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GENETIC VARIABILITY AND HERITABILITY FOR YIELD AND YIELD-ASSOCIATED TRAITS OF WHEAT GENOTYPES IN PESHAWAR VALLEY

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ABSTRACT

Knowledge of heritability is important for plant breeders to develop effective selection strategies. This experiment was conducted to estimate genetic variability, heritability and genetic progress in bread wheat genotypes at the University of Agriculture, Peshawar, Pakistan during the 2019/20 growing season. Planting material comprising 12 advanced bread wheat lines was grown in a three-replicate, complete block design. Data were recorded on plant height, spike length, spikelet spikelet-1, spike density, spikelet spike-1 grains, 1000 grain weight, biological yield, grain yield and harvest index. The results showed significant variation for all traits among the wheat genotypes tested. This suggested the existence of reasonable genetic variability among the tested wheat genotypes. Mean data for plant height ranged from 79 cm to 99 cm, for spikelet length from 7.4 cm to 10 cm, and for spikelet^{-1} from 15.13 to 18.63. Similarly, the mean data for spike density ranged from 1.59 to 2.33, for grain spike^{-1} from 29 to 59, and the 1000-grain weight from 27.80 g to 44.77 g. The mean data for the biological yield varied between 4776 kg ha-1 and 6090 kg ha-1, the grain yield between 1810 kg ha-1 and 2716 kg ha-1 and the harvest index between 33% and 54%. The tallest plant was recorded for genotype AUPG01 (99 cm), the maximum spike length was observed for AUPG06 (10 cm), the maximum number of spikelets spike-1 was recorded for AUPG11 (18.63), the value of high spike density became recorded for AUPG03 (2.30), the maximum number of grains spike-1 was observed for AUPG12 (50.47), the maximum weight of 1000 grains was recorded for AUPG07 (44.77 g), the biological yield was maximum for AUPG01 (6090 kg ha-1). In contrast, the grain yield for AUPG07 was maximum (2716 kg ha^{-1}) and the harvest index was recorded for AUPG07 as maximum (54.32%). Wheat genotype AUPG07 outperformed grain yield, while AUPG03 showed a higher biological yield. Maximum spike length, as well as high grain spike^{-1}, were recorded for AUPG06. AUPG07 was observed for the highest 1000-grain weight. Among the genotypes, AUPG02 was distinguished by dwarf traits. The AUPG07 and AUPG06 genotypes resulted in superior grain yield among the genotypes. The heritability for different traits ranged from 0.36 to 0.88. The highest heritability in the broadest sense, coupled with moderate to high genetic advancement, was recorded for plant height, grain spike^{-1}, biological yield, and grain yield. These results could be helpful for wheat breeders to use the most promising wheat genotypes from this study in future breeding programs to improve wheat cultivars.

Keywords: Genetic variability, heritability, genetic advance, yield traits

INTRODUCTION

Bread wheat (Triticum aestivum L.) belongs to the Poaceae/Gramineae family. There are several types of wheat, but the most common and vital is hexaploid because it is grown in a variety of forms around the world for human consumption purposes (Debasis and Khurana 2001). In recent years, almost 95% of the wheat species grown worldwide are bread wheat ($2n = 6x = 42$). By any measure, wheat has become an important cereal crop, providing more calories than other crops. It is a staple of some countries like Pakistan and some others countries, which is why it is considered the king of all cereal. Wheat is grown almost all over the world, accounts for about 30% of the cereal area and provides 20% of the calories for the human population (Khan et al., 2015). In 2019, wheat was grown on 215 million hectares worldwide with a total production of 765 million tons and an average yield of 34254 kg ha-1 (FAO 2018). China was the world's largest wheat producer, while Pakistan ranked eighth in production.

In Pakistan, wheat was grown on 8.79 million hectares with a total production of 25.07 million tons and an average yield of 2850 kg ha-1 (FAO, 2018). The total wheat acreage in Khyber Pakhtunkhwa in 2018-19 was 0.74 million hectares, producing 1.13 million tons of grain with an average yield of 1795 kg/ha (GOP, 2018). Bread wheat gain much consideration as a staple meal for the high population of the world in the form of different backed food products and others.

Bread wheat is considered a staple food for the world's high population in the form of foods with various baking mixes and others. To meet the needs of Pakistan's developing population, wheat genotypes need to be genetically enhanced to produce high yields. Heritability is the ratio of genotypic variance to total phenotypic variance. Broad-sense heritability is the ratio of genetic variance to the total phenotypic variance, while heritability in the narrow sense is the ratio of additive genetic variance to the total variance within the population (Burton 1951). (Mahmud and Kramer 1951).

In plants, breeding heritability plays an important role, i.e. based on the presence of heritability, the performance of the next generation of a population predicts decision-making and decision-making. Based on genetic diversity, many crop species have been studied considering qualitative and quantitative traits to select parents with large genetic distance for the hybridization process (Shekhawat et al., 2001; Arega et al., 2007; Haydar et al., 2007; Ahmadi Zadeh et al., 2011; Daniel et al., 2011). Information about a trait and its heritability lets the breeder know that he can estimate the selection response based on the performance of the succeeding generation (Larik et al., 1989).

Genetic advances and a high heritability score predict and clarify whether selection occurs among genotypes that would be much more effective for yield and yield components (Ghandorah & Shawaf, 1993). Various studies have been carried out by different researchers showing that heredity alone is not always sufficient for the selection process in an advanced generation, which must be complemented by sufficient genetic progress (Memon et al., 2007; Mangi et al., 2008).

For plant breeders, heritability estimation is very useful for selecting elite genotypes from homozygous lines, which is a good index of transmission of a particular trait from parents to their offspring. When estimating heritability with genetic progress compared to estimating heritability alone in predicting genetic gain under selection (Burton and Devane 1953). Heritability estimation shows the degree to which character is passed from parents to offspring and is a more valuable genetic trait used along with other parameters to predict genetic gain after a specific trait selection. Heritability is a parameter often used in setting up breeding programs and forming selection indices. This study was designed to evaluate 12 bread wheat genotypes with the specific objectives of determining genetic variability in bread wheat genotypes, estimating heritability and genetic progress for yield and yield-related traits, and identifying high-yielding wheat genotypes for a future breeding program.

The objectives of the study were to:

- Determine genetic variability in bread wheat genotypes.
- Estimate heritability and genetic progress for yield and yield-related traits.
- Identify high-yielding wheat genotypes for future breeding programs.
- Provide recommendations for the use of promising wheat genotypes in breeding programs.

MATERIALS AND METHODS

The present study was conducted to assess twelve wheat genotypes to estimate heritability and genetic progress for various key plant attributes at the New Experimental Research Farm, The University of Agriculture in 2019-20 (Table 1). Planting material consisting of twelve wheat varieties was grown under randomized complete block design (RCBD) in three replications. Each entry consisted of two rows with a row length of 3 meters and a row-to-row spacing of 0.30 m. Standard agronomic practices were followed from the day of sowing to harvesting.

Statistical Analysis

Field data for various plant traits were subjected to Analysis of Variance (ANOVA) following Steel and Torie (1997). Means were separated at a 5% level of probability using the least significant test (LSD) upon significant differences among genotypes, heritability and genetic advance were also estimated.

Table 1. List of genotypes used in the experiment.

S.No.	Genotypes
1	AUPG01
2	AUPG02
3	AUPG03
4	AUPG04
5	AUPG05
6	AUPG06
7	AUPG07
8	AUPG08
9	AUPG09
10	AUPG10
11	AUPG11
12	AUPG12

Estimation of Heritability

Heritability in a broad sense was estimated as the ratio of genotypic to phenotypic variance (Singh and Ceccarelli, 1996). Broad sense heritability was computed with the help of the following formula.

$Vg = (Mg-Me) / r$

$V_e =$ Me (error mean square)

$Vp = Vg + Ve$

$h^2 = Vg/Vp$

Where,

h^2 (B.S) = Heritability.

Vg = Genotypic variance.

Vp = Phenotypic Variance.

The heritability was categorized as low, moderate and high as given by Robinson et al. (1949).

0-30: Low

30-60: Moderate

60 and above: High

Genetic Advance

The genetic advance was calculated following Allard (1960), as under: -

$$G.\ A = \delta_p \times h^2 \times i$$

Where,

δ_p = standard deviation of phenotypic variance

h^2 = broad sense heritability in fraction.

i = selection intensity.

The value of i = 1.755 (at 10 % selection pressure) was used in this study.

RESULTS AND DISCUSSION

The present study was performed to estimate heritability and genetic progression for various important plant attributes of 12 bread wheat genotypes. Data on plant height, spike length, spike weight, spikelets per spike, kernels per spike, spike density, 1000 kernel weight, biological yield, grain yield and harvest index were documented. Mean squares, mean values, LSD, genotypic and phenotypic variances, heritability, and genetic progress scores for all traits are presented in Tables (2–8), which are described as follows:

Plant Height (cm)

Analysis of variance revealed highly significant (P≤0.01) differences in plant height between genotypes (Table 2). The coefficients of variation (CV) and coefficients of determination (R2) for plant height were 2.62% and 0.92, respectively. The height of plants for a set of 12 genotypes ranged from 79.4 cm to 99.9 cm. The minimum (79 cm) was recorded for AUPG02 while the maximum height (99.9 cm) was recorded for AUPG01 (Table 3). The least significant difference (LSD 5%) for plant height was 3.89 cm. Heritability and genetic advancement for plant height were 0.88 and 12.52 cm, respectively. High heritability and moderate genetic advancement (Table 8) indicated that selection by plant height would be an appropriate criterion. In the present study, plant height heritability value was high and genetic progress was moderate. These results contradict the early researchers like Kamboj (2003), Memon et al. (2007) and Khan and Naqvi (2011) who reported high heritability and low genetic progression for plant height. Conflicting results could be due to differences in the genetic material used in the studies.

Spike length (cm)

Analysis of variance revealed highly significant (P≤0.01) differences in spike length between genotypes (Table 2). The coefficients of variation (CV) and coefficients of determination (R2) for spike length were 7.58% and 0.68, respectively. The length of the spike for genotypes ranged from 7.4 cm to 10.0 cm. The minimum spike length (7.37 cm) was recorded for AUPG02, while the maximum spike length (10.0 cm) was recorded for AUPG06 and AUPG07 (Table 3). The least significant difference (LSD 5%) for spike length was 1.12 cm. Heritability and genetic advance for spike length were 0.50 and 1.02 cm, respectively. Moderate heritability and low genetic advance (Table 8) indicated that care should be taken in spike length selection. In the present study, the heritability value for spike length was moderate and genetic advancement was low. These results contradict the early researchers like Kamboj (2003), Memon et al. (2007) and Khan and Naqvi (2011) who reported high heritability and low genetic advance for spike length. Conflicting results could be due to differences in the genetic material used in the studies.

Spike weight (g)

Significant (P ≤ 0.01) differences between genotypes for spike weight were observed (Table 2). The estimated coefficients of variation (CV) and coefficients of determination (R2) for spike weight were 11.72 and 0.92, respectively. Mean weight average values range from 1.15 g to 2.33 g. The minimum mean weight (1.15 g) was recorded for AUPG05, followed by AUPG09, which were not statistically different from each other. The maximum spike weight (2.33 g) was noted for AUPG07 (Table 3). The least significant difference (LSD 5%) for spike weight was 0.35 g. High heritability (0.89) for spike weight coupled with low genetic advancement (1.18 g) was estimated (Table 8). Kihrizi et al. (2010) reported these results, where heritability was also high for spike weights in bread wheat associated with low genetic advance.

Spikelets spike^{-1}

Mean square values for spikelets per spike showed highly significant (P≤ 0.01) differences between genotypes for spikelet spikelet-1 (Table 2). The estimated coefficients of variation (CV) and coefficients of determination (R2) for spike weight were 1.39 and 0.96, respectively. Spikelets per spike range from 15.13 to 18.63 among genotypes. The maximum number of spikelets per spike (18.63) was recorded for AUPG11 and the minimum number of spikelets per spike (15.13) was recorded for AUPG09 (Table 3). The least significant difference (LSD 5%) for spikelets per spike was 0.38. The heritability for spikelets per spike was high at 0.94 with a low genetic advance of 2.02 spikelets (Table 8). This trait expresses a high heritability value, indicating that the environment does not influence this trait and selection would be much more effective in the next few generations. Our results contrast Abinasa et al. (2011) who reported moderate heritability for this trait. In agreement with the results of Memon et al. (2007) who reported high heritability and showed dissimilarity to our results in having greater genetic advance for the number of spikelets per spike. On the other hand, Ajmal et al. (2009).

Number of grains spike^{-1}

Remarkably, highly significant (P ≤ 0.01) differences between the genotypes for the number of grains per ear were recorded (Table 4). The estimated coefficients of variation (CV) and determination coefficients (R2) for grains per spike were 14.56 and 0.75, respectively. The number of kernels per ear ranged from 29.60 to 59.40. The maximum number of grains per spike (59.40) was recorded for AUPG06 and the minimum number of grains per spike (29.60) was recorded for AUPG08 (Table 5). The least significant difference (LSD 5%) for grains per spike was 10.05 grains. The heritability for the number of kernels per ear was 0.62 coupled with a genetic advance of 10.66 (Table 8). The results show high heritability and low genetic progress for the number of kernels per ear. Eid (2009), Aycieck and Yildirim (2006) reported low heritability estimates for the number of kernels per ear in their studies. While Gupta and Verma (2000) and Haq et al. (2008). Ajmal et al. (2010) reported high heritability with moderate genetic advance for this parameter.

Spike density

Mean square values indicated significant ($P \leq 0.05$) differences between genotypes for spike density (Table 4). The estimated coefficients of variation (CV) and coefficients of determination (R2) for spike density were 11.93 and 0.59, respectively. Mean peak density values ranged from 1.59 to 2.33 (Table 5). The maximum spike density value (2.33) was recorded for AUPG03, while the minimum spike density value (1.59) was recorded for AUPG10. The least significant difference (LSD 5%) for spike density was 0.38. The observed heritability was 0.38 with a genetic advance value of 0.21 for spike density (Table 8), showing moderate heritability and low genetic advance. These results indicated that care should be taken in selecting spike density.

1000-grain weight (g)

Highly significant ($P \leq 0.01$) differences between genotypes for 1000-grain weight (Table 4). The coefficients of variation (CV) and coefficients of determination (R2) estimated for 1000 grain weight were 11.11 and 0.76, respectively. The mean 1000-grain weight for the genotypes ranged from 27.80 to 44.77 g. A maximum weight of 1000 grains (44.77 g) and a minimum weight of 1000 grains (27.80 g) for AUPG05 was recorded for AUPG07 (Table 5). The least significant difference (LSD 5%) for the 1000-grain weight was 6.87 g. The heritability observed was 0.64 with a genetic advance value of 7.82 g (Table 8), showing moderate heritability and low genetic advance. These results are also consistent with some of the earlier findings by Haq et al. (2008), Ferdous et al. (2000), Eid (2009) and Yadav et al. (2011) they also reported high heritability for the 1000 grain weight. However, these results contradict early researchers such as Gupta and Verma (2000), who reported moderate heritability and little genetic progress for a 1000-grain weight. The differences could be due to the genetic material used or the environmental conditions in the study.

Biological yield

Analysis of variance revealed significant (P≤0.01) differences between genotypes for biological yield (Table 6). The estimated coefficients of variation (CV) and coefficient of determination (R^2) for biological yield were 2.95 and 0.84, respectively. The mean values for the biological yield were between 4776.67 kg ha^{-1} and 6090.33 kg ha^{-1} (Table 7). The minimum biological yield (4776.67 kg ha^{-1}) was recorded for AUPG03, while the maximum biological yield (6090.33 kg ha^{-1}) was recorded for AUPG01 (Table 7). The least significant difference (LSD 5%) for biological yield was 260.90 kg ha-1. The heritability value for the biological yield was 0.81 with a genetic advance of 515.14 kg ha^{-1} (Table 8). Based on the results, the biological yield shows high heritability and the highest value of genetic advance. The high value of heritability and genetic advance confirmed the results of Gupta and Verma (2000) and Yadav et al. (2011) for biological yield.

Grain yield

Notable Difference (P ≤0.01) Differences between genotypes for grain yield (Table 6). The estimated coefficients of variation (CV) and coefficient of determination (R2) for grain yield were 3.34 and 0.95, respectively. Average grain yields ranged from 1810 kg ha^{-1} to 2716.67 kg ha^{-1}. Maximum grain yield (2716.67 kg ha-1) was recorded for AUPG07 while minimum grain yield (1810 kg ha^{-1}) was recorded for AUPG09 (Table 7). The least significant difference (LSD 5%) for grain yield was 125.98 kg ha^{-1}. The heritability for grain yield was 0.92 and the genetic advancement score was 453.14 (Table 8), indicating high heritability and genetic advance. A high estimate of heritability and genetic advance provides information for effective selection. These results confirm the results of Khan and Naqvi (2009), Mangi et al. (2010), Ajmal et al. (2009) and Haq et al. (2008) who observed high heritability of grain yield.

Harvest index

Analysis of variance showed a significant (P≤ 0.05) difference in harvest index between genotypes (Table 6). The estimated coefficients of variation (CV) and coefficients of determination

(R2) for spike weight were 16.04 and 0.59, respectively. The mean values for the harvest index were between 33.89 and 54.32%. The maximum harvest index (54.32%) was recorded for AUPG07, while the minimum harvest index (33.89%) was recorded for AUPG09 (Table 7). The crop index's least significant difference (LSD 5%) was 11.17%. Heritability was estimated at 0.36 coupled with low genetic advance rated at 5.09% (Table 8). Low heritability and low genetic advance were recorded for the harvest index. Gupta and Verma (2000) reported low heritability of the harvest index. Ferdous et al. (2009) and Sharma (2007) reported high genetic advance, while Yadav et al. (2011) reported high heritability for the harvest index.

Table 2. **Mean squares for plant height, spike length, spike weight, and spikelets per spike of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20**

SOV	DF	Plant height	Spike length	Spike weight	Spikelets spike^{-1}
REP	2	13.36	0.20	0.01	0.03
GENO	12	130.85**	1.86**	1.17**	3.09**
ERROR	24	5.55	0.45	0.05	0.05
CV (%)	--	2.62	7.58	11.72	1.39
R^2	--	0.92	0.68	0.92	0.96

** = Significant at 1% probability level.

Table 3. **Mean values for plant height, spike length, spike weight, and spikelets per spike of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.**

Genotypes	Plant height (cm)	Spike length (cm)	Spike weight (g)	Spikelets spike^{-1} (no.)
AUPG01	99.00	8.77	2.11	16.25
AUPG02	79.00	7.37	1.93	15.88
AUPG03	79.67	7.63	2.09	17.50
AUPG04	94.00	8.87	2.00	17.25
AUPG05	97.00	8.93	1.15	17.88
AUPG06	91.33	10.00	1.39	16.38
AUPG07	92.00	9.90	2.23	17.50
AUPG08	92.33	8.63	1.94	15.88
AUPG09	85.00	9.23	1.25	15.13
AUPG10	97.00	9.90	2.22	15.75
AUPG11	82.00	8.67	2.06	18.63
AUPG12	89.00	8.77	1.31	15.88
LSD (5%)	3.89	1.12	0.35	0.32

Table 4. **Mean squares for grains per spike, 1000-grain weight, and spike density of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.**

SOV	DF	Grains spike^{-1}	Spike density	1000 GWT
REP	2	10.15	0.02	1.14
GENO	12	221.95**	0.14*	110.25**
ERROR	24	37.11	0.05	17.34
CV (%)	--	14.56	11.92	11.11
R^2	--	0.75	0.58	0.76

*,** = Significant at 5 and 1% probability levels, respectively

Table 5. **Mean values for grains per spike, 1000 grain weight, and spike density of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.**

GENO	Grains spike^{-1} (no.)	Spike density (no.)	1000 GWT (g)
AUPG01	43.07	1.86	34.33
AUPG02	48.40	2.16	37.47
AUPG03	42.40	2.30	42.33
AUPG04	38.60	1.95	43.33
AUPG05	31.07	2.01	27.80
AUPG06	59.40	1.64	28.47
AUPG07	39.20	1.79	44.77
AUPG08	29.67	1.87	33.13
AUPG09	30.20	1.64	39.67
AUPG10	40.93	1.59	40.23
AUPG11	48.33	2.15	42.80
AUPG12	50.47	1.81	41.27
LSD (5%)	10.05	0.38	6.87

Table 6. Mean squares for biological yield, grain yield, and harvest index of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.

SOV	DF	Biological yield	Grain yield	Harvest index
REP	2	40000.00	30588.88	40.08
GENO	12	344204.75**	222886.03**	118.75*
ERROR	24	25000.00	5828.66	45.84
CV (%)	--	2.96	3.34	16.04
R^2	--	0.87	0.96	0.59

*' ** = Significant at 5 and 1% probability levels, respectively

Table 7. Mean values for biological yield, grain yield, and harvest index of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.

GENO	Biological yield (Kg ha^{-1})	Grain yield (Kg ha^{-1})	Harvest index
AUPG01	6090.33	2176.67	35.75
AUPG02	5528.33	2431.33	45.65
AUPG03	4776.67	2508.00	51.82
AUPG04	5641.67	2698.67	47.33
AUPG05	5150.83	2446.80	41.78
AUPG06	5278.17	2246.50	42.33
AUPG07	5001.67	2716.67	54.32
AUPG08	5733.17	2194.83	38.33
AUPG09	5111.67	1810.00	33.89
AUPG10	5243.17	2118.17	40.40
AUPG11	5306.67	1938.33	34.08
AUPG12	5341.67	2080.00	40.69
LSD (5%)	260.90	125.98	11.17

Table 8. **Genotypic variance, phenotypic variance, heritability, and genetic advance for spike length, spike weight, spikelets per spike, grains per spike, 1000-grain weight, spike density, biological yield, grain yield, and harvest index of 12 wheat genotypes evaluated at the University of Agriculture, Peshawar during 2019-20.**

Parameter	Vg	Ve	Vp	H^2	GA
Plant height	41.76	5.55	47.32	0.88	12.57
Spike length	0.47	0.45	0.92	0.50	1.01
Spike weight	0.37	0.05	0.42	0.89	1.10
Spikelets spike^{-1}	1.01	0.05	1.07	0.94	2.02
Grains spike^{-1}	61.62	37.11	98.72	0.62	10.67
1000 GWT	30.97	17.34	48.31	0.64	7.83
Spike density	0.03	0.05	0.08	0.38	0.21
Biological yield	106401.58	25000.00	131401.58	0.81	515.14
Grain yield	72352.45	5828.66	78181.12	0.93	454.13
Harvest index	24.30	45.84	70.14	0.36	5.09

h^2 = Heritability GA = Genetic Advance

CONCLUSIONS AND RECOMMENDATIONS

Based on the findings of the current research work, the following conclusions and recommendations for use in future breeding programs were made.
The outcome of the present study showed a wide range of variability among the wheat genotypes. Among these

- Desirable minimum plant height was observed for AUPG02.
- Genotype AUPG07, followed by AUPG06 and AUPG04 out-yielded all other genotypes due highest performances for grain yield. It is, therefore, recommended that these genotypes could be included in further breeding programmes.
- Genotypes AUPG07 and AUPG04 had higher 1000-grain weights.
- High heritability coupled with moderate to high genetic advance was recorded for plant height, grains spike^{-1}, biological yield, and grain yield, providing room for future improvement.

Implications of the study's findings for wheat farmers and breeders:

- The study identified significant genetic variability among the tested wheat genotypes, indicating the potential for improving yield and yield-associated traits in wheat crops.
- The findings provide valuable information for wheat breeders to select and use the most promising genotypes in future breeding programs to develop improved wheat cultivars.
- The study highlighted specific genotypes, such as AUPG07, AUPG06, and AUPG04, that outperformed others in terms of grain yield, suggesting their potential for inclusion in breeding programs.
- The heritability estimates for traits like plant height, grain spike-1, biological yield, and grain yield were moderate to high, indicating the possibility of genetic improvement through selection.
- The results can guide wheat farmers in selecting suitable wheat genotypes for cultivation, considering traits like plant height, grain yield, and harvest index.

Future research directions that can build on the findings of the study:

- Conduct further studies to identify the specific genetic factors responsible for the observed variability in yield and yield-associated traits in wheat genotypes. This can help in understanding the underlying mechanisms and facilitate targeted breeding efforts.

- Investigate the relationship between genetic variability and environmental factors to determine the stability of the identified genotypes across different growing conditions. This can provide insights into genotype-by-environment interactions and help in developing adaptable wheat cultivars.

- Explore the potential of incorporating high-performing genotypes, such as AUPG07, AUPG06, and AUPG04, into breeding programs to enhance grain yield. This can be done through hybridization or introgression of desirable traits from these genotypes into elite breeding lines.

- Assess the performance of the identified genotypes in field trials and on-farm evaluations to validate their potential for practical application. This can provide more reliable data on their agronomic performance and yield stability.

- Investigate the genetic basis of other important traits, such as disease resistance, drought tolerance, and nutrient use efficiency, in the identified genotypes. This can contribute to the development of improved wheat varieties with multiple desirable traits.

- Conduct comparative studies to evaluate the performance of the identified genotypes against existing commercial cultivars to assess their superiority and potential for commercial adoption.

LITERATURE CITED

Abinasa, M., A. Ayana, and G. Bultosa 2011. Genetic variability, heritability, and trait association in durum wheat (*Triticum turgidum* L var. durum) genotypes. African J. Agri. Res. 6(17): 3972-3979.

Ahmadi zadeh, M., H. Shahbazi, M. Valizadeh, and M. Zaefizadeh 2011. Genetic diversity of durum wheat landraces using multivariate analysis under normal irrigation and drought stress conditions. African J. Agri. Res. 6(10): 2294-2302.

Arega, G., M. Hussein, and H. Singh 2007. Genetic divergence in selected durum wheat genotypes of Ethiopian plasma. African J. Crop Sci. 15(2): 67-72.

Ajmal, S. U., N. Zakir, and M. Y. Mujahid 2009. Estimation of genetic parameters and character association in wheat. J. Agri. Biol. Sci. 1(1): 15-18.

Allard, R. W. 1960. Principles of Plant Breeding. John Wiley & Sons, Inc.

Aycicek, M., and T. Yildirim 2006. Heritability of yield and some yield components in bread wheat (Triticum aestivum L.) genotypes. Bangladesh J. Bot. 35(1): 17-22.

Burton, W. G., and E. H. Devane 1953. Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material. Agron. J. 45: 478-481.

Daniel, H., M. Mebrahtom, and G. Tsige 2011. Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. J. Cent. Eur. Agric. 12(2): 344-352.

Debasis, P., and P. Khurana 2001. Wheat biotechnology: A minireview. Electron. J. Biotechnol. 4(2): 1-29.

Eid, M. H. 2009. Estimating heritability and genetic advance of yield traits in wheat (Triticum aestivum L.) under drought conditions. Int. J. Genet. Biol. 1(7): 115-120.

FBS. 2010. Federal Bureau of Statistics. Economic survey. Gov. Pakistan, Islamabad.

Food and Agriculture Organization 2018.

Ferdous, M. F., A. K. M. Shamsuddin, D. Hasan, and M. M. R. Bhuiyan 2009. Performance and variability for yield and yield contributing characters in spring wheat. J. Bangladesh Agric. Univ. 8(2): 195-197.

El-Shawaf, I. I. S. 1993. Genetic variability, heritability estimates, and predicted genetic advance for some characters in faba bean. J. King Saud Univ. Wheat J. Agric. Res. 28(3): 193-200.

Gupta, S. K., and S. R. Verma 2000. Variability, heritability, and genetic advance under normal and rainfed conditions in durum wheat (Triticum durum_desj). Indian J. Agric. Res. 34(2): 122-125.

Haq, W. U., M. F. Malik, M. Rashid, M. Munir, and Z. Akram 2008. Evaluation and estimation of heritability and genetic advancement for yield-related attributes in wheat lines. Pak. J. Bot. 40: 1699-1702.

Haydar, A., M. B. Ahmed, M. M. Hannan, M. A. Razvy, M. A. Mandal, M. Salahin, R. Karim, and M. Hossain 2007. Analysis of genetic diversity in some potato varieties grown in Bangladesh. Middle-East J. Sci. Res. 2(3-4): 143-145.

Kihrizi, D., K. Cheghamirza, M. Kakaei, R. Mohammadi, and A. Ebadi 2010. Heritability and genetic gain of some morphophysiological variables of durum wheat (Triticum turgidum var. durum). African J. Biotechnol. 9(30): 4687-4691.

Kamboj, R. K. 2003. Skewness, heritability, and genetic advance in two F2 populations of bread wheat (Triticum aestivum L. Em Thell.). Madras Agric. J. 90(7-9).

Khan, A. S., I. Salam, and Z. Ali 2003. Heritability of various morphological traits in wheat. Int. J. Agric. Biol. 5(2): 138-140.

Khan, N., and F. N. Naqvi 2011. Heritability of morphological traits in bread wheat advanced lines under irrigated and non-irrigated conditions. Asian J. Agric. Sci.

Khan, O. U., I. Fahid, and T. S. Muhammad 2015. Heritability analysis for yield-associated traits in wheat (Triticum aestivum L.). Sci. Technol. Dev. 34(4): 260-264.

Larik, A. S., H. M. I. Hafiz, and A. M. Khushk 1989. Estimation of genetic parameters in wheat populations derived from inter/cultivar hybridization. Pak. Phyton 1: 51-56.

Mangi, S. L., M. L. Sial, B. A. Ansari, M. A. Arain, K. A. Laghari, and A. M. Mirbahar 2010. Heritability studies for grain yield and yield components in F3 segregating generation of spring wheat. Pak. J. Bot. 42(3): 1807-1813.

Mahmud, I., and H. H. Kramer 1951. Segregation for yield, height, and maturity following a soybean cross. Agron. J. 43: 605-609.

Memon, S., M. D. Qureshi, B. A. Ansari, and M. A. Sial 2007. Genetic heritability for grain yield and its related characters in spring wheat (Triticum aestivum L.). Pak. J. Bot. 39(5): 1503-1509.

Sharma, S. N., and Y. Sharma 2007. Estimates of variation and heritability of some quantitative and quality characters in Triticum turgidum L. ssp. durum (Desf.). Acta Agron. Hung. 55(2): 261-264.

Shekhawat, U. S., P. Vijay, and D. L. Singhania 2001. Genetic divergence in barley (Hordeum vulgare L.). Indian J. Agric. Res. 35(2): 121-123.

Mangi, S. A., M. A. Sial, B. A. Ansari, M. A. Arain, K. A. Laghari, and A. A. Mirbahar 2008. Heritability studies for grain yield and yield components in F3 segregating generation of spring wheat. Pak. J. Bot. 42(3): 1807-1813.

Steel, R. G. D., and J. H. Torrie 1997. Analysis of covariance. In Principles and Procedures of Statistics: A Biometrical Approach (pp. 401-437). McGraw-Hill.

Yadav, A. K., R. K. Maan, S. Kumar, and P. Kumar 2011. Heritability variability and genetic advance for quantitative characters in hexaploid wheat (Triticum aestivum). Electron. J. Plant Breed. 2(3): 40-405.