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GENETIC ANALYSIS OF YIELD RELATED TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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ABSTRACT

To study genetic behavior of yield and related traits Diallel analysis were carried out to evaluate the performance of eight wheat genotypes; viz., Fakhar e Sarhad, Ghaznavi-98, Takbeer, Tatara-98, SQ-92, ICP-3, Sare-3 and Dera-98, in a 8 × 8 diallel combinations. Data were collected on plant height, days to 50% heading, days to maturity, flag leaf area, fertile tillers plant^{-1} and grain yield plant^{-1}. Highly significant differences were observed among the genotypes for all the traits studied except flag leaf area. In diallel analysis additive effect "a" was highly significant for all the studied traits. The dominant effect "b" was non significant for all the traits except grain yield plant^{-1}. Analysis of genetic components revealed that additive genetic variations (D) were also significant for all the studied parameters except grain yield plant^{-1}. While dominant genetic variations (H) were significant in plant height, tillers plant^{-1} and grain yield plant^{-1} and was non-significant for other parameters. It was suggested from results that plant height, tillers plant^{-1} and grain yield plant^{-1} may be used as selection criteria traits for the improvement of wheat grain yield under water deficit conditions.

Keywords: Diallel, Wheat, Genetic Components, Dominance, Additive, Heritability

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. In our country, wheat is currently

grown on 9.0 million hectare land with annual production of 23.8 million tons. The present per capita consumption of wheat is 37.5 kg per anum [1]. Because of the rapid increase in the population growth rate, the demand for wheat is also increasing. On the other hand, land and water resources are being declined because of urbanization and industrialization. It is therefore, an intense need to increase wheat production within the available resources in order to meet the increasing demand for food. Thus the wheat breeders are concentrating to improve the yield potential by developing new cultivars having desirable genetic makeup to control the consumption pressure of ever increasing population [2-5]. 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 [6-8]. 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 [5, 9]. Various statistical analysis techniques help plant breeder for the selection of high yield crop genotypes [10-13]. Estimates of gene effects have a direct impact on the method of hybridization and selection to be adopted in breeding programs. Investigation of genetic parameters is useful in understanding the genetic consequences of hybridization and inbreeding. The present study was thus conducted to investigate the genetic background and to get information on gene action of these genotypes and their crosses before starting a systematic breeding program.

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 x 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). The experiment was replicated thrice in randomized complete block design (RCBD). All the F1s 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 plant height (cm), days to 50% heading, days to physiological maturity, flag leaf area (cm^2), fertile tillers $plant^{-1}$, and grain yield $plant^{-1}$ (g). The data collected were subjected to analysis of variance according to Steel and Torrie [14]. Diallel analysis [15] 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 [16, 17] and Mather and Jinks [15]. 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

All the data subjected to analysis of variance under rainfed conditions (Table 1) revealed highly significant differences for all the characters studied, except flag leaf area. Diallel analysis was carried out for those characters that showed significant genotypic variations.

PLANT HEIGHT

Analysis of variance for plant height (Table 2) revealed highly significant and greater amount of additive effect "a" variation while effect of dominance "b" was non significant. Components "b_1", showing the absence of directional dominance "b_2", "b_3" were non significant displaying, symmetry of gene distribution and specific genes respectively, for these parameters. Maternal effect "c" and reciprocal effect "d" were non significant, so no need of retesting "a" component and "b". It is revealed that additive effect D was significant while dominance effect H_1 was non-significant (Table 3). These results are similar to Wagorie *et al*., [18] who reported additive gene action for plant height. Variations due to dominant effect of genes

correlated with gene distribution H_2 was significant. The value of h^2 was significant, showing the presence of overall dominance effect due to heterozygous loci affecting the trait. While environmental effect E was also significant. Average degree of dominance showed the presence of additive gene action, as it is less than 1. Broad sense heritability estimates were high (Table 3) while narrow sense heritability was 51% under same conditions. This shows that half of the total inherited genetic portion was of dominance nature and half of additive nature. Ma, [19] and Dagustu, [8] also reported average estimates for broad sense heritability for plant height.

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

SOV	D.F.	Plant height (cm)	Days to heading	Days to maturity	Flag leaf area	Fetile tillers plant-1	Grain yield plant-1
Rep	2	19.92 ns	1.60ns	129.79*	186.91*	30.32*	22.33ns
Genotypes	63	50.97**	15.70**	7.19**	23.77ns	12.13**	63.22**
Error	126	19.65	1.89	3.19	23.67	8.25	49.58

***=Significant at 5% probability level, **=Significant at 1% probability level**

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

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	1537.05	219.57	7.51**	-	-
B	28	784.61	28.02	1.34ns		
b_1	1	305.04	305.04	3.87ns		
b_2	7	98.52	14.07	0.73ns		
b_3	20	381.04	19.05	1.02ns		
C	7	144.87	20.69	2.63ns		
D	21	744.72	35.46	1.88ns		
Total	63	3211.28				
a × blocks	14	409.14	29.22			
b_1 × blocks	2	157.61	78.80			
b_2 × blocks	14	269.69	19.26			
b_3 × blocks	40	740.32	18.50			
b × blocks	56	1167.62	20.85			
c × blocks	14	109.87	7.84			
d × blocks	42	790.51	18.82			
Total × blocks	126	2477.15				

*** $P \leq 0.05$ ** $P \leq 0.01$, 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 3: Estimates of genetic components of variation for plant height under rainfed conditions

Components	Means	Standard errors
D	18.28*	0.21
H_1	4.17ns	0.50
H_2	5.57*	0.44
F	0.23ns	0.52
h^2	41.61*	0.29
E	6.55*	0.07
$(H_1/D)^{1/2}$	0.47	
$H_2/4H_1$	0.33	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$	1.02	
Heritability (ns)	51.17	
Heritability (bs)	59.73	

*** 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**

DAYS TO HEADING

Complete analysis of variance following Mather and Jinks [15] for days to heading under rainfed conditions (Table 4) showed that the item "a" which measures additive gene effects, was highly significant and accounted for a highly proportion of the total variation. The overall dominance component "b" was non significant. Likewise significant "b_1" item indicated the directional dominance deviation of the genes. Symmetry of gene distribution among parents was represented by non significant "b_2" component. Non significant "b3" item shows the absence of the effect of specific genes. Influence of maternal effect (component "c") was highly significant, therefore requiring retesting of "a" item which turned non significant after retesting, while reciprocal effect (component "d") was non significant therefore no need of retesting of component b. The estimates of genetic components of variation exhibited (Table 5) the significant value of D component showed that days to heading were under the control of additive gene effect, while H component was non significant showing the absence of dominance effect. Additive gene action for this trait has also been reported by Singh *et al*., [20]. F value was also non significant. Unequal values of H_1 and H_2 indicated the presence of positive and negative alleles in unequal frequencies as H_1 shows the variation due to dominant effect of genes, while H_2 shows the variation due to dominant effect of genes correlated with gene distribution. This was also supported by the ratio of $H_2/4H_1$ that was less than 0.25. It was suggested that when genes are equally distributed among the parents, this value is equal to 0.25 [21]. Significant value of h^2 indicated the presence of overall dominance effect due to heterozygous loci affecting the expression of this trait. Presence of additive gene action was indicated by the value of average degree of dominance, which was less than 1 (when the value of average degree of dominance is more than 1, it shows dominance effect of gene action). The environmental component of variation E was significant. Rehman *et al*., [22] also reported high estimates of broad and narrow sense heritabilities for days to heading. High narrow and broad sense heritability estimates were also recorded (Table 5). Heritability in broad sense estimates the genetic proportion (additive + dominant + interaction) of the total phenotypic variation while heritability in narrow sense estimates only the additive proportion. Thus, broad-sense heritability estimates eventually are greater than narrow sense heritability. Thus in days to heading heritability were of additive nature.

Table 4: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for days to 50% heading

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	590.986	84.42	40.26**	1.43ns	-
B	28	69.92	2.49	1.64ns		
b1	1	24.91	24.91	25.32*		
b2	7	20.71	2.95	2.09ns		
b3	20	24.285	1.21	0.77ns		
C	7	234.33	33.47	28.12**		
D	21	60.50	2.88	1.12ns		
Total	63	955.74				
a × blocks	14	29.35	2.09			
b1 × blocks	2	1.96	0.98			
b2 × blocks	14	19.81	1.41			
b3 × blocks	40	63	1.57			
b × blocks	56	84.78	1.51			
c × blocks	14	16.66	1.19			
d × blocks	42	108	2.57			
Total × blocks	126	238.80				

*** 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 days to 50% heading under rainfed conditions

Components	Means	Standard errors
D	7.58*	0.21
H_1	0.67ns	0.50
H_2	0.40ns	0.44
F	0.97ns	0.52
h^2	3.35*	0.29
E	0.63*	0.07
$(H_1/D)^{1/2}$	0.29	
$H_2/4H_1$	0.15	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} –F$	1.55	
Heritability (ns)	822.46	
Heritability (bs)	84.88	

*** 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**

DAYS TO PHYSIOLOGICAL MATURITY

Analysis of variance for days to maturity (Table 6) showed highly significant additive "a" effect, while dominance effect "b" was non significant showing that additive effect was more than dominance effect. However, directional dominance "b_1" was absent which shows the deviation of the F_1s from their mid parental value. Non significant "b_2" shows the symmetry of gene distribution among parents, and "b_3" indicating no role of specific gene effects. Maternal effect "c" and reciprocal effect "d" were also non significant. Therefore no need of retesting the items a and b against c and d. Components of genetic variation (Table 7) depicted that additive D variation was significant while dominance H_1 and H_2 were non significant, unequal and negative as well. The value of H_2/H_4 was positive which for the

distribution of positive and negative alleles in the parents in rainfed conditions. Similarly F value was non significant and negative which shows that dominant genes were less frequent in the parents. The value of h^2 was non significant. However, significant value of E depicted the influence of the environment on the expression of this trait under water stressed conditions. The value of average degree of dominance is 1.02 indicating the presence of over dominant gene action. The narrow sense heritability was 50.55%, which shows the greater portion of additive inheriting variation. The results are suggesting that considerable involvement of both additive and dominant variation in the inheritance of days to maturity under rainfed conditions [23].

Table 6: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for days to maturity

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	251.78	35.98	8.06**	-	-
B	28	65.88	2.35	0.98ns		
b1	1	5.63	5.63	1.81ns		
b2	7	21.95	3.13	1.08ns		
b3	20	38.29	1.91	0.87ns		
C	7	50.45	7.20	1.96ns		
D	21	85.20	4.05	1.10ns		
Total	63	453.32				
a × blocks	14	62.43	4.45			
b1 × blocks	2	6.20	3.10			
b2 × blocks	14	40.53	2.89			
b3 × blocks	40	87.58	2.18			
b × blocks	56	134.32	2.39			
c × blocks	14	51.41	3.67			
d × blocks	42	154.91	3.68			
Total × blocks	126	403.09				

*** 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 7: Estimates of genetic components of variation for days to maturity under rainfed conditions

Components	Means	Standard errors
D	2.25*	0.12
H_1	-2.32ns	0.28
H_2	-1.88ns	0.24
F	-0.80ns	0.29
h^2	0.06ns	0.16
E	1.72*	0.04
$(H_1/D)^{1/2}$	1.02	
$H_2/4H_1$	0.19	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} –F$	0.45	
Heritability (ns)	50.51	
Heritability (bs)	32.05	

*** 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**

FLAG LEAF AREA

The results of flag leaf area were found non significant. Therefore its analysis was not been carried out (Table 1).

FERTILE TILLERS PLANT^{-1}

After carrying out formal diallel analysis (Table 8) it was observed that only the additive genetic effects "a" component were highly significant with unequal frequency of dominant genes among the parents and absence of directional dominance "b_1", maternal and reciprocal effects were non significant, i.e., c and d. so no need of retesting a and b against c and d. Genetic components of variation were computed (Table 9), and both additives D as well as dominant H_1 values were significant while H_2 was non significant. These results are in close agreement to Prodanovic, [24]. Rabbani *et al*., [25] and Inamullah *et al*., [26] also found similar genetic behavior of fertile tillers plant^{-1} and other morphological traits in his study. This value shows the distribution of positive and negative alleles in unequal frequencies among the parents. This was also supported by the ratio of $H_2/4H_1$ which was less than 0.25 as we know that this value will be 0.25 in case when the genes are equally distributed and in that case the value is 0.10. The significant value of F showed the greater frequency of dominant genes over recessive genes. The value of h_2 was significant, showing a substantial role of dominance effects at the heterozygous loci. Presence of over dominant gene action was indicated by the value of average degree of dominance, which was greater than 1. Environmental variation was also significant in fertile tillers plant^{-1}. Estimates of narrow and broad sense heritabilities showed that the inherited genetic variation was mainly contributed through dominance. Their values were 16.54 for narrow sense and 31.53 for broad sense.

Table 8: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for fertile tillers plant^{-1}

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	176.55	25.22	4.424**	-	-
B	28	346.16	12.30	1.18ns		
b1	1	50.84	50.84	5.27ns		
b2	7	160.75	22.94	1.50ns		
b3	20	134.56	6.72	0.76ns		
C	7	95.29	13.63	1.03ns		
D	21	146.31	6.96	1.50ns		
Total	63	764.32				
a × blocks	14	79.80	5.700			
b1 × blocks	2	19.27	9.635			
b2 × blocks	14	213.37	15.240			
b3 × blocks	40	349.85	8.746			
b × blocks	56	582.49	10.401			
c × blocks	14	183.65	13.118			
d × blocks	42	194.07	4.620			
Total × blocks	126	1040.02				

*** 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 9: Estimates of genetic components of variation for fertile tillers plant^{-1} under rainfed conditions

Components	Means	Standard errors
D	4.05*	1.17
H_1	6.10*	2.70
H_2	2.50ns	2.35
F	6.25*	2.77
h^2	6.16*	1.57
E	2.86*	0.39
$(H_1/D)^{1/2}$	1.22	
$H_2/4H_1$	0.10	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} –F$	4.39	
Heritability (ns)	16.54	
Heritability (bs)	31.50	

*** Value is significant when it exceeds 1.96 when it is divided by its std.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**

GRAIN YIELD PLANT^{-1}

Formal diallel analysis of variance for grain yield plant^{-1} under rainfed conditions (Table 10) revealed highly significant additive "a" and dominant "b" gene effects, the latter being maximum in magnitude. Highly significant b_2 value indicated the different distribution of genes among the parents while highly significant b_3 value displayed the important effect of specific genes. Maternal c and reciprocal effect d were also highly significant. After retesting the a and b against c and d. after retesting significance of a components remained unchanged indicating that maternal effects did not influence the additive genetic effects. All highly significant items have no response to retesting showing that reciprocal effects invalidated them. These findings are in close agreement with the previous findings of Inamullah *et al*., [26]. The estimates of genetic components of variation (Table 11) depicted that additive D genetic effect was non significant while dominant H genetic component was significant and positive as well. H_1 and H_2 values were necessarily equal in magnitude displaying uniformity of distribution of positive and negative alleles among parents. This was supported by $H_2/4H_1$ ratio (0.33), which was close to 0.25. F value was negative and non significant but ratio of dominant to recessive gene (1.55) suggested the greater frequency of dominant alleles. Value of h^2 was significant. Presence of additive gene action was indicated by the value of average of dominance (0.29 less than 1). Broad sense heritability was much greater than the narrow sense one variation. Ahmad *et al*., [23] and Misra *et al*., [27] also obtained same genetic behavior for grain yield plant^{-1} in different generations of bread wheat.

Table 10: Mean squares and degree of freedom for the analysis of variance of 8 × 8 diallel for grain yield plant^{-1}

Source	df	SS	MS	F	Re-testing against	
					C	D
A	7	532.57	76.08	4.424**	-	-
B	28	2157.66	77.06	1.18ns		
b1	1	1.81	1.81	5.27ns		
b2	7	210.31	30.04	1.50ns		
b3	20	1945.54	97.28	0.76ns		
C	7	308.13	44.02	1.03ns		
D	21	984.27	46.87	1.50ns		
Total	63	3982.62				
a x blocks	14	759.24	54.23			
b1 x blocks	2	79.25	39.62			
b2 x blocks	14	562.15	40.15			
b3 x blocks	40	1704.65	42.62			
b x blocks	56	2346.06	41.89			
c x blocks	14	807.63	57.69			
d x blocks	42	2334.09	55.57			
Total x blocks	126	6247.02				

*** 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 11: Estimates of genetic components of variation for grain yield plant^{-1} under rainfed conditions

Components	Means	Standard errors
D	-7.62ns	5.47
H_1	13.83*	12.59
H_2	18.60*	10.95
F	-14.64ns	12.94
h^2	-6.90*	7.34
E	6.57*	1.82
$(H_1/D)^{1/2}$	0.29	
$H_2/4H_1$	0.33	
$(4DH_1)^{1/2} + F/(4DH_1)^{1/2} – F$	1.55	
Heritability (ns)	0.05	
Heritability (bs)	0.26	

*** 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 genetic component of additive **D** effect were significant for days to heading, days to maturity, plant height, tillers plant^{-1} while the component for dominance **H** was found significant for plant height, tillers plant^{-1} and grain yield plant^{-1}. It was suggested that the traits days to heading, days to maturity, plant height, tillers plant^{-1} may be use for selecting genotypes to develop synthetic varieties while plant height, tillers plant^{-1} and grain yield plant^{-1} may be used to develop hybrid wheat under water deficit condition.

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