Genetic Variability and Character Association Study for Yield Enhancement in Bread Wheat (*Triticum aestivum* L.)

ABSTRACT

The present investigation was conducted to examine the 20 Bread Wheat genotypes along with 2 checks to study the genetic parameters, correlation and genetic diversity. The experiment was carried out in main experimental station of Agricultural Research Farm, Rama University (U.P), Mandhana, Kanpur during Rabi Season, 2020-21 in Randomized Block Design (RBD) with three replications. Analysis of variance showed highly significant differences among 20 Bread Wheat for 11 characters studied. On the basis of mean performance, genotype HPAN 111exhibited high grain yield per plant over the check.Genotypic coefficient of variation (GCV) was recorded highest for Biological yield per plant (15.073%). Phenotypic Coefficient of Variation (PCV) was recorded highest for Biological yield per plant (16.316%). Environmental coefficient of variation (ECV) was recorded highest for Effective tiller per plant (13.591%). High heritability was observed for most of the traits and it was noted highest for Biological yield per plant (85.4%). Genetic advancement was recorded highest for Biological yield per plant (643.733%). The high Genetic advance as per cent of mean was recorded for Biological yield per plant (28.687%). Grain yield per plant shows Significant Positive Correlation with Biological yield per plant (0.8803**) at genotypic and phenotypic level.

Key words: Bread Wheat, genetic parameters, correlation

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[1] INTRODUCTION

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Wheat(*Triticumaestivum*L.)isoneofthemostimportantcerealscrops of the world as well as India. It is cultivated under various growing condition of soil and climate. It is second most important food crops after rice and most prominent crop in Rabi season in India. It contributes

around 35% in cereal crops and described as **'King of Cereals'** because of high trade and area it covered at global level, it was cultivated over 214.79 million ha and production of 735.18 million tones with an average productivity of 34.22 quintals per hectare (FAOSTAT, 2018). In India, Wheat has second rank after paddy both in area and production, occupying 29.14 million ha acreage area with production of 102.19 million tones and the productivity of 35.07 quintals per hectare (IIWBR, 2018-19).

The optimum temperature for wheat growth is 25°C with minimum and maximum growth temperatures of 30°C to 40°C and 30°C to 32°C, respectively (Briggle, 1980). Cultivars of widely differing pedigree are grown under varied conditions of soil and climate and show wide trait variation.

Grain yield is a complex polygenic character with great genetic, physic-morphological,ecologicalandPathological dependence. The hereditarypotential of a cultivar/genotype depends upon stability and yielding. Genetically, yield contributing attributes i.e. yield components, (productive tiller, number of grains, 1000 grain weight etc.), there genetic nature and magnitude of association areresponsibleforrealizationofyieldpotentialinfluencedbychangingagro climatic condition. Thus it is essential to accumulate information on these aspectstoresolveandquantifytheirmodeofcontributiontograinyield.Presence of genetic variability is a pre-requisite of any breeding programme aimed at developing varieties with high yield potential and yieldstability.

For genetic manipulation of quality as well as grain yield in cereals, there is need to examine the nature of genetic variability for the quality constituents and yield related attributes. This aspect need an extensive investigation, as most of the quality components of wheat are having reverse relationship with yield.

The idea of heritability which offers an index of the transmissibility to measurethegeneticrelationshipofacharacterinthepopulation,if heritabilityof a character is high it should be fairly easy to improve that trait. Genetic advance estimates give an idea of

improvement in the mean performance of the selected families over the base populations. Correlation coefficient analysis appears to be quiet powerful tool to understand the interrelationship of various yieldattributes. Consequently path coefficient analysis was considered as the most common and useful statistical method used for this purpose and it can also be used to estimate the quantitative impact of direct and indirect effects caused by one or other components of grain yield and their relationship between thesecomponents.Breeding/Identification of high yielding wheat lines of good quality associated with resistance biotic and abiotic factors is the prime objective of wheat important. Knowledge of pattern of existing genetic variability, trend of character association, help researcher to identify important character and development of high yielding wheat lines.

In order to increase the efficacy of germplasm the information on genetic basis of variation for economically in the desirable character relies mainly upon identificationofgeneticallysuperiorandsuitablegenotypes.Selectionofprogeny and its breeding depend upon the genetic variability in a population (Ajmal*et al*. 2009).

[2] MATERIALS ANDMETHODS

The Present Investigation was conducted during Rabi, 2020-21.The materials used for present investigation comprised of 20 bread wheatgenotypes collectedfromFaculty of Agricultural Sciences and Allied Industries, Rama University, Mandhana, Kanpur.

Table No. 1: Name of wheat genotypes

S.No.	Genotypes Name	S.No.	Genotypes Name
1	HPST-16-17-07	**11**	HPAN 147
2	HPST-16-17-15	**12**	HPAN 164
3	HPST-16-17-16	**13**	HPAN 42
4	BHU 25	**14**	HPAN 57
5	BHU 31	**15**	HPAN 65
6	Zincol	**16**	HPAN 111
7	Ankur	**17**	HPAN 127
8	PBW Zn 1	**18**	CRD Genhun 1
9	WB 02	**19**	PBW 677
10	HPAN 101	**20**	HD 2967

All the 20 genotypes were grown in Randomized Block Design (RBD) with 3

replications.Ineachreplication,genotypesweresownin2rowsof1-meterlength with row to row and plant to plant spacing of 20 cm and 10 cm respectively.Theexperiment was sown on December 03, 2020. Agronomic practices and plant protection measures were followed to raise a good crop.

[3] RESULTS AND DISCUSSION

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The present investigation was carried out to estimate the nature and magnitude of variability parameters, characters associations and genetic divergence among 20 genotypes of Bread Wheat for 11 characters. The experiment was laid out in Randomized Completely Block Design (RBD) with 2 replications during Rabi, 2020-21. The experiment data obtained was subjected to statistical analysis.

[3.1]. ANALYSIS OF VARIANCE (ANOVA)

The Analysis of variance (ANOVA) indicated that the mean sum of squares due to genotypes were highly significant for all the traits *viz.*, Days to 50% flowering, Days to maturity, Plant height (cm), Number of effective tillers per plant, Length of main spike (cm), Number of spikelet's per spike, Number of grains per spike, Thousand seed weight (g), Biological yield per plant (g), Grain yield per plant (g), Harvest index (%). The mean sum of squares due to replication showed non-significant differences for all the traits under study indicating good homogeneity among replications. Mean sum of square from analysis of variance for various traits are given in Table.

The similar observation have been reported by Tahmasebi*et al.* (2013), Mollasadeghi*et al.* (2013) and Lal*et al.* (2009), Sabit*et al.* (2017), Kaddem*et al.* (2014), Mecha*et al.* (2016), Ghuttai *et al.* (2015).

[3.2]. MEAN PERFORMANCE OF THE GENOTYPES

Mean performance of genotypes and range for all the 11 characters are presented in Table.

TABLE No.2: Means Table

Variety	DFF	DM	PH	ETP	SL	SPS	GPS	BYP	GYP	HI	TSW
HPST-	84.00	118.0	100.0	5.50	13.00	21.00	58.5	2050	780	36.9867	48.83

16-17-07											
HPST-16-17-15	83.00	117.0	97.5	4.50	13.50	22.00	52.5	2200	620	28.63	47.4267
HPST-16-17-16	82.50	116.5	92.5	5.50	13.50	20.00	56.5	1570	625	41.3033	48.5167
BHU 25	82.50	116.5	100.0	5.00	13.00	20.00	49.5	2245	790	35.1767	46.6767
BHU 31	81.50	116.0	90.0	6.00	13.00	20.00	50.5	1610	620	38.6867	47.65
Zincol	82.00	116.0	87.5	4.50	13.50	22.00	59.5	1970	670	34.4867	48.9167
Ankur	83.00	117.0	97.5	4.50	12.50	20.00	61.5	2730	830	30.63	48.71
PBW Zn 1	81.50	118.0	100.0	5.50	13.00	19.00	59.5	2630	860	32.4867	48.85
WB 02	81.00	117.0	95.0	5.00	12.50	20.00	70.5	2530	850	33.6567	50.04
HPAN 101	82.00	115.5	97.5	4.00	12.50	20.00	61.0	2380	730	31.41	47.89
HPAN 147	82.00	115.5	95.0	6.50	14.00	23.00	54.0	2300	960	42.8067	48.9467
HPAN 164	82.00	117.0	92.5	4.50	11.50	18.00	69.0	2050	730	35.9667	49.9367
HPAN 42	81.50	117.5	97.5	5.00	13.00	19.00	54.0	2100	670	32.5133	48.98
HPAN 57	81.00	117.5	87.5	5.50	13.50	21.00	54.5	2400	850	35.42	47.66
HPAN 65	81.00	116.5	87.5	4.50	13.00	20.00	62.5	2780	860	31.3467	48.9567
HPAN 111	83.00	116.0	95.0	4.00	12.50	19.00	59.5	2540	965	38.22	48.7367
HPAN 127	84.00	116.0	95.0	6.00	12.50	19.00	52.0	2070	700	33.8867	47.55
CRD Genhun 1	81.50	118.5	95.0	5.50	14.00	23.00	54.5	2240	710	30.5467	46.9
PBW 677	82.50	117.5	95.0	5.50	12.50	18.00	46.5	2790	900	32.38	43.99
HD 2967	85.00	118.5	97.5	4.00	13.50	21.00	58.5	1695	640	37.8733	47.64
Mean	82.325	116.9	94.75	5.05	13.00	20.25	57.225	2244	768	34.7207	48.1402
Min.	81.00	115.5	87.5	4.00	11.50	18.00	46.5	1570	620	28.63	43.99
Max.	85.00	118.5	100	6.50	14.00	23.00	70.5	2790	965	42.8067	50.04
C.V.	1.0662	1.2209	3.4773	13.5907	5.5806	7.5617	10.9728	10.8163	12.2331	13.4159	2.3988
S.E.(m)	0.5068	0.824	1.9022	0.3963	0.4189	0.8841	3.6253	140.1331	54.242	2.6893	0.6667
C.D. 5%	1.4508	-	5.4459	1.1344	1.1991	2.531	10.3789	401.1906	155.2908	7.6994	1.9087

Days to flowering ranged from 81 days (WB 02, HPAN 57, HPAN 65) to 85 days (HD 2967) with a mean value of 82.325 days.Days to maturity ranged from 115.5 days (HPAN 101, HPAN 147) to 118.5 days (CRD Genhun 1, HD 2967) with a mean value of 116.9 days.The plant height ranged from 87.5 cm (Zincol, HPAN 57, HPAN 65) to 100 cm (HPST-16-17-07, BHU 25, PBW Zn 1) with mean value of 94.75 cm.Number of effective tillers per plant is one of the important yield determining trait among all traits under study. The mean of effective tillers per plant was 5.05 and it ranges from 4 (HPAN 101, HPAN 111, HD 2967) to 6.5 (HPAN 147).The mean value for length of main spike was noted as 13 cm with a range from 11.5 cm (HPAN 164) to 14 cm (HPAN 147, CRD Genhun 1).The number of spikelet's per spike ranged from 18 (HPAN 164, PBW 677) to 23 (HPAN 147, CRD Genhun 1) with a mean value of 20.25.Number of grains per spike ranged from 46.5(PBW 677) to 70.5 (WB 02) with a mean value of 57.225.The mean value for 1000-grains weight was 48.1402g and it ranged from 43.99g (PBW 677) to 50.04g (WB 02).Harvest Index had mean value of 34.7207% and it ranges from 28.63% (HPST-16-17-15) to 42.8067% (HPAN 147). Biological yield per plant ranged from 1570 g (HPST-16-17-16) to 2790g (PBW 677) with a mean value of 2244g.

Grain yield per plant was minimum 620g (HPST-16-17-15, BHU 31) while it was maximum for genotype HPAN 111(965g) with mean value of 768g.

The findings were quite similar to as reported by Kabir *et al.* (2017) for biological yield per plant. Tsegaye *et al.* (2012) for harvest index. Rajpoot *et al.* (2013) for days to 50% flowering, days to maturity, grain yield per plant. Rajpoot *et al.* (2013) and Ghuttai *et al.* (2015) for plant height, grain per spike, spike length.

[3.3]. GENETIC VARIABILITY PARAMETERS

The parameters of genetic variability viz., Phenotypic Coefficient of Variation (%), Genotypic Coefficient of Variation (%), Efficient Coefficient of Variation (%), Heritability (%) in broad sense, Genetic advancement5% and Genetic advance as percent of mean 5% for each traits are presented in Table.

Table No.3: Genetic Parameter

Character	Hbs %	ECV	GCV	PCV	GA 5%	GA as % of mean 5%
DFF	78.40	1.066	1.174	1.326	1.764	2.143
DM	20.90	1.221	0.362	0.792	0.398	0.340
PH	77.90	3.477	3.771	4.272	6.496	6.856
ETP	70.00	13.591	11.991	14.330	1.044	20.669
SL	52.40	5.581	3.379	4.669	0.655	5.038
SPS	62.60	7.562	5.653	7.143	1.866	9.217
GPS	64.30	10.973	8.505	10.605	8.040	14.050
BYP	85.40	10.816	15.073	16.316	643.733	28.687
GYP	76.60	12.233	12.771	14.594	176.804	23.021
HI	48.10	13.416	7.458	10.753	3.700	10.657
TSW	75.00	2.399	2.400	2.771	2.061	4.282

[3.4.1]. Phenotypic Coefficient of Variation (PCV)

The Phenotypic Coefficient of Variation (PCV) was higher in magnitude than that of genotypic coefficient of variation for all the characters under study. The highest PCV was recorded for biological yield per plant followed by grain yield per plant, number of effective tillers per plant, harvest index, grain per spike and spikelet's per spike. The characters viz.,days to maturity, daysto 50% flowering, thousand seed weight, plant height and spike length showed low phenotypic coefficient of variation.

Tiwari*et al.* (2016), Desheva and Kyosev (2015), Singh and Upadhyay (2013), Rajdeeep*et al.* (2014), Chethana*et al.* (2017) also find the highest PCV for most of the character like grain yield per plant, biological yield per plant and lowest for spike length, days to maturity.

[3.4.2]. Genotypic Coefficient of Variation (GCV)

Genotypic coefficient of variation (GCV) was recorded highest for biological yield per plant followed by grain yield per plant, effective tiller per plant, number of grains per spike, and harvest index. The characters viz.,days to maturity, days to 50% flowering, thousand seed weight, spike length, plant height, and spikelet's per spike exhibited low genotypic coefficient of variation.

Ali and Abdulla (2016), Sharaan*et al.* (2017), Arya *et al.* (2017), Bisht and Gahalin

(2009) reported high estimates of GCV for grain yield per plant, effective tiller per plant. Mecha*et al.* (2016), Chimdesa*et al.* (2017) reported low GCV for spikelet's per spike, plant height.

[3.4.3]. Efficient Coefficient of Variation (ECV)

Efficient coefficient of variation (ECV) was recorded highest foreffective tiller per plant followed by harvest index, grain yield per plant (12.233%),number of grains per spike (10.973%) and biological yield per plant (10.816%). The characters viz.,days to 50% flowering (1.066%), days to maturity (1.221%), thousand seed weight (2.399%), plant height (3.477%), spike length (5.581%) and spikelet's per spike (7.562%) exhibited low efficient coefficient of variation.Rajpoot *et al.* (2013), Desheva and Kyosev (2015) also find similar observations.

[3.4.4]. Heritability (h^2)

Broad sense heritability was estimated for all the characters under study. High heritability was observed for most of the traits and it was noted highest forbiological yield per plantfollowed bydays to 50% flowering,plant height, grain yield per plant,thousand seed weight,effective tiller per plant, grain per spike, spikelet's per spike. However,days to maturity, harvest index and spike length exhibited low estimates of heritability.

Bhushan *et al.* (2013) for biological yield per plant,Chethana *et al* (2017) plant height and spike length.Shah *et al.* (2017) for plant height and thousand seed weight.Sabit*et al.* (2017) high heritability for biological yield per plant.Wahid Abdul and KarimShahla (2014)reported high heritability for plant height.

[3.4.5]. Genetic advancement 5%

Genetic advancement was recorded highest for biological yield per plant followed bygrain yield per plantand the characters viz.,days to maturity, spike length, effective tiller per plant, days to 50% flowering,spikelet's per spike, thousand seed weight, harvest indexplant height, grain per spikeexhibited low genetic advancement.

Shah *et al.* (2017), Kumar *et al.* (2017), Bhusan*et al.* (2013) reported high genetic

advancement for biological yield per plant. Chimdesa*et al.* (2017), Suleiman *et al.* (2014) for grain yield per plant.

[3.4.6]. Genetic advance as per cent of mean 5%

The high Genetic advance as per cent of mean was recorded for biological yield per plantfollowed by grain yield per plant, effective tiller per plant, number of grains per spike, and harvest index. The characters viz.,days to maturity (0.34%),days to 50% flowering (2.143%), thousand seed weight, spike length, plant height, spikelet's per spikeexhibited low genetic advance as per cent of mean.

Suleiman *et al.* (2014), Mecha*et al.* (2016) reported high genetic advancement as percent of mean for grain yield per plant. Kumar *et al.* (2017), Sharaan*et al.* (2017) for biological yield per plant.

[4]. Genotypic and phenotypic correlation coefficient analysis

Correlation coefficient at Phenotypic and Genotypic levels were estimated using 11 characters in 20 genotypes of bread wheat to study the degree of mutual relationship between yields and its component traits. The estimates are present in Table. Perusal of the results revealed that the estimates of genotypic correlation coefficients were higher in magnitude than their corresponding correlation coefficient at phenotypic level.

Table No.4: Genotypical Correlation Matrix

Traits	Level	DFF	DM	PH	ETP	SL	SPS	GPS	BYP	HI	TSW	GYP
DFF	*G*	**1.000**	-0.086	0.701**	-0.139	0.041	0.046	-0.210	-0.374	0.050	-0.229	-0.389
	P	**1.000**	0.151	0.466**	-0.188	-0.040	-0.004	-0.179	-0.328	0.182	-0.203	-0.228
DM	*G*		**1.000**	0.911**	0.342	0.425	-0.058	-0.176	-0.061	-0.735**	-0.531**	-0.883**
	P		**1.000**	0.309	-0.031	0.164	0.039	0.011	0.032	-0.286	-0.175	-0.110
PH	*G*			**1.000**	-0.247	-0.224	-0.182	-0.219	0.075	-0.056	-0.192	0.109
	P			**1.000**	-0.063	-0.107	-0.101	-0.102	0.102	-0.162	-0.115	0.044
ETP	*G*				**1.000**	0.363	0.041	-0.717**	-0.166	0.784**	-0.256	0.239
	P				**1.000**	0.330	0.163	-0.482**	-0.150	0.362	-0.185	0.107
SL	*G*					**1.000**	0.977**	-0.714**	-0.417	0.270	-0.191	-0.375
	P					**1.000**	0.839	-0.425	-0.269	0.190	-0.158	-0.163
SPS	*G*						**1.000**	-0.273	-0.340	0.114	-0.010	-0.313
	P						**1.000**	-0.127	-0.212	0.089	0.046	-0.141
GPS	*G*							**1.000**	0.225	0.016	0.735**	0.272
	P							**1.000**	0.161	-0.056	0.792	0.134
BYP	*G*								1.000	-0.648**	-0.126	0.880**
	P								1.000	-0.525**	-0.104	0.785**
HI	*G*									**1.000**	0.461**	-0.223
	P									**1.000**	0.213	0.095
TSW	*G*										1.000	0.109
	P										1.000	0.027
GYP	*G*											**1.000**
	P											**1.000**

Genotypic and phenotypic Correlation

Days to flowering shows significantpositive correlation with plant height.Non-significant positive correlation with harvest index, spikelet's per spike, spike length.Non-significant negative correlation with grain yield per plant, biological yield per plant, thousand seed weight, grain per spike , effective tiller per plant, days to maturity.Days to maturity shows significant positive correlation with plant height.Significant negative correlation with grain yield per plant, harvest index, thousand seed weight.Non-significant positive correlation with spike length, effective tiller per plant.Non-significant negative correlation with grain per spike, biological yield per plant, spikelet's per spike.Plant height showsnon-significant positive correlation with grain yield per plant, biological yield per plant.Non-significant negative correlation with effective tiller per plant, spike length, grain per spike, thousand seed weight, spikelet's per spike, harvest index.

Effective tiller per plant shows significant positive correlation with harvest index.Significant negative correlation with grain per spike.Non-significant positive correlation with spike length, grain yield per plant, spikelet's per spike.Non-significant negative correlation with thousand seed weight and biological yield per plant.Spike length shows Significant Positive Correlation with Spikelet's per spike.Significant negative correlation with Grain per spike.Non-Significant Positive Correlation with harvest index. Non-Significant negative correlation with biological yield per plant, grain yield per plant andthousand seed weight.Spikelet's per spike shows Non-Significant Positive Correlation with harvest index.Non-Significant negative correlation with biological yield per plant, grain yield per plant, grain per spike andthousand seed weight.Grains per spike shows Significant Positive Correlation with thousand seed weight. Non-Significant positive correlation with grain yield per plant, biological yield per plant (0.2253),harvest index.Biological yield per plant shows Significant Positive Correlation with grain yield per plant.Significant negative correlation with harvest index.Non-Significant negative with thousand seed weight.

Harvest index shows Significant Positive Correlation with thousand seed weight.Non-Significant Negative Correlation withgrain yield per plant.Thousand seed weight shows Non-Significant Positive Correlation with grain yield per plant.Grain yield per plant shows Significant Positive Correlation with biological yield per plant.Significant Negative Correlation with days to maturity.Non-Significant Positive Correlation with grain per spike, effective tiller per plant, plant height, thousand seed weight. Non-Significant Negative Correlation with days to 50% flowering, spike length, spikelet's per spike and harvest index.

Fellahi*et al.* (2013), Sulaiman*et al.* (2014), Kaddem*et al.* (2014), Rahman *et al.* (2016), Sabit*et al.* (2017) also agreed with the similar finding.

[5]. REFERENCES

Comment [M34]: Make sure all the references you cited them in your manuscript please delete for example Baloch et al. were not found in the body of your manuscript but you put them in the references list.

Arya, V. K., Singh, J., Kumar, L., Kumar, R., Kumar, P. and Chand, P., (2017).Geneticvariabilityanddiversityanalysisforyieldanditscomponentsinwheat(*Triticumaestivum*L.).*Indian JournalofAgriculturalResearch*, 51(2):128-134.

Baloch, M., Baloch, A. W., Siyal, N. A., Baloch, S. N., Soomro, A. A., Baloch, S. K.and Gandahi, N. (2016).HeterosisAnalysis inF1HybridsofBreadWheat.SindhUniv.*Res.Jour.(Sci.Ser.)*48(2);261-264.

David, G. and Adams, P. (1985).Crops of the Drier Regions of the Tropics LongmanClusterPp- 96-98.

Devesh,P.,Moitra,K.P.,Shukla,R.S.,Shukla,S.S.,Pandey,S.,andArya,G.(2018).AnalysisofVariability,HeritabilityandGeneticAdvanceofYield,itsComponentsandQualityTraits in Wheat, *IJAEB*: 3(2):855-859.

Desale, C. S., Mehta, D.R. and Singh, A. P. (2014). Combining ability analysis in breadwheat.*JournalofWheatResearch*,6(1):25-28.

Dholariya, N. D., Akabari, V. R., Patel, J. V. and Chovatia, V. P. (2014).Combiningabilityandgeneactionstudyforgrainyieldanditsattributingtraitsinbreadwheat.*ElectronicJournalofPlantBreeding*,5(3):402-407.

Dutamo, D., Alamerew, S., Eticha, F. and Assefa, E. (2015).Genetic Variability inBread Wheat (*Triticum aestivum* L.)Germplasm for Yield and Yield ComponentTraits.*JournalofBiology, AgricultureandHealthcare*,Vol.5(17).

Farshadfar,E.andEstehghari,M.R.(2014).Estimationofgeneticarchitectureforagro-morphological characters in common wheat. *International Journal of Biosciences*,5(6):140-147.

Gale,M.D.andYoussefian,S.(1985).Dwarfingenes inwheat, *ProgressinPlantBreeding* 3(2):517- 520.

.

Gelalcha,S.andHanchinal,R.R.(2013).Correlationandpathanalysisinyieldandyieldcomponentsinspringbreadwheat(*Triticumaestivum*L.)genotypesunderirrigatedconditioninSouthernIndia.*AfricanJournalofAgriculturalResearch*,8(24):3186-3192.

Ghaffar,M.,Khan,S.andKhan,W.(2018).Geneticvariabilityanalysisofwheat(*Triticumaestivum*L.)genotypesforyieldandrelatedparameters.*PureAppl.Biol.*,7(2):547- 555.

Ghallab, K. H., Sharran, A. A. N. and Al-SayedShalby, N. A.N. (2016). Geneticparametersforyieldandyieldcomponentstraitsofsomewheatgenotypesgrowninnewlyreclaimedsoils.*InternationalJournalofAgronomyandAgricultural Research*,9(4):1-8.

Hassan, M. S., El-Said, R. A. R. and Abd-El-Haleem, S. H. M. (2013).Estimation ofHeritabilityandVarianceComponentsforSomeQuantitativeTraitsinBreadWheat(*Triticum aestivum L.*).*WorldAppliedSciencesJournal*,27(8):944-949.

Ishaq, M., Ahmad, G., Afridi, K., Ali, M., Khan,T.U., Shah, I. A., Ahmad, B., Ahmad, N.,Ahmad, I., Saleem, A. and Miraj, M. (2018). Combining ability and inheritancestudiesformorphologicalandyieldcontributingattributesthroughline×testermatingdesigninwheat*(Triticum aestivum*L.*).PureAppl.Biol.*, 7(1):160-168.

Jadoon, S. A., Mohammad, F., Ullah, H. and Khalil, I. H. (2012).Geneaction for pre and postharvesttraitsinF_2 wheatpopulations. .*Qscienceconnect*:pp. 2-5.

Kalhoro, F. A., Rajpar, A. A., Kalhoro, S. A., Mahar, A., Ali, A., Otho, S. A., Soomro, R.N., Ali, F. and Baloch, Z. A. (2015). Heterosis and combing ability in F_1 populationofhexaploid wheat(*Triticumaestivum*L.).*AmericanJournalofPlantSciences*,6,1011-1026.

Khan,N.andNaqvi,F.N.(2012).CorrelationandPathCoefficientAnalysis inWheatGenotypes under Irrigated and Non-Irrigated Conditions. *Asian Journal ofAgriculturalSciences*, 4(5):346-351.

Kumar, A., Kumar, A., Singh, G. and Tiwari, K .N. (2017).Stability analysis fordifferent agro morphological traits under different temperature regimes in breadwheat(*Triticumaestivum*L.),*Environ. LifeSci.*10(3) 270-274.