IJBPAS, May, 2017, 6(5): 999-1008

ISSN: 2277–4998

International Journal of Biology, Pharmacy and Allied Sciences (IJBPAS)

'A Bridge Between Laboratory and Reader'

www.ijbpas.com

INHERITANCE OF QUANTITATIVE TRAITS IN *TRITICUM AESTIVUM*

SALMAN S, ALI S, SAYAL OU, RAMZAN I AND JAMIL A

Department of Plant Breeding & genetics, Faculty of Agriculture, Gomal University, Dera Ismail Khan

***Corresponding author:** ishratramzan35@yahoo.com

Received 1st Dec. 2016; Revised 4th Feb. 2017; Accepted 5th March 2017; Available online 1st May 2017

ABSTRACT

Diallel analysis is a good mean of studying genetic behavior of traits. This experiment was conducted at KPK Agricultural University, Peshawar to evaluate the performance of eight wheat genotypes; viz., Fakhar e sarhad, Ghaznavi-98, Takbeer, Tatara-98, SQ-92, ICP-3, Sarc-3 and Dera-98, in a 8 × 8 diallel combinations under rainfed conditions. Data were collected on spike length, harvest index, 1000-grain weight and biological yield. Highly significant differences were observed among the genotypes for all the traits studied. In diallel analysis additive effect "a" was highly significant for all the studied traits except harvest index and biological yield. The dominant effect "b" was non-significant for all the traits except biological yield, harvest index and 1000-grain weight. Analysis of genetic components revealed that additive genetic variations (D) were also significant for all the studied parameters except harvest index. While dominant genetic variations (H) were significant in 1000-grain weight and biological yield and was non-significant for other parameters. The results suggested that the selection of higher yield wheat genotypes on the basis of spike length, harvest index, 1000-grain weight and biological yield may be helpful to improve grain yield under water deficit conditions.

Keywords: *Triticum aestivum*, diallel analysis, rainfed, geen action, additive, dominance

INTRODUCTION

Wheat has played a key role in the men's economic and social development. Wheat is a crop of global importance in area cultivated and production. It is a main source of energy to human population and is one of the richest source of nutrients. Due to the major role in farming system, a large number of plant breeders have been engaged in the improvement throughout the world to meet the requirements of rapidly growing population. It is grown on 8307 thousand hectares with total production of 21.708 million tons and an average of 2.615 tons ha^{-1} [1]. Grain yield is a complex trait made up of the interaction between different yield components and environmental effects. Because of these complex interactions it is difficult to improve yield through breeding (especially in the early generations) if yield is the only factor recorded, suggesting that component traits should also be used as selection criteria for yield improvement [2, 3]. This is the reason why it is necessary to know the genetic architecture of yield components [4-6]. The quantitative traits are controlled by few major genes and a number of polygene. The major genes exert larger whereas the polygenes (also called minor genes) produce small effect in controlling of a quantitative trait [7-9]. The analysis of morphological and yield traits provides an opportunity to plant breeder for selecting higher yield crop plant genotypes [10-12]. Estimates of gene effects have a direct impact on the method of hybridization and selection to be adopted in breeding programs. Wheat evaluations in Pakistan have so far been focused on the genetic research and development of cultivars under irrigated environments. It is now to evaluate wheat under rainfed conditions to get answers to the problems of breeding for the non-irrigated or rainfed areas of the country. Thus the aim of the study was to investigate the genetic background and to get information on gene action of these genotypes and their crosses before starting a systematic breeding program for rainfed areas.

MATERIALS AND METHODS

The experiment was conducted in the experimental area of the Department of Plant Breeding and Genetics, Faculty of Agriculture Gomal University D.I. Khan during 2013-14. Eight wheat genotypes, viz., Dera-98, Fakhar e sarhad, ghaznavi-98, ICP-3, Takbeer, Tatara-98, SQ-92 and Sarc-3 were crossed in all possible combinations in an 8 × 8 diallel fashion during the crop season 2013-14. During the cropping season 2013-14, the experiment was conducted to utilize and analyze the performance of all the genotypes (including 8 parents and their 56 F_1s hybrids) under rainfed conditions. The experiment in rainfed conditions received only one irrigation just after planting. The experiment was replicated thrice in randomized complete block design (RCBD).

All the F_1s along with their parents were planted. Each treatment consisted of two row plot with the row length of 2.5 meters. Each row consisted of approximately 15 plants, with a plant to plant and row to row distance of 15 and 30 cm respectively. All other cultural practices including hoeing, weeding, fertilizer etc were carried out for the experiment to reduce the experimental error. Data were collected on spike length (cm), harvest index (%), 1000-grain weight (g) and biological yield (g). The data collected were subjected to analysis of variance according to Steel and Torrie [13]. Diallel analysis [14] was carried out after an ordinary analysis of variance to determine whether significant variation existed among genotypes for the character under consideration. Only the presence of significant differences allowed proceeding further for diallel analysis. The genetic components of variation were calculated using the procedures given by Hayman [15,16] and Mather and Jinks [14]. The genetic parameters calculated were additive variation (D), variation due to dominant effect of genes (H_1), variation due to dominant effect of genes correlated for gene distribution (H_2), relative frequency of dominant and recessive alleles (F), overall dominance effect of heterozygous loci, environmental variance (E), average degree of dominance, proportion of genes with positive and negative effects in the parents ($H_2/4H_1$), proportion of dominant and recessive genes in the parents and heritability (broad and narrow sense).

RESULTS AND DISCUSSIONS

Analysis were carried out on the data recorded on spike length (cm), harvest index (%), 1000-grain weight (g) and biological yield (g) on 56 F_1s to investigate the genetic information on various aspects under rainfed conditions. Analysis of variance was carried out according to the Steel and Torrie [13]. Those parameters where significant, differences observed and further analyzed comparing diallel analysis [14-16]. All the data subjected to analysis of variance under rainfed conditions (Table 1) revealed highly significant differences for all the characters studied. Diallel analysis was carried out for those characters that showed significant genotypic variations. Because only the presence of significant differences allows processing further for diallel analysis.

SPIKE LENGTH

Analysis of variance for spike length (Table 2) depicted that additive component ***"a"*** was highly significant and dominance component "b" was non-significant. Directional dominance deviations of the genes "b_1" were non-significant, while the highly significant

"b_2" showed the gene distribution among parents was asymmetrical. Effect of specific genes was found non-significant, i.e., *"b_3"* Maternal *"c"* and reciprocal *"d"* effects were found non-significant. Re-testing of *"a"* and *"b"* against *c* and *d* is not required. Increase of genetic component of variation the D was found significant and dominant H component of variation were found non-significant (Table 3). Unequal and non-significant values of H1, H2 and Value of H2/4H1 presented the distribution of positive and negative alleles among parents. F value was negative and non-significant. This clearly indicates the greater frequency of recessive genes than dominant gene among parents. Presence of additive gene action was indicated by the value of average degree of dominance, and its value was 0.17.Broad sense heritability estimates was 52.89% (Table 3) while narrow sense heritability was 57.20% under same conditions. This shows that half of the total inherited genetic portion was of dominance nature and half of additive nature [3,5].

1000-GRAIN WEIGHT

Data subjected to analysis of variance for 1000-grain weight (Table 4) revealed that highly significant "a" and "b" indicating the presence of both additive and dominance effects. The directional dominance "b_1" was only significant and a symmetrical gene distribution (as *"b_2"* was non-significant). The non-significant *"c"* and *"d"* items showed absences of both maternal and reciprocal effects. Retesting of *"a"* and *"b"* is not needed. Components of genetic variation (Table 5) indicating that D additive and dominant H component 0f variation both were significant. The value of $H_2/4H_1$ indicating the distribution of positive and negative genes among parents its value was 0.23, which was close to specific value 0.25 so the genes are equally distributed among the parents. The value of F was significant and showing the greater frequency of dominance over recessive genes. Dominance effect of heterozygous loci was found significant, displaying the substantial role of dominance effects due to heterogeneity at loci. The value of average degree of dominance was 0.86 which was less than 1 indicating that the additive effect was more than dominant effect. High broad sense heritability indicated the greater amount of dominant genetic variation in the total inherited genetic variation of the trait [5]. The values of broad sense heritability and narrow sense heritability were 68.63 and 44.53 respectively.

Table 1: Analysis of variance for the characters under rainfed conditions

Character	Reps.	Genotypes	Error
	d.f = 2	d.f = 63	d.f = 126
Spike length (cm)	0.53 ns	1.27**	0.61
Harvest index (%),	11.60 ns	68.36**	32.88
1000-grain weight (g)	2.15 ns	15.61**	5.491
Biological yield (kg)	94197	97465**	24291

**=Significant at 5% probability level

Table 2: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for spike length

Source	df	SS	MS	F	Re-testing against	
					C	d
A	7	46.39	6.62	7.26**	-	-
B	28	14.15	0.50	1.17ns		
b_1	1	0.73	0.73	7.19ns		
b_2	7	6.73	0.96	4.87**		
b_3	20	6.68	0.33	0.63ns		
C	7	6.36	0.90	1.62ns		
D	21	13.68	0.64	0.86ns		
Total	63	80.57				
a × blocks	14	12.76	0.91			
b_1 × blocks	2	0.20	0.10			
b_2 × blocks	14	2.76	0.19			
b_3 × blocks	40	21.17	0.52			
b × blocks	56	24.10	0.43			
c × blocks	14	9.63	0.68			
d × blocks	42	31.56	0.75			
Total × blocks	126	78.19				

* P ≤ 0.05 ** P ≤ 0.01, F-ratio. Each item is treated against its own block interaction, Re-testing against c and d mean squares, a= additive gene effect, b= dominance gene effect, b1= directional dominance deviation, b2= gene distribution among the parents, b3= effect of specific genes, c= maternal effect, d= reciprocal effect

Table 3: Estimates of genetic components of variation for spike length under rainfed conditions

Components	Means	Standard errors
D	0.35*	0.03
H_1	0.01ns	0.03
H_2	-0.07ns	0.64
F	-0.06ns	0.07
h^2	0.01ns	0.04
E	0.20*	0.01
$(H_1/D)^{1/2}$	0.17	
$H_2/4H_1$	-1.76	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$	0.31	
Heritability (ns)	57.19	
Heritability (bs)	52.89	

* Value is significant when it exceeds 1.96 when it is divided by its standard error, ns non significant, D. measures additive effect, H1 and H2 measures dominance effect, F determines frequencies of dominant to recessive alleles in parents, h2 determines the overall dominance effect due to heterozygous loci, E shows environmental effect

Table 4: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for 1000-grain weight

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	470.53	67.21	10.34**	-	-
B	28	386.31	13.79	2.32**		
b1	1	264.89	264.82	47.19*		
b2	7	49.38	7.05	1.44ns		
b3	20	72.04	3.60	0.57ns		
C	7	70.94	10.13	1.32ns		
D	21	56.00	2.66	0.69ns		
Total	63	983.80				
a × blocks	14	90.98	6.49			
b1 × blocks	2	11.22	5.61			

b2 × blocks	14	68.47	4.89			
b3 × blocks	40	252.42	6.31			
b × blocks	56	332.13	5.93			
c × blocks	14	107.04	7.64			
d × blocks	42	161.64	3.84			
Total × blocks	126	691.80				

*** P ≤ 0.05 ** P ≤ 0.01, F-ratio. Each item is treated against its own block interaction, Re-testing against c and d mean squares, a= additive gene effect, b= dominance gene effect, b1= directional dominance deviation, b2= gene distribution among the parents, b3= effect of specific genes, c= maternal effect, d= reciprocal effect**

Table 5: Estimates of genetic components of variation for 1000-grain weight under rainfed conditions

Components	Means	Standard errors
D	7.78*	0.58
H_1	5.97*	1.35
H_2	5.57*	1.17
F	3.03*	1.38
h^2	37.8*	0.78
E	1.81*	0.19
$(H_1/D)^{1/2}$	0.87	
$H_2/4H_1$	0.23	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} – F$	1.57	
Heritability (ns)	44.53+	
Heritability (bs)	68.63	

*** Value is significant when it exceeds 1.96 when it is divided by its standard error, ns non significant, D. measures additive effect, H1 and H2 measures dominance effect, F determines frequencies of dominant to recessive alleles in parents, h2 determines the overall dominance effect due to heterozygous loci, E shows environmental effect**

HARVEST INDEX

Data subjected to analysis of variance for harvest index (Table 6) indicated that item ***"a"*** was non-significant, while the item "b" for dominance effect was highly significant. The item "b_1", e, was non-significant; it means that directional dominance is absent. The component "b_2", which is for asymmetrical distribution of genes, was also significant. The item "b_3" was highly significant showing high specific gene effect. Maternal effect was non-significant while reciprocal effect was only significant. When we have retested the item *"a"* and *"b"* we revealed that maternal effect was highly significant for additive effect and was non-significant for all others components in case of reciprocal effect. Components of genetic variation (Table 7) showed that both additive and dominant components of variation were non-significant. The value of H_2/H_41 was 0.21, which shows the distribution genes among parents. F value was also non-significant. Net dominance effect of heterozygous loci was found negative and non-significant, i.e., h^2. The value of average degree of dominance was 6.90 showing the over dominant effect. Heritability estimates shows that narrow sense heritability was 7.9, while the broad sense heritability, was 42.9. It means that dominance effect governed the whole genetic variation [17,18]. Various researchers have found similar results which showed that the selection of higher yield wheat genotypes may be developed through selection on the basis of harvest index [19-22].

Table 6: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for harvest index

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	480.66	68.665	1.47ns	-	
B	28	2031.01	72.536	2.43**		1.39ns
b1	1	0.13	0.132	0.00ns		0.00ns
b2	7	366.73	52.390	3.34*		1.00ns
b3	20	1664.14	83.207	2.37**		1.59ns
C	7	700.31	100.044	1.65ns		
D	21	1094.84	52.135	2.24*		
Total	63	4306.82				
a × blocks	14	651.77	46.55			
b1 × blocks	2	45.68	22.84			
b2 × blocks	14	219.29	15.66			
b3 × blocks	40	1401.00	35.02			
b × blocks	56	1665.98	29.74			
c × blocks	14	848.08	60.57			
d × blocks	42	977.32	23.26			
Total × blocks	126	4143.16				

* $P \leq 0.05$ ** $P \leq 0.01$, F-ratio. Each item is treated against its own block interaction, Re-testing against c and d mean squares, a= additive gene effect, b= dominance gene effect, b1= directional dominance deviation, b2= gene distribution among the parents, b3= effect of specific genes, c= maternal effect, d= reciprocal effect.

Table 7: Estimates of genetic components of variation for harvest index under rainfed conditions

Components	Means	Standard errors
D	-0.66ns	8.39
H_1	31.61ns	19.81
H_2	26.65ns	16.81
F	1.28ns	19.21
h^2	-4.72ns	11.23
E	10.84*	2.80
$(H_1/D)^{1/2}$	6.90	
$H_2/4H_1$	0.21	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$	1.32	
Heritability (ns)	7.91	
Heritability (bs)	42.92	

* Value is significant when it exceeds 1.96 when it is divided by its standard error, ns non significant, D. measures additive effect, H1 and H2 measures dominance effect, F determines frequencies of dominant to recessive alleles in parents, h2 determines the overall dominance effect due to heterozygous loci, E shows environmental effect

BIOLOGICAL YIELD

Diallel analysis of variance (Table 8) revealed that item "a" was non-significant while item *"b"* (for dominance) was highly significant. The item "b_1" was non-significant showing the absence of directional dominance. While the component *"b_2"* for asymmetry of gene distribution was also highly significant. The component *"b_3"* for specific gene distribution was also highly significant which shows the important role of dominant gene. Maternal effect *"c"* was only significant and reciprocal effect *"d"* was highly significant. Re-testing of *"a"* and *"b"* showed non-significant for all the components. Genetic components of variation (table 9) revealed that both additives D and dominance variation H were significant. The H_1 and H_2 values suggested the asymmetry of positive and negative gene distribution among parents. Its value was supported by the ratio $H_2/4H_1$ that was less than 0.25 which is fixed value for gene distribution. F value was positive and significant while the value of h_2 was non-significant. The E was also significant.

Presence of over-dominant effect of genes was indicated by the value of average degree of dominance. Heritability estimates for narrow sense was too low than broad sense and their ratios were (ns 5.31 and bs 63.33) showing that genetic variation governed by dominance effects. These findings are in close agreement with the previous findings of Inamullah *et al*., [22]. Broad sense heritability was much greater than the narrow sense one variation. Ahmad *et al*., [17] also obtained same genetic behavior for grain yield plant^{-1} in different generations of bread wheat. Biological yield plays an important role in selecting higher yield wheat genotypes [23, 24].

Table 8: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for biological yield

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	383341.7	54763.10	1.17ns	0.412ns	
B	28	2960100	105717.90	9.26**		1.22ns
b1	1	22344.05	22344.05	7.08ns		0.25ns
b2	7	1190919	170131.30	15.56**		1.97ns
b3	20	1746837	87341.83	7.28**		1.01ns
C	7	988141.7	141163.10	2.84*		
D	21	1808742	86130.56	3.37**		
Total	63	6140325				
a × blocks	14	653927.1	46709.08			
b1 × blocks	2	6309.97	3154.98			
b2 × blocks	14	153028.5	10930.61			
b3 × blocks	40	479639.7	11990.99			
b × blocks	56	638978.1	11410.32			
c × blocks	14	695408.3	49672.02			
d × blocks	42	1072358	25532.34			
Total × blocks	126	3060672				

* $P \leq 0.05$ ** $P \leq 0.01$, F-ratio. Each item is treated against its own block interaction, Re-testing against c and d mean squares, a= additive gene effect, b= dominance gene effect, b1= directional dominance deviation, b2= gene distribution among the parents, b3= effect of specific genes, c= maternal effect, d= reciprocal effect

Table 9: Estimates of genetic components of variation for biological yield under rainfed conditions

Components	Means	Standard errors
D	51549.80*	12516.52
H_1	89743.35*	28901.61
H_2	53556.34*	25145.04
F	85288.49*	29707.11
h^2	-443.22ns	16821.93
E	8461.11*	4190.84
$(H_1/D)^{1/2}$	1.31	
$H_2/4H_1$	0.14	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$	4.36	
Heritability (ns)	5.30	
Heritability (bs)	63.33	

*** Value is significant when it exceeds 1.96 when it is divided by its standard error, ns non significant, D. measures additive effect, H1 and H2 measures dominance effect, F determines frequencies of dominant to recessive alleles in parents, h2 determines the overall dominance effect due to heterozygous loci, E shows environmental effect**

CONCLUSIONS

The results of prescribed study revealed that the spike length, harvest index, 1000-grain weight and biological yield traits are the potential criteria for improvement of yield of wheat under water deficit condition.

REFERENCES

[1] Government of Pakistan. (2005-2006). Year Book, Agricultural Statistics of Pakistan. Ministry of Food, Agriculture and Livestock, Islamabad. P. 55.

[2] Novoselovic, D., Marijana Baric, G. Drezner1, J. Gunjaca and A. Lalic. (2004). Quantitative inheritance of some wheat plant traits. Genetics and Molecular Biology, 27 (1): 92-98.

[3] Farooq, J., Khaliq, I., Ali, M. A., Kashif, M., Rehman, A. U., Naveed, M., ... & Farooq, A. (2011). Inheritance pattern of yield attributes in spring wheat at grain filling stage under different temperature regimes. *Australian Journal of Crop Science*, *5*(13), 1745.

[4] Misra SC, Rao VS, Dixit RN, Surve VD and Patil VP (1994) Genetic control of yield and its components in breadwheat. Indian Journal of Genetics 54:77-82.

[5] Farooq, J., Khaliq, I., Kashif, M., Ali, Q., & Mahpara, S. (2011). Genetic analysis of relative cell injury percentage and some yield contributing traits in wheat under normal and heat stress conditions. Chilean Journal of Agricultural Research, 71(4), 511.

[6] Mahmood, Z., Afzal, M., Ahmad, M., Munir, MA., Ali, MI., Sharif, MN., and Maqbool, R. (2016). Genetic analysis for morphological traits of *Euphorbia helioscopia*. Bull. Bio. All. Sci. Res., 1:5.

[7] Ali, MI., Mahmood, Z., Ahmad, M., Afzal, M., Munir, MA., Sharif, MN., and Shakeel, A. (2016). Genetic variability in *Cirsium arvensei* under different environmental conditions. Bull. Bio. All. Sci. Res., 1:3.

[8] Gai, J.Y. and J. K. Wang. (1998). Genetic system of quantitative traits in plants. Theor Appl Genet. 97: 1162-1168.

[9] Munir, MA., Ahmad, M., Ali, MI., Mahmood, Z., Afzal, M., Sharif, MN., and Aslam, M. (2016). Correlation and regression analysis of morphological traits in *Rumex dentatus*. Bull. Bio. All. Sci. Res., 1:2.

[10] Ahmad, M., Munir, MA., Mahmood, Z., Ali, MI., Afzal, M., Sharif, MN., and Khan, TM. (2016). Multivariate analysis for morphological traits of *Convulvularis arvensis*. Bull. Bio. All. Sci. Res., 1:4.

[11] Ahmad, A., and Tahir, M. (2017). Role of Zinc Sulphate for Maize (*Zea mays* L.) and Mungbean (*Vigna radiata* L. Wilczek) yield improvement: A review. Bull. Bio. All. Sci. Res., 2:1.

[12] Afzal, M., Ali, MI., Munir, MA., Ahmad, M., Mahmood, Z., Sharif, MN., and Aslam, M. (2016). Genetic association among morphological traits of *Lepidium draba*. Bull. Bio. All. Sci. Res., 1:1.

[13] Steel, R. G. D. and J. H. Torrie. (1984). Principles and procedures of statistics. McGraw-Hill book Co., Inc., New York, USA.

[14] Mather, K. and J. L. Jinks. (1982). Introduction to biometrical genetics. Chapman and Hall Ltd. London.

[15] Hayman, B. I. (1954a). The theory and analysis of diallel crosses. Genetics 32: 789-809.

[16] Hayman, B. I. (1954b). The analysis of variance of diallel crosses. Biometerics 10: 235-245.

[17] Ahmad, F., F. Mohammad, M. Bashir, saifullah and H. Khan. (2007). Inheritance of important traits in bread wheat over different planting dates using diallel analysis. Sarhad. J. Agric. 23(4):

[18] Prodanovic, S. (1993). Genetic values of F1 hybrids obtained in diallel crosses. Review of Res. Work at the Faculty of Agric., Belgrade 38(2): 25-37 (Wheat and Barley and Tritical Abstr. 11(6): 5292; 1994).

[19] Wagorie, W. W., O. Stolen and R. Ostiz. (1998). Combining ability analysis in bread wheat adapted to the east Africa highland. Wheat information service (Denmark). 8T: 39-41.

[20] Ma, S. F. (1988). An analysis of combining ability and heritability for agronomic characters in spring wheat parents. Ningxia J. Agro Forest. Sci. And Tech. 5: 22-24 (Pl. Br. Abstr, 59(5): 5546, 1989.

[21] Singh, R. K. and B. D. Chaudhary. (1985). Biometrical methods in Quantitative Genetic Analysis. Kalyani Pub., Ludhiana, New Delhi, Revised Ed. Pp. 102-118.

[22] Inamullah, H. Ahmad, F. Mohammad, S. U. Din, G. Hassan and R. Gul. (2006). Diallel analysis of the inheritance pattern of agronomic traits of bread wheat. Pak. J. Bot. 38(4): 1169-1175.

[23] Dagustu, N. (2008). Genetic analysis of grain yield per spike and some other agronomic traits in diallel crosses of bread wheat (Triticum aestivum L.). Turk. J. Agric. 32: 249-258.

[24] Rabbani, G., M. Munir, S. U. K. Ajmal, F. U. Hassan,G. Shabir and A. Mahmood. (2009). Inheritance of yield attributes in bread wheat under irrigated and rainfed conditions. Sarhad. J. Agric. 25(3): 429-439.