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GENETIC VARIABILITY AND CORRELATION STUDIES IN WHEAT ADVANCED LINES FOR YIELD IMPROVEMENT

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Abstract

The current research was conducted with the objective to estimate evaluation of variability, genetic advance and correlations in wheat. Sixty-four wheat advance lines were grown in alpha lattice designed during 2022-2023 at Cereal Crops Research Institute (CCRI), Pirsabak Nowshera, Pakistan. Significant differences among genotypes were recorded shown through analysis of variance. For majority of the variables, significant differences among genotypes were recorded shown through analysis of variance. Days to maturity ranged from 164 days to172 days, spike length ranged from 9cm-12cm, spike weight ranged from 3-5 g, spikelet per spike ranged from 16-23, peduncle length ranged from 40-16 cm, chlorophyll content ranged from 42-55 and grain yield from 3240 kg/ ha to 6051 kg/ ha. Genetic variance is higher than environmental variance for the traits. Regarding values highest heritability recorded for peduncle length (0.83), while lowest heritability recorded for days to maturity (0.79). Maximum phenotypic coefficient of variation value recorded for spike weight (15.69), while for days to maturity recorded value was (0.88) while lowest value recorded for grain yield (0.27). Maximum value of genetic gain recorded for peduncle length (5.48) and it was minimum for spike weight (0.61). The findings indicated strong and positive link spikelet per spike and spike length. This indicates that early maturity of wheat may affect yield since the plant may not have enough time to develop the necessary expression.

INTRODUCTION

Wheat is self-pollinating annual plant belongs to the family gramineae having chromosome number 2n=6x=42, [AABBDD] (hexaploid) and is widely cultivated worldwide [18]. Wheat ranks first in total cultivated area and second in total production among cereal crops globally, however it is the third most significant cereal food crop in the world after maize and rice [4]. Globally, wheat is cultivated on about 218.22 million hectares, with an estimated total production of 765.53 million tonnes in the 2018/2019 cropping season [17]. In the 2020/2021 season, its production of 5.48 million tonnes fell short of the

annual consumption of about 6.7 million tonnes. Globally, 79% of total wheat production comes from China, United States of America, Turkey, Canada, Australia, India and Argentina accounting to approximately 751 million tons per annum [4].

Yield gains in wheat are currently estimated at wheat is a staple source of nutrients for about 40% of the population worldwide [8]. A great source of dietary fibre, micronutrients, minerals, vitamins and fats (lipids), among other nutrients. When a little amount of animal or legume protein is added to it, it becomes even more nutrient-rich [14]. A diet based primarily on wheat is richer in fibre than a diet focusing primarily on meat. About 0.5 to 1% per year which is below than 2.4% required to satisfy global demand [3]**.** The world population is growing rapidly, which has raised demand for wheat. In order to meet the growing population's need for food, more food must be produced globally, which can only be done by increasing cereal crop production [1].

The low yield per hectare is caused by a number of problems, including a lack of high-yielding cultivars that can be acclimated to a variety of agroecologist around the country. Grain yield response in wheat is influenced by several agronomic and physiological traits [12]. Agronomic traits such as plant height, total biomass, number of kernels per spike, thousand seed weight, grain weight per spike and physiological traits s chlorophyll content, water-soluble carbohydrates have contributed to grain yield improvement in wheat [7]. Hence, the first step in the development of varieties is assessing the genetic variability of available genotypes for the characters of interest [20]. Increasing wheat production is one of the options for meeting the country's internal demand. Numerous yield related characteristics of bread wheat exhibit genetic development, heritability and variability as described by [20]. High genetic progress and broad heritability show an important contribution which demonstrate an important role of additional genetic variation to the production of the traits [12]. The degree of genetic variability is considered as an important factor, which is an essential prerequisite for successful hybridization aimed at obtaining high yielding generations. The large range of variability in the population provides an opportunity to select genotypes with a variety of desirable traits [3]. Genetic advance can be considered as a final assessment of the improvement according to the applied selection pressure on the materials. High heritability coupled with high genetic advance for different yield elements indicate a better opportunity to select highly productive genotypes [16]. As a result, the current study was carried out with the goal of determining the genetic variability, genetic advance and their correlation of wheat genotypes based on their agro-morphological characteristics.

Materials and Methods

The investigation entitled "Evaluation of Variability, Genetic advancement and their Correlation in Wheat (*Triticum aestivum* L.) "was conducted during 2022-2023 at Cereal Crops Research Institute (CCRI), Pirsabak Nowshera, Pakistan. A total of 64 advence lines including 02 check varieties were used in the present study. The crop was sown in four rows of 3-meter length with three replicates in a Randomized Block Design (RBD). At the proper time and according to each protocol's instructions, data were collected. Four plants from middle rows of plot were selected randomly and tagged to record the data of different morpho- agronomical traits *viz.,* days to maturity, spike length, spike weight, spikelet per spike, chlorophyll content, grain yield and peduncle length.

Statistical analysis

The mean performance of individual genotypes was used for statistical analysis. The approach recommended by Steel and Torri (1980) was used to analyze data variance to distinguish between means, the least significant difference (LSD) test was applied. The ANOVA and correlation between features were determined using Software Statics version 8.1. The formula adopted by Allard (1960) was used to calculate heritability (h^{-1}) in the broadest meaning for all traits. Genetic advance as percent of mean of each character was worked out adopting the formula given by Johnson *et al.* (1955). Correlation analysis among yield and yield-related traits was performed as suggested by (Kwon and Torrie, 1964).

RESULTS AND DISCUSSION

Table 4.1. ANOVA for 06 parameters of 64 wheat advanced lines during the year of 2022-2023 at CCRI, Pirsabak Nowshera.

SOV	DF	DTM	SL	SWT	SPS	PL	CC	GY (kg ha^{-1}
Block	1.00	242.00	0.09	0.03	7.97	10.87	12.69	274540.50
Genotype	63	4.018	0.488	0.54	4.56	41.37	12.29	685588.56
Error	49	0.42	0.33	0.06	1.08	3.86	3.32	118256.81
CV%	-	0.39	5.37	7.24	5.71	6.25	3.74	8.35

Table 4.2. Estimate of variance genotype, environmental, phenotypic coefficient of variation (genotypic and phenotypic) heritability, genetic, PCV, GCV, selection intensity and genetic gain computed for 6 important traits for wheat advance lines during 2022-2023 at CCRI, Pirsabak, Nowshera.

Traits	GV	VE	VP	GCV	PCV	H^2	SI	Genetic gain
DTM	1.78	0.42	2.20	0.79	0.88	0.81	1.40	1.68
SL	0.61	0.33	0.93	7.32	9.08	0.65	1.40	0.88
SWT	0.24	0.07	0.31	13.92	15.69	0.79	1.40	0.61
SPS	1.73	1.08	2.81	7.21	9.20	0.61	1.40	1.44
PL	18.52	3.86	22.37	13.68	15.04	0.83	1.40	5.48
CC	4.51	3.32	0.93	7.32	9.08	0.65	1.40	0.88
GY (kg ha^{-1})	285386.58	118256.81	121.00	12.97	0.27	2358.57	1.40	36321.93

(GV= Genotypic variance, VE= Environmental variance, VP= Phenotypic variance, GCV= genotypic coefficient of variance, PCV= Phenotypic coefficient of variance, h^2 = Broad sense heritability, SI = Selection intensity).

Table 4.3. Simple correlation among 06 important traits of 64 bread wheat advance lines including check cultivars evaluated during year 2022-2023 at CCRI, Pirsabak Nowshera.

Traits	DM	SPL	SPS	PL	SW	CC	GY
DM	1	-0.001	0.13	-0.08	0.01	0.05	-0.09
SPL		1	0.34**	0.01	0.07	0.01	0.09
SPS			1	-0.03	-0.04	0.15	-0.09

PL				1.00	-0.05	0.06	0.30**
SW					1	0.07	0.06
CC						1	0.24**
GY							1

(*and**, significant at 5% and 1% level of probability, respectively.

Days to maturity (no)

Phenotypic variance for days to maturity were 2.20, which is more than that of environmental variance 0.42. Magnitude of GCV (0.79) is less then PCV (0.88). Days to maturity sense heritability was similarly higher (0.81). (Siyal *et al.,* 2021) reported comparable findings and demonstrated that days to maturity affect wheat output. Days to maturity showed weak positive relation with spikelet per spike (r=0.13), spike weight (r=0.01) and chlorophyll content (r=0.05), while spike length (r=-0.001), peduncle length (r=-0.08), thousand grain yield (r=-0.01) exhibited weak negative association with days to maturity. Rathod and Gawand 2019) reported same result for days to maturity.

Spike length (cm)

For spike length phenotypic variance was (0.93) and variances due to environment (0.33) was greater than in magnitude then the estimated variances due to genetic variance (0.61). The GCV (7.32) was also smaller than the PCV (9.08) in magnitude. The broad sense heritability (0.65) is due to the fact that the level of variability is lower and the impact of the environment is stronger on spike length. Spike length demonstrated a strong positive association with spikelets per spike (r= 0.34**), while weak positive correlation with pendule length (r=0.01), spike weight (r=0.07) and chlorophyll content (r=0.04). However, there was a non-significant negative connection between spike length and days to maturity (r= -0.001). Our findings on spike length closely match those of (Khan *et al.,* 2015) on spikelets per spike, which demonstrated a positive and highly significant association (r=0.34*).

Spike weight

For the spike weight the overall phenotypic variance (0.31) was cooperatively higher in magnitude then the genotypic variance (0.24). However, the genotypic variance's percentage contribution was substantially higher than the environmental variance's (0.07). Similarly, to this, the broad sense heritability was (0.79). Our results are comparable to those of (Farshadfar and Estehghari, 2014), who found moderate broad sense heritability among wheat lines and considerable differences for the grain weight spike^{-1}.

Spike weight exhibited non-significant positive association with chlorophyll content (r=0. 06), spike length (r= 0.07) and days to maturity (r= 0.01), however spike weight showed non-significant negative correlation with peduncle length (r= - 0.05) and days to maturity (r= - 0.08).

Spikelet per spike

According to (Table 4.2) for spikelets spike, genetic variation (1.73) was marginally larger than environmental variance (1.08), but that overall phenotypic variance (2.81) was higher. Similar to this, the GCV and PCV for the aforementioned characteristic were 7.21 and 9.20, respectively, given a heritability in the wide sense of 0.61. Broad sense heritability of was (0.61) for spikelet per spike and the Coefficient of variation (CV) for spikelet per spike was 5.71.

Spikelets per spike exhibited highly positive association with spike length (r= 0.34**), while showed unremarkable positive correlation with days to maturity (r= 0.13),), chlorophyll content (r= 0.15. Contrarily, there is no significant negative association between spike weight (r=-0.04) and peduncle length (r=-0.03). Zakirullah *et al.,* 2017) reported a similar finding.

Peduncle length (cm)

For peduncle length, genetic variance (18.52) was marginally higher than environmental variance (3.86), according to table 4.2, however, the phenotypic variance as a whole (13.68) was larger. Similar to this, the GCV and PCV for the aforementioned attribute were 13.68 and 15.04, respectively. With a broad sense heritability of 0.83. According to table 4.2, the peduncle length's coefficient of variation (CV) was 6.25.

Peduncle length showed non-significant positive relation with spike length (r= 0.01), chlorophyll content (r= 0.06). Peduncle length showed strong and positive correlation with spike length at both levels which is in contradiction with (Farooq *et al.,* 2018).

Chlorophyll content

Phenotypic variance (0.93) and variances due to environmental (3.32) was higher than in magnitude then the estimated variances due to genetic variances (4.51). The GCV (7.32) was also smaller than the PCV (9.08) in magnitude. Because environmental factors have a bigger impact on chlorophyll content than the magnitude of variability, the broad sense heritability (0.65) is justified. Coefficient of Variation (CV) for leaf chlorophyll content was 3.74. Content suggests that the influence of environmental factors on these traits (Arya *et al.,* 2005) noted comparable results. Chlorophyll content showed an extremely substantial positive connection (r= 309** and 988*, respectively). While showed non-significant positive correlation with days to maturity (r= 0.05), spike length (r= 0.01), spikelet per spike (r= 0.15), peduncle length (r= 0.06) and spike weight (r= 0.07). Only a non-significant negative connection (r=-0.04) with chlorophyll concentration was observed. similar result was reported by (Guendouz and K. Maamari 2012).

Grain yield (kg ha^{-1})

Analysis of grain yield variance among the genotypes under investigation revealed it to be highly significant ((P≤0.10). Recorded Coefficient of Variation (CV %) for grain yield was (8.35). heritability estimates (238.57). Environmental variance (118256.81) was less than estimated genetic variance (285386.58). Plant height and grain yield showed a highly significant (P≤0.01) and favorable connection with flag leaf area (r=0.09) and tiller demonstrated a weakly positive association between grain yield, while non-significant negative was recorded for thousands grain yield (r= - 0.09). These results validated the findings from (Mahpara *et al.,* 2018).

CONCULSION

Out of the total 64 genotypes, Genotype AWL24 were showed best performance in peduncle length, while genotype AWL53 identified for maximum chlorophyll content. For the majority of traits, high genotypic variance vs environmental variance implied that the variation was within the control of genetic expression of the genotypes and would be sustained.in the current study revealed that chlorophyll positive correlation most the traits.

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