.13	5.09
No of tillers plant^{-1}	3.58	1.96	18.67	25.22	54.80	2.14	19.75
Spike density	0.14	0.04	166.32	91.30	30.13	0.23	17.05
Spike length	3.53	2.34	22.88	18.62	66.23	2.56	23.54
1000-grain weight	158.34	155.26	2.68	2.66	98.05	25.42	72.07

Table 4. ANOVA for different yield related traits.

Parameters	Range	Mean	MS	SE (2 means)	SE of Mean
Grain yield plant^{-1}	17.67	22.81	62.3633**	1.9950	1.4107
No of grains spike^{-1}	31.33	45.35	250.124**	1.9778	1.3985
No of spikelet spike^{-1}	6.33	22.23	9.49222**	1.8694	1.3219
No of tillers plant^{-1}	5.87	10.82	7.50281**	1.0385	0.7343
Spike density	0.78	0.69	0.22556**	0.2560	0.1810
Spike length	6.56	10.89	8.21529**	0.8920	0.6307
1000 grain weight	58.33	35.27	468.861**	1.4340	1.0140