

## Research Article

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# Heritability and genetic variability estimates in F<sub>3</sub> populations of bread wheat (*Triticum aestivum* L.)

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### Abstract

The wheat breeders are concentrating to improve the yield potential of bread wheat by developing new varieties with desirable genetic makeup in order to overcome the consumption pressure of the ever-increasing human population. For resolving this situation, research was carried out on eight F<sub>3</sub> populations along with their six parents grown in the Experimental Field. The experiment was carried out in a Randomized Complete Block Design with four replications. The characters studied were; plant height (cm), peduncle length (cm), tiller plant<sup>-1</sup>, spike length (cm), spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup>, seed index (g), grain yield plant<sup>-1</sup> (g), biological yield plant<sup>-1</sup> (g) and harvest index (%). The analysis of variance revealed significant differences among genotypes, hybrids and parents vs. hybrids for all the traits studied. Such results signified the worth of breeding material for further exploitation. The present research indicated that based on average performance, F<sub>3</sub> populations performed better than their parents for most of the traits studied. It means transgressive segregants were present in F<sub>3</sub> populations. If the selection of such potential plants is successful, then they may be utilized for further improvement of bread wheat. The genetic parameters of F<sub>3</sub> progenies indicated that cross TJ-83 x TD-1 displayed higher heritability estimates coupled with more genetic gains for plant height, spike length, spikelets per spike and grains per spike; TJ-83 x Sarsabz for tillers per plant and biological yield plant<sup>-1</sup>; TJ-83 x Moomal for peduncle length, grain yield per plant and harvest index and Moomal x TD-1 for seed index. These F<sub>3</sub> populations may be kept on priority for selection from subsequent filial generations to improve the studied traits in bread wheat.

**Keywords:** Genetic advance; Genetic variability; Heritability; Wheat

### Introduction

Wheat breeders are emphasizing the potential to increase the yield of bread wheat by developing new varieties with the desired genetic makeup to overcome the increasing

consumption pressure of the population [1]. Therefore, the increase in production and output is still the main goal of the prehistoric period and current breeding programs. Genetic manipulation of plant traits is the

best way to increase wheat yield [2, 3]. Grain yield is a product of many yield components, including most economic characteristics. Yield components and their inherent physiological mechanisms interact with crop growth environments and management practices to increase grain yield  $\text{ha}^{-1}$ . The researchers found significant differences in the bread wheat genotypes of the yield components [4, 5]. This variation in yield between varieties indicates that there is a genetic variation between wheat varieties, which is responsible for the success of the breeding program [6]. Among other reasons, food production is strongly influenced by many genetic factors and environmental fluctuations [7].

The heritability estimate determines the extent to which a character is passed from one generation to the next and is a more valuable genetic attribute used with other parameters to predict genetic gain after a particular feature selection [8]. It is speculated that the higher the estimate of heritability, the simpler the selection procedure [9]. It has been emphasized that hereditary power alone is not sufficient to substantially improve the overall selection of late generations unless accompanied by substantial genetic advancement [10]. Estimates of heritability and genetic progression provide parents with knowledge of the inheritance of their offspring and their response to selection. Heritability and genetic progression values help breeders make choices more effective and predict choice responses [11]. For this purpose, genetic information about yield and its components is important for breeders to select and develop new and high yield cultivars. This is why selective genetic manipulation becomes extremely important [12]. In order to select the desired genotype, knowledge of the extent of gene action and variation in the breeding material is important for successful breeding programs

[13, 14]. In the wheat yield improvement program, the selection based on phenotypic variation is not efficient unless the genetic variation of the breeding material is fully evaluated and utilized. Therefore, it is necessary to obtain information on phenotypic and genotypic differences, hereditary and genetic progression. Several studies conducted at different locations in Ethiopia assessed genetic variability between tested bread wheat genotypes [1, 4]. Therefore, this study aimed to study the heritability of  $F_3$  progeny yield and its components and to understand how many phenotypic differences have been passed on to future generations. Therefore, the purpose of this study was to estimate the heritability in the broad sense and the genetic progress of the bread wheat  $F_3$  population to obtain yield and yield-related traits.

#### **Materials and methods**

Eight  $F_3$  populations along with their six parents viz. Sunhri, PBGST-1, Sarsabz, TD-1, TJ-83, and Moomal were grown in the growing season. The experiment was carried out in Randomized Complete Block Design with four replications. At maturity, fifteen plants per genotype from each replication were randomly tagged as treated index plants for recording the data on plant height (cm), peduncle length (cm), Tillers per plant, spike length (cm), Spikelets per pike, Grains per spike, seed index (1000 grain wt, g), Grain yield per plant (g), biological yield (g) and harvest index (%). The data were analyzed according to the statistical technique outlined by Gomez and Gomez [15] through Statistix 8.1 computer software so as to work-out the differences among the genotypes for various traits. The Phenotypic variance usually combines the genotype variance with the environmental variance. Genetic variance has three major components: the additive genetic variance, dominance variance, and epistatic variance. The portion of phenotypic variance that is

due to differences in the environments to which the individuals in a population have been exposed is called environmental variance. The genetic, phenotypic, environmental variances, broad-sense heritability ( $h^2$ ) and expected response to selection were estimated according to the procedure adopted by Baloch et al. [16]. All the inputs are given, and cultural practices were done according to the recommendations of the wheat crop.

L.S.D at  $P \leq 0.05$  for pairwise comparisons was used to determine the critical differences between the mean of genotypes consisted of seven parents and their eight  $F_3$  progenies by using the following formula:

L.S.D (5%) = S.E xt value by using error degrees of freedom

$$\text{Where S.E} = \sqrt{\frac{2MSE}{r}}$$

## Results

### Analysis of variance

The genetic improvement of any crop species depends on the size of the genetic variation and the heritability of the yield and its contribution characteristics. The purpose

**Table 1. Mean squares from analysis of variance for various quantitative traits in wheat genotypes**

Traits	Replication	Genotypes	Parents (P)	$F_3$ hybrids (H)	P vs. H	Error
	(D.F= 3)	(D.F= 13)	(D.F= 5)	(D.F= 7)	(D.F= 1)	(D.F= 39)
Plant height	11.25	433.85**	905.27**	80.74**	548.501**	3.845
Peduncle length	2.08	78.09**	131.87**	15.32**	248.579**	0.837
Tillers per plant	0.01	0.71**	0.75**	0.59**	1.323**	0.037
Spike length	0.16	4.62**	4.25**	1.83**	25.889**	0.139
Spikelets per pike	0.50	14.04**	20.21**	5.40**	43.645**	0.397
Grains per spike	7.77	77.43**	127.91**	41.04**	79.801**	6.608
Seed index	3.79	60.24**	81.86**	21.94**	216.786**	3.593
Grain yield per plant	3.25	7.88**	6.23**	2.23**	55.677**	0.721
Biological yield per plant	16.15	32.72**	31.33**	15.24**	162.044**	3.726
Harvest index	3.64	53.73**	47.99**	41.62**	167.212**	6.131

\*\* = Significant at 1% probability level

of this study was to assess the genetic variance, generalized heritability, and genetic progression under the 20% selection pressure of the wheat  $F_3$  population, for 10 important traits. The results regarding the genetic parameters are listed in graphs 1 to 10. The analysis of variance in table 1 reveals significant differences between the parents of all traits studied and the  $F_3$  population, indicating the presence of genetic variability between the parent and its  $F_3$  progeny. The characteristics of the study were: plant height, spike length, tillers per plant, ear length, spikelet per spike, Grains per spike, seed index (1000-grain weight), grain yield per plant, biomass yield per plant and harvest index. After finding that the mean square differences are significantly different, the data is further processed to determine genetic parameters. Researchers also found significant differences in various polygenic traits of the bread wheat genotype (*Triticum aestivum* L.) [17]. The average performance of the parent and  $F_3$  hybrids shown in table 2. In graphs 1 to 10 their genetic parameters are presented.

### Mean performance of parents and their F<sub>3</sub> progenies

The average performance of the different traits of the 6 parents and their 8 F<sub>3</sub> populations is shown in table 2. The results indicate that for most of the studied traits, the F<sub>3</sub> progeny gave an average higher than their parental mean. The parental line TD-1 showed the smallest plants (58.1 cm), while Sarsabz produced the tallest plants (102.9 cm) compared to the other parents. In the F<sub>3</sub> progeny, the shortest plant (75.4 cm) was observed in the cross TD-1 x Sarsabz, while the TJ-83 x Sarsabz produced the highest plant (91.5 cm), followed by Moomal x TD-1 (90.1 cm). In the parental line, the lower peduncle length was measured in TD-1 (25.9), followed by TJ-83 (26.0 cm), and the highest value was given by Sarsabz (39.5 cm). The offspring TD-1 x Sarsabz showed the lowest value (33.8). The highest value was shown by TJ-83 x Sarsabz (40.0 cm), followed by Sarsabz x Moomal (38.3). The maximum is the tiller produced by the parent TD-1 (5.6), followed by PGBST-01 (5.2), and the minimum tiller is observed in Moomal (4.4). From the offspring, Sunhari x TD-1 (5.9) produced the most bifurcation, followed by TJ-83 x Sarsabz (5.7), while the minimum bifurcation was generated by TJ-83 x Moomal and TJ-83 x TD-1 (4.8). In the parent, the maximum ear length (12.9 cm) recorded in PGBST-1 was obtained from Sarsabz (12.4 cm), and the smallest spike was measured by TD-1 (10.2). In hybridization, the highest value of ear length was recorded by TJ-83 x Moomal (13.9 cm), and the second-highest value was recorded in PGBST-01 x TD-1 (13.2 cm). The lowest value was crossed by Sunhari x TD-1 recording (12.0 cm). The results further show that the largest spikelets per ear are noted in Sarsabz (21.7), followed by PGBST-1 (19.1), and the minimum of TD-1 (15.3) in the parents. The F<sub>3</sub> hybrid Sarsabz x Moomal (20.82) is the highest level in

hybrid, followed by Moomal x TD-1 (20.8), and a small value of this trait was observed in the cross TD-1 x Sarsabz (17.4). The Moomal variety produced the largest number of grains per panicle (63.0), the combined results were the same as Sarsabz (63.0), and TD-1 (49.3) was the smallest. Hybrid Moomal x TD-1 (64.07) calculates the maximum particle size for each ear, followed by Sarsabz x Moomal (63.20), and the minimum is derived from two hybrids TJ-83 x Moomal and TD-1 x Sarsabz (55.3). The parental line PGBST-1 weighted highest seed index (37.0g), then TD-1 (31.1 g), the lowest is given by Sarsabz (26.6 g). The maximum seed index in the isolated population was weighted by PGBST-1 x TD-1 (37.5 g), weighted by Moomal x TD-1 (35.8 g), and recorded by Sunhari x TD-1 (30.4 g). value. For the trait yield per plant, the maximum kernel weight was observed in the parental PGBST-1 (7.7 g), followed by Sarsabz (7.5 g), and the minimum kernel weight was recorded in Moomal (4.7 g). The progeny from Moomal x TD-1 (9.52 g) showed the maximum grain yield per plant, followed by TJ-83 x Moomal (8.8 g), and TJ-83 x TD-1 and TD-1 x Sarsabz produced the smallest but similar yield (7.3, 7.3g). Regarding the biomass yield per plant, Sarsabz produced a maximum (21.3 g), followed by PGBST-1 (18.0 g), while Moomal produced 13.7 g. The offspring Moomal x TD-1 produced the maximum harvest index (22.0%), followed by two F<sub>3</sub> hybrids, such as Sunhari x TD-1, TJ-83 x Sarsabz (21.5, 21.4%), and the minimum value was expressed in TD-1 x Sarsabz. In the parental line, PGBST-1 had the highest (43.1%) harvest index, Sunhari (40.5%) ranked second, and TJ-83 (33.9%) had the lowest. The highest percentage of the harvest index came from the cross TJ-83 x Moomal (46.9%), then the cross TD-1 x Sarsabz (45.2%), and the lowest from TJ-83 x Sarsabz (38.1%).

**Table 2. Mean performance of parents and F<sub>3</sub> populations of wheat for plant height (cm), peduncle length (cm), Tillers per plant, spike length (cm) and spikelets spike, Grains per spike, seed index (g), Grain yield per plant (g), Biological yield per plant(g) and harvest index**

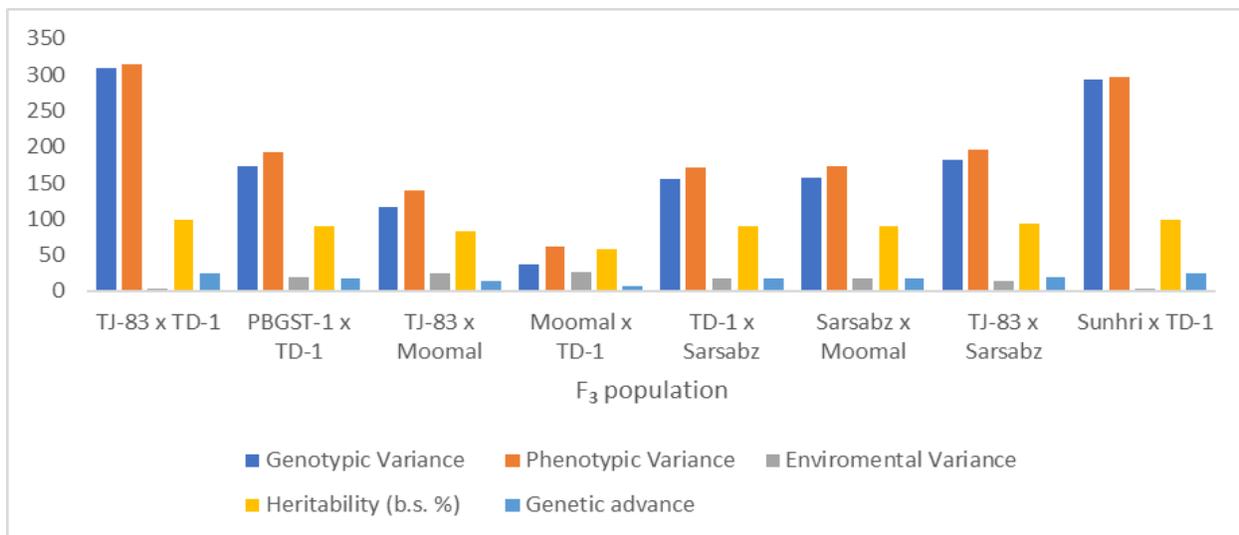
Genotypes (Parents and F <sub>3</sub> hybrids)	Characters							Grain yield per plant	Biological yield per plant	Harvest index
	Plant height (cm)	Peduncle length (cm)	Tillers per plant	Spike length	Spikelets per pike	Grains per spike	Seed index			
	<b>Parents</b>									
Sunhari	81.0	33.2	4.7	10.6	17.6	51.8	30.7	6.1	15.3	40.5
PBGST-1	82.1	33.5	5.2	12.9	19.1	58.2	37.0	7.7	18.0	43.1
Sarsabz	102.9	39.5	5.2	12.4	21.7	63.0	26.6	7.5	21.3	35.8
TD-1	58.1	25.9	5.6	10.2	15.0	49.3	31.1	6.2	16.0	38.6
TJ-83	68.5	26.0	4.9	11.8	17.9	55.9	24.1	4.8	14.3	33.9
Moomal	80.9	37.7	4.4	11.2	16.7	63.0	27.5	4.7	13.7	35.7
Average	78.9	32.6	5.0	11.5	18.0	56.8	29.5	6.1	16.4	37.9
	<b>F<sub>3</sub> hybrids</b>									
TJ-83 x TD-1	84.4	37.9	4.8	12.5	20.7	58.9	34.1	7.3	18.8	39.0
PBGST-1 x TD-1	83.2	34.4	5.2	13.2	19.4	59.7	37.5	8.3	20.9	39.8
TJ-83 x Moomal	88.1	36.9	4.8	13.9	20.6	55.3	34.1	8.8	18.7	46.9
Moomal x TD-1	90.1	37.2	5.6	13.4	20.8	64.0	35.8	9.5	22.0	43.1
TD-1 x Sarsabz	75.4	33.8	5.5	12.2	17.4	55.3	32.0	7.3	16.3	45.2
Sarsabz x Moomal	83.2	38.3	5.3	13.6	20.82	63.2	31.5	7.7	19.3	39.8
TJ-83 x Sarsabz	91.5	40.0	5.7	12.7	19.6	60.1	32.9	8.2	21.4	38.1
Sunhari x TD-1	84.3	37.2	5.9	12.0	19.1	57.8	30.4	8.5	21.5	39.5
Average	85.0	36.9	5.3	12.9	19.8	59.2	33.5	8.2	19.8	41.4
LSD (5%)	2.8	1.3	0.2	0.5	0.9	3.6	2.7	1.2	2.7	3.5

**Genetic parameters of F<sub>3</sub> populations**

**Plant height**

Graph 1 shows the genetic, phenotypic, environmental variance, heritability estimates and genetic advance for plant height. The results further revealed that F<sub>3</sub> populations showed wider range of phenotypic ( $\sigma^2_p = 62.4$  to 313.7) and genetic variances ( $\sigma^2_g = 36.1$  to 310.2) and estimated moderate to high heritability for this trait. The highest heritability with maximum

genetic advances were observed in progenies TJ-83 x TD-1 (98.8%, 24.5) closely followed by Sunhri x TD-1 (98.7%, 23.8), yet lowest heritability was observed in cross Moomal x TD-1 (57.5%, 6.3). On individual population basis, their phenotypic variances were very closer to their respective genotypic variances, consequently higher heritability estimates were recorded ranging from 57.5 to 98.8%.

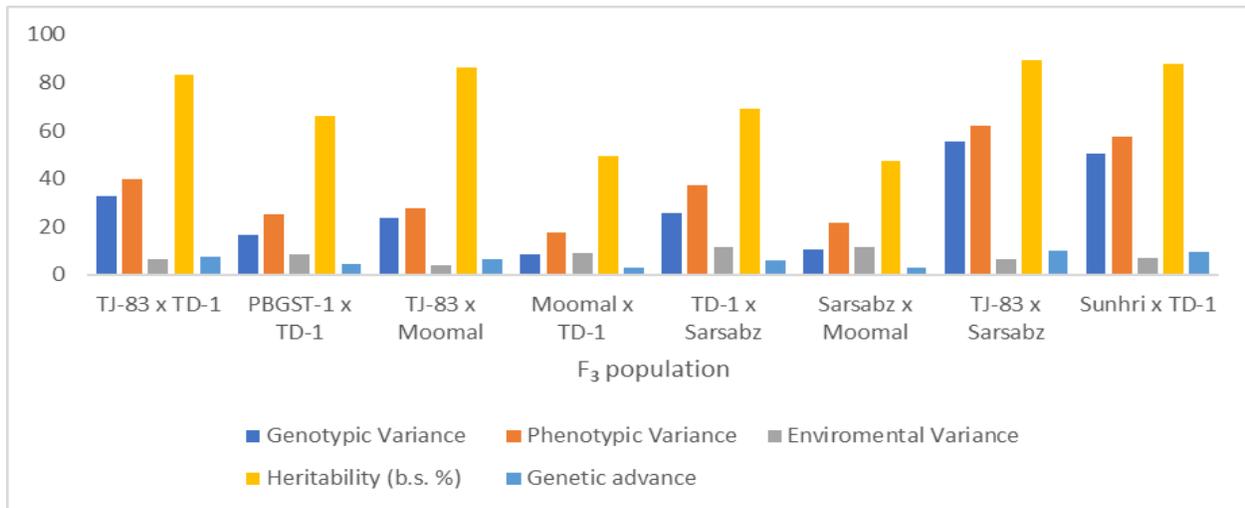


**Graph 1. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Plant height**

**Peduncle length**

Graph 2 describes the genetic variance ( $\sigma^2_g$ ), phenotypic variance ( $\sigma^2_p$ ), environmental variance ( $\sigma^2_e$ ), heritability estimates (b.s.), and genetic progression of peduncle length. The results showed that the F<sub>3</sub> population expressed a broader genotype variance ( $\sigma^2_g = 8.5$  to 55.6). The F<sub>3</sub> population also expressed a moderate to

high heritability estimate for this feature. The maximum heritability and the highest hereditary progression were estimated from the cross TJ-83xSarsabz (89.5%, 9.8), while the minimal heritability was observed in the cross Sarsabz x Moomal (47.4%). However, the lowest genetic progression was calculated from the progeny Moomal x TD-1 (2.8).

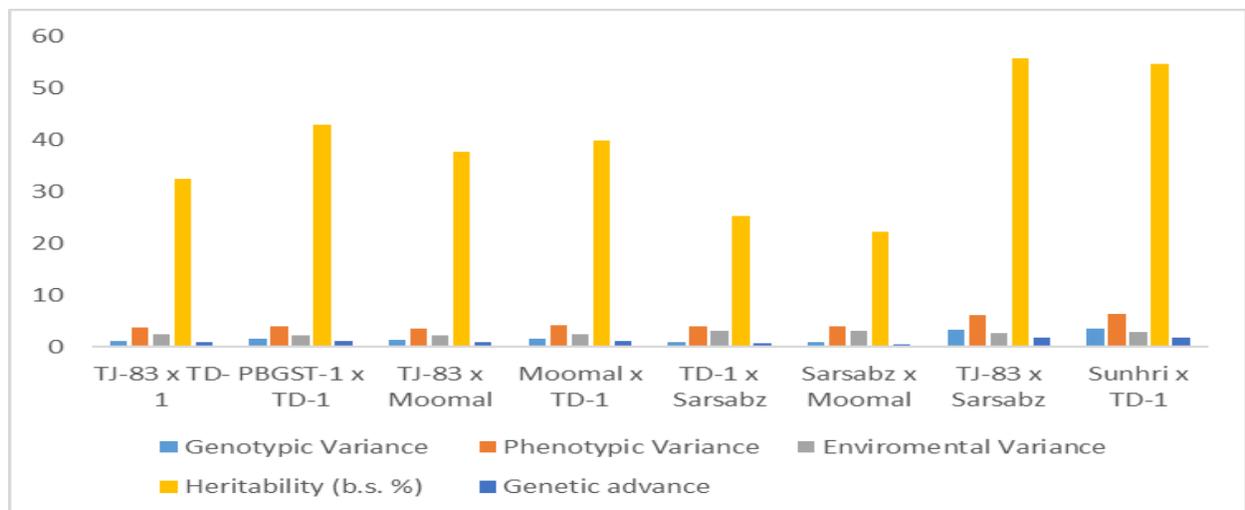


**Graph 2. Heritability estimates and genetic advance of eight F<sub>3</sub> populations for of bread wheat for Peduncle length**

### Tillers per plant

Genetic parameters such as phenotype ( $\sigma^2_p$ ), genotype ( $\sigma^2_g$ ) and environmental ( $\sigma^2_e$ ) variance, heritability estimates (bs) and genetic progression of each plant tiller are shown in graph 3. The results showed that F<sub>3</sub> hybrids exhibited different phenotypic variation ranges ( $\sigma^2_p = 17.3$  to 62.1). Low to moderate heritability was observed for the tillering of each plant. The

highest heritability with the greatest genetic progression was measured in F<sub>3</sub> progeny like TJ-83 x Sarsabz (55.6%, 1.94). However, minimal heritability with low genetic progression was observed in the cross Sarsabz x Moomal (22.3%, 0.6). Phenotypic variation in the F<sub>3</sub> population is usually twice as high as its corresponding genetic variation, so almost all populations have lower heritabilities.

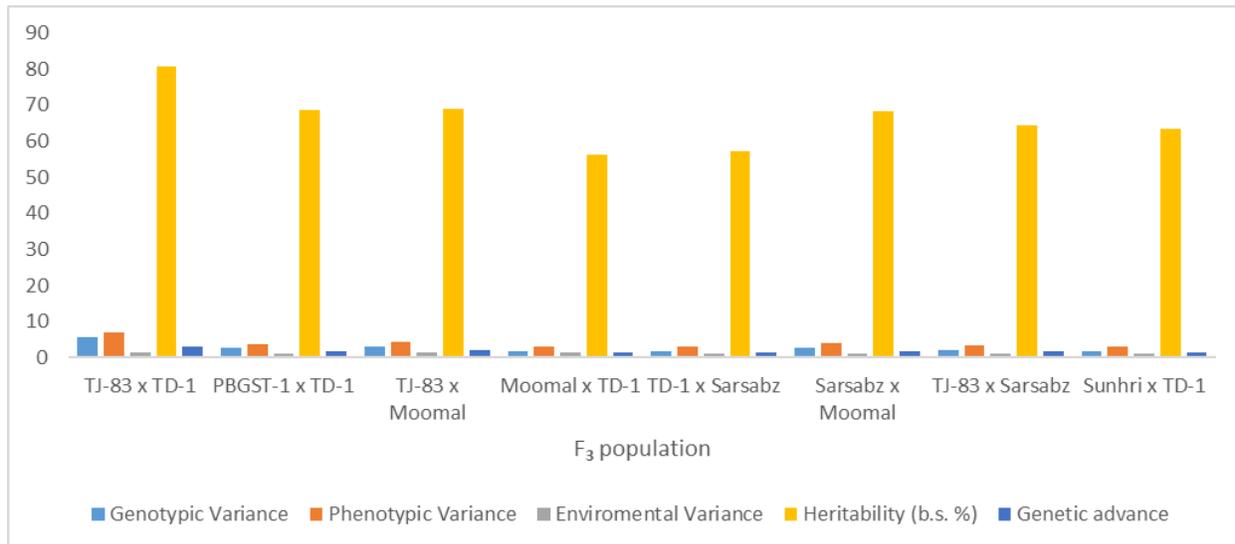


**Graph 3. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Tillers per plant**

**Spike length**

In the case of spike length graph 4, the genotype, phenotype and environmental variation range were  $\sigma^2_g = 1.6$  to  $5.6$ ,  $\sigma^2_p = 2.9$  to  $6.9$  and  $\sigma^2_e = 1.2$  to  $1.4$ , respectively. Crossover TJ-83×TD-1 showed the highest heritability (80.7%), which was associated

with higher genetic progression (2.9), followed by TJ-83×Moomal (68.9%) and genetic progression of 2.0. However, the lowest heritability (56.1%) was estimated by the progeny Moomal x TD-1, and the lowest genetic progression was estimated by the progeny TD-1×Sarsabz (1.3).

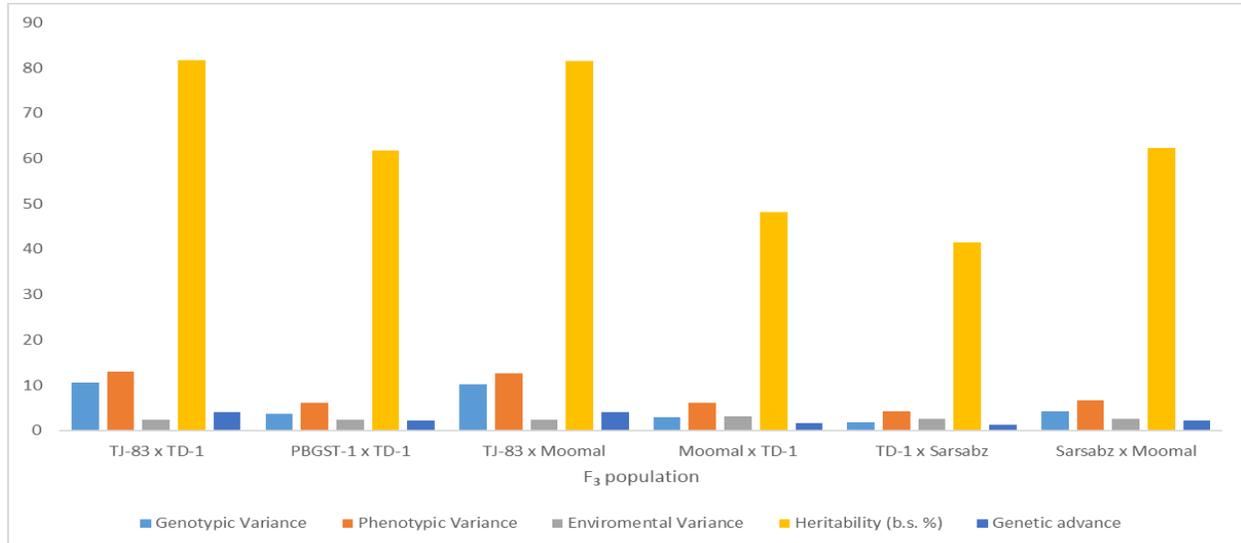


**Graph 4. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Spike length**

**Spikelets per pike**

High and moderate heritability of spikelets per ear was observed. The genotypes ( $\sigma^2_g = 1.7$  to  $10.6$ ), the phenotype ( $\sigma^2_p = 3.3$  to  $13.0$ ) and the environmental variance ( $\sigma^2_e = 1.64$  to  $3.9$ ) were recorded and listed in graph 5. High heritability (81.6%) plus high showed genetic progression by crossover TJ-83 x TD-1 (4.1). However, the lowest heritability is estimated by the offspring

Sunhari x TD-1 (40.3). The minimum genetic progression is estimated to be cross TD-1 x Sarsabz (1.2). Two populations, TJ-83×TD-1 and TJ-83×Moomal, which express very close genetic and phenotypic variations, provide higher estimates of heredity (above 80%). A population with a low heritability variance for its phenotypic variation recorded a low heritability estimate for spikelet spike<sup>-1</sup>.



**Graph 5. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Spikelets per pike**

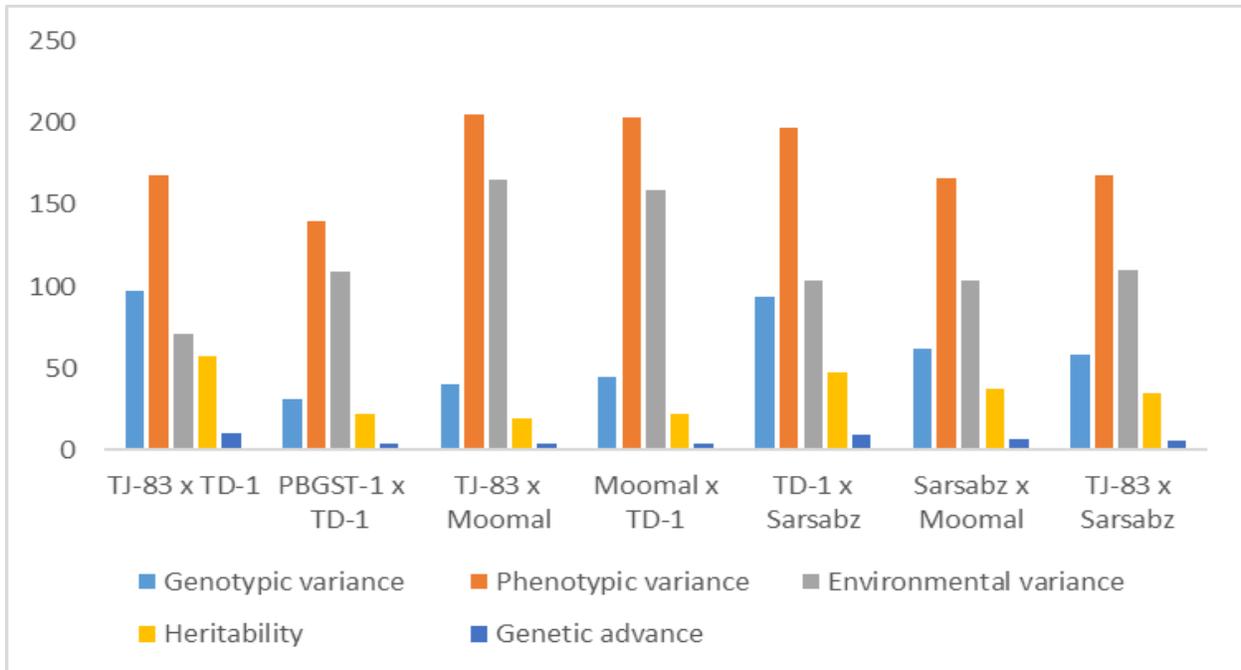
### Grains per spike

The low to moderate heritability of the number of grains per panicle in the F<sub>3</sub> population was estimated. The variance of genotype ranged from  $\sigma^2_g=30.7\sim 96.8$ , the variance of phenotype was  $\sigma^2_p=121.2\sim 204.9$ , and the environmental variance was  $\sigma^2_e=71.3\sim 164.7$ . The F<sub>3</sub> from the cross TJ-83×TD-1 represents the largest but moderate heritability (57.6%), with the highest genetic progress (10.4), followed by TD-1×Sarsabz, the heritability rate is 47.4%, and the genetic progression is 9.31. However, TJ-83×Moomal (19.6%) recorded minimal heritability, but the lowest genetic progression was observed in cross-PBGST-1×TD-1 (3.6). Almost all F<sub>3</sub> populations provide low heritability estimates because environmental differences are greater than their genotypic differences and the boundaries of genetic differences ultimately

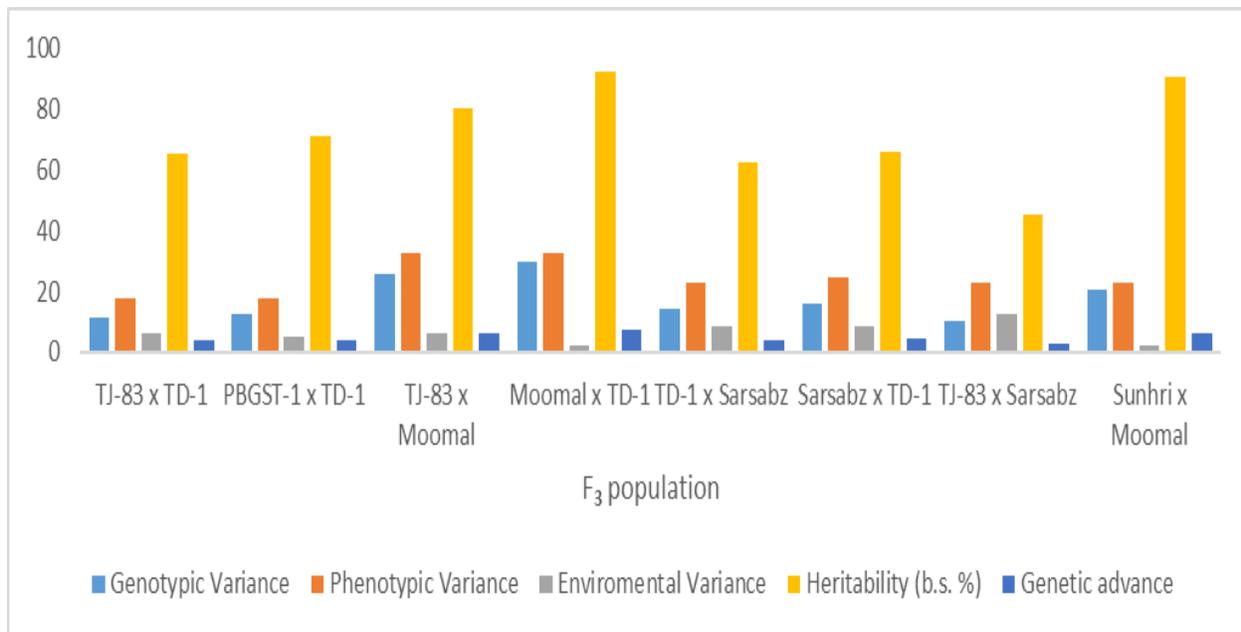
lead to a reduction in heritability estimates (Graph 6).

### Seed index

The characteristic seed index represents a high to medium heritability estimate. The genetic variance ranged from  $\sigma^2_g = 11.4$  to 29.9; the phenotypic variance was  $\sigma^2_p = 17.6$  to 32.4, and the environmental variance was  $\sigma^2_e = 2.1$  to 12.5. The highest heritability was tested in crossover Moomal x TD-1 (92.4%) and maximum genetic progression (7.3) and crossover Sunhari x TD-1 (90.4%). However, the minimal heritability comes from the offspring of the cross TJ-83×Sarsabz (45.4%) and the lowest genetic progression (3.0). Populations with large genetic differences provide relatively more genetic progression, indicating that the added genes control the seed index in these offspring (Graph 7).



**Graph 6. Heritability estimates and genetic advances of eight F<sub>3</sub> populations of bread wheat for Grains per spike**

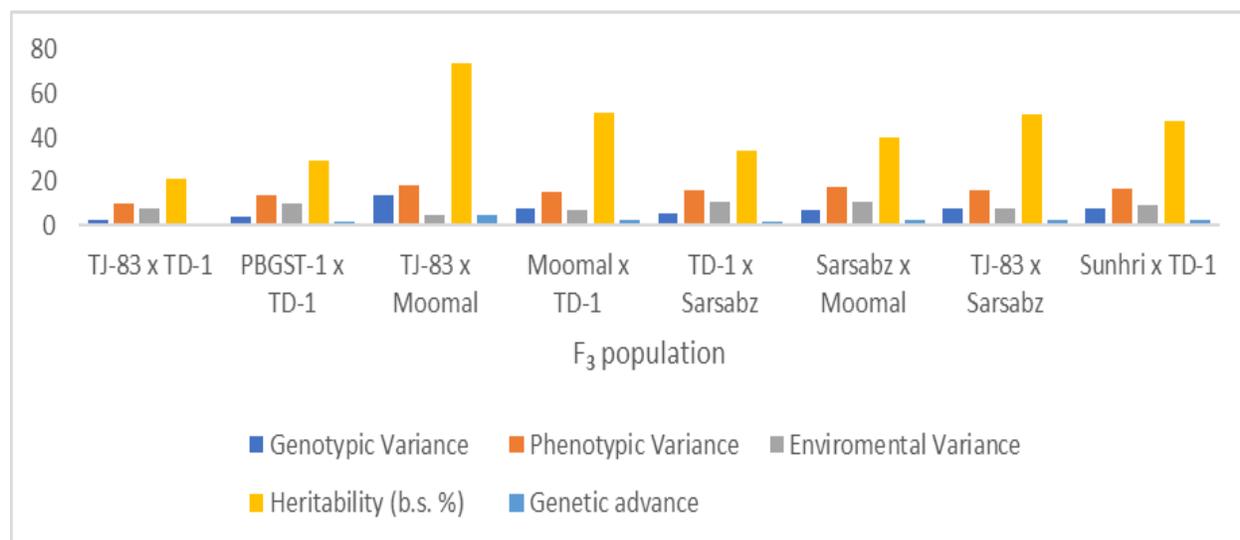


**Graph 7. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Seed index (1000-grain wt.)**

### Grain yield per plant

A low to high heritability estimate was observed for each plant's grain yield (Graph 8). Genotype differences ranged from 2.1 to 13.4, phenotypic differences ranged from 9.86 to 18.1, and environmental differences ranged from 4.7 to 10.9. Low heritability estimates were recorded because the genotype differences in the F<sub>3</sub> population were much lower than their respective phenotypic variations. However, the highest

heritability (4.40) was observed in the progeny TJ-83 x Moomal (73.6%) associated with the greatest genetic progression. The minimum heritability was estimated in the offspring TJ-83 x TD-1 (21.5%) and minimal genetic progression (0.9). In general, almost all F<sub>3</sub> populations exhibit low heritability, thus indicating that environmental differences are not effectively controlled.

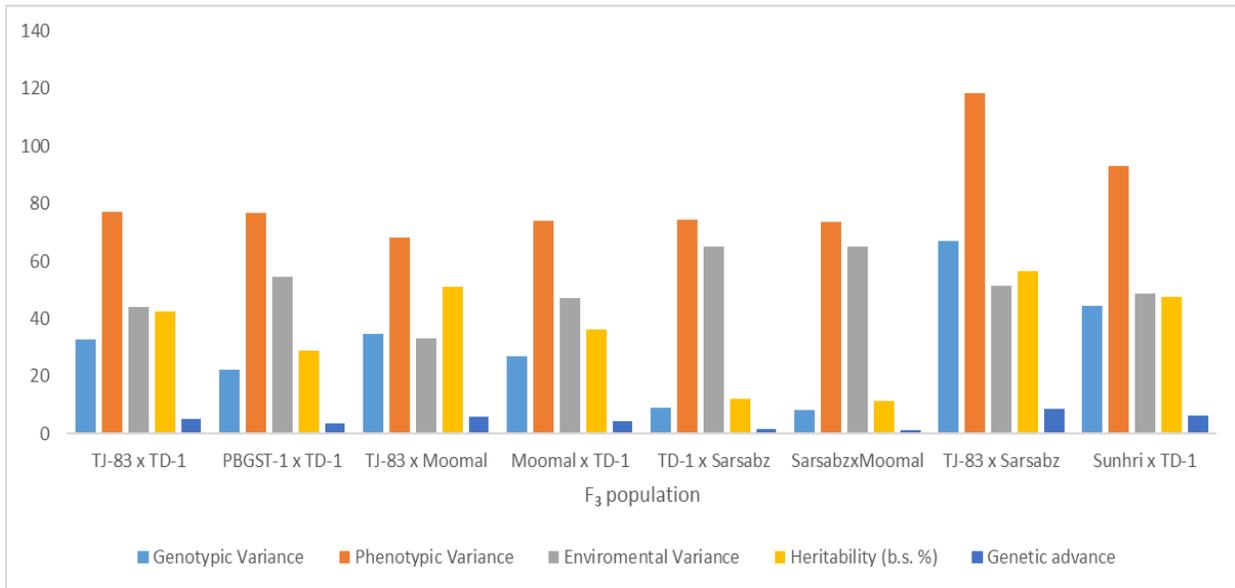


**Graph 8. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Grain yield per plant**

### Biological yield per plant

The F<sub>3</sub> progeny of the biological yield of each plant was estimated to have a moderate to low heritability (Graph 9). The genetic variance ranged from 8.3 to 67.1; the phenotypic differences ranged from 68.0 to 118.4, and the environmental differences ranged from 33.2 to 65.2. The highest heritability (56.6%) and the highest genetic progression (8.6) were observed after TJ-83×Sarsabz crosses, followed by TJ-

83×Moomal (51.1%). However, the minimum heritability was estimated to be cross Sarsabz x TD-1 (11.3%) and the lowest genetic progression (1.3). Except for a small number of people, most of them estimate that the genetic yield of per plant is low. These results indicate that selection can be postponed increasing the biomass production of per plant until later segregation.

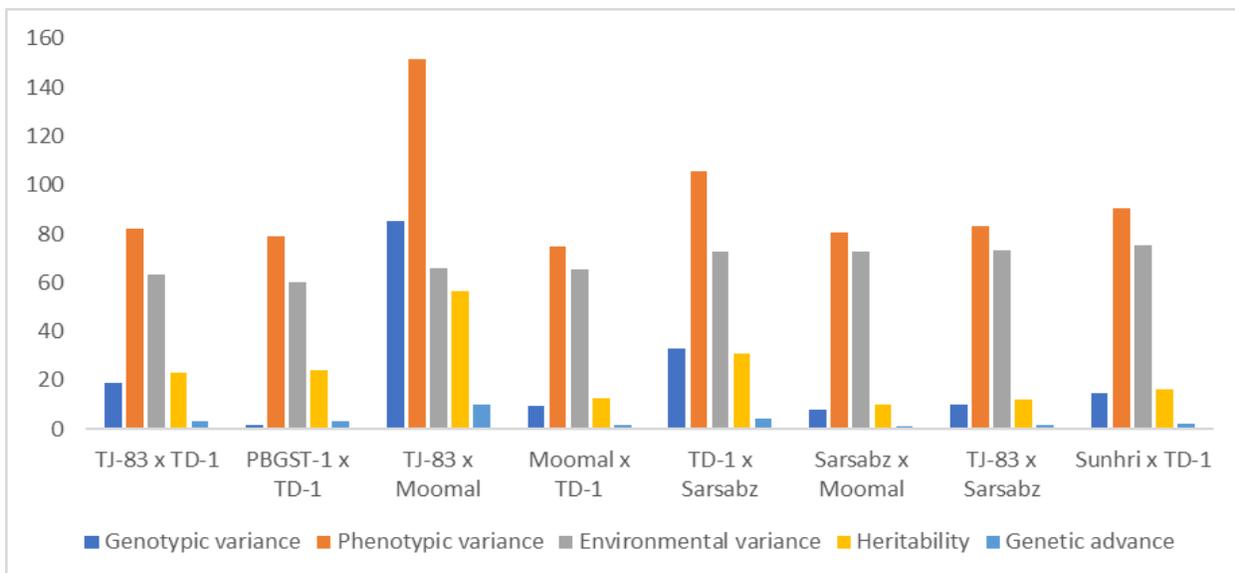


**Graph 9. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Biological yield**

**Harvest index**

Observe the moderate heritability estimates for the harvest index as shown in (Graph 10). The variance range is recorded in the following manner. Genotypes ranged from 8.0 to 85.4; phenotypes ranged from 74.9 to 151.3, and the environment ranged from

60.2 to 75.4. The highest heritability (57.0%) was shown by crossover TJ-83 x Moomal and maximum genetic progression (11.0), while the minimum heritability (10.0%) was represented by cross Sarsabz x TD-1 with the lowest genetic progression (1.3).



**Graph 10. Heritability estimates and genetic advance of eight F<sub>3</sub> populations of bread wheat for Harvest index**

## Discussion

### Plant height

Most researchers believe that plant height is a polygenic trait due to the genetic pattern in the isolated population. Among wheat, semi-dwarf plants with high productivity are more desirable. The results in table 2 indicate that pro-Sarsabz produced the tallest plant (102.9 cm) compared to the other parental lines and F<sub>3</sub> progeny, while TD-1 produced the shortest plant (58.1 cm). In the cross, the offspring TJ-83 x Sarsabz produces the tallest plant, 91.5 cm long, while the shortest plant is recorded by TD-1 x Sarsabz (75.4 cm). The results shown in (Graph 1) indicate that the maximum (98.8%) of the heritability associated with high plant height (24.5) of plant height is represented by the offspring TJ-83 x TD-1. However, other F<sub>3</sub> progeny showed moderate to high heritability estimates and considerable genetic gain. Our results are consistent with the other's findings [3, 17-19] they also studied genetic parameters and recorded higher genotypic variability; medium to high heritability values and plant height greater inheritance the combination of progress. They also observed highly significant differences between parents and hybrids. Existing results with higher heritability estimates and significant genetic progression indicate that plant height is primarily controlled by additive genes, so direct selection may be effective in isolated generations. Furthermore, the results indicate that offspring with ideal genetic parameters TJ-83 x TD-1, Sunhari x TD-1, TJ-83 x Sarsabz, PBGST-1 x TD-1, Sarsabz x Moomal and TD-1 x Sarsabz may be Breeding materials are selected for selection to increase the plant height of subsequent generations.

### Peduncle length

Peduncle length is a portion of wheat plant which is measured from top node to the base of spike. The mean performance shown in

table 2 indicated that among the parents, longest peduncle length (39.5cm) was produced by Sarsabz; while parent TD-1 measured shortest peduncle length measuring 25.9cm. Among F<sub>3</sub> progenies, TJ-83 x Sarsabz produced longest peduncle length (40.0cm) and shortest by TD-1 x Sarsabz (33.8). Results regarding genetic parameters presented in graph 2 demonstrated that the progenies displayed moderate to high heritability and genetic advances. The highest heritability percentage ( $h^2=89.5\%$ ) associated with greater genetic advance (GA=9.8) were expressed by the progeny TJ-83 x Sarsabz. The current results are consistent with the results of other researchers who also recorded the high heritability of inflorescence length [3, 20-22].

### Tillers per plant

Tiller is the main yield component and has a direct impact on food production, so this improvement in characteristics will ultimately increase food production. Regarding the average performance, the parental line TD-1 produced maximum tillers per plant (5.6) closely followed by PBGST-1 (5.2), while parent Moomal produced minimum tillers plant<sup>-1</sup> (4.4). Among the F<sub>3</sub> progenies, cross Sunhari x TD-1 recorded maximum tillers per plant (5.2), while minimum tillers plant<sup>-1</sup> (4.8) were produced by TJ-83 x Moomal and TJ-83 x TD-1. The results presented in graph 3 regarding genetic parameters revealed that most of the F<sub>3</sub> progenies displayed appreciable amount of genetic variability and low to moderate values of heritability, however progenies from cross TJ-83 x Sarsabz expressed highest heritability percentage ( $h^2=55.6\%$ ) with greater genetic advance (GA=1.94), while minimum ( $h^2=22.3$ ) was shown by progenies Sarsabz x Moomal coupled with generic advance of 0.62. Results generally suggested that the F<sub>3</sub> progenies from the crosses like TJ-83 x

Sarsabz and Sunhari x TD-1 may be the choice segregating material for selection to improve the tillers per plant. Similar to our results, significant genetic variation and low to moderate heritability estimates for tillering of each plant were also observed [3, 18, 23].

### **Spike length**

On average, among the parents, PBGST-1 exhibited maximum spike length (12.97cm), while minimum spike length was measured by parent TD-1 (10.2cm). Among the F<sub>3</sub> populations TJ-83 x Moomal produced longer spikes (13.8cm) closely followed by Sarsabz x Moomal (13.6cm). The results regarding phenotypic variance ( $\sigma^2_p$ ), genetic variance ( $\sigma^2_g$ ), environmental variance ( $\sigma^2_e$ ), heritability percentage in broad sense ( $h^2_{b.s}$ ) and genetic advance (GA) summarized in graph 4 revealed that F<sub>3</sub> populations showed considerable amount of genetic variability. However progenies from cross TJ-83 x TD-1 displayed highest heritability ( $h^2=80.9\%$ ) coupled with maximum genetic advance (GA=2.9). The other F<sub>3</sub> progenies like TJ-83 x Moomal ( $h^2=68.9\%$ ), PBGST-1 x TD-1 ( $h^2=68.7\%$ ) and Sarsabz x Moomal ( $h^2=68.3\%$ ) also exhibited higher heritability estimates. Present results are in conformity with those who also observed higher heritability percentage for spike length and controlled by additive genetic factors [3, 20, 24, 25].

### **Spikelets per spike**

The spikelets of each ear steadily promote the grain yield of wheat. Therefore, plant breeders and researchers suggest that spikelets per ear are indeed a good standard for selecting high-yielding wheat varieties. The mean performance of genotypes, shown in table 2 indicated that, among the parents, maximum spikelets per spike (21.7) were produced by Sarsabz. Whilst among the F<sub>3</sub> progenies, Sarsabz x Moomal (20.82) closely followed by Moomal x TD-1 (20.8) and TJ-83 x TD-1 (20.70) recorded a higher

number of spikelets per spike. Results regarding genetic parameters presented in graph 5 demonstrated that the several F<sub>3</sub> progenies exhibited moderate to high heritability and genetic advances. The highest heritability percentage ( $h^2=81.7\%$ ) associated with greater genetic advance (GA=4.1) were expressed by the progenies from cross TJ-83 x TD-1. These results suggested that the progenies TJ-83 x TD-1 and TJ-83 x Moomal with desirable genetic parameters may be considered valuable breeding material for selection of desirable plants in further filial generations to improve this trait. Our findings are consistent with the findings of who observed a moderate to high heritability of spikelets per ear [3, 20, 11, 17].

### **Grains spike<sup>-1</sup>**

The number of grains per spike<sup>-1</sup> is the main yield component, so an increase in the number of grains per panicle will eventually increase the yield of wheat. Based on mean performance, parent Moomal counted maximum grains per spike (63.04), closely followed by Sarsabz (63.0). The genetic parameters presented in graph 6 demonstrated that most of the progenies expressed moderate to low heritability percentages in broad sense indicating the presence of substantial genetic variability. The progenies from crosses TJ-83 x TD-1 displayed the highest percentage of heritability in broad sense (57.6%) coupled with higher genetic advance (10.7). Further, these results suggested that the progenies TJ-83 x TD-1 and TD-1 x Sarsabz may be the choice segregating populations to improve grains per spike. Others also noted the low-medium heritability of the number of grains per panicle [20, 26-28].

### **Seed index (thousand-grain weight)**

Seed index is also a polygenic trait that imposes great impact on grain yield in wheat. The parental mean value for seed index ranged from 24.2 to 37.1g, while the

mean value in  $F_3$  progenies ranged from 30.4 to 37.5g. Results in graph 7 representing the genetic parameters for seed index revealed that almost all the  $F_3$  progenies displayed moderate to high heritability estimates, however maximum heritability percentage in broad sense ( $h^2=92.4\%$ ) and maximum genetic advance ( $GA=7.4$ ) were manifested by progenies Moomal x TD-1 followed by Sunhari x Moomal ( $h^2=90.5\%$ ,  $GA=6.1$ ). Results suggested that  $F_3$  progenies from crosses Moomal x TD-1, Sunhari x Moomal and TJ-83 x Moomal may be the choice breeding material for selection to improve the seed index of wheat. Former workers, their research yielded similar results [3, 19, 20, 25].

#### **Grain yield per plant**

Yield is still the most important of all characteristics in any crop variety. The grain yield per plant largely depends on four factors, i.e. spike length, spikelets spike<sup>-1</sup>, grains spike<sup>-1</sup> and seed index. Based on mean performance presented in table 2, the result indicated that parent PBGST-1 produced maximum grain yield per plant (7.7g) followed by Sarsabz (7.5g). Whilst among the  $F_3$  progenies, Moomal x TD-1 exhibited highest mean value (9.5g). Results regarding genetic parameters presented in graph 8 demonstrated that the progenies displayed low to high heritability estimates and genetic advances. The maximum heritability percentage ( $h^2=73.7\%$ ) associated with greater genetic advance ( $GA=4.4$ ) were expressed by progenies from cross TJ-83 x Moomal. These results suggested that the progenies TJ-83 x Moomal, Moomal x TD-1 and TJ-83 x Sarsabz with desirable genetic parameters may be considered as valuable breeding populations for selection in further filial generations for the improvement of grain yield plant<sup>-1</sup>. Similar results were observed [3, 25, 26, 28].

#### **Biological yield per plant**

Based on mean performance, parent Sarsabz gave maximum biological yield plant<sup>-1</sup> (21.3g), whereas, among the  $F_3$  progenies, the top ranker was Moomal x TD-1 (22.05g). The genetic parameters presented in graph 9 established that most of the progenies expressed low heritability percentages in the broad sense therefore selection for biological yield plant<sup>-1</sup> may carry out in later segregating generations. The progenies from the crosses TJ-83 x Sarsabz displayed highest heritability percentage in broad sense (56.6%) coupled with maximum genetic advance (8.6). The other  $F_3$  progenies such as TJ-83 x Moomal ( $h^2=51.5\%$ ) and Sunhari x TD-1 ( $h^2=47.6\%$ ) also exhibited higher but moderate heritability estimate. The current results are consistent with the results of other researchers they also observed a moderate heritability of individual plant biomass [3, 19, 20].

#### **Harvest index**

Harvest index is also a polygenic trait that has direct impact on grain yield of wheat. The parental mean value for harvest index ranged from 33.9% to 43.1%, while the mean value in  $F_3$  progenies varied from 38.1% to 46.9%. Results shown in graph 10 representing the genetic parameters for harvest index revealed that almost all the  $F_3$  progenies displayed low to moderate heritability estimates, however highest heritability percentage in broad sense ( $h^2=57.0\%$ ) and maximum genetic advance ( $GA=11.0$ ) were manifested by progenies from cross TJ-83 x Moomal, while Sarsabz x TD-1 expressed lowest heritability percentage in broad sense ( $h^2=10.0\%$ ) which was also associated with the lowest genetic advance (1.3). Our findings are consistent with the findings of another researcher they also observed a low to moderate heritability of the seed index in a broad sense [3, 19, 20].

## Conclusion

Result as a whole indicated that most of the F<sub>3</sub> progenies displayed considerable hereditary variation which resulted into high amount heritability observes, and a considerable amount of foretelling genetic gains, suggested that lines under present work trustworthy subjected to phenotypic isolating for desirable segregants from subsequent filial generations so as to improve studied traits in bread wheat. The study generally indicates the genetic variation between the genotypes studied. Most of them have high heritability and genetic, so direct selection has good results for these populations.

## Authors' contributions

Conceived and designed the experiments: MM Nizamani, Performed the experiments: MM Nizamani, FG Nizamani, AA Khokhar, RA Rind, A Mehmood & M Nizamani, Analyzed the data: MM Nizamani, Contributed reagents/ materials/ analysis tools: MM Nizamani, Wrote the paper: MM Nizamani & RA Rind.

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