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ELUCIDATION OF INDIGENOUS WHEAT BREEDING LINES FOR GRAIN YILED AND YIELD RELATED TRAITS

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Abstract

Improving grain yield is the principal objective of wheat breeding program for its commercial cultivation. Therefore, in the presented study, we evaluated 100 indigenous wheat genotypes including three commercial checks for seed yield and some potential yield related parameters. Results indicated significant difference among studied wheat breeding lines for plant height, heading days, maturity days, and length of spike, peduncle length, tillers meter⁻², spikelets/spike, and number of grains spike⁻¹, 1000-grain weight and grain yield plot⁻¹. Wheat genotype UCA-95 gained maximum 1000-grain weight i.e. 48.41 g in minimum maturity days (136.50). Similarly, maximum plant height (97.91 cm), tillers m⁻² (403.00), spike length (14.85 cm), number of grains spike⁻¹ (62.32) and grain yield plot⁻¹ (2033.5 g) were recorded for UCA-77, UCA-67, UCA-88, UCA-42 and UCA-14, respectively. These breeding lines proved better grain yielder than commercial checks. Furthermore, high heritability (BS) and high genetic advance values were found for tillers m⁻² and grain yield plot⁻¹ which revealed that these two parameters were potential traits for seed yield improvement in studied wheat breeding lines. Inter-relationship among potential traits revealed that grain yield plot⁻¹ exhibited positive genetic association with peduncle length, plant height and spikelet/spike. Thus, it is suggested that wheat accessions which showed better performance than checks should be promoted for varietal development procedures and potential traits having positively significant relationship with wheat grain yield should be used in wheat breeding program.

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Introduction

Bread wheat has got a distinctive position among all the cereals being cultivated throughout the world. Wheat is the only crop which provides more nutrition for the world population and important for sustaining food security. Wheat is a principal leading crop of Pakistan and its importance is increasing rapidly due to its consumption as daily food (Laghari *et al.*, 2010; Akhtar *et al.*, 2018).

It is the basic food of peoples of Pakistan. It contributes 72% of the total calories intake with per capita consumption is 125 kg per year (Khan *et al.*, 2015, Khokhar *et al.*, 2019). Wheat covers the area of about 37% of the total area and 70 % of Rabi crops in Pakistan (Economic Survey of Pakistan, 2018).

Regardless of its outstanding position in cereal grains there is noteworthy yield gap existing in wheat production associated to top wheat producing countries of this sphere. The break in yield is related to different stresses (biotic and abiotic) which are dangerous for crop throughout its life cycle.

The success of wheat breeding depends on the availability of genetic variation among wheat plant traits and its efficient utilization.

The main task of wheat breeders is to develop high yield potential wheat cultivars for diverse climatic environments and cultural practices at fields of farmers. Cultivars adaptability is checked by its relation with various environments. A variety is considered much adaptive which shows less variation in yield components (Akram et al., 2009). Selection of genotypes that are adapted to the stress and nonstress conditions is the main target while varieties selected for high yield in non-stress condition may not show more yield under stress. So, variety which is tolerant to stress condition should be estimated in stress before selection. Thus, wheat yield can only be increased through improved productive genotypes that have resistance to different stresses. Wheat fulfils 21% caloric requirement and 20% protein requirements of 4.5 billion people and mostly these people belong to developing countries as reported by Braun *et al.* (2010). Therefore, reported study was carried out to assess indigenous wheat germplasm for grain yield potential and yield related potential plant traits with ultimate objective to increase wheat production through selection of the best performing wheat genotypes having high yield and disease resistance to improve wheat grain production.

Materials and methods

The experiment was conducted during November 2016-17 evaluate 100 wheat breeding to lines/cultivars in College of Agriculture, University of Sargodha. Experimental material (Table 1) comprised of 97 advance wheat lines/varieties along with three commercial checks (Faisalabad 2008, Punjab 2011and Galaxy 2013) were grown in Alpha Lattice design having two repeats. Plot size for each genotype was kept as 4.8 m². At proper stage data were collected by taking fine random plants from each plot in each repeat for plant height, heading days, length of spike, maturity days, peduncle length, tillers meter-², spikelets/spike, grains spike⁻¹, 1000-grains weight and grain yield plot-1.

Analysis of variance of plant traits under study were calculated to observe the significance of these traits by using Statistix 8.1. Genotypic (Vg) and phenotypic (Vp) variances and broad sense heritability (h^{2}_{BS}) were calculated from ANOVA Table. Correlation coefficients for different studied characters were also estimated (Kwon and Torrie (1964). Heritability (BS) was estimated as out lined by Singh and Chaudhary (1985). Genetic advance (GA) was calculated as developed by Sleper and Poehlman, (2006). Path analysis was done as proposed by Dewey and Lu (1959) to observe inter relationship among different yield contributed plant parameters.

Results and discussion

Analysis of variance

Mean square values of yield contributing parameters are presented in Table 2. Results of this study exposed that wheat genotypes showed significant difference among themselves for reported potential traits.

Genotype	Parentage	Genotype	Parentage	Genotype	Parentage
UCA-1	Yecora/Galaxy-13	UCA-35	Lasani-08/Frontana	UCA-69	SA-42/King bird/Inq-91
UCA-2	Inq91/Australian donar	UCA-36	Pavon	UCA-70	SA-42/Shafaq-06
UCA-3	Inq-91/Babax	UCA-37	ERA	UCA-71	MH-97/ Chakwal-50
UCA-4	Babax/Sehar-06	UCA-38	Sehar-06/ERA	UCA-73	Inq-91/GD-188
UCA-5	Pak-81/ERA	UCA-39	Sehar-06	UCA-74	Koh-97/GD-116
UCA-6	Pasban-90	UCA-40	Inq-91	UCA-75	SA-42/MH-97
UCA-7	Pak-81/Frontana	UCA-41	SA-42/Nacozari	UCA-76	Chenab-70/Sehar-06
UCA-8	Yecora/Fsd-08	UCA-42	Inq-91/Millat-11	UCA-77	Watan/ERA
UCA-9	Millat-11	UCA-43	Sehar-06/Inq-91	UCA-78	Ujala-15
UCA-10	SA-42/Prula	UCA-44	Inq-91/Lasani-08	UCA-79	Sr-39/Pb-11
UCA-11	AAS-2002/WL-711	UCA-45	Inq-91/AAS-11	UCA-80	Millat-11/Advance line E1
UCA-12	NAC/THAC/3*PN	UCA-46	Inq-91/AARI-11	UCA-81	Pb-11/Advance
UCA-13	Babax/SA42/MH97	UCA-47	Kohenoor	UCA-82	3VAskar/G3031//90A204
UCA-14	SA-42/Inq-91	UCA-48	Kohenoor/Fsd-08	UCA-83	MH-97/Huites
UCA-15	NAC/Mirlo	UCA-49	SA-42/Pak-81	UCA-84	Lu26/Jun's/HP1744
UCA-16	SA-42/ERA	UCA-50	Inq-91/Frontana	UCA-85	Fretz/WBLL/TACUPET
UCA-17	SA-42Australian donar	UCA-51	AAS-2002/SA-42	UCA-86	SH88/MH97
UCA-18	Shafaq/WL-711	UCA-52	Lasani-08/WL-711	UCA-87	PBW343/Lu26/Nac
UCA-19	Chakwal -86/ V-8724	UCA-53	Pb-11/Nacozari	UCA-88	NE9511/Lasani-08
UCA-20	WL-711/Inq-91	UCA-54	Pasban-90/Sehar-06	UCA-89	AS-2002/Iqbal-2000/MTS22
UCA-21	Kohenoor/Lasani-08	UCA-55	Trap-1	UCA-90	Weaver/CMH955//NA66/AGA
UCA-22	M.T.S.8/2/Inq91	UCA-56	Pb-11/Trap-1	UCA-91	CB-517/CB-520
UCA-23	Seher-06/Inq-91	UCA-57	Yecora/Lasani-08	UCA-92	V95200/Pari 73
UCA-24	Kohenoor/Inq-9128.	UCA-58	Pb-76/Kanbra	UCA-93	Hp-1744/Lu26/KEA
UCA-25	Frontana	UCA-59	CIMMYT E-29	UCA-94	Shafaq-06/Fsd-08
UCA-26	Pb-11/Frontana	UCA-60	AAS-2002/M.T.S.	UCA-95	Nodnol/Lasani-08
UCA-27	Sehar-06/Pavon	UCA-61	Sehar-06/Shafaq	UCA-96	Fsd-08/Bhakar-02
UCA-28	Inq-91/Pb-11	UCA-62	AARI-11/Millat-11	UCA-97	Fret2/WBLL//TACUPET
UCA-29	Pasban-90/Pb-11	UCA-63	NAC/THAC/3/PVN/Mirlo	UCA-98	Punjab-2011 (check)
UCA-30	Pb-11/Millat-11	UCA-64	SA-42/Millat-11	UCA-99	Faisalabad-2008 (check)
UCA-31	3-Vascar/G-303	UCA-65	Pb-11/King Bird	UCA-100	Galaxy-2013 (check)
UCA-32	Sehar-06/Frontana	UCA-66	Pb-11/Babax		
UCA-33	Lasani-08/ERA	UCA-67	Sehar-06/Millat-11		
UCA-34	Lasani-08/Pavon	UCA-68	CIMMYT E-88		

Table 1. List of wheat genotypes with parentage.

The maximum plant height (97.91 cm) was recorded from UCA-77 while 75.66 cm height was recorded for UCA-7. UCA-67 displayed maximum (403.00) while UCA-2 exhibited minimum (161) number of tillers m⁻² in studied genotypes. Similarly, wheat genotype UCA-50 showed maximum (108.50) heading days and UCA-18 showed (93.50) minimum heading days. Regarding peduncle length, maximum length (42.83 cm) was observed in UCA-22, while minimum length (26.66 cm.) was calculated in UCA-29. In case of length of spike, UCA-88 gained highest (14.85 cm) while UCA-90 attained lowest (10.15 cm) spike of length. In case of number of spikelets/spike UCA-24 gained maximum (20.85) while UCA-88 had minimum (14.80) spikelets/spike. Wheat genotype UCA-95 gained maximum 1000-grain weight whereas UCA-62 reported lowest grain weight (33.00 g).

The minimum maturity days (128.00) was observed from UCA-95, while highest days to maturity (136.50 days) were reported in UCA-71. Regarding number of grains spike⁻¹ genotype UCA-42 obtained maximum grains (62.32) and minimum grains (32.15) were examined in UCA-99 (Pb-11 as check). UCA-14 gained the highest grain yield plot⁻¹ (2033.5 g) while minimum plot yield (1023.5 g) was found in UCA-67. This indicated that enough genetic variation was present in studied wheat breeding lines for grain yield

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contributing traits. Thus, selection of high yielding wheat genotypes would be possible based on these traits. It was further suggested that these potential plant parameters should be considered at the time of selection of desired plants in segregating population. Our results get support from Baloch *et al.*, (2013), Muhammad *et al.*, (2014), Khan *et al.*, (2015), Birhanu *et al.*, (2016), Zerga *et al.*, (2016), Akhtar *et al.*, 2018 and Khokhar *et al.*, 2019. Their experimental results are similar with our findings.

Plant traits	Genotypes	Replications	Error
	(g-1) 99	(r-1) 1	(g-1)(r-1) 99
Heading days	13.55^{**}	$0.02^{ m NS}$	0.89
Plant height	47.62**	79.23	29.36
Peduncle length	13.99**	30.91	2.09
Length of spike	2.08**	0.14 ^{NS}	0.056
Maturity days	9.28**	0.50 NS	0.63
Tillers m ⁻²	3463.36**	79.23 ^{NS}	66.71
Spikelets per spike	3.90**	0.14 ^{NS}	0.37
Grain spike ⁻¹	64.98**	1.40 ^{NS}	2.83
1000-seed weight	30.58**	7.99 ^{NS}	1.67
Grain yield plot ⁻¹	122948.00**	2429.00	237.00

Table 2. Mean squares values of 100 wheat lines/varieties for grain yield and related traits.

** = Highly significant (P \leq 0.01) & NS = Non-Significant.

Genetic variability, broad sense heritability (h_{BS}^{2}) and genetic advance (GA)

The results exposed that plant traits tillers m⁻², thousand grain weight, maturity days, grains spike⁻¹ and grain yield plot⁻¹ showed high h^{2} _(BS) and GA in most of the wheat genotypes under study (Table 3). Length of spike length and heading days also exposed

good $h^{2}_{(BS)}$ and expected gain in next generation. This indicated that selection on the basis of above said traits would be fruitful to enhance grain yield in these wheat genotypes. Furthermore, these traits would also be beneficial in the selection of plants in early generations. Rahman *et al.*, (2016) and Akhtar *et al.*, (2018) also described such types of results.

Table 3. Estimates of genetic variability, heritability and genetic advance of lines/varieties.

Plant traits	V_{G}	V p	H ² (BS)	GA
Plant height	9.13	38.49	23.72	2.54
Tillers m ⁻²	1698.32	1765.03	96.22	70.01
Heading days	6.33	7.22	87.67	4.08
Peduncle length	5.95	8.04	74	3.63
Length of spike	0.97	1.11	87.70	1.59
Spikelet's per spike	1.77	2.14	82.68	2.09
1000-grain weight	14.45	16.13	89.61	6.23
Maturity days	8.65	9.28	93.19	4.92
Grains spike ⁻¹	31.08	33.91	91.65	9.24
Grain yield plot ⁻¹	61355.5	61592.5	99.58	428.03

Correlation coefficients and path analysis

Correlation coefficients and path analysis of studied plant traits are presented in Tables 4 and 5. Correlation coefficients exposed positively significant relationship of plant height with tillers m⁻², spikelets per spike, grain yield plot⁻¹ and peduncle length at genotypically and phenotypically, while it displayed strong positive genetic association with 1000-grain weight. This revealed that to some extent plant height had significantly positive impact to improve these parameters in wheat which were directly correlated to enhance seed yield in wheat. However, negative relationship of plant height with different plant traits was also observed which indicated that these traits did not helpful to enhance seed yield. Therefore, carefully selection should be done to improve grain yield in studied genotypes. Remaining studied traits showed non-significant but positive or negative relationship with plant height in studied wheat genotypes. However, path coefficients displayed direct positive effect of plant height on length of spike, grains spike⁻¹ and maturity days. The findings of this experiment are in accordance with experimental results of Kalimullah *et al.*, (2012), Baloch *et al.*, (2013) and Akhtar *et al.*, (2018).

Traits		Plant	Tillers	Heading	Peduncle	Length	Spikelets	1000-grain	Maturity days	Grains spike-1
		height	m-2	days	length	of spike	per spike	weight		
Tillers m ⁻²	\mathbf{r}_{g}	0.27^{*}								
	\mathbf{r}_{p}	0.24*								
Heading days	\mathbf{r}_{g}	0.10	-0.23*							
	\mathbf{r}_{p}	0.09	-0.17							
Peduncle length	\mathbf{r}_{g}	0.66**	0.50**	-0.05						
	\mathbf{r}_{p}	0.62*	0.32**	-0.05						
Length of spike	\mathbf{r}_{g}	-0.22*	-0.29*	0.03	-0.47**					
	\mathbf{r}_{p}	-0.15	-0.21*	0.01	-0.24*					
Spikelets per	\mathbf{r}_{g}	0.60**	0.37*	0.40**	0.28*	-0.05				
spike	\mathbf{r}_{p}	0.46**	0.16	0.34**	0.23*	0.02				
1000-grain	\mathbf{r}_{g}	0.14*	0.14*	-0.04	0.04	-0.20*	0.05			
weight	\mathbf{r}_{p}	0.11	0.09	-0.04	0.03	-0.16	0.05			
Maturity days	\mathbf{r}_{g}	-0.20*	-0.37**	0.19*	0.06	-0.06	-0.25**	-0.25**		
	\mathbf{r}_{p}	-0.14	-0.28**	0.19	0.04	-0.04	-0.20*	-0.25*		
Grains spike-1	\mathbf{r}_{g}	-0.16*	0.00	-0.27**	0.02	0.07	-0.45**	-0.01	-0.02	
	\mathbf{r}_{p}	-0.13	-0.02	-0.26**	0.02	0.05	-0.38*	-0.01	-0.02	
Grain yield plot-1	\mathbf{r}_{g}	0.26**	-0.27**	0.00	0.15*	0.01	0.14*	-0.02	-0.01	-0.21**
	\mathbf{r}_{p}	0.21^{*}	-0.20*	0.00	0.12	0.01	0.12	-0.02	-0.01	-0.21*

Tillers meter⁻² revealed strong positive interrelationship with peduncle length, thousand grain weight and spikelets per spike. However, it exposed significantly negative association with length of spike, maturity days and grain yield plot⁻¹. Path analysis suggested that tillers m⁻² had direct positive effects on peduncle length, thousand grain weight and spikelets per spike (Baloch *et al.*, 2013).

Heading days only presented strong positive interrelationship with spikelets per spike phenotypically and genotypically. This trait also displayed significant and positive genetic correlation with maturity days. While it revealed significantly negative association with grains spike⁻¹. Path analysis study exhibited that this trait had direct positive effect on length of spike, spikelets per spike and maturity days (Anwar *et al.*, 2009).

Peduncle length presented significantly positive relationship with grain yield plot⁻¹ and spikelets per spike but it exhibited significantly negative impact on spike length genotypically and phenotypically. Other studied plant parameters exposed positively non-significant relationship with peduncle length. Under path coefficient analysis this trait exerted direct positive effect on 1000-grain weight, maturity days, spikelets per spike and grains spike⁻¹ which ultimately contributed to grain yield. The results of this experiment are in agreement with Baloch *et al.*,

(2013) for such types of findings in wheat.

Length of spike revealed significant but negative genetic relationship with the plant height, tillers m⁻², 1000-grain weight and peduncle length. The remaining parameters showed either positive or negative relationship with spike length but nonsignificant. This negative relationship displayed that selection would not be productive in studied wheat genotypes based on this trait. However, path analysis showed that this trait had direct positive impact on grains spike⁻¹ to improve grain yield (Anwar *et al.*, (2009). Our results are in contrary with Kalimullah *et al.*, (2012).

Fable 5. Path	analysis fo	r grin yield	and potential	traits in wheat.
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Variables	Plant height	Tillers m ⁻²	Heading	Peduncle	Length of	Spikelets per	1000-grain	Maturity days	Grains spike-1	Residual
			days	length	spike	spike	weight			
Plant height	0	0.127432	0.036466	0.007	-0.01896	0.155517	-0.06757	-0.0197	-0.01019	1.11994
Tillers m ⁻²	-0.06603	0	-0.06888	0.003613	-0.02655	0.054093	-0.05528	-0.0394	-0.00157	1.11994
Heading days	-0.02446	-0.12212	0	-0.00056	0.001264	0.114947	0.024569	0.026735	-0.02037	1.11994
Peduncle length	-0.16141	0.265482	-0.02026	0	-0.03034	0.077759	-0.01843	0.005628	0.001567	1.11994
Length of spike	0.053803	-0.15398	0.012155	-0.00531	0	0.006762	0.098276	-0.00563	0.003918	1.11994
Spikelets per spike	-0.14674	0.196457	0.162069	0.003161	-0.00632	0	-0.03071	-0.02814	-0.02978	1.11994
1000-grain weight	-0.03424	0.074335	-0.01621	0.000452	-0.02528	0.016904	0	-0.03518	-0.00078	1.11994
Maturity days	0.048912	-0.19646	0.076983	0.000677	-0.00759	-0.08452	0.153557	0	-0.00157	1.11994
Grains spike ⁻¹	0.03913	0	-0.1094	0.000226	0.008849	-0.15214	0.006142	-0.00281	0	1.11994

Spikelets per spike exposed strong genetic relationship with grain yield plot⁻¹ while it showed significant but negative relationship with grains spike⁻¹ and maturity days, and Path coefficient study stated that this trait had direct positive effect on 1000-grain weight. Our results are in accordance with Mohibullah *et al.* (2011).

Thousand grain weight is an important plant trait. In this study it exhibited significantly positive association with tillers meter⁻² and plant height at genotypically but it indicated significantly negative interrelationship with maturity days at both levels.

The remaining traits showed either positive or negative relationship with spike length but nonsignificant. Our findings get support from Baloch *et al.*, (2013) and Rahman *et al.*, (2016) results.

The affiliation between maturity days and heading days was observed significantly positive genotypically under this study. The remaining traits showed either positive or negative relationship with spike length but non-significant. Under path coefficient analysis it was observed that maturity days had direct negative impact on grains spike⁻¹.

Grains spike⁻¹ exhibited significant negative genetic inter-relationship with grain yield plot⁻¹ genotypically and phenotypically.

Path coefficient analysis reported that grains spike⁻¹ had direct positive impact on plant height, peduncle length, 1000-grain weight and length of spike to enhance seed yield in wheat. The obtained results are in accordance with the findings of Said *et al.* (2014).

Grain yield plot⁻¹ displayed significantly positive inter-relationship with plant height, peduncle length and spikelets per spike in this study while it exhibited strong negative correlation with tillers m⁻² and grains spike⁻¹. Kalimullah *et al.* (2012) and Baloch *et al.*, (2013) also reported such types of findings in wheat. However, our results regarding negative interrelationship with grain yield plot⁻¹ with tillers m⁻² and grains spike⁻¹ were contrary with these researchers who reported strong positive association with grain yield.

These may be due to environmental effects like soil fertility, plant competition, moisture conditions or mismanagement during data collection for that specific trait.

Conclusion

It is concluded that advanced wheat breeding lines that performed better than existing commercial wheat varieties for the studied plant traits, should be forwarded for varietal developmental procedures. Potential traits like Plant Height, Tillers per meter square, Spikelets per spike, Heading days and 1000grain weight which showed strong positive genetic association with grain yield along with high heritability (h^2) and genetic advance (GA) in present study, would be used extensively during selection process in early generations. However, careful selection should be done for those traitswhich disclosed negative association with wheat grain yield.

References

Akhtar N, Waseem A, Mehmood T, Bano S, Raza A, Aziz A. 2018. Gene action appraisal for seed yield and related traits in bread wheat (*Triticum aestivum* L.). Journal of Animal and Plant Sciences. **28**, 1457-1465.

Akram Z, Ajmal SU, Shabbir G, Munir M, Cheema NM. 2009. Inheritance mechanism of some yield components in bread wheat. Pakistan Journal of Agriculture Research **22**, 1-8.

Anwar J, Ali MA, Hussain M, Sabir W, Khan MA, Zulkiffal M, Abdullah M. 2009. Assessment of yield criteria in bread wheat through correlation and path analysis. The journal of animal and plant science **19**, 185-188.

Baloch MJ, Baloch E, Jatoi WA, Veesar NF. 2013. Correlation and heritability of yield and yield attributing traits in wheat (*Triticum aestivum* L.) Pakistan Journal of Agriculture, Engineering and Veterinary Science **29**, 96-105.

Birhanu M, Alamerew S, Assefa A, Assefa E, Dutamo D. 2016. Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Bread Wheat (*Triticum aestivum* L.) Genotypes. Global Journal of Frontier Science Research **16**, 1067-1073. **Braun HJ, Atlin G, Payne T.** 2010. Multi-location testing as a tool to identify plant response to global climate change. In: Reynolds, CRP. (ed.). Climate change and crop production, CABI, London, UK.

Dewey RD, Lu KH. 1959. A correlation and phenotypic correlation analysis of some quality character and yield of seed cotton in upland cotton (*Triticum aestivum* L.). Journal of Biological Sciences **4**, 235-236.

Economic Survey of Pakistan. 2018. Ministry of Food, Agriculture and Livestock, Federal Bureau of Statistics Islamabad, Pakistan.

Kalimullah, Khan SJ, Irfaq M, Rahman HU. 2012. Genetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. The Journal of Animal and Plant Science. 22, 330-333.

Khan WU, Mohammad F, Khan FU, Zafar FZ, Ghuttai G. 2015. Correlation Studies among Productions Traits in Bread Wheat under Rainfed Conditions. American-Eurasian Journal of Agriculture and Environmental Science 15, 2057-2063.

Khokhar MI, Javed K, Ikram ul Haq, Akhtar N, Habib I, Anwar MJ. 2019. Genetic study for improvement of various yield attributing traits in wheat. Journal of Agriculture Research **57**, 73-80.

Kwon S, Tirrie J. 1964. Heritability and interrelationship among traits of two soybean populations. Crop Science **4**, 196-198.

Laghari KA, Sial MA, Arain MA, Dahot MA, Mangrio MS, Pirzada AJ. 2010. Comparative Performance of Wheat Advance Lines for Yield and its Associated Traits. World Applied Sciences Journal **8**, 34-37.

Mohibullah M, Rabbani MA, Jehan S, Amin ZA, Ghazanfar-ullah, 2011. Genetic variability and

Int. J. Biosci.

correlation analysis of bread wheat (*Triticum aestivum* L.) accessions. Pakistan Journal of Botany. **43**, 2717-2720.

Muhammad S, Hussain I, Din RU, Tanveer SK, Qamar M, Abbas SH. 2014. Physio-agronomic Traits Evaluation of Wheat Genotypes for Adaptability under Rainfed Conditions. Sarhad Journal of Agriculture **30**, 211-217.

Rahman M, Barma NCD, Biswas BK, Khan AA, Rahman J. 2016. Study on morpho-physiological traits in spring wheat (*Triticum aestivum* L.) under rainfed condition. Bangladesh Journal of Agriculture Research **41**, 235-250.

Said S, Khan SJ, Khan J, Khan R, Khan I. 2014. Genetic Variability Studies in Bread Wheat (*Triticum* *aestivum* L.) Accessions. Pakistan Journal of Agriculture **3**, 142-157.

Singh RK, Chaudhary BD. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Puplishers, Ludhiana, New Delhi, p 318.

Sleeper DA, **Poelhman JM.** 2006. Breeding Field Crops, 5th ed. Panima Pub., New Delhi, 75-76.

Zerga K, Mekbib F, Dessalegn T. 2016. Genetic Variability, Heritability and Genetic Advance in Bread Wheat (*Triticum aestivum* L.) Genotypes at Gurage Zone, Ethiopia. International Journal of Microbiology and Biotechnology **1**, 1-9.