Original Article
DOI: https://doi.org/10.70749/ijbr.v2i02.134

INDUS JOURNAL OF BIOSCIENCE RESEARCH
https://induspublishers.com/IJBR
ISSN: 2960-2793/ 2960-2807

OPEN ACCESS

Evaluation of Variability, Genetic Advancement and their Correlation in *Triticum Aestivum* L.

Amna Naz[1], Abdur Rauf[1], Mamoona Bibi[1], Yaseen[1], Iqra Ambreen[1], Syeda Khushnood[1], Khayyam Aziz[1], Haseeba[1], Zarghoona[1], Khilwat Afridi[2], Aisha Siddique[3]

[1]Department of Botany, Abdul Wali Khan University Mardan, KP, Pakistan.
[2]Plant Breeding and Genetics, University of Agriculture, Peshawar, KP, Pakistan.
3Department of Microbiology, Women University, Mardan, KP, Pakistan.

ARTICLE INFO

Keywords

Wheat, Correlation, Genetic Coefficient of Variation, Phenotypic Coefficient of Variation, Genetic Advance, Variability

Corresponding Author: Amna Naz
Department of Botany, Abdul Wali Khan University Mardan, KP, Pakistan.
Email: Amnaorakzai0449@gmail.com

Declaration

Author's Contributions: All authors contributed to the study and approved the final manuscript.
Conflict of Interest: The authors declare no conflict of interest.
Funding: No funding received.

Article History
Received: 3-10-2024
Revised: 12-10-2024
Accepted: 22-10-2024

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. Days to heading ranged from 116 days to138 days, flag leaf area ranged from 18cm2-40cm2, plant height ranged from 84 cm -111 cm, tiller m-2 ranged from 136-424, grain yield from 3240 kg/ ha to 6051 kg/ ha and thousand grain weight ranged from 31g-52 g. Maximum value of GCV reported for tiller per spike (20.2), while minimum value recorded for days to heading (2.70), while high PCV value recorded for1000 grain weight was (25.02), while lowest value recorded for grain yield (0.27). Magnitude of heritability was higher for grain yield (2358) and it was recorded moderate for thousand grain weight (0.50). Maximum value of genetic gain recorded for tiller-2 (65.38) and it was minimum for days to heading (3.73). The findings indicated strong and positive link between grain yield with plant height (r=0.30**), days to heading have a negative correlation with qualities that contribute to production, such as grain yield and 1000-grain weight.

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 [21]. 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 [6]. 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 [20], 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 [6]. Accounting to approximately 751 million tons per annum [23].

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 [18]. A diet based primarily on wheat is richer in fibre than a diet focusing primarily on meat [22]. 0.5 to 1% per year which is below than 2.4% required to satisfy global demand [5]**.** 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 [15]. 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 [17]. 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 [17]. 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 [24]. 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 [19]. 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 Bread 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 heading, flag leaf area, plant height, tiller per square, grain yield and 1000 grain weight.

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 1

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

SOV	DF	DH	FLA	PH	TM^{-2}	GY (kg ha^{-1})	TGWT
Block	1.00	900.47	342.00	67.57	1176.13	274540.50	56.98
Genotype	63	28.35	55.70	74.04	8435.80	685588.56	53.71
Error	49	6.07	13.51	1.75	1783.59	118256.81	19.92
CV%	-	2.00	12.78	1.38	14.76	8.35	10.66

Table 2 Estimate of variance genotype, environmental, phenotypic coefficient of variation (genotypic and

phenotypic) heritability, Phenotypic coefficient of variation, Genotypic coefficient of avariation, selection intensity and genetic gain computed for six important traits for wheat advance lines during 2022-2023 at CCRI, Pirsabak, Nowshera.

Table 2

Traits	GV	VE	VP	GCV	PCV	H^2	SI	Genetic gain
DH	11.00	6.07	17.08	2.70	3.36	0.64	1.40	3.73
FLA	20.72	13.51	34.23	15.83	20.35	0.61	1.40	4.96
PH	35.84	1.75	37.59	6.23	6.38	0.95	1.40	8.18
T^{-2}	3344.45	1783.59	5128.04	20.21	25.02	0.65	1.40	65.38
GY (kg ha^{-1})	285386.58	118256.81	121.00	12.97	0.27	2358.57	1.40	36321.93
TGWT	20.24	19.92	40.16	10.75	15.14	0.50	1.40	4.47

(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 3

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

Traits	DH	FLA	TGWT	PH	TIL	GY
DH	1	-0.13	-0.19*	-0.22*	-0.02	-0.09
FLA		1	-0.06	0.34**	-0.10	0.09
TGWT			1	-0.04	-0.02	-0.09
PH				1	0.09	0.30**
T					1	0.06
GY						1

Days to Heading (no)

The data's statistical analysis reveals highly significant differences (P≤0.10) in the number of days to heading among the tested advance wheat lines (62) and the control cultivars.Genetic variation (11.00) was lower than the total phenotypic variance for days to heading, although it was higher than the independent effect of environmental variance (6.07). The estimated values of 2.70 and 3.36 respectively, for the genotypic coefficient of variation and phenotypic coefficient of variation also suggested a limited range of variability. The estimations of the broad sense heritability, which were recorded for the days to heading, were (0.64%). (Rahman *et al.*, 2016) also indicated that days to heading is genetically controlled and taken into consideration and highlighted similar heritability Days to heading and days to maturity showed highly significant or negative relationship with flag leaf area (r=- 0.13) and tiller and grain yield (r=- 0.09). However, days to heading had strong negative correlation with thousand grain yield (r=-0.19*) and plant height (r=-0.22*). Days to heading revealed weak and negative association with flag leaf area (r = -0.13), (Khan *et al.*, 2015) was also discovered that there was a weak negative association between the days' heading and the flag leaf area.

Flag Leaf Area (cm^2)

Taking into account all variables, an examination of flag leaf area revealed a significantly significant difference between advance wheat lines (62) and check cultivars (02). Genetic variation (11.00) was lower than the total phenotypic variance for days to heading, although it was higher than the independent effect of environmental variance (6.07). The estimated values of 2.70 and 3.36 respectively, for the genotypic coefficient of variation and phenotypic coefficient of variation, also suggested a limited range of variability. coefficient of variation for flag leaf area was (12.78) and heritability was (0.61). Significant positive associations (r=0.34*) and r=10.9*) between leaf area and plant height. But show negative correlation with, grain yield (r=.09), thousand grain weight (r=-0.06*) and tiller (r=-0.10). Our results substantially resemble those of (Khan *et al.,* 2015) in terms of the connection between flag leaf area and plant height (r= 0.34**).

Plant Height (cm)

Mean value for plant height varied from 85-112. The overall phenotypic variance (37.59) for the plant height was substantially larger in magnitude than the genotypic variance (35.48). The findings of this study support (Rahman *et al.,* 2016) findings, which also shown similar outcomes in wheat bread. For the same attribute, broad sense heritability was 0.95, while the genotypic and phenotypic coefficients of variance were (6.23) and (6.28) respectively. Plant height revealed highly positive strong association with flag leaf area (r=0.34**), while showed non-significant positive correlation with tiller (r=0.09), whereas plant height had non-significant negative correlation with thousand grain yield (r=-0.04) while, weak and negative association with days to heading (r=-0.22*). Our research backs up (Jamali and Jamali's 2008) findings, which likewise indicated a significant relationship between plant height and spike length.

Tillers Per Plot

Wheat genotypes tillers m^{-2} ranged from 136-424. The Coefficient of Variation (CV) for tillers m^{-2} was 14%. Phenotypic variance for tiller m^{-2} were 5128.04, which is more than that of environmental variance 1783.59. Magnitude of genotypic coefficient of variation (20.21) is less then phenotypic coefficient of variation (25.02). Similarly, broad sense heritability was higher (0.65) tiller.

Tillers revealed non-significant positive relation with plant height (r=0.09), while tillers exhibit non-significant negative association with thousand grain weight (r= -0.02), flag leaf area (r= -0.10) and days to heading (r= -0.02). Tiller showed unremarkable and positive association with grain yield (r = 0.06), Waqas *et al.,* 2014) noted same result for tillers per plot.

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).

Thousand Grain Weight (gm)

For the 1000-grain yield weight, the analysis of variance revealed extremely significant (P≤0.10) variation among all the genotypes examined. Estimates of genetic variance (20.24) for 1000 grain weight were higher than the equivalent environmental variance (19.92). The phenotypic coefficient of variation (15.140) for the aforementioned attribute was slightly higher than the genotypic coefficient of variation (10.75). Estimates of broad sense heritability (0.50) as recorded for 1000 grans weight, described 10.66 Coefficient of Variation (CV %) for thousand grain weight. 1000-grain weight showed highly significant negatively association with days to heading (r=-0.19*), while flag leaf area (r=-0.06), plant height (r=-0.04) and tiller (r=- 02) showed unremarkable negative association with 1000-grain weight. Higher grain output was found to be directly related with higher grain weight, according to (Kamaran *et a*l., 2019). (Bilgrami *et al.,* 2018) reported similar results. 1000-grain weight revealed a highly significant and positive connection with peduncle length (r=34**).

CONCULSION

Out of the total 64 genotypes, genotype AWL5 line recorded best for maximum flag leaf area and plant height. On the other hand, genotype AWL34 were found best line for tiller. Genotype AWL24 were showed best performance in thousand grain weight, while genotype AWL53 identified for maximum in grain yield. 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. The current study revealed that grain yield was highly and positive correlation with plant height (r=0.30**).

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