



E-ISSN: 2278-4136

P-ISSN: 2349-8234

JPP 2019; 8(5): 1036-1041

Received: 10-07-2019

Accepted: 12-08-2019

Sebghatullah SayedpoorAgricultural Research Institute
of Afghanistan (ARIA), Kabul,
Afghanistan**Ibrahim Hassani**Agricultural Research Institute
of Afghanistan (ARIA), Kabul,
Afghanistan**Attifullah Shinwari**Advisory Office to the President
on Agriculture and Development
(ADA), Kabul, Afghanistan

Assessment of genetic variability among bread wheat (*Triticum aestivum* L.) genotypes

Sebghatullah Sayedpoor, Ibrahim Hassani and Attifullah Shinwari

Abstract

Twenty bread wheat genotypes were tested at Uttar Pradesh, India in 2012/13, with the objective of assessing the extent of genetic variation and correlation of wheat genotypes in yield and yield components traits using randomized complete block design. Data collected for 12 agronomic characters were subjected to analysis of variance which revealed significant differences among the genotypes for all the characters. The broad sense heritability (H^2) ranged from 38% (for spike length) to 99 % (for test weight), while genetic advance as percent of mean (GAM) from 4.71 (for spike length) to 27.34% (for test weight). The genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) differences were low in magnitude for days to heading days to flowering and days to maturity, and H^2 values were coupled with moderate to high GAM. This suggests selection based on phenotype of the lines could be effective to improve these characters. Interestingly, genotype K-911 showed superior performance under Agro-climatic condition of Uttar Pradesh, India. It exhibited highest grain yield, highest number of tillers per plant and less number of days to maturity (early in maturity) which is important for rice-wheat based cropping system. It also showed escaping mechanism against high temperature, and resistance against pest and disease which can be used for development of new varieties. Grain yield was positively and significantly correlated with test weight (0.65), harvest index (0.41), and positively and non-significantly with plant height (0.15), days to maturity (0.23) and days to flowering (0.12), of which test weight (0.65) and harvest index (0.41) had the highest positive direct effect on grain yield. Thus, selection for higher mean test weight and harvest index could be considered simultaneously for selection of higher grain yield.

Keywords: Bread wheat, correlation, genetic coefficient of variation, genetic advance, and heritability

Introduction

The presence of genetic variability and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Genetic variability refers to the genetic distance between species or between populations within a species. Smaller genetic distances indicate a close genetic relationship where as large genetic distances indicate a more distant genetic relationship. It is a challenging task before the breeders to enhance the present level of production as the growing population of the country will require much more food as compared to the present day requirement. It is not possible to increase the area under production. Hence, only alternative is to increase the productivity by evolving superior varieties and better management of crop production to cope up with increasing demands of food.

Wheat is the staple food of Afghans and occupies about 2.5 million hectares with an average production of about five million tons annually (Persaud, 2012; Akbar Waziri *et al.*, 2013) [18, 26]. Wheat yield in Afghanistan is relatively lower than other countries in the region. Lack of adequate number of resistant varieties for different production environments is one of the major reasons for this. International Maize and Wheat Improvement Centre (CIMMYT) in collaboration with Agricultural Research Institute of Afghanistan (ARIA) have been working to identify suitable high yielding wheat varieties for Afghanistan. CIMMYT, ARIA and other stake holders have successfully released about 34 new wheat varieties in the country before 2000 (Obaidi *et al.*, 2017) [16]. The success of a crop improvement program depends upon the amount of genetic variability existed in the germplasm. To bring the heritable improvements in economic characters through selection and breeding, estimation of genetic parameters must be made before starting a program. There are different techniques available to compute the genetic parameters and the index of transmissibility of characters. Heritability estimates provides information about the extent to which a particular character can be transmitted to the successive generations. Knowledge of heritability of a trait thus guides a plant breeder to predict behavior of succeeding generations and helps to predict the response to selection. Therefore, an experiment was conducted to identify the quantitative characters for selection

Corresponding Author:**Sebghatullah Sayedpoor**Agricultural Research Institute
of Afghanistan (ARIA), Kabul,
Afghanistan

breeding in wheat under agro climatic conditions of Allahabad, U P, India.

Material and Methods

The experimental material comprising of 20 genotypes including two checks, were grown under randomized block design (RBD) with three replications, during rabi 2012-2013. The experimental field was divided into 3 blocks of equal size and each block possesses 20 plots. Each genotype was accommodated in a two row of 2 meter length spaced at 25 cm with a approximate plant to plant distance of 5 cm. The sowing was done on December 5th 2012. Thinning was done to maintain a plant to plant spacing of 5cm. The recommended dose of N: P: K was applied. All the recommended agronomic practices were followed to raise a healthy crop. The artificial irrigation was given at CRI stage, grain filling stage and milking stage where as other requirement of water was fulfilled through natural precipitation. Two manual weeding were done after 35 and 65 days of sowing. Harvesting was done by serrated sickles when the grains were dried enough and had turned to straw color. Each genotypes harvested were kept in different tagged bags. Harvested wheat was dried on sun for two days and was threshed by beating with sticks.

The experimental data on various quantitative traits was collected on five randomly selected plants per plot (except for days to flowering and days to maturity, where the observation

were recorded on plant basis) in each replications for all 20 genotype. The experimental observations on all genotypes in each replication were recorded for:

Physio-morphological traits

DTH-Days to 50% heading, PHM-Plant height at maturity, DTF-Days to 50% Flowering, FLL-Flag leaf Length, FLW-Flag Leaf width, PM-Days to physiological maturity,

Yield attributing traits

ET-Effective tillers, SL-Spikelet's length (cm), B.Y. - Biological yield (ton/ha), GY-Grain yield (ton/ha), HI-Harvest index, TGW- Thousand grain weight (gm) (Kandel *et al.*, 2018) [12]:

Harvest index was calculated as per the formula (Huhn 2008).

$$H.I. = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Where,

Economic yield = Grain yield (g)

Biological yield = Total plant yield (g)

The plant materials were obtained from Allahabad Agricultural Institute -Deemed University (AAIDU). The list of 41 genotypes included in the study is presented in Table 1.

Table 1: List of experimental genotypes of wheat varieties

S.No	Genotypes Name	Resources	S.No	Genotypes Name	Resources
01	K -910-4	CSAU&T, Kanpur	11	AAI-16	SHIATS, Allahabad
02	K -612	CSAU&T, Kanpur	12	NW-6007	NDUA&T, Faizabad
03	K -910-30	CSAU&T, Kanpur	13	NW-1014 (C)	NDUA&T, Faizabad
04	SVPW-1	SVPUA& T, Meerut	14	K -9162 (C)	CSAU&T, Kanpur
05	K -512	CSAU&T, Kanpur	15	K -307	CSAU&T, Kanpur
06	K -607	CSAU&T, Kanpur	16	AAI 1101 (Halna X VWTH-08-14)	SHIATS, Allahabad
07	K -911	CSAU&T, Kanpur	17	AAI 1102 (K-816 X VWTH-0814)	SHIATS, Allahabad
08	HUW-468	BHU, Varanasi	18	AAI 1103 (Halna X K-9423)	SHIATS, Allahabad
09	AAI-11	SHIATS, Allahabad	19	AAI 1104 (K-816 X K-8962)	SHIATS, Allahabad
10	AAI-13	SHIATS, Allahabad	20	AAI 1105 (Halna X K-9533)	SHIATS, Allahabad

Statistical Analysis

The data were analyzed using INDOSTAT software for computation of

Analysis of Variance (ANOVA)

The analysis of variance of experimental design was performed to test the significance of differences between genotypes for all the characters with fixed effect model.

Standard error of mean

Standard error of mean was calculated by the following formula.

$$S.E.M = \sqrt{2EMS/r}$$

Critical difference

Critical difference was calculated by the following formula.

$$C.D. = \sqrt{2EMS/r} \times t_{\text{edf at } 5\%}$$

Where, r = Number of replications, EMS = Error mean sum of squares, t =Table value of 't' at error degrees of freedom at 0.05 level of significance.

Genotypic variance

The genotypic variance (VG or σ_g^2) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was

$$VG = V_t - EMS/r$$

Where, V_t = MSS due to treatment and EMS= Error mean sum of squares.

Environmental or error variance

The environmental variance (VE or σ_e^2) is the variance due to environmental deviation.

$$VE = EMS$$

Phenotypic variance

VP = Genotypic variance (VG) + Error variance (VE)

Coefficient of variation

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

CV (%) = (Standard deviation/ Mean) x 100

The formulae used to calculate PCV, GCV and ECV were given by Burton (1952).

PCV (%) = (Phenotypic standard deviation/Grand Mean) x 100 = $(\sqrt{VP / X}) \times 100 =$

GCV (%) = (Genotypic standard deviation/Grand mean) x 100 = $(\sqrt{VG / X}) \times 100 =$

ECV (%) = (Error standard deviation/ Grand mean) x 100 = $(\sqrt{VE/X}) \times 100 =$

Heritability (broad sense)

It was calculated by the formula given by Lush (1949) [15] and Burton and Devane (1953) [7].

$$h^2 = \frac{VG}{VP} \times 100$$

Where, VG = genotypic variance, VP = phenotypic variance.

Correlation coefficient analysis

Single correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting following formula given by Al-Jibouri *et al.* (1958) [1].

Genotypic correlation between traits X and Y:

$$R_{xy}(g) = (\sigma_g^2(xy) / \sqrt{\sigma_g^2(x) \times \sigma_g^2(y)})$$

Phenotypic correlation between traits X and Y:

$$R_{xy}(p) = (\sigma_p^2(xy) / \sqrt{\sigma_p^2(x) \times \sigma_p^2(y)})$$

Where, $\sigma_g^2(xy)$ = Genotypic covariance between X and Y:

Results and Discussion

Various genetic parameters like means, standard deviations, variances, coefficient of variability, heritability, estimate and genetic advance values for various quantitative traits in 20 wheat genotypes were investigated during 2013. The mean value of 12 characters for 20 genotypes is presented in Appendix Table 1. Genotypes had in between 67.00 to 87.00 days to heading and 119 to 133 days to maturity with a mean of 67 and 125 days, respectively. The result showed a wide range of variations for days to heading and maturity. Grain yield per plant showed that it ranged from 19.56 to 12.45 g with mean value of 14.14 g. Maximum grain yield per plant was recorded for the genotypes K-911 (19.53 g) followed by SVPW-1 (19.50 g), NW-6007 (19.20g) and NW-1014 (C) (18.46g) whereas minimum grain yield per plant was recorded for AAI 1101 (12.45 g) and AAI-13 (13.43 g) and AAI 1104 (14.10g). Higher grain yield always a demand for providing food security to everyone. These findings of grain yield per plant are in accordance with the findings of Singh *et al.* (2010) who, reported high grain yield per plant in their studies.

Maximum plant height was recorded in genotype NW-6007 (113.07 cm). The maximum spike length was recorded in genotype AAI-11 (17 cm). The findings of spike length are in accordance with the findings of Gupta *et al.* (2004). On the other hand the maximum tillers per plant were recorded in genotype NW 1014 (14.70 cm). The maximum biological yield per plant was recorded in a genotype viz. K-910-4 (48.00 g). The maximum harvest index was recorded in genotype K-910-30 (52.58). The maximum 1000 seed / test weight was recorded in genotype K-9162 (42.57 g). Weight of 1000 grains of particular genotypes indicated its potential to

show better yield per plant Phadnawis *et al.* (2002) [19], and Khan *et al.* (2005). Maximum grain yield per plant was recorded in genotype K-911 (19.53 g).

The maximum flag leaf length value was recorded in genotype AAI 1105 (28.60cm). However, the maximum flag leaf width was recorded in genotype HUW-468 (1.75cm).

The mean sum of squares showed significant differences at 5%* and 1%** levels respectively, among 20 wheat genotypes for all the quantitative traits under study (table 2). The wide range of variation was observed for all the traits which offer scope of selection for development of desirable genotypes of wheat crop. Several researchers reported significant differences among bread wheat genotypes studied (Kifle *et al.*, 2016; Arya *et al.*, 2017; Tesfaye *et al.*, 2016; Birhanu *et al.*, 2016) [14, 2, 25, 3].

Table 2: Analysis of variance for 12 characters of wheat

S. No.	Characters	Mean sum of squares		
		Replication (df=2)	Treatment (df= 19)	Error (df= 38)
1	Days to 50% Heading	0.450	112.15**	3.36
2	Days to 50% Flowering	1.05	95.94**	3.48
3	Flag Leaf Length	0.13	22.42**	1.45
4	Flag Leaf Width	0.003	0.046**	0.05
5	Tillers/ Plant	1.046	10.23**	2.39
6	Spike Length	3.18	2.91*	1.01
7	Plant Height	3.07	306.08**	7.11
8	Days to Maturity	5.01	35.27**	3.20
9	Grain Yield/ Plant	0.77	12.15**	1.50
10	Biological Yield	2.73	43.17**	7.95
11	Harvest index%	8.03	63.69**	19.52
12	1000 seed / test Weight	0.18	62.02**	0.30

Significant at 5%*, and 1% ** level respectively,

Estimation of variability components

The estimate of phenotype coefficient of variation (PCV) for all the traits ranged from 2.98 (days to maturity) to 20.97 (tillers per plant). Maximum phenotypic coefficient of variation was observed for tillers per plant (20.97) followed by harvest index (13.36), test weight (13.47), grain yield per plant (13.11), and biological yield (11.04), while minimum PCV was exhibited in days to maturity (2.98), followed by days to 50% flowering (7.04) and days to 50% heading (8.09). A perusal of genetic coefficient of variation (GCV) revealed that it ranged from 2.98 (days to maturity) to 20.97 (tillers per plant). Maximum genotypic coefficient of variation was observed for tillers per plant (15.18), followed by test weight (13.37), flag leaf length (12.08) and grain yield (10.99), while minimum genetic coefficient of variation (GCV) was recorded in days to maturity (2.61) followed by spike length (5.22), days to 50% flowering (6.67) and days to 50% heading (7.74). This indicated less environmental influence on the expression of all the attributes. Similar findings were also reported by Singh *et al.* (2010), Sharma and Garg (2002) [27, 9], who have also observed the PCV values were higher than GCV values for different quantitative characters in wheat.

Estimation of Heritability and Genetic Advance

In the present investigation, heritability and genetic advance have been worked out for the twelve quantitative characters and are presented in table 3. Maximum heritability was recorded in test weight (0.99), flag leaf width (0.97) plant height (0.93), days to 50% heading (0.92), days to 50% flowering (0.90) and flag leaf length (0.83), whereas minimum heritability was recorded in spike length (0.38)

followed by harvest index (0.43), tillers per plant (0.52%), biological yield (0.60) and grain yield per plant (0.70).

High values indicate that heritability may be due to higher contribution of genetic component. High heritability estimates were also reported by Shah (1998) [22] and Bergale *et al.* (2001) [4] for 1000 grain weight, Asif *et al.* (2004) [2] for plant height, Khumkar *et al.* (2001) [13] for chlorophyll content, Rasal *et al.* (2008) [20] and Shankarrao *et al.* (2010) [23] has also observed high value of heritability for grain yield and its components in wheat.

Heritability alone provides no indication of amount of genetic improvement that would result from selection of individual genotypes hence knowledge about genetic advance coupled with heritability is most useful. Genetic advance is the improvement in the mean of selected family over the base population (Johnson *et al.*, 1955) [11].

Characters exhibiting high heritability may not be necessarily gives high genetic advance Johnson *et al.*, (1955) [11]. It showed that high heritability should be accompanied with high genetic advance to arrive at more reliable conclusion. The breeder should be cautious in making selection based on heritability as it includes both additive and non-additive gene effect a perusal of genetic advance (table 4.3) revealed that it was high for plant height (19.87), days to 50% heading (11.87), days to 50% flowering (10.84), test weight (9.28) and biological yield (5.45) and low genetic advance was observed for flag leaf width (0.25), followed by spike length (1.02), tillers per plant and (2.42), grain yield per plant (3.25). The heritability estimates coupled with expected genetic advance indicate the mode of gene action in the expression of traits

which helps in choosing an appropriate breeding methodology. High heritability along with high genetic advance was registered for plant height (0.93, 19.87), days to 50% heading (0.92, 11.87) and days to 50% flowering (0.90, 10.84) suggesting predominance of additive gene action in the expression of these traits. High heritability with moderate genetic advance was registered for test weight (0.99, 9.28), suggesting predominance of additive and non-additive gene action in the expression of these traits therefore, these character can be improved by mass selection and other breeding method based on progeny testing. Similar results in wheat have been also reported Panwar *et al.* (2002) [19]. However character like, flag leaf length (0.83, 4.96) and flag leaf width (0.97, 0.25) possessed high heritability with low genetic advance, suggesting non additive gene action in the expression of these traits. The high heritability the traits were due to favorable influence of environment rather than genotypic and selection for these traits may not be rewarding similar were reported by Panwar and Singh (2000) [17] for plant height, number of tillers per plant exhibited higher heritability.

Correlation of grain yield with other characters

The heritable association between two variables is known as genotypic correlation. This type of correlation may be either due to pleiotropic actions of genes or due to linkage. The information of genotypic correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement by selecting the characters of a pair that is genetically correlated.

Table 3: Estimation of genetic variability and genetic parameters for 12 characters

S. No.	Characters	σ^2_g	σ^2_p	GCV	PCV	h^2 (bs) %	GA	GA as % of mean
1	Days to 50% Heading	36.26	39.63	7.74	8.09	0.92	11.87	15.25
2	Days to 50% Flowering.	30.82	34.31	6.67	7.04	0.90	10.84	13.03
3	Flag Leaf Length	6.99	8.44	12.08	13.27	0.83	4.96	22.64
4	Flag Leaf Width	0.02	0.02	7.81	7.95	0.97	0.25	15.81
5	Tillers/ Plant	2.63	5.02	15.18	20.97	0.52	2.42	22.64
6	Spike Length	0.63	1.65	5.22	8.42	0.38	1.02	6.66
7	Plant Hight	99.66	106.77	10.66	11.04	0.93	19.87	21.22
8	Days to Maturity	10.69	13.90	2.61	2.98	0.77	5.91	4.71
9	Grain Yield/ Plant	3.55	5.05	10.99	13.11	0.70	3.25	18.98
10	Biological Yield	11.74	19.69	8.53	11.04	0.60	5.45	13.57
11	Harvest index%	14.72	34.25	8.94	13.63	0.43	5.18	12.07
12	Test Weight	20.57	20.88	13.37	13.47	0.99	9.28	27.34

σ^2_g = Genetic variance, σ^2_p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h^2 = heritability broad sense, GA = Genetic advance.

Table 4: Positive and significant estimates of correlation of these characters with grain yield indicate strong association of these traits with grain yield

S. No.	Characters	DH	DF	FLL	FLW	TPP	SL	PH	DM	BY	HI	TW	GY
1	Days to 50% Heading	1.00	0.94**	0.41**	0.15	-0.23	0.39*	0.43**	0.39*	-0.01	0.04	-0.22	0.04
2	Days to 50% flowering		1.00	0.44**	0.34**	-0.19	0.44**	0.43**	0.49**	0.01	0.10	-0.15	0.12
3	Flag leaf length			1.00	0.13	-0.31*	0.53**	0.77**	0.58**	-0.001	0.003	0.29 *	0.04
4	Flag leaf width				1.00	0.04	0.31*	0.35*	0.29*	0.15	0.02	0.16	0.12
5	Tillers per plant					1.00	-0.15	-0.38*	-0.43**	0.03	-0.03	-0.41*	0.02
6	Spike Length						1.00	0.51**	0.49**	0.05	0.03	0.23	0.09
7	Plant height							1.00	0.57**	0.02	0.14	0.44**	0.15
8	Days to maturity								1.00	0.24	0.03	0.21	0.23
9	Biological yield									1.00	-0.41*	-0.14	0.11
10	Harvest index										1.00	0.26*	0.41**
11	Test weight											1.00	0.65**
12	Grain yield												1.00

*, ** Significant at 5%, 1% levels of significance respectively, DH=Days to 50% Heading, DF= Days to 50% flowering, FLL=Flag leaf length, FLW=Flag leaf width, TPP=Tillers per plant, SL= Spike Length, PH= Plant height, DM=Days to maturity, BY= Biological yield, HI= Harvest index, TW=Test weight, GY=Grain yield.

Grain yield per plant showed positive significant genotypic correlation with harvest index (0.82**) and test weight (0.43**), while negative significant correlation with flag leaf width (-0.23*). Positive and significant estimates of correlation of these characters with grain yield indicate strong association of these traits with grain yield (table 4). Therefore, by increasing the value of these traits, seed yield may also be increased simultaneously, suggesting that selection for these traits will be useful in improving seed yield. The positive but non – significant correlation showed with days to 50% heading (0.05), days to 50% flowering (0.13), flag leaf width (0.15), flag leaf length (0.05), tillers per plant (0.05), spike length (0.24), plant height (0.19), days to maturity (0.32) and biological yield (0.15). These findings are in accordance to findings of Dawit Tsegaye *et al.* (2012) [5] and Sultana *et al.* (2005) [21].

Conclusion

The study indicated the presence of wide genetic variation among the wheat genotypes which can be exploited to develop high yielding varieties with desirable grain quality and early maturity in the study area and similar agro-ecologies, where terminal moisture stress is the major constraint of wheat production. Moderate GCV coupled with moderate PCV (10 to 20%) was observed for grain yield and test weight, indicating the effectiveness of selection based on the phenotypic performance of the genotypes. High heritability (>80%) coupled with moderate genetic advance as percent of mean (10 to 20%) was observed for days to heading, days to flowering and plant height. This implies that the variation observed was mainly under genetic control and the possibility of progress from selection. In general, in the context of plant breeding, traits that exhibited good GCV, H² and GAM would be useful as a base for selection; hence days to heading, days to flowering, plant height, grain yield and test weight were identified as the major contributors. K-911 was found superior yielding genotype under agro climatic condition of Allahabad, U. P., India. Secondly, this genotype exhibited highest seed / grain yield along with high number of tillers per plant, and early maturity (fewer days to maturity). Thirdly, the same genotype showed inbuilt escaping mechanism against high temperature. Fourthly, the same genotype showed tolerance / resistance against pest and disease infestation. Fifthly, it was concluded that the gene pool of genotype K -911 is a unique and complex gene pool suitable for the improvement of multiple traits and environments. Grain yield had positive and highly significant correlation with test weight and harvest index which highest positive direct effect on grain yield was exerted by test weight followed by harvest index both. Therefore, selection for high mean values of test weight / 1000 kernel weight and harvest index could be considered as the simultaneous selection of genotypes for high gain yield.

References

1. Al-Jibouri NA, Miller RA, Robinson HP. Genotypic and environmental variances and covariances in upland cotton. *Gecrosses of interspecific origin*. *Agronomy Journal*. 1958; 50:133.
2. Arya VK, Singh J, Kumar L, Kumar P, Chand P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian J Agric. Res.* 2017; 51(2):128-134.
3. Asif M, Mujahid MY, Kisana NS, Mustafa SZ, Ahmad I. Heritability, genetic variability and path coefficient of

some traits in spring wheat. *Sarhad Journal of Agriculture*. 2004; 20(1):87-91.

4. Birhanu M, Sentayehu A, Alemayehu A, Ermias A, Dargicho D. Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes. *Glob. J Sci. Front. Res.* 2016; 16(7):12-15.
5. Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS. Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat (*Triticum aestivum* L.). *Madras Journal of Agriculture*. 2001; 88(7/9):457-461.
6. Dawit Tsegaye, Tadesse Dessalegn, Yigzaw Dessalegn, Getnet Share. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* Desf). *Agricultural Research and Reviews*. 2012; 1(4):107-112.
7. Danaïl Kahrizi, Kianoosh Cheghamirza1, Mehdi Kakaei, Reza Mohammadi, Abdolghafar Ebadi. Heritability and genetic gain of some morpho-physiological variables of durum wheat (*Triticum turgidum* var. *durum*). *African Journal of Biotechnology*. 2010; 9(30):4687-4691.
8. Devenand Burton GW. Estimating heritability in tall fescue (*Restuca arundian*) from replicated clonal material. *Agronomy Journal*. 1953; 45(1):478-481.
9. Donald CM, J Hamblin. The biological yield and harvest index of cereals as agronomic and plant breeding criteria. *Advanced Agronomy*. 1976; 28:361-405.
10. Garg DK, Sharma AK. Genetic variability in wheat (*Triticum aestivum* L.) crosses under different normal and saline environments. *Annals*. 2002; 23(3):497-499.
11. Gupta RS, Singh RP, Trwari DK. Analysis of heritability and genetic advance in bread wheat (*Triticum aestivum* L.). *Advances in plant science*. 2004; 17(1):303-305.
12. Johnson RE, Robinson HW, Comstock HF. Estimate of genetics and environment variability in soybean. *Agronomy Journal*. 1955; 47:314-318.
13. Kandel M, Bastola A, Sapkota P, Chaudhary O, Dhakal P, Chalise P *et al.* Analysis of Genetic Diversity among the Different Wheat (*Triticum aestivum* L.) Genotypes. *Turkish J of Agriculture and N. Science*. 2018; 5(2):180-185.
14. Khumkar MS, Chaudhary HB, Deshmukh PS. Genetic variability and association of morpho-physiological characters with grain yield in late sown wheat (*Triticum aestivum* L.). *Annals of Agriculture Research*. 2001; 22(2):217-220.
15. Kifle Z, Firew M, Tadesse D. Estimation of association among growth and yield related traits in bread wheat (*Triticum aestivum* L.) genotypes at Gurage Zone, Ethiopia. *Int. J Plant Breed. Crop Sci.* 2016; 3(2):126-132.
16. Lush JL. Inter se, correlation and regression of characters proceedings of American Society of Animal Production. 1949; 33:293-301.
17. Obaidi MQ, Mohmand Elias, Azmatyar MH, Sharma R. Two new wheat varieties for irrigated conditions of Afghanistan. *Af. J of Agriculture Research*. 2017; 12(17):1483-1485.
18. Panwar D, Singh I. Genetic variability and character association of some yield components in winter x spring nursery of wheat. *Advanced Plant Science*. 2000; 8(1):95-99.
19. Panwar SV, Patil SC Nalik, Jombhale VM. Genetic variability and heritability in wheat. *Journal of*

- Maharashtra Agriculture University. 2002; 27(3):324-325.
20. Persaud S. Long term growth Prospects for Wheat Production in Afghanistan. Retrieved from, 2012. http://www.ers.usda.gov/media/193523/whs11101_1_.pdf
 21. Phadnawis BN, Khatod JP, Vitkare DG, Shivankar RS, Nagone AH. Genetic variability and correlation coefficient studies in durum wheat. *Annals of Plant Physiology*. 2002; 6(2):115-118.
 22. Rasal PN, Bhoite KD, Godekar DA. Genetic variability and genetic advance in durum wheat. *Journal of Maharashtra Agriculture University*. 2008; 33(1):102-103.
 23. Sultana R, Malik SK. Genetic variability and character association between yield and yield attributing traits in bread wheat, (*Triticum aestivum* L.). *Annals*. 2005; 26(1):118-125.
 24. Shah MA. Genetic studies for grain and temperature attributes in bread wheat (*Triticum aestivum* L.). *Indian Journal of Agriculture Research*. 1998; 32(2):105-110.
 25. Shankarrao BS, Mukherjee S, Pal AK, De DK. Estimation of variability for yield parameters in Bread Wheat (*Triticum aestivum* L.) grown in Gangetic West Bengal. *Electronic Journal of Plant Breeding*. 2010; 1(4):764-768.
 26. Sultana R, Malik SK. Genetic variability and character association between yield and yield attributing traits in bread wheat, (*Triticum aestivum* L.). *Annals*. 2005; 26(1):118-125.
 27. Singh SK, Singh Ayodhya, Singh Archana, Tomar Anjali, Sharma Shubhashni. Studies on heritability and genetic advance for some quantitative traits in wheat (*Triticum aestivum* L.). *Flora and Fauna (Jhansi)*. 2010; 16(1):21-25.32 ref.
 28. Tesfaye W, Firdisa E, Sentayehu A, Ermias A, Dargicho D. Genetic variability, heritability and genetic advance for yield and yield related traits in Durumwheat (*Triticum durum* L.) accessions. *Sky J Agric. Res*. 2016; 5(3):42-47.
 29. Waziri A, Habibi A, Manan AR, Rabbani H, Kamalzai H, Alawi KS *et al*. Making Afghanistan wheat secure by 2022. *eWIS*, No. 2013; 116:12-14.