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Genetic Variability Analysis and Correlation Studies of Bread Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

In the present investigation, fifty four bread wheat (*Triticum aestivum* L.) genotypes were evaluated for estimation of the genetic variability and its potential of each genotype under normal spring condition in Kabul Afghanistan in two years consequently (2020 and 2021). Analysis of variance revealed that genotypes possess significant genetic variability among all traits. For all the studied traits, mean squares showed the presence of significant variation among the genotypes. Higher values of PCV and GCV indicated that there was high variability exiting among the genotypes. The higher values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (GCV) were recorded for grain yield (GCV = 11.93% and PCV = 16.15%) followed by thousands grains (GCV=7.53% and PCV=8.15%). The highest heritability (0.94) was indicated in grain yield in the year 2021 followed by thousand grains (0.85) whereas the plant height (0.70) observed in (2020). The values of genetic advance were recorded low to moderate for all parameters. A highly significant positive correlation was observed among yield and harvest index and showed the significant difference for others except number of effective tiller per m^2, on contrary the negative non-significant correlation was observed for effective tiller per m^2 (-0.07). Grain yield with biological yield revealed a non-significant correlation (0.04), similarly days to heading revealed a non-significant negative correlation with grain yield (-0.05) respectively. From the study suggested that all the traits showing significant correlation with grain yield needs better attention for increasing yield in future wheat breeding programs.

***Keywords*:** Bread wheat, Broad sense heritability, Genetic advance, Correlation coefficients

Introduction

Wheat (*Triticum aestivum* L.) is the most important grain and is being used as a staple food for more than one third of the world. Development of the varieties with high potential that having desirable combination of characters is always the main objective of wheat breeding programme. The studies of the genetic association and identification of genetic variability between various genotypes are essential for wheat improvements as well for breeders, because the crosses between dissimilar parents permit a huge segregation and the grouping of various favorable alleles (Bered et al. 2002). Wheat is the second important cereal crop after rice in the world and that is a source of nutrition for 35% of the world population and currently ranks first among cultivated plants in terms of cultivation area and production. Wheat is the first most important cereal crop of Afghanistan and plays a vital role in food and nutritional security.

Wheat cultivated under diverse agroclimatic conditions and showed wide variations in productivity from region to region, as crop becomes restricted due to sudden fluctuations in environmental changes. The main objective of a crop breeding programme is to develop varieties that perform well over a broad spectrum of environments. Further, a variety having wide or good adaptability is one which gives consistently superior performance over several environments (Frey 1964). The quantitative trait like yield mainly dependent on Genotype × Environment interaction as it obscure the interpretation of genetic experiments and makes predictions difficult. In such circumstances it is difficult to select and suggest one better genotype across various locations. A wider adapted genotype performs consistently over a wider range of environment. To ensure valid genotype recommendation and to identify promising genotypes, a breeder should conduct multi location yield trials across different environments (Soleman et al. 2018).

Grain yield in wheat is a complex character and is depend on its component traits. For genetic manipulation of grain yield, quality and other characters in wheat, there is a need to examine the nature of genetic variability for the yield related attributes and quality traits. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) helps to choose the potential genotype and heritability along with genetic advance would be more useful tool in predicting the resultant effect for selection of best genotypes for yield. Path coefficient analysis was used by plant breeders to help identify traits that could be useful as a selection criterion for improving crop yield. The path coefficient divides correlation coefficients into direct and indirect effects within the correlation system of traits. When there is a genetic correlation between two traits, the selection for one of them will produce a change in the other trait. In other words, the response of the correlation to the act of selection will take place.

Path parameters show a direct effectof the independent variable in the dependent variable, as well as an indirect effect of the independent variable in the dependent variable through another independent variable (Hadi et al. 2018). Keeping these things in the view, the present investigation was made to assess genotypes with the objectives, to estimate the variability, heritability and genetic advance for yield and yield components traits in wheat.

Materials and Methods

The experimental materials consisting of 54 genotypes including checks. The experiment was conducted at Research Station of Agricultural Research Institute of Afghanistan in spring season of the year 2020 and 2021. The experiment was carried out in a Randomized Block Design (RBD) under irrigated conditions with two replications. Each line was sown in 6 rows of 3 meter long and 20 cm apart. The recommended packages of practices were followed to raise the good crop. Sowing was done by hand drilling.

The observations, namely, days to heading, days to maturity, grain yield and biological yield were recorded on plot basis whereas, data for the traits such as plant height, spike length, number of spikelets per spike, number of grains per spike were recorded on randomly selected five plants per genotype per replication. The number of effective tillers was recorded by counting effective tillers of per meter square row length. The thousand grain weights were recorded by counting 1000 seeds per genotype per replication and weigh.

The mean performance of individual genotypes was used for statistical analysis. Statistical analysis of recorded phenotypic data was performed using a computer based statistical package program. To test the difference among the genotypes, the analysis of variance was worked out separately for each character as per method suggested by Fisher (1954). Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were calculated as per the standard formula suggested by Burton and Devane (1953). Heritability in broad sense was calculated as the ratio of genotypic variance (Vg) to phenotypic variance (Vp) and expressed in percentage (Falconer, 1981). Genetic advance as percent of mean of each character was worked out adopting the formula given by Johnson et al. (1955). Genetic gain (GG) is the genetic advance expressed as per cent of mean. It was estimated by using the formula of Johnson et al. (1955). Similarly, path analyses were carried out using the method suggested by Dewey and Lu (1959).

Results and Discussion

Analysis of variance

The analysis of variance was worked out to test the differences among genotypes by F-test. It was carried out according to the procedure of Randomized Complete Block Design.The analysis of variance (ANOVA) indicated for both years highly significant differences among the genotypes for days to heading flowering, days to maturity, effective tillers/m^2, plant height, spike length, number of spikelets per spike, number of grains per, grain yield, 1000 grain weight, biological yield, and harvest index (Table 1.) revealed the existence of sufficient genetic variability in all the traits the genotypes under study. The genotypes showed significant different in characters suggested for the next year as the best genotypes. Significant differences among the genotypes for different morphological and quality traits were also earlier reported by Singh et al. (2013), Singh et al. (2014), Kumar et al. (2016) and Gauravrajsinh (2021) in wheat crop.

Heritability (Broad sense) and genetic advance

The estimates of broad-sense heritability in percent have been presented in Table 2. The heritability estimates in broad sense were quite high for most of the characters indicated that strong genetic nature for all the traits. The higher heritability implied that selection for most of the traits might be effective in this set of genotypes. The characters namely, grain yield per plot was showed highest value (h^2=0.94) in 2021, and followed by 1000 grains yield (h^2=0.85) in 2020 number of spikelets per spike, plant height and weight per ear have high heritable.

The high heritability indicate that the characters were less influenced by environment, the similar results were also found by Bharat et al. (2012), Liu and Ma (1994), Deswal et al. (1996). High estimates of heritability coupled with high genetic advance were observed for plant height, thousand grain weight biological yield per plant and grain yield which indicated that above characters was governed by additive gene action and as such expected to exhibit improvement by direct selection. Similar findings were also reported by Bhushan et al. (2013) and Nukasani et al. (2013).

The estimates of genetic advance as percent of the mean are presented in Table 2. It revealed that the highest genetic advance as percent of mean was recorded for grain yield (27.7%) followed by biological yield (25.6%) during the year 2021.

Genotypic and phenotypic variability

The study revealed, phenotypic coefficient of variation (PCV) were higher than their corresponding genotypic coefficient of variation (GCV) for all the quantitative traits among the genotypes in both the years i.e. 2020 and 2021. This indicates that the characters were influenced by the environment. The selection on the basis of phenotype alone can be effective for the traits where variation between PCV and GCV were less means less influenced by the environment. (Table 3). Higher values of PCV and GCV indicated that there was high Variability exiting among the genotypes that consequently showed.

The higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for grain yield (11.9%) and (PCV= 16.2%) followed by thousands grain weight (GCV=7.54% and PCV=8.16%), biological yield (GCV=7.20% and PCV=7.20%), effective tillers per plant (GCV=6.63% and PCV=11.5%), plant height (GCV=6.28% and PCV=7.47%), number of grain per spike (GCV=5.44% and PCV=8.63%), number of spikelets per spike (GCV=5.25% and PCV=8.07%), spike length (GCV=4.43% and PCV=6.54%) in 2020, similarly for 2021 also higher value of PCV and GCV were recorded in grain yield (PCV=13.9%) and (GCV=14.4%) followed by effective tiller per m^2 (GCV=9.43%) and (PCV=11.5%) indicating better opportunity for improvement in these traits through selection. A range of GCV (6.93% to 28.24%) and PCV (7.62% to 28.57%) were reported by Girnam et al. (2018). Though a range of PCV (0.81% to 9.07%) and GCV (0.50% to 8.08%) reported by Kumar et al. (2016). The other researchers namely Singh et al. (2013) and Singh et al. (2014) also reported high value of PCV and GCV for grain yield and tillers per plant in wheat. High phenotypic and genotypic coefficient of variation for grain yield, harvest index and tillers per plant were also reported by Kumar et al. (2016).

Correlation coefficient analysis

Correlation coefficient is the mutual association between variables without implying any cause and effect relationship. Simple correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting following formulae given by Al- Jibouri et al. (1958). Genotypic correlation analysis was conducted between different morphological traits and it was observed that most of them showed a significant correlation coefficient at 0.01 or 0.05 level of significance (Table 3). The yield and related traits was expressed different trends in relationship among the traits.

Grain yield showed significant positive association with harvest index (0.97**), plant height (0.73**), number of grain per spike (0.3*) spike length (0.21*), number of spikelets per spike (0.48*), thousand grains weight (0.21) and similarly, noticed there was no significant positive relationship between effective tillers per m^2 (-0.07) and biological yield (0.04), other researchers also reported the results like Ahmad Khan, et al. (2017). Ahmad et al. (2016), reported significant and positive association between grain yield and flag leaf area, tillers per plant and 1000-grain weight. Significant positive association of grain yield with tillers per plant and plant height was previously noticed by Masood et al. (2014).

Similarly, Iftikhar et al. (2013) also noticed positive association of yield with flag leaf area, grains per spike and 1000-grain weight. Similarly, significant positive relationship of grain yield and flag leaf area was also observed by Hussain et al. (2013). Rehman et al. (2015) also reported positive association between1000-grain weight and plant height, spike length, grains spike^{-1} and grain yield.

Conclusions

The results of the study showed that significant variations were present among the genotypes for different traits.

The heritability values were observed high for grain yield per plot in 2021 and thousands grain weight in 2020 and moderately showed for others while the lower heritability observed for days to heading. The genetic advance were observed low to moderate, which is an indicator that non-additive gene action was controlling the expressions of these characters.

Furthermore, the genotypic correlation revealed positive correlation of grain yield with harvest index and plant height at highly significant and shows the significant correlation with number of grain per spike, number spikelets per spike and spike length. It suggesting that more importance should be given to these traits for improving the yield in wheat.

The analysis of variance for grain yield and its contributing components namely days to 50% flowering, days to maturity, productive tillers, plant height, spike length, spikelets pet spike, grains per spikelet, biological yield, harvest index, 1000 grain weight, grain yield and gluten content showed highly significant differences (at<1% level of significance) among the genotypes under present study. High heritability along with high genetic advance and high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for grain yield (g), biological yield (g), harvest index (%), spike length (cm) and 1000 grain weight (g) indicated substantial contribution of additive gene action in the expression and thus selection would be effective for genetic improvement of these traits for improving grain yield in wheat.

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Table 1. Analysis of variance (ANOVA) for yield and yield contributing traits in bread wheat genotypes for the year 2020 and 2021

Traits	Replication (d.f=1)		Treatments (d.f=53)		Error (d.f=53)		F. ratio	
Years	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**
DH	0.75	0.453704	4.204228*	3.0330**	2.61792	0.3971	1.6059	7.6379
DM	2.37	1.564815	1.452131**	3.1273**	0.57791	0.62141	2.5127	5.0326
ET	7566.8	984.037	2393.301**	2015.6*	1191.75	183.433	2.0082	10.988
PH	3.703	11.3425	62.50874**	41.321**	10.7791	6.62561	5.799	6.2367
SL	0.280	1.33333	0.563636**	0.3962**	0.20933	0.06918	2.6925	5.7273
NSS	0.593	6.11564	3.695318**	1.8792**	1.49825	0.84696	2.4664	2.2188
NGS	27.0	0.59259	19.18239**	6.1481*	8.26415	1.10202	2.3212	5.5789
GY	0.046	0.00128	0.208105**	0.15986*	0.06116	0.00506	3.4025	31.536
TSW	28.99	0.00037	22.3988**	17.5744*	1.77361	2.88923	12.628	6.0827
BY	0.0048	0.006379	0.745992*	0.92374*	0.42661	0.06587	1.7486	14.023
HI	39.64	4.304371	22.2473***	15.7751*	8.74909	3.29260	2.5428	4.7911

DH= Days to heading, DM= Days to maturity, ET= Effective number of tillers per meter square, PH= Plant height, SL= Spike length, NSS= Number of spikelets per spike, NGS= Number of grains per spike, GY= Grain yield per plot, BY= Biological yield per plot, HI= Harvest index

Table 2. Mean, range, heritability (BS), genetic advance and coefficient of variation for yield and yield attributing traits of bread wheat genotypes for the year 2020 and 2021.

Traits	Mean		Range				Heritability (Broad sense)		Genetic Advance as % of Mean		Coefficient of Variation (%)			
			Maximum		Minimum						GCV		PCV	
Year	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**	**2020**	**2021**
DH	72	69	78	73	67	66	0.23	0.77	1.22	2.99	1.23	1.65	2.56	1.89
DM	114	112	116	115	113	110	0.43	0.67	0.78	1.69	0.58	1.00	0.88	1.23
ET	370	321	419	389	293	242	0.34	0.83	7.91	17.7	6.63	9.43	11.5	10.3
PH	81.0	78.9	92.5	90.0	62.5	70	0.71	0.72	10.86	9.25	6.28	5.28	7.47	6.20
SL	9.5	9.2	10.5	10.3	8.3	8.3	0.46	0.70	6.18	7.62	4.43	4.41	6.54	5.26
NSS	20.0	17.8	22	20.5	16	16	0.42	0.38	7.03	5.13	5.25	4.05	8.07	6.58
NGS	42.9	40.5	51.5	46.5	38	37	0.40	0.70	7.07	6.75	5.44	3.93	8.63	4.71
GY	2.27	2.00	2.86	2.43	1.53	1.37	0.55	0.94	18.2	27.7	11.9	13.9	16.2	14.4
TSW	42.6	41.3	49.2	48.0	34.9	36.0	0.85	0.72	14.3	11.4	7.54	6.56	8.16	7.74
BY	5.55	4.92	6.93	6.40	4.14	3.36	0.27	0.87	7.75	25.6	7.20	13.3	7.20	14.3
HI	40.9	40.8	47.1	47.6	31.8	32.3	0.44	0.65	8.64	4.16	6.36	6.13	9.63	7.57

DH= Days to heading, DM= Days to maturity, ET= Effective number of tillers per meter square, PH= Plant height, SL= Spike length, NSS= Number of spikelets per spike, NGS= Number of grains per spike, GY= Grain yield per plot, BY= Biological yield per plot, HI= Harvest index

Table 3. Genotypic correlation coefficients of yield and yield related traits

DH	DM	ET	PH	SL	NSS	NGS	TSW	BY	HI	GY
DH	1	-0.30	0.02	-0.04	0.48**	0.029	0.44*	-0.00	0.15*	-0.05
DM	-0.30*	1	-0.14	-0.07	-0.12	-0.47	-0.31	-0.06	-0.41*	0.23*
ET	0.02	-0.14	1	0.66**	0.37*	0.34*	0.26	0.18*	0.93**	0.26*
PH	-0.04	-0.07	0.66**	1	0.17	0.41*	-0.22	0.41*	0.59**	-0.32*
SL	0.48**	-0.12	0.37*	0.17	1	0.60*	0.20	0.24*	0.78**	-0.07
NSS	0.02	-0.47	0.34*	0.41*	0.60**	1	-0.16	0.12	0.51*	-0.18
NGS	0.44	-0.31	0.26*	-0.22	0.20*	-0.16	1	-0.26	0.43*	-0.11
TSW	-0.00	-0.06	0.18*	0.41*	0.24*	0.12	-0.26	1	0.19*	-0.10
BY	0.15	-0.41	0.93**	0.59*	0.78**	0.51	0.43*	0.19	1	0.28*
HI	-0.05	0.23*	0.26*	-0.32	-0.07	-0.18	-0.11	-0.10	0.28	1
GY	0.17*	-0.07	0.73**	0.21*	0.48*	0.30*	0.21*	0.04	0.97**	0.73**

The significant was tested at 0.05% and 0.01%

DH= Days to heading, DM= Days to maturity, ET= Effective number of tillers per meter square, PH= Plant height, SL= Spike length, NSS= Number of spikelets per spike, NGS= Number of grains per spike, GY= Grain yield per plot, BY= Biological yield per plot, HI= Harvest index

References

Khan AS and Hassan G, (2017). Heritability and correlation studies of yield and yield related traits in bread wheat. Sarhad J Agric 33(1):103-107

Ahmad I, Mahmood N and Khan N, (2016). Genetics analysis for five important morphological attributes in wheat. J Anim & Pl Sci, 26(3):725-730

Al-Jibouri HA, Miller PA and Robinson HF, (1958). Genetic and environmental variances and co-variances in upland cotton cross of interspecific origin. Agronomy J, 50:633-37

Bharat B, Gaurav SS, Kumar R, Pal R, Panday MA, Kumar S, Bharti S, Nagar S and Rahul VP, (2012). Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). Environ & Ecology, 31(2):405-407

Bhushan B, Bharti S, Ojha A, Pandey M, Gaurav SS, Tyagi BS and Singh G, (2013). Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. J Wheat Res, 5(1):21-26

Burton GW and Devane EH, (1953). Estimating heritability in all fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy J, 45:478-481

Dewey DR and Lu KH, (1959). A correlation and path analysis of components of crested wheat grass seed production. Agronomy J, 51:515-518

Falconer DS, (1981) Introduction to quantitative genetics. 2nd Edition, Longman Group Ltd., London, 1-133.

Fisher RA, (1954). Statistical methods for research workers. 12th Edition, Biological Monograph and Manuals, 5:130-131.

Frey, (1964). Adaptation reaction of oat strains selected under stress and non-stress environmental conditions. Crop Sci. 4:55-58.

Girnam S, Pradeep K, Ravi K and Gangwar LK, (2018). Genetic diversity analysis for various morphological and quality traits in bread wheat (*Triticum aestivum* L.). J Appl and Natural Sci, 10 (1):24-29

Hadi BH, AL-Maliky RJM, Zaid MA and Hassan WA, (2018). Estimation of some genetic parameters in bread wheat *Triticum aestivum* L. for Wasit and Diwaniyya locations. Euphrates J Agri Sci, 10(1):194-203

Iftikhar RSB, Hussain I, Khaliq and Smiullah, (2013). Study of inheritance for grain yield and related traits in bread wheat (*Triticum aestivum* L.). SABRAO J. Breed. Genet. 45 (2):283-290

Johnson HW, Robinson AE and Comstock RE, (1955). Estimates of genetic and environmental variability in soybeans. Agronomy J, 47:314-318.

Kumar P, Singh G, Kumar S, Kumar A and Ojha A, (2016). Genetic analysis of grain yield and its contributing traits for their implications in improvement of bread wheat cultivars. J Applied and Natural Sci, 8:350-357

Masood SA, Ahmad S, Kashif M and Ali Q, (2014). Correlation analysis for grain and its contributing traits in wheat (*Triticum aestivum* L.). Natural Sci. 12(11):168-176

Nukasani V, Potdukhe NR, Bharad S, Deshmukh S and Shinde SM, (2013). Genetic variability, correlation and path analysis in wheat. J Wheat Res, 5(2):48-51

Rehman, S, Abid MA, Bilal M, Ashraf J, Liaqat S, Ahmed RI and Qanmber G, (2015). Genotype by trait analysis and estimates of heritability of wheat (*Triticum aestivum* L.) under drought and control conditions. Bas. Res. J. Agric. Sci. Rev. 4(4):127-134

Singh G, Kulshreshtha N, Singh BN, Setter TL, Singh MK, Saharan MS, Tyagi BS, Verma Ajay and Sharma I, (2014). Germplasm characterization, association and clustering for salinity and water-logging tolerance in bread wheat (*Triticum aestivum*). Indian Journal of Agricultural Sciences, 84:1102-10

Singh MK, Sharma PK, Tyagi BS and Singh G, (2013). Genetic analysis for morphological traits and protein content in bread wheat (*Triticum aestivum* L.) under normal and heat stress environments. Ind J Genet and Pl Breeding, 73:320-324

Soleman M, (2010). Performance of yield and stability of wheat genotypes under high stress environments. Arid L and Agril Sci, 21(1):81-92

Vaghela GK, Patel JM, Parthsinh R and Gokulakrishnan M, (2021). Assessment of genetic variability and character association for morpho-chemical traits in bread wheat (*Triticum aestivum* L.). Emergent Life Sci Res 7(1):14-20