



Genetic Analysis of Some Quantitatively Inherited Plant Traits in Spring Wheat (*Triticum aestivum* L.)

Shahzadi Mahpara¹, Muhammad Ishaq Asif Rehmani², Muhammad Kamran Qureshi³, Safdar Hussain², Javaid Iqbal², Muhammad Shahnawaz¹

¹Department of Plant Breeding and Genetics, Ghazi University, Dera Ghazi Khan

²Department of Agronomy, Ghazi University, Dera Ghazi Khan

³Department of Plant Breeding and Genetics, BZU Multan

ABSTRACT

This experiment was conducted to find out genetic effects for some quantitatively inherited plant traits using six generations viz., parents, their first and second filial generations and their backcrosses (BC-I, BC-II) of two wheat crosses namely, Mairaj-08 × Blue Silver (cross-I) and Faisalabad-08 × DH-60 (cross-II). Generation mean analysis through scaling test (A,B,C,D) was performed which highlighted the presence of non-allelic gene interaction in many plant studied traits in both crosses due to differences in origin of all parents involved. So, a six parameter model was applied to estimate the characteristics of gene action in these plant traits except in 1000-grains weight. Additive gene action was controlling many plant traits in both crosses except for days to maturity, plant height, spike density in cross-I while number of spikelet spike⁻¹, number of grains spike⁻¹ and grain yield plant⁻¹ in cross-II. It is concluded that most of the traits in Faisalabad-08 × DH-60 were under control of additive gene action so this cross may be utilized for high grain yield in future wheat enhancement breeding program.

[Shahzadi Mahpara, Muhammad Ishaq Asif Rehmani, Muhammad Kamran Qureshi, Safdar Hussain, Javaid Iqbal, Muhammad Shahnawaz. **Genetic Analysis of Some Quantitatively Inherited Plant Traits in Spring Wheat (*Triticum aestivum* L.)**. *Life Sci J* 2022;19(10):50-58]. ISSN 1097-8135 (print); ISSN 2372-613X (online). <http://www.lifesciencesite.com>. 07.doi:[10.7537/marslsj191022.07](https://doi.org/10.7537/marslsj191022.07).

Key words: Wheat, Epistasis, Generation mean analysis, Plant traits, Gene action, Additive gene interaction, Grain yield.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most diversified and popular crop among cereals (Abbasi et al., 2014). Wheat fulfils dietary requirements of 30% people worldwide and provides about 50% food calories and protein requirements for the humans. In Pakistan, wheat is the primary food commodity and is included in daily diet. Wheat was cultivated on an area of 9.04 million hectares, producing 25.3 million tons with an average yield of 2.79 tons ha⁻¹ (Government of Pakistan, 2013) which is not sufficient to fulfil the requirements of rapidly growing population. Moreover changing climatic conditions and management issues are resulting in lower wheat production (Asseng et al., 2015; Ata-Ul-Karim et al., 2015; Dogar et al., 2016; Ali et al., 2017; Ashraf et al., 2017; Kaur et al., 2017). So, there is a requisite to improve this situation by increasing per acre yield of wheat. For this purpose, exploring of new potential genotypes with wider adaptability by utilizing existing wheat germplasm is the suitable approach to increase wheat production (Reynolds et al., 2009; Parry et al., 2010; Reynolds et al., 2011) and can be effectively utilized in Pakistan.

Grain yield is a plant trait that is regulated by multigenes and these genes are involved in interactions of genotypic and environmental variance. Genetic variability and genetic analysis determines the behavior and expression of these genes in a genetic population (Singh et al., 2003; Abbasi et al., 2014). Improvement in grain yield through breeding is complicated if yield is the solely factor recorded, so it is suggested that its related traits/ components should also be used as selection criteria for yield improvement. So, it is essential to know the architecture of crop yield components (Misra et al., 1994; Ahmad et al., 2011; Dwivedi et al., 2012). Gene effects consisting of additive (d), mean (m), and dominance (h) gene effects and non-allelic gene interactions including additive × additive (i), dominance × dominance (l) and additive × dominance are more important. Generation means analysis is one of the reliable biometrical techniques. It is a very useful method to compute gene effects and gene interactions responsible for inheritance of yield and its components (Singh and Singh, 1992; Dwivedi et al., 2012).

Thus, the current experiment was performed to get information about genetic variability, gene action

and genetic interaction for various plant traits in two wheat crosses. This information can be used for further wheat breeding program to enhance grain yield.

MATERIALS AND METHODS

Plant Materials

Two spring wheat (*Triticumaestivum*L.) crosses viz., Mairaj-08 × Blue silver and Faisalabad-08 × DH-60 were used as genetic materials in this experiment.

Parentage of two crosses under study

Genotypes	Parentage
Mairaj-08	PTS/3/TOB/LFN//BB/4/BB/HD-832-5//ONXGV/ALD'S'/HPO'S'BR-3385-3B-1B-0B
Blue silver	I153.388/AN//YT54/N10B/3/LR/4/B4946.A.4.18.2.1Y/Y53//3*Y20II18 427-0PAK
Faisalabad-08	PBW65/2*PASTOR
DH-60	OPATA (Double Haploid)

Seeds of P₁, P₂ and F₁ generations for both crosses were provided by the Department of Plant Breeding & Genetics, Ghazi University, D G. Khan and F₂ (by seeds of F₁ plants), BC₁ plants were developed by crossing between plants of F₁ and P₁ and BC₂ were developed by crossing between F₁ hybrids and P₂ plants. At maturity, seeds of each generation were kept separately for comparison. So, seeds of obtained from six basic generations i.e. parent cultivars (P₁, P₂), first and second filial generations (F₁, F₂), first and second backcrosses (BC₁, BC₂) of both crosses were planted and arranged in a randomized complete block design (RCBD) with three replications, at Research area of Ghazi University, Dera Ghazi Khan, Pakistan during the winter season, 2011-12. Each plot was 2 meters long keeping row-to-row distance 30 cm and plant-to-plant distance of 10 cm.

Evaluation of various plant traits

On maturity, data was collected for various plant traits including days to heading, days to maturity, number of tillers plant⁻¹, plant height (cm) at maturity, spike length (cm), peduncle length (cm), number of spikelet spike⁻¹, spike density, number of grains spike⁻¹, 1000-grains weight (g), grain yield plant⁻¹ (g) were collected and processed for further analysis.

Statistical and genetic analysis

The data were first analyzed to find the differences among six generations by ANOVA Table as described by Steel et al., (1997)(Steel et al., 1997). Before considering the biometrical analysis, as well as, the scaling test (A, B, C and D) means for all six generations were tested by LSD test for studied characters to detect the presence of epistasis as described earlier (Mather and Jinks, 1977). The simple model (m, d, and h) for genetic analysis was applied when epistasis was absent, while in case of non-allelic

interaction the analysis was performed for estimation the inter-action types involved using six-parameter genetic model i.e., (m, d, h, i, j, and l) as described earlier (Hayman, 1958).

RESULTS AND DISCUSSION

The data collected for various plant traits were subjected to analysis of variance (ANOVA) for both crosses. Mairaj-08 × Blue Silver cross showed highly significant differences for all six pedigrees ($P \leq 0.01$; Table 1) for various plant traits except for days to maturity. The traits that showed highly significant difference are days to heading, plant height, number of tillers plant⁻¹, peduncle length, number of grains spike⁻¹, number of spikelet spike⁻¹, spike length, spike density, 1000-grains weight and grain yield plant⁻¹. Table 2 shows genetic variability in Faisalabad-08 × DH-60 for all plant traits. It indicated six generations of both crosses possessed genetic differences for all plant traits under study. Similar, findings were also reported. It was found that genetic variability exists in wheat and other crops for various quantitative plant traits (Mahpara et al., 2008; Kotal et al., 2010; Rabbani et al., 2011; Sami-Ul-Allah et al., 2011; Shabbir et al., 2011; Irshad et al., 2012; Jatoti et al., 2014; Mahpara et al., 2015; Saleem et al., 2015). It means that further genetic analysis was applicable for all the traits.

Scaling tests

As the ANOVA table for both crosses showed significant difference in all genotypes for plant traits under study, the generation mean analysis was used for these traits for the assessment of gene action. The scaling tests are of great importance in generation means analysis as they explain whether epistasis is prevailing or not and which model of generation means analysis is fit. There are four type of scaling tests as given by (Mather and Jinks, 1977). If any of the scaling

tests is significant, it means that epistasis must be present among the traits. If all the four scaling tests are non-significant, epistasis will be absent and a three parameters model is applicable in this situation. In the present study, a six parameters model is selected for the estimation of gene action and genetic effects. The results of the scaling tests applied for the two crosses being studied in the current research are shown in tables (Table 3) for both crosses (Mairaj-08 × Blue Silver and Faisalabad-08 × DH-60).

In Mairaj-08 × Blue Silver cross, results from table 3 revealed that four scaling tests (A, B, C and D) were significant for plant traits studied. The scaling tests A, B and D were significant for days to maturity while the scaling tests A, C and D were significant for plant height. For the trait, grain yield plant⁻¹ scaling test A and C were significant. For number of grains spike⁻¹, C and D were significant, while the scaling tests A and D were significant for peduncle length. All these traits exhibited epistasis type of gene interaction because of significance of scaling tests for all traits except for 1000-grains weight, which possessed non-significant results for scaling tests. So, it can be concluded that in 1000-grains weight, epistasis was absent.

In Faisalabad-08 × DH-60 cross, the results of scaling tests (Table 4) highlighted significant four types of scaling tests (A, B, C and D) for plant height and peduncle length. Scaling tests A, B and C for days to maturity and days to heading were found significant, whereas for spike density A, C and D were found significant. Moreover, A and D scaling tests were significant for number of tillers plant⁻¹ and spike length, B and C tests were significant for number of grains spike⁻¹, number of spikelet spike⁻¹ and 1000-grains weight. For grain yield plant⁻¹, the results of scaling tests were significant for the A and C. These significant results for plant traits were in agreement with (Magda and El-Rahman, 2013).

Estimation of genetic components

Generation means analysis is the technique used to investigate the prevalence of gene effects including additive (d), dominance (h) and genetic interactions including additive × additive (i), additive × dominance (j) and dominance × dominance (l). For this purpose, scaling tests were applied initially to assess the presence or absence of non-allelic genetic interactions. The significance of any scaling test confirms the presence of epistasis in the experimental material. When any of the scaling tests was found significant for any plant trait, a six parameters model of generation means analysis was selected for further study.

Types of gene action estimated by generation mean as genetic effects in six parameters model and their results were presented in table 5. As scaling tests were significant for all the traits studied except for 1000-

grains weight in Mairaj-08 × Blue Silver cross, so six parameters model was applied for these traits but for 1000-grains weight, three parameters model was adopted to estimate gene action and gene interaction. In the second cross (Faisalabad-08 × DH-60), scaling tests for all plant traits were significant so six parameters model was applied to estimate gene effects for these traits.

Significant values for the estimated values of mean effects (m) indicated that all the studied characters were quantitatively inherited. The additive gene effects (d) were positively or negatively significant for all traits studied except for days to maturity, plant height, spike density, number of grains per spike and grain yield per plant in Mairaj-08 × Blue Silver cross (Table6). While in the second cross, additive effects were significant for plant traits studied except for number of spikelet per spike, number of grains per spike, 1000-grains weight and grain yield per plant. Dominance genetic effects were found significant for days to heading, days to maturity, plant height, peduncle length, spike length, spike density, number of grains per spike and 1000-grains weight in the first cross (Mairaj-08 × Blue Silver). In the second cross (Faisalabad-08 × DH-60), plant height, peduncle length, spike density, number of grains per spike and 1000-grains weight were found to be significant which suggests the potential for further improvement in these traits by selection of their progenies. Values of dominance gene effects were greater than values of additive gene effects, which suggest that pedigree selection is useful breeding procedure for improving population. However, negative dominance values found in many plant traits indicated that alleles controlling high value were dominant over alleles controlling high value. These results were in agreement with the earlier reports (Khattab et al., 2001; Khattab et al., 2010).

Significant values of additive × additive interaction; an epistatic type of gene effects “i”, were observed in all plant traits under observation in the cross-I except 1000-grains weight and grain yield per plant (Table 5). Similarly, in the cross-II, “I” value was significant for all traits except for days to heading, number of spikelet per spike, number of grains per spike, 1000-grains weight and grain yield per plant. Additive × dominance epistatic gene effects “j” were found significant in almost all plant traits in both crosses except for number of spikelet per spike, 1000-grains weight and grain yield per plant. Negative value in some plant traits for “j” indicated dispersion of genes in parents. In dominance × dominance type of epistatic gene effects “l” were found to be significant in many plant traits. Whereas, “l” value was found non-significant for plant height, number of spikelet per spike, 1000-grains weight and grain yield per plant for

the cross-I while in the cross-II, most of the plant traits were significant whether positive or negative except in number of spikelet per spike, number of grains per spike, 1000-grains weight and grain yield per plant. These findings were also in favor of findings of some researchers like , Farag (2009) and (Khattab et al., 2001; Khattab et al., 2010). Opposite signs of ‘h’ and ‘l’ were found in many plant traits suggesting duplicate type of non-allelic gene interaction while complementary epistasis type of genetic effects were found in all plant traits. Thus, inheritance of all plant traits was controlled by additive and non-additive gene effects with greater values of dominance gene effects than additive in most of plant traits.

For the assessment of genetic control mechanism for grain yield plant⁻¹, a six parameters model of generation means analysis was applied for grain yield plant⁻¹ in Mairaj-08 × Blue Silver. These results showed that the mean and additive genetic parameters were significant and fully valid for the evaluation of gene action. The genetic parameters, additive and additive × additive, were most influential for the control of this trait. Similar findings were reported earlier ((Ali et al., 1999; Ullah et al., 2010; Anwar et al., 2011). Contrarily Erkul et al., (2011) reported contribution of both additive and dominance effects in controlling inheritance of grain yield plant⁻¹(Erkul et al., 2010).

In case of Faisalabad-08 × DH-60 cross genetic analysis of grain yield plant⁻¹ expressed that only one parameter i.e. mean (m) was found valid for the estimation of gene action and type of epistasis with additive and additive × additive epistasis was more prominent (Khattab et al., 2010). Therefore, mass selection or progeny selection is best for the improvement in such situations. For grain yield plant⁻¹ in Faisalabad-08 × DH-60 cross, the results of generation means analysis exposed the dominance and dominance × dominance gene interactions showed opposite signs. This indicated that there was duplicate epistasis for grain yield plant⁻¹.

CONCLUSION

It is concluded that in cross Faisalabad-08 × DH-60, maximum plant traits like days to heading, days to maturity, plant height, number of tillers per plant, peduncle length, spike length, spike density were controlled by additive gene action so this cross may be utilized for high grain yield in future wheat yield improvement breeding program.

Table1. Analysis of variance for yield and its related traits in Mairaj-08×Blue silver cross

S.O.V	DF	Days to heading	Days to maturity	Plant height	Peduncle length	No. of tillers/plant	Spike length	No. of spikelet/s pike	Spike density	No. of grains/spike	1000-grain wt.	Grain yield/plant
Blocks	2	14.57**	7.60**	2.31 ^{ns}	1.57 ^{ns}	0.30 ^{ns}	2.89 ^{ns}	2.50 ^{ns}	0.01 ^{ns}	1.03 ^{ns}	0.52 ^{ns}	1.32 ^{ns}
Generations	5	43.80**	20.64	9.97**	4.89*	4.78*	14.91*	16.11**	8.79**	25.50**	9.68**	21.85**
Error	10	1.78	1.67	26.27	8.21	5.22	0.34	0.62	0.007	3.09	2.81	5.76
Total	17	461.78	214.00	1694.07	308.49	180.18	30.76	60.15	0.39	432.56	166.81	703.07

*significant at t = 0.025; ns = non-significant; DF = degree of freedom

Table2. Analysis of variance for yield and its related traits in Faisalabad-08×DH-60 cross

S.O.V	DF	Days to heading	Days to maturity	Plant height	Peduncle length	No. of tillers/plant	No. of spikelet/spike	No. of grains/spike	1000-grain wt.	Spike length	Grain yield/plant	Spike density
Blocks	2	1.63 ^{ns}	0.86 ^{ns}	20.25**	2.16 ^{ns}	0.17 ^{ns}	8.40**	0.73 ^{ns}	0.28 ^{ns}	3.70 ^{ns}	5.93*	0.42 ^{ns}
Generations	5	32.88**	41.42**	7.01*	12.69**	8.63**	12.65**	15.43**	5.45**	7.98**	12.46**	41.42**
Error	10	6.83	6.25	18.07	8.99	3.54	0.32	12.77	5.88	0.53	2.62	0.004
Total	17	1214	1368.94	2267.62	699.67	189.49	28.74	1131.35	222.52	30.36	220.93	0.72

*significant at t = 0.025; ns = non-significant; DF = degree of freedom

Table 3. Scaling tests for yield and its related traits in Mairaj-08×Blue silver cross

Scaling tests	DF	Days to heading	Days to maturity	Plant height	No. of tillers /plant	Peduncle length	Spike length	No. of spikelet /spike	Spike density	No. of grains/spike	1000-grains wt.	Grain yield /plant
A	89	12.91*	27.03*	5.96*	-2.15*	4.95*	2.42*	4.43*	3.04*	1.67 ^{ns}	0.13 ^{ns}	2.64*
B	89	23.33*	14.61*	1.12 ^{ns}	-5.64*	1.29 ^{ns}	-3.20*	2.68*	11.05*	1.25 ^{ns}	0.80 ^{ns}	1.27 ^{ns}
C	239	5.61*	0	13.57*	-2.32*	-1.45 ^{ns}	8.41*	9.63*	-5.21*	-2.21*	0.57 ^{ns}	6.30*
D	209	-24.24*	-19.83*	3.62*	3.24*	-5.80*	8.13*	2.29*	-13.88*	-3.68*	-0.28 ^{ns}	1.84 ^{ns}

*significant at $t = 0.025$; ns = non-significant; DF = degree of freedom

Table 4. Scaling tests for yield and its related traits in Faisalabad-08×DH-60 cross

Scaling tests	DF	Days to heading	Days to maturity	Plant height	No. of tillers /plant	Peduncle length	Spike length	No. of spikelet /spike	Spike density	No. of grains/spike	1000-grains wt.	Grain yield /plant
A	89	33.91*	31.14*	-3.24*	-9.13*	-3.25*	-8.10*	1.12 ^{ns}	30.80*	-0.03 ^{ns}	0.68 ^{ns}	2.39*
B	89	18.44*	19.01*	-7.44*	-0.05 ^{ns}	-6.67*	1.52 ^{ns}	2.30*	1.21 ^{ns}	2.55*	2.17*	1.56 ^{ns}
C	239	26.41*	30.34*	5.96*	-0.70 ^{ns}	4.03*	0.85 ^{ns}	3.53*	7.01*	4.34*	2.39*	4.09*
D	209	-1.34 ^{ns}	-1.49 ^{ns}	11.91*	4.23*	11.26*	5.46*	0.24 ^{ns}	-24.38*	1.69 ^{ns}	-0.63 ^{ns}	1.76 ^{ns}

*significant at $t = 0.025$; ns = non-significant; DF = degree of freedom

Table 5. Six-parameters model for estimation of genetic parameters in Mairaj-08 × Blue silver (1) and Faisalabad-08 x DH-60 (2) for various plant studied traits

Characters	Cross	Genetic effects					
		m	d	H	i	j	l
DF		239	299	629	539	359	629
Days to heading	1	2234.50*	-4.15*	20.91*	24.24*	-3.69*	-24.98*
	2	269.44*	8.36*	-2.57*	1.34	21.04*	-18.34*
Days to maturity	1	528.32*	-1.00	16.32*	19.83*	3.57*	-26.28*
	2	441.44*	6.71*	-5.12*	1.49*	20.79*	-18.32*
Plant height	1	134.43*	-0.07	-3.86*	-3.62*	3.77*	-0.65
	2	88.82*	-2.56*	-13.03*	-11.91*	2.76*	10.94*
No. of tillers/plant	1	28.38*	3.52*	-2.62*	-3.24*	2.61*	4.68*
	2	30.67*	-4.92*	-3.25*	-4.23*	-5.40*	4.93*
Peduncle length	1	89.96*	2.57*	7.07*	5.80*	3.34*	-5.46*
	2	70.25*	-3.00*	-11.50*	-11.27*	2.83*	10.19*
Spike length	1	79.32*	3.21*	-6.28*	-8.13*	4.31*	5.23*
	2	114.63*	-7.67*	-5.17*	-5.46*	-7.71*	5.16*
No. of spikelet per spike	1	136.42*	2.36*	-1.28	-2.29*	-0.09	-1.17
	2	124.32*	1.16	1.07	-0.24	-0.61	-1.07
Spike density	1	159.57*	-0.89	11.95*	13.87*	-9.10*	-13.76*
	2	1000.90*	32.84*	27.17*	24.37*	22.53*	-25.65*
No. of grains per spike	1	46.92*	2.37*	4.91*	3.85*	0.20	-3.22*
	2	65.67*	-1.26	0.71	-1.68	-1.97*	-0.02
1000-grains weight	1	10.24*	7.07*	0.99*			
	2	66.28*	-0.57	1.75	0.63	-1.59	-1.44
Grain yield per plant	1	66.73*	2.62*	0.60	-1.84	1.31	-0.47
	2	20.44*	1.63	-0.96	-1.76	0.72	-0.02

*significant at t = 0.025; ns = non-significant; DF = degree of freedom

References

- [1]. Abbasi, S., A. Baghizadeh, G. Mohammadi-Nejad, B. Nakhoda. 2014. Genetic analysis of grain yield and its components in bread wheat (*Triticum aestivum* L.). *Annual Research & Review in Biology*. 4(24): 3636.
- [2]. Ahmad, F., S. Khan, S.Q. Ahmad, H. Khan, A. Khan, F. Muhammad. 2011. Genetic analysis of some quantitative traits in bread wheat across environments. *African Journal of Agricultural Research*. 6(3): 686-692.
- [3]. Ali, S.A., L. Tedone, G. De Mastro. 2017. Climate Variability Impact on Wheat Production in Europe: Adaptation and Mitigation Strategies. In: Ahmed, M., Stockle, C.O. (Eds.), *Quantification of Climate Variability, Adaptation and Mitigation for Agricultural Sustainability*. Springer International Publishing, Cham, pp. 251-321.
- [4]. Ali, Z., A.S. Khan, T.M. Khan. 1999. Gene action for plant height, grain yield and its components in spring wheat. *Pak. J. Biol. Sci*. 2(4): 1561-1563.
- [5]. Anwar, J., M. Akbar, M. Hussain, S. Asghar, J. Ahmad, M. Owais. 2011. Combining ability estimates for grain yield in wheat. *Journal of Agricultural Research*. 49(4): 437-445.
- [6]. Ashraf, R., Fayyaz-ul-Hassan, M. Ahmed, G. Shabbir. 2017. Wheat Physiological Response Under Drought. In: Ahmed, M., Stockle, C.O. (Eds.), *Quantification of Climate Variability, Adaptation and Mitigation for Agricultural Sustainability*. Springer International Publishing, Cham, pp. 211-231.
- [7]. Asseng, S., F. Ewert, P. Martre, R.P. Rotter, D.B. Lobell, D. Cammarano, B.A. Kimball, M.J. Ottman, G.W. Wall, J.W. White, M.P. Reynolds, P.D. Alderman, P.V.V. Prasad, P.K. Aggarwal, J. Anothai, B. Basso, C. Biernath, A.J. Challinor, G. De Sanctis, J. Doltra, E. Fereres, M. Garcia-Vila, S. Gayler, G. Hoogenboom, L.A. Hunt, R.C. Izaurralde, M. Jabloun, C.D. Jones, K.C. Kersebaum, A.K. Koehler, C. Muller, S. Naresh Kumar, C. Nendel, G. O'Leary, J.E. Olesen, T. Palosuo, E. Priesack, E. Eyshi Rezaei, A.C. Ruane, M.A. Semenov, I. Shcherbak, C. Stockle, P. Stratonovitch, T. Streck, I. Supit, F. Tao, P.J. Thorburn, K. Waha, E. Wang, D. Wallach, J. Wolf, Z. Zhao, Y. Zhu. 2015. Rising temperatures reduce global wheat production. *Nature Clim. Change*. 5(2): 143-147.
- [8]. Ata-Ul-Karim, S.T., N. Akbar, E. Ullah. 2015. Improvement in Wheat Crop Growth and Grain Yield under Different Planting Techniques in Faisalabad Zone. *Journal of Environmental and Agricultural Sciences*. 5: 71-79.
- [9]. Dogar, M.H., S. Akhtar, M. Hussain. 2016. Factors affecting yield gap in different wheat varieties in Southern Punjab. *Journal of Environmental and Agricultural Sciences*. 7: 42-47.
- [10]. Dwivedi, D., P. Pandey, R. Krishana. 2012. Genetic analysis of some quantitative traits in wheat (*Triticum aestivum* L.). *Current Advances in Agricultural Sciences*. 4(2): 159-162.
- [11]. Erkul, A., U. Aydin, C. Konak. 2010. Inheritance of yield and yield components in a bread wheat (*Triticum aestivum* L.) cross. *Turkish Journal of Field Crops*. 15(2): 137-140.
- [12]. Hayman, B.I. 1958. The Theory and Analysis of Diallel Crosses. II. *Genetics*. 43(1): 63-85.
- [13]. Irshad, M., I. Khaliq, A.-S. Khan, A. Ali. 2012. Genetic studies for some agronomic traits in spring wheat under heat stress. *Pak. J. Agri. Sci*. 49(1): 11-20.
- [14]. Jatoi, W., M. Baloch, N. Khan, M. Munir, A. Khakwani, N. Vessar, S. Panhwar, S. Gul. 2014. Heterosis for yield and physiological traits in wheat under water stress conditions. *J. Anim. Plant Sci*. 24(1): 252-261.
- [15]. Kaur, A., P.K. Sraw, S.S. Kukal. 2017. Climatic Variability Impact on Wheat-Based Cropping Systems of South Asia: Adaptation and Mitigation. In: Ahmed, M., Stockle, C.O. (Eds.), *Quantification of Climate Variability, Adaptation and Mitigation for Agricultural Sustainability*. Springer International Publishing, Cham, pp. 353-370.
- [16]. Khattab, S., R. Esmail, A. Al-Ansary. 2010. Genetical analysis of some quantitative traits in bread wheat (*Triticum aestivum* L.). *NY Sci. J*. 3(11): 152-157.
- [17]. Khattab, S., A. Shaheen, S. Afiah. 2001. Genetic behavior of some metric traits in four bread wheat crosses under normal and saline conditions. *J. Agric. Sci. Mansoura Univ*. 26(1): 217-229.
- [18]. Kotal, B.D., A. Das, B. Choudhury. 2010. Genetic variability and association of characters in wheat (*Triticum aestivum* L.). *Asian J. Crop Sci*. 2(3): 155-160.
- [19]. Magda, E., A. El-Rahman. 2013. Estimation of some genetic parameters through generation mean analysis in three bread wheat crosses. *Alex Journal of Agricultural Research*. 58(3): 183-195.
- [20]. Mahpara, S., Z. Ali, M. Ahsan. 2008. Combining ability analysis for yield and yield related traits among wheat varieties and their F1 hybrids. *Int. J. Agric. Biol. Sci*. 10: 599-604.

- [21]. Mahpara, S., Z. Ali, J. Farooq, S. Hussain, R. Bibi. 2015. Heterosis and Heterobeltiosis Analysis for Spike and its Related Attributes in Different Wheat Crosses. *Pakistan Journal of Nutrition*. 14(7): 396.
- [22]. Mather, K., J.L. Jinks. 1977. Interaction of genotype and environment. *Introduction to Biometrical Genetics*. Springer US, Boston, MA, pp. 130-162.
- [23]. Misra, S., V. Rao, R. Dixit, V. Surve, V. Patil. 1994. Genetic control of yield and its components in breadwheat. *The Indian Journal of Genetics and Plant Breeding*. 54(1): 77-82.
- [24]. Parry, M.A.J., M. Reynolds, M.E. Salvucci, C. Raines, P.J. Andralojc, X.-G. Zhu, G.D. Price, A.G. Condon, R.T. Furbank. 2010. Raising yield potential of wheat. II. Increasing photosynthetic capacity and efficiency. *J. Exp. Bot*.
- [25]. Rabbani, G., A. Mahmood, G. Shabbir, K.N. Shah, A. Naeem-ud-Din. 2011. Gene action in some yield attributes of bread wheat under two water regimes. *Pak. J. Bot*. 43(2): 1141-1156.
- [26]. Reynolds, M., D. Bonnett, S.C. Chapman, R.T. Furbank, Y. Manès, D.E. Mather, M.A.J. Parry. 2011. Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. *J. Exp. Bot*. 62(2): 439-452.
- [27]. Reynolds, M., M.J. Foulkes, G.A. Slafer, P. Berry, M.A.J. Parry, J.W. Snape, W.J. Angus. 2009. Raising yield potential in wheat. *J. Exp. Bot*.
- [28]. Saleem, M.Y., M. Asghar, Q. Iqbal. 2015. Analysis of genetic proximity in tomato (*Solanum lycopersicum* L.) genotypes. *Journal of Environmental and Agricultural Sciences*. 3: 08-13.
- [29]. Sami-UI-Allah, A. Khan, W. Ashfaq. 2011. Genetic analysis of physio-morphological traits in bread wheat (*Triticum aestivum* L.) under water stress conditions. *Cereal Research Communications*. 39(4): 544-550.
- [30]. Shabbir, G., N.H. Ahmad, Z. Akram, M.I. Tabassum. 2011. Genetic behavior and analysis of some yield traits in wheat (*Triticumaestivum* L.) genotypes. *J. Agric. Res*. 49(1): 1-9.
- [31]. Singh, H.P., D.R. Batish, R.K. Kohli. 2003. Allelopathic Interactions and Allelochemicals: New Possibilities for Sustainable Weed Management. *Crit. Rev. Plant Sci*. 22(3-4): 239-311.
- [32]. Singh, R., S. Singh. 1992. Estimation of genetic parameters through generation mean analysis in breadwheat. *The Indian Journal of Genetics and Plant Breeding*. 52(4): 369-375.
- [33]. Steel, R., J. Torrie, D. Dickey. 1997. *Principles and procedures of statistics: a biometrical approach*. McGraw-Hill, New York, NY, USA.
- [34]. Ullah, S., A.S. Khan, A. Raza, S. Sadique. 2010. Gene action analysis of yield and yield related traits in spring wheat (*Triticum aestivum*). *Int. J. Agric. Biol*. 12(1): 125-128.

10/8/2022