Agriculture Association of Textile Chemical and Critical Reviews Journal (2025) 107-112

AATCC Review

13 December 2024: Received
26 February 2025: Revised
19 March 2025: Accepted
22 March 2025: Available Online

https://aatcc.peerjournals.net/

Original Research Article Open Access

Genetic variability for yield and yield attributing traits in Advance wheat breeding lines evaluated under Temperate Ecology

Asra Rashid[1], F. A. Sheikh[2], Anand Kumar[3*], Shabir. H. Wani[2*], R. R. Mir[1], Mohd Altaf Wani[1], Shazia Farooq[4] and Shashank Mishra[5]

[1]*Division of Genetics and Plant Breeding, Faculty of Agriculture, Wadura, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Jammu & Kashmir, India*

[2]*Mountain Research Centre for Field Crops, Khudwani, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Jammu & Kashmir, India*

[3]*Faculty of Agricultural Sciences, GLA University, Mathura-281406, Uttar Pradesh, India*

[4]*Division of Plant Pathology, Faculty of Agriculture, Wadura, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Jammu & Kashmir, India*

[5]*Department of Plant Pathology, Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipurum, Meerut, India*

ABSTRACT

The present study was conducted to determine variability for complex traits of yield and yield attributes by measuring different morphologically related metric traits and evaluation of the traits that are closely related to yield. Grain yield showed high heritability along with high genetic advance yield and the characters which high heritability along with high genetic advance and genetic gain were spike length, 1000-grain weight, spikelet per spike, grains per spike, seed size, awn length, peduncle length, and stem weight would be effective for selection in the breeding programme. However, highest estimates of heritability (b.s.) accompanied by high genetic advance as per cent of mean were recorded for grain yield/ ha. The estimates of genotypic coefficient of variation (GCV) were highest for grain yield (35.24%) followed by 1000 grain weight (23.42%), grains per spike (19. 34%) and a number of spikelet spike (19.32%).It is obvious that yield is a polygenic trait that results from the contribution of many interacting factors. The phenotypic and genotypic correlations for yield and yield attributing traits revealed that grain yield exhibited positive and highly significant genotypic and phenotypic correlation with 1000 grain weight, grains per spike, and spikelets per spike but exhibited negative and significant genotypic and phenotypic correlation with days to flowering and days to maturity. The highest indirect positive effects of a number of grains per spike on grain yield was recorded via a number of spikelets per spike (0.368) followed by spike length (0.136) and flag leaf length (0.123) whereas grains per spike recorded a moderate negative indirect effect via length breadth ratio (-0.014), awn length (-0.011) and peduncle length (-0.145) on grain yield. This study offers treasured acumens for breeders and researchers working on enhancing wheat productivity to meet the mounting demands of increasing human population

Keywords: *Genetic variability, genotypic and phenotypic coefficients of variation, heritability, genetic advance, correlation path coefficients, advanced breeding lines and temperate ecology*

INTRODUCTION

Wheat (*Triticum sp.*) known as king of cereals is a self-pollinating annual crop belonging to the family Poaceae. The wheat crop is grown all around the globe for its food, feed and fuel (Singhania *et al.,* 2014). Wheat contributes about 55% of carbohydrates and 20% calories to the global population. Wheat unlike other cereal crops contains gluten in high amount, the protein that is necessary for the elasticity of dough and excellent bread-making quality, and is a major source of essential micronutrients such as Fe and Zn (Velu*et al.*, 2017). As per area and production globally, wheat ranks first among cereals and third in terms of productivity after maize and rice, with a total production of 731.55 million metric tonnes and productivity of 3.39 metric tonnes per hectare grown on about 215.87 million hectares of land (Anonymous, 2019). With 106.21 million tonnes, India ranks second in wheat production grown over an area of 29.319 million hectares (Anonymous, 2019). The northern Indian states like Uttar Pradesh has largest share in area with 9.75 million hectares (32%) followed by Madhya Pradesh (18.75%), Punjab (11.48%), Rajasthan (9.74%), Haryana (8.36%), Bihar (6.82%) contribute about 87.15 percent of the total wheat production in the country (Anonymous, 2017). Moreover, wheat ranks third both in area and production after rice and maize in the UT of J&K where it is cultivated on an area of 368 lakh hectares with a production of 5.40 million tonnes and productivity of 1.94 tonnes per hectare(Anonymous, 2018). Major area under wheat cultivation is in Jammu region (273 thousand ha), as compared to Kashmir valley (96 thousand ha), because of the climatic constraints and lack of early maturing varieties that could fit in rice-wheat rotation in Kashmir valley.

To meet the food requirements of the growing world population which is expected to reach 9.8 billion by 2050, we need to

---

Corresponding Author: **Shabir. H. Wani and Anand Kumar*

DOI: https://doi.org/10.21276/AATCCReview.2025.13.02.107

continuously increase the yield. We need to develop such varieties that can withstand all such stresses that hamper the yield. During freedom Indian agriculture situation was terrible, as only 6.46 million tonnes of wheat was produced which was not ample to bring about the food necessities forthe prevailing population. With the mutual exertions of multidisciplinary research, India became the second-largest wheat producer in the world (Dronamraju, 2008). Still, there is need to increase wheat productivity to feedever increasing population of the country.

Characterization of genetic variation within natural populations and among breeding lines is considered very important and crucial for effective conservation and exploitation of genetic resources for crop improvement programs. To improve the genetic diversity in the germplasm it is important to know the extent of already existing genetic variability in the germplasm. To increase the productivity of wheat, the breeding programme should be potent and develop climate resilient crop especially for biotic and abiotic resistant. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits. Correlation studies along with path analysis provide a better understanding of the association of different characters. Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixet&Dubey, 1984).

MATERIALS AND METHODS

The research was conducted during *rabi* season (2018-2019) over two locations one at research farm of the Division of Genetics and Plant Breeding, Faculty of Agriculture, Wadura SKUAST-K, Sopore and at Mountain Research Centre for Field Crops (MRCFC), Khudwani. The research was carried out to obtain information on the genetic variability related to lodging and yield and yield attributing traits. Among 23 genotypes, 21 genotypes were advance wheat breeding lines from IIWR and 2 genotypes were Shalimar Wheat -1 and Shalimar Wheat -2 from SKUAST-K.

LIST OF GENOTYPES USED UNDER STUDY

S. No.	Code	Genotype	Source
1	G1	NHIVT-1	IIWR,Karnal
2	G2	NHIVT-2	IIWR, Karnal
3	G3	NHIVT-3	IIWR,Karnal
4	G4	NHIVT 1804	IIWR, Karnal
5	G5	NHIVT 1805	IIWR, Karnal
6	G6	NHIVT 1806	IIWR, Karnal
7	G7	NHIVT 1807	IIWR, Karnal
8	G8	NHIVT 1808	IIWR, Karnal
9	G9	NHIVT 1809	IIWR, Karnal
10	G10	NHIVT 1810	IIWR, Karnal
11	G11	NHIVT 1811	IIWR, Karnal
12	G12	NHIVT 1812	IIWR, Karnal
13	G13	NHIVT 1813	IIWR, Karnal
14	G14	NHIVT 1814	IIWR, Karnal
15	G15	NHIVT 1815	IIWR, Karnal
16	G16	NHIVT 1816	IIWR, Karnal
17	G17	NHAVT 1817	IIWR, Karnal
18	G18	NHAVT 1818	IIWR, Karnal
19	G19	NHAVT 1819	IIWR, Karnal
20	G20	NHAVT 1820	IIWR, Karnal
21	G21	NHAVT 1821	IIWR, Karnal
22	G22	Shalimar Wheat-1	SKUAST-K
23	G23	Shalimar Wheat-2	SKUAST-K

The experimental set up was laid out in RBD with four replications at each location with land dimensions of 4.5 m^2. On plot basis the data was collected for different morphological quantitative traits. From central rows five plants were selected from each plot on a random basis at each genotype during different stages of vegetative and reproductive growth. Observations were recorded for the characters includes Plant height (cm), Stem height (cm), Days to 50 % flowering, Flag leaf length (cm),Flag leaf width (cm), Peduncle length (cm) ,Awn length (cm),Spike length (cm) , Number of spikelet spike^1, Days to maturity , Grains spike-^{1} , Seed size (L:B ratio) , Grain yield, 1000 - Grain weight , Protein content (%).

STATISTICAL ANALYSIS

Though the study was taken over two locations, the G×E interaction was non-significant as calculated by F- test of homogeneity. The pooled data of the two locations was subjected to further statistical analysis using software like R , Window stat version 9.0. To get a reliable estimation of heritability pooled data of the two locations was subjected to further statistical analysis using softwareslike R,Window stat version 9.0. Theanalysis was based on the statistical model as per the standard procedure by Panse andSukhatme (1978). The coefficient of variation for different characters was estimated by a formula as suggested by Burton and De-Vane (1953). Heritability for the present study was calculated in a broad sense by adopting the formula as suggested by Hanson *et al.* (1956). The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard.

$$\text{Genetic gain} = \frac{\text{Genetic advance (R)}}{X} \times 100$$

Where,

X = Mean of character. Estimation of genotypic and phenotypic variance and covariance's were substituted in the following formula suggested by Johnson et al. (1955) to calculate the correlation coefficient between possible pairs of characters. Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixet&Dubey, 1984).

RESULT AND DISCUSSION

The pooled analysis of variance (Table 1) revealed the existence of significant variability among the genotype for morphological and yield-related traits *viz*., grain yield per hectare, 1000 grain weight, grain per spike, days to 50% flowering, days to maturity, length /breadth ratio, plant height, stem height, spike length, spikelets per spike, flag leaf length, flag leaf width, peduncle length and awn length. Significant differences have been reported among wheat genotypes for yield and yield attributing traits (Baranwal*et al*. 2012.,Çifci 2012., Khan *et al.,* 2013; Singh and Upadhyay, 2013). The estimates of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) (Table 2) for morphological and yield-attributing traits studied showed that PCV was higher than GCV thus indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors. The estimates of the genotypic coefficient of variation (GCV) were highest for grain yield (35.24%) followed by 1000 grain weight (23.42%), grains per spike (19. 34%) and number of spikelet spike (19.32%).

Moreover, high heritability estimates (broad sense) were observed to be high (= or >80%) for maximum traits (Table 2) except spike length (42.25 %) and peduncle length (77.92%). However, highest estimates of heritability (b.s.) accompanied by high genetic advance as per cent of mean were recorded for grain yield/ ha followed by 1000 - grain weight, number of grains / spike, number of spikelet/ spike, awn length, seed size (l/b ratio), peduncle length, stem weight, flag leaf width, and plant height. These results are following the findings of Singh and Upadhyay (2013), Amin *et al*. (2015) and Khiabani*et al*. (2015).The high heritability accompanied with moderate genetic advance for plant height in wheat is desired for selection of short plant height because taller plants are likely to lodge and need more energy to transport photosynthates to the grains in wheat (Çifci, 2012., Degewione*et al*., 2013). Spikelets per spike and number of grains per spike also need to be considered for selection due to high heritability with high genetic gain to increase grain yield in wheat (Mohammadi*et al.,* 2011). Though grain yield exhibited high heritability and high genetic advance but direct selection for this trait would not be effective due to its quantitative nature (Yadav*et al*., 2014; Ibrahim *et al.,* 2012).

The phenotypic and genotypic correlations for yield and yield attributing traits (Table 3) revealed that grain yield exhibited positive and highly significant genotypic and phenotypic correlation with 1000 grain weight, grains per spike, spikelets per spike but exhibited negative and significant genotypic and phenotypic correlation with days to flowering and days to maturity. Grain yield is a complex trait and can be improved by selecting traits significantly related to this trait. Grain yield has recorded a highly significant positive association with grains per spike and with thousand kernel weight (Surma*et al*., 2012).

According to Kearsey and Pooni (1996), the positive correlation of these characters with grain yield resulted from the presence of strong coupling linkage of genes or the characters may be the result of pleiotropic genes that control these characters in the same direction. The grain yield also showed negative non-significant association with plant height and protein content. The non-significant association of grain yield with plant height was also reported by Singh (2014).

Grain yield exhibited a significant but negative association with days to maturity. In field crops at physiological maturity, the crop attains the maximum seed dry weight. However, 1000-grain weight showed a highly significant and negative correlation with days to maturity and days to 50% flowering. The physiological maturity of the crop is very important as at maturity the crop is subjected to different stresses like lodging, pre-harvest sprouting, hail and biological stresses which results in reductions in yield (Calderini*et al*., 2000). These stresses result in a yield loss up to 10% (Bauder, 2001).

The path analysis allows the partitioning of the genotypic association into direct and indirect effects with the grain yield as a_dependent variable. The direct and indirect effects of seven different traits on grain yield (Table 4) revealed that number of grains per spike had highest direct effect (0.521) on grain yield/ha followed by number of spikelets per spike (0.483). These direct effects are mainly responsible for the positive association of these characters with grain yield/ha. The high indirect positive effects of number of grains per spike on grain yield was recorded via a number of spikelets per spike (0.368) followed by spike length (0.136) and flag leaf length (0.123) whereas grains per spike recorded a moderate negative indirect effect via length breadth ratio (-0.014), awn length (-0.011) and peduncle length (-0.145) on grain yield. The results revealed that number of grains per spike may be used as direct selection criteria in any breeding program aimed to increase grain yield. The number of spikelets per spike had high a direct effect (0.483) on grain yield /ha and indirect positive effects via a number of grains per spike (0.201) followed by flag leaf length (0.156) and spike length (0.136) whereas number of spikelets per spike recorded a moderate negative indirect effect via length breadth ratio (-0.007), awn length (-0.005) and peduncle length (-0.072) on grain yield. The results revealed that a number of spikelets per spike may also be used as direct selection criteria in any breeding program aimed to increase grain yield. Mecha*et al*. (2016) reported spike length, number of spikelets per spike, grains per spike, thousand seed weight and biomass yield had a positive direct effect on grain yield. Fellahi*et al*. (2013) and Gelalcha and Hanchinal (2013) also reported similar results.The direct effects of the remaining characters *viz*., flag leaf length, awn length, spike length, peduncle length, and length breadth ratio were very low and non-significant indicating their negligible direct contribution towards grain.

Table 1: Analysis of Variance (NOVA) for yield and yield attributing traits in wheat

Source	D.f	GPH	1000 gw	GPS	DTF	DTM	LB	PH	SH	SPS	FLL	FLW	PL	AL	SL	PTN
Replication	3	1.0	2.8	2.82	3.4	14.0	0.002**	4.86	18.3	0.70	5.423	0.04*	49.22**	0.76*	1.21	9.31**
Genotypes	22	742**	378**	227.23**	128.3**	146**	0.21**	145.10*	177.1*	56.81**	8.39**	0.076**	82.39**	5.61**	3.22**	1.41**
ENV	1	0.9	59.9*	28.17*	1480.9**	4423.7**	0.24	90.44**	345.1**	7.04*	1.58	0.020	64.57**	0.66	0.107	0.88
G*E	22	32**	41.6**	25.42**	118.5**	158**	0.008	119.96**	82.3**	6.36**	8.95**	0.024**	37.73**	0.79**	1.68**	1.72**
Pooled error	135	5.6	5.9	4.79	1.9	4.0	0.0006	60.3	7.0	1.20	2.43	0.011	5.45	0.21	0.82	0.70

**, ** significant at 0.05 and 0.01 per cent level respectively*

Table 2: Selection par

Traits	Range			Variance			Coefficient of variance		Selection parameters		
	Mean	Min	Max	Ev	GV	PV	GCV	PCV	H (bs) (%)	GA (5%)	GA as (%) of mean
GPH	38.47	29.41	55.85	5.6	184.1	189.7	35.24	35.79	97.04	27.52	71.55
1000gw	41.16	33.51	53.51	5.9	93.02	98.92	23.42	24.14	94.03	19.25	46.78
GPS	38.51	33	48.51	4.79	55.61	60.4	19.34	20.17	92.06	14.73	38.26
SPS	19.25	17.06	24.25	1.21	13.9	15.11	19.32	20.15	91.99	7.35	38.19
SL	9.84	8.76	10.86	0.82	0.6	1.42	7.82	12.09	42.25	1.03	10.52
L/b	1.77	1.31	2.91	0.0006	0.05	0.05	12.99	12.99	98.91	0.46	26.47
DTF	185.92	173.12	188	1.9	31.6	33.5	3.02	3.10	94.32	11.23	6.04
DTM	245.66	232.75	248.88	4	35.5	39.5	2.42	2.55	89.87	11.62	4.73
PH	90.14	81.38	96.25	6.51	34.65	41.16	6.52	7.11	84.18	11.11	12.33
SH	80.06	74.13	88.63	7	42.52	49.52	8.14	8.78	85.86	12.43	15.53
PL	37.01	31.25	41	5.45	19.23	24.68	11.83	13.40	77.92	7.96	21.51
FLL	21.91	20.61	23.81	2.43	1.49	3.92	5.56	8.99	38.01	1.54	7.04
FLW	1.58	1.41	1.77	0.011	0.016	0.02	7.59	10.12	59.63	0.19	12.43
AL	6.04	4.52	7.79	0.21	1.35	1.56	19.20	20.52	86.53	2.21	36.59
Ptn	10.31	9.36	11.09	0.71	0.17	0.88	3.97	9.11	19.77	0.38	3.71

**, ** significant at 0.05 and 0.01 per cent level respectively*

Table 3: Genetic Correlations (above diagonal) and phenotypic correlation (below diagonal) for yield and yield attributing traits of Wheat

Traits	GPH	1000gw	GPS	SPS	SL	LB	DTF	DTM	PH	SH	PL	FLL	FLW	AL	PTN
GPH	1	0.992**	0.989**	0.989**	-0.248	-0.28	-0.555**	-0.512**	-0.304	-0.305	0.167	-0.127	0.292	-0.176	-0.102
1000Gw	0.985**	1	0.998**	0.998**	-0.191	-0.29	-0.513*	-0.471*	0.264	-0.295	0.120	-0.118	0.287	-0.164	0.015
GPS	0.983**	0.996**	1	0.999**	-0.169	-0.32	-0.513*	-0.475*	-0.247	-0.286	0.130	-0.101	0.280	-0.212	0.015
SPS	0.983**	0.996**	1.00**	1	-0.169	0.321	-0.513*	-0.473*	-0.247	-0.286	0.130	-0.101	0.280	-0.212	0.015
SL	-0.249	-0.202	-0.184	-0.184	1	0.254	0.803**	0.870**	-0.157	-0.188	0.520*	0.764*	-0.570**	-0.015	0.122
LB	-0.176	-0.138	-0.158	-0.158	0.379	1	0.210	0.187	-0.059	0.056	-0.260	0.010	0.060	0.172	-0.396
DTF	-0.540**	-0.493*	-0.495*	-0.495*	0.649*	0.211	1	0.978**	0.139	0.063	-0.540**	0.420*	-0.415*	0.174	0.193
DTM	-0.502**	-0.458*	-0.461*	-0.461*	0.705*	0.211	0.966**	1	0.121	0.027	-0.555**	0.473*	-0.415*	0.124	0.192
PH	-0.292	-0.253	-0.235	-0.235	-0.094	-0.135	0.125	0.106	1	0.999**	0.257	0.267	-0.011	0.040	0.454
SH	-0.267	-0.254	-0.236	-0.236	-0.142	-0.104	0.042	0.017	0.954**	1	0.357	0.193	0.066	0.042	0.197
PL	0.195	0.160	0.173	0.173	0.584*	-0.466	-0.530**	-0.527**	0.238	0.318	1	0.153	0.685**	-0.216	-0.223
FLL	-0.129	-0.102	-0.093	-0.093	0.529*	0.151	0.373*	0.411*	0.210	0.211	0.190	1	-0.245	-0.413*	0.202
FLW	0.374	0.408	0.403	0.403	-0.37018**	-0.360	-0.394*	-0.389*	-0.059	-0.013	0.537**	-0.004	1	0.362	-0.216
AL	-0.114	-0.089	-0.125	-0.125	-0.01017	0.006	0.147	0.103	0.018	-0.014	-0.231	-0.266*	0.141	1	0.213
PTN	-0.182	-0.124	-0.130	-0.130	-0.02877	0.076	0.199	0.208	0.429	0.272	-0.116	-0.040	-0.034	0.305	1

**, ** significant at 0.05 and 0.01 per cent level respectivel*

Table 4:Direct (diagonal) and indirect (off diagonal) effect of seven variable traits on grain yield in wheat

Traits	GPS	SPS	L/B	FLL	AL	SL	PL	Genotypic correlation coefficient of grain yield q/ha
GPS	0.521	0.368	-0.014	0.123	-0.011	0.136	-0.145	0.989**
SPS	0.201	0.483	-0.007	0.156	-0.005	0.068	-0.072	0.989**
L/B	-0.079	-0.110	-0.001	0.027	-0.001	0.012	-0.013	-0.288
FLL	0.120	0.001	-0.091	0.091	-0.170	0.028	-0.045	-0.127
AL	-0.160	-0.038	0.000	-0.031	0.025	0.001	0.007	-0.176
SL	-0.078	0.168	0.000	-0.026	-0.200	-0.049	0.046	-0.248
PL	0.012	0.120	-0.002	0.149	-0.008	0.160	-0.321	0.167

Residual effect = 0.0132

***significant at 0.01 percent level respectively*

Where asGPPa=grains per plant, GPPo=grains per plot, GPH=grains per hectare, 1000gw=1000 grain weight, GPS=grain per spike, DTF=days

CONCLUSION

The results obtained from diverse genotypes and their combination exhibited. The analysis of variance revealed the existence of significant variance among 23 genotypes of traits related to lodging and yield and yield attributing traits. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits in all traits except seed size ratio (12%) showed equal PCV & GCV. High heritability with high genetic advance indicates maximum contribution of additive gene action in the expression of character and improvement would be possible for direct selection in grain yield per hectare. 1000 grain weight, grains per spike , spikelet per spike, flag leaf length, stem weight per cm showed a highly significant and positive correlation with grain yield. Genotypic and phenotypic correlation coefficients revealed that the grain yield had a positive and highly significant association with 1000-grain weight, grains per spike, spikelets per spike. Path coefficient analysis result indicated spikelets per spike followed by seed size revealed direct, positive and significant association with grain yield at molecular level. The best genotypes possessing good yield among tested materials areNHIVT 1804, NHIVT 1813, NHIVT 1810. It isassumed that these traits can increase the yield of bread wheat. It is proved by study that these characters and their combination may improve the yield further to meet the growing demand of rising population in India.

Acknowledgments

The authors are thankful to the anonymous reviewers for their careful read.

Conflicts of Interest

The authors declare that no conflict of interest exists

References

1. Amin, M. F., Hasan, M., Barma, N. C. D., Rahman, M. M. and Hasan, M. M. 2015. Variability and heritability analysis in spring wheat (*Triticumaestivum* L.) genotypes.*Bangladesh Journal of Agricultural Research*40(3), 435-450.

2. Anonymous, 2017.Directorate of wheat research, *Directorate of wheat Perspective Plan Vision* pp. 2025.

3. Anonymous, 2018. Digest of statistics*, Directorate of Economics and Statistics,* Government of Jammu and Kashmir.

4. Anonymous, 2019.Agriculture statistics, *Directorate of Economics and Statistics*, Department of Agriculture Coorporation and Farmers Welfare.

5. Baranwal, D. K., Mishra, V. K., Vishwakarma, M. K., Yadav, P. S. and Arun, B. 2012. Studies on genetic variability, correlation and path analysis for yield and yield contributing traits in wheat (*T. aestivum* L.).*Plant Archives*, 12, 99-104.

6. Bauder, J. 2001.Irrigating with limited water supplies.*Montana State University Communications Services.Montana Hall. Bozeman, MT* 59717. USA.

7. Burton, G. W. and Devane, E. H. 1953. Estimating heritability in tall fescue (*Festucaarundinacea*) from replicated clonal material. *Agronomy Journal*45(10): 478-481.

8. Calderini, D. F. and Reynolds, M. P. 2000.Changes in grain weight as a consequence of de-graining treatments at pre and post anthesis in synthetic hexaploid lines of wheat (*Triticum durum* T. tauschii*).*Australia journal Plant Physiology*27: 183-191.

10. Çifci, E. A. 2012. Estimate of heterosis, correlation and path analysis for grain yield per spike and some agronomic traits on durum wheat (*T. durum*). *The Journal of Animal and Plant Sciences*22(3): 747-752.

11. Degewione, A., Dejene, T. and Sharif, M. 2013.Genetic variability and trait association in bread wheat (*Triticumaestivum L.)* genotypes.*International Research Journal of Agricultural Sciences*1(2): 19-29.

12. Dixet, P. and D.K. Dubey. 1984. Path analysis in lentil (Lens culinaris Med.). Lens Newsletter, 11: 15-17.

13. Dronamraju, K. R. 2008. Emerging consequences of biotechnology: biodiversity loss and IPR issues. *World Scientific, Singapore, Science*460: 978-981.

14. Fellahi, Z., Hannachi, A. and Bouzerzour, H. 2013. Correlation between traits and path analysis coefficient for grain yield and other quantitative traits in bread wheat under semi arid conditions.*Journal of Agriculture andSustainability*3(1): 16-26.

15. Gelalcha, S. and Hanchinal, R. R. 2013. Correlation and path analysis in yield and yield components in spring bread wheat (*Triticumaestivum*L.) genotypes under irrigated condition in Southern India. *African Journal ofAgricultural Research*8(24): 3186-3192.

16. Hanson, C. H., Rabinson, H. E. and Comstock, R. E. 1956.Biometrical studies of yield is segregating population of Korean lespedeza. *Agronomy Journal*48: 268-272.

17. Ibrahim, M., Ullah, H., Ahmad, B. and Inamullah-Malik, M. F. A. 2012.Effect of incremental dose of Phosphorous and Sulphur upon yield and protein content of Wheat.*Biological Diversity and Conservation*5(3): 76-81

18. Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955.Estimates of genetic and environmental variability in soybean.*Agronomy Journal*47: 314-318.

19. Kearsey, M. J. P. and Pooni, H. S. 1996.The genetical analysis of quantitative traits. Chapman and Hall, London, Weinhein, New York pp. 381.

20. Khan, A. A., Alam, M. A., Alam, M. K., Alam, M. J. and Sarker, Z. I. 2013.Correlation and path analysis of durum wheat (*Triticumturgidum* L. var. *Durum)*.*Bangladesh Journal of Agricultural Research*38(3): 515-521.

21. Khiabani, B. N., Aharizad, S. and Mohammadi, S. A. 2015. Genetic analysis of grain yield and plant height in full diallel crosses of bread wheat. *Biological Forum An International Journal*7(1): 1164-1172.

22. Mecha, B., Alamerew, S., Assefa, A., Assefa, E. and Dutamo, D. 2016. Genetic variability, heritability and genetic advance for yield and yield related traits in bread wheat (*TriticumAestivum*L.) genotypes. *GlobalJournal of Science Frontier Research: Agriculture and Veterinary* 16: 7.

23. Mohammadi, M., Karimizadeh, R., Shefazadeh, M. K. and Sadeghzadeh, B. 2011.Statistical analysis of durum wheat yield under semi-warm dry land condition.*Australian Journal of Crop Science* 5(10): 1292-1297.

23. Panse, V. G. and Sukhatme, P. V. 1967.Statistical methods for agricultural workers. ICAR, Pub. (IInd Ed.), New Delhi.

24. Singh, B. and Upadhyay, P. K. 2013.Genetic variability, correlation and path analysis in wheat (*Triticumaestivum* L.). Indian Research *Journal of Genetics and Biotechnology*5(3): 197-202.

25. Singh, S. 2014. Genetic variation for protein content and its association with yield related traits in recombinant inbred lines (RILs) population of bread wheat (*Triticumaestivum*L. *Em. Thell)*. M. Sc. Thesis, CCSHAU, Hisar.

26. Singhania, R. R., Saini, J. K., Saini, R., Adsul, M., Mathur, A. and Gupta, R. 2014.Bioethanol production from wheat straw via enzymatic route employingpenicillium janthinellum cellulase. *Bioresource. Technology*169: 490-495.

27. Surma, M., Adamski, T., Banaszak, Z., Kaczmarek, Z., Kuczyńska, H., Majcher, M. and Krystkowiak, K. 2012.Effect of genotype, environment and their interaction on quality parameters of wheat breeding lines of diverse grain hardness.*Plant Production Science*15(3): 192-203.

28. Velu, G., Guzman, C., Mondal, S., Autrique, J. E., Huerta, J. and Singh, R. P. 2017.Effect of drought and elevated temperature on grain zinc and iron concentrations in CIMMYT spring wheat.*Journal of Cereal Science* 69: 182-186.

29. Yadav, S. K., Singh, A. K., Baghel, S. S., Jarman, M. and Singh, A. K. 2014.Assessment of Genetic variability and Diversity for Yield and its Contributing Traits among CIMMYT Based Wheat Germplasm.*Journal of Wheat Research*6(2): 154-159.