Research Article

Inheritance Studies of Yield and Yield Related Traits in Bread Wheat Genotypes

Sher Nawab Khan* and Ghulam Hassan

Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, Khyber Pakhthunkhwa, Pakistan.

Abstract | Plants contribute almost 93% of food and among the crops wheat has the largest contribution of about 80% to the total global cereal production. Eight wheat cultivars including a land race were crossed in 8×8 full diallel fashion during 2014-15 wheat growing season. In the succeeding crop season all the 56 F1 hybrids and their parents were evaluated during 2015-16 to study inheritance pattern of yield and yield related traits at Peshawar-Pakistan. Data were generated on spikelets spike^{-1}, spike length (cm), days to heading and grain yield plant^{-1}. Significant differences were present for all the studied parameters. In diallel analysis highly significant dominant (b) and additive (a) genetic effects were detected for all the parameters except spikelets spike^{-1}. Scaling test for the adequacy of the model was complete to partially adequate for the studied parameters. Similarly, both dominant (H) and additive (D) genetic components were observed significant for the studied characters. Moderate to high broad and narrow sense heritability was recorded for the studied traits which indicated the expression of additive gene effect for controlling the inheritance of these traits.

Introduction

Among the cereal crops bread wheat is the most common staple food in Pakistan due to its wider adoptability and unique chemical and physical properties (Minhas et al., 2014). The average wheat yield of Pakistan is however lower than developed countries (Pervez et al., 2014). To ensure food security of growing population management of resources such as breeder's efforts for the production of high yielding varieties are very important (Irshad et al., 2014; Ullah et al., 2010). Development of high and stable yielding varieties for target environment required information of gene action of yield components which allow better choice of breeding methods to select genetically suitable parents (Ljubičić et al., 2017). Among the mating designs diallel is a useful tool for genetic analysis and computation of components of variations and nature of gene action (Ahmad et al., 2011). The diallel cross technique was developed for the first time by Hayman (1954a) and Jinks (1954) to study F_1 generation for important genetic information of plants to devise suitable breeding strategies (Minhas et al., 2014). Diallel is a set of crosses produced by mating selected homozygous genotypes in all combination. The "n" number of genotypes crossed in such pattern produce "n²" progeny families (Singh and Chaudhury, 1985) which provides perfect information about significant non-additive or additive variation (Ahmad et al., 2017). The present study was design to extract genetic information and mode of gene action for yield and yield traits using F1 cross combinations derived from diallel mating design in wheat.

Materials and Methods

In this study eight wheat (*Triticum aestivum* L.) genotypes i.e. Atta-Habib (AH), Lalma-13 (Lal-13), Tatara-96 (Tat-96), Punjab-11 (PJ-11), Pirsabak-2005 (PS-05), Pirsabak-2013 (PS-13), Janbaz (JB) and a land race Khatakwal (KW) were crossed in 8×8 full diallel fashion during 2014-15 wheat crop growing season. In the next crop growing season during 2015-16 parents along with their 56 F_1 hybrids were evaluated for yield and yield associated traits at The University of Agriculture, Peshawar. Data were recorded on spike length (cm), spikelets spike^{-1}, days to 50% heading and grain yield plant^{-1} (g). Analysis of variance (ANOVA) was conducted according to Steel et al. (1980). On the basis of significant genotypic differences additive-dominance model was applied, as described by Mather and Jinks (1977). After ordinary analysis of variance, according to Hayman (1954a) and Jinks (1954) genetic components of variance were computed. In graphical representation a regression line was draw within the limiting parabola using variance (Vr) and covariance (Wr) as described Mather and Jinks (1982). The trail was conducted in a randomized complete block (RCB) design with three replications. Each entry was comprised of two rows having row length of 2 meters while row to row and plant to plant distances were maintained 30 and 15 cm, respectively. Recommended inputs and standard agronomic practices were applied. Data were recorded on spike length (cm), spikelets spike^{-1}, days to 50% heading and grain yield plant-1 (g). Analysis of variance (ANOVA) was conducted according to Steel et al. (1980). On the basis of significant genotypic differences additive-dominance model was applied, as described by Mather and Jinks (1977). After ordinary analysis of variance, according to Hayman (1954a) and Jinks (1954) genetic components of variance were computed. In graphical representation a regression line was drawn within the limiting parabola using variance (Vr) and covariance (Wr) as described Mather and Jinks (1982).

Results and Discussion

Significant variation among the genotypes was observed for all the studied characters (Table 1). Similar findings of significant variation among different wheat cultivars for various traits have also been reported by Ahmad et al. (2016).

Days to 50% heading

Additive gene effect 'a' and dominance component 'b' were highly significant for days to heading (Table 3). The overall dominance component 'b' was smaller than additive component in magnitude which shows important role of dominant genes on days to heading. Directional dominance deviation b1 and maternal effect 'c' was observed non-significant. Highly significant b2 indicated asymmetry of gene distribution. Similarly, controlling the inheritance significant b3 showed vital role of specific genes. Reciprocal component 'd' was also recorded highly significant and required re-testing of 'b' component against 'd'. After re-testing highly significant items b, b2, b3 and non-significant b1 remain unchanged and suggested that reciprocal effects did not affected asymmetry of gene distribution among the parents (Table 3). Similar findings of additive gene distribution for days to heading were also published by Singh et al. (2004) and Farooq et al. (2014) while, studied gene action of quantitative characters in different wheat genotypes. Both scaling tests of additive-dominance model was carried out according to Mather and Jinks (1982). Regression analysis invalidated the model but uniformity of Vr and Wr showed adequacy of the model and remain partially adequate for this trait (Table 2).

Table 1: *Analysis of variance for various traits.*

	Reps	Genotypes	Error	CV%
Character	(d.f= 2)	(d.f= 63)	(d.f=126)	
Days to heading	5.86	8.58**	1.34	0.97
Spike length	2.63	1.22**	0.33	5.28
Spklets spike^{-1}	0.52	4.35**	1.55	6.39
Grain yield plant $^{-1}$	11.16	36.88**	2.83	6.33

**: *P < 0.01*

Table 2: *Adequacy test of 8 × 8 diallel cross of wheat genotypes.*

Characters	Uniformity of Wr and Vr (t²)	Regression analysis		Remarks
		b = 0	b = 1	
Days to heading	0.040[nS]	2.191[ns]	0.818[ns]	Model was partially adequate
Spike length	1.113[ns]	4.753**	-0.759[ns]	Model was fully adequate
Spikelets spike^{-1}	1.435[ns]	3.098*	-0.556[ns]	Model was fully adequate
Grain yield plant^{-1}	0.047[ns]	2.983*	0.564[ns]	Model was fully adequate

*: *significant;* ****:** *highly significant and* **ns:** *non-significant;* **Wr:** *Covariance of array;* **Vr:** *variance of array,* **t²:** *test of uniformity of Wr and Vr;* **b:** *regression coefficient.*
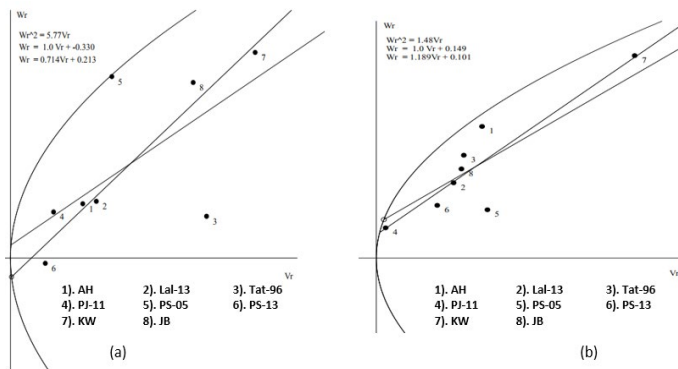
Figure 1: *Wr/Vr graphs,* **a)** *Days to heading, and* **b)** *Spike length.*

Significant dominant (H) and additive (D) components suggested contribution of both dominant and additive gene for days to heading. However, the magnitude of D was observed smaller than H which showed preponderance of dominance genes. Unequal distribution of negative and positive alleles was confirmed by unequal values of H_1 and H_2 which was further confirmed by $H_2/4H_1$ ratio having value less than 0.25. According to Singh and Chaudhury (1985), $H_2/4H_1$ ratio should be equal to 0.25 in case of equal genes distribution. The role of dominant genes for days to heading was confirmed by positive and significant value (5.30) of F, which was also supported by dominant to recessive genes ratio (2.42). Non-significant h^2 values indicated absence of overall dominance effects due to heterozygous loci. Dominant to recessive ratio was more than 1 which shows the importance and greater percentage of dominant genes. Non-significant E indicated the absence of environmental effects. Average degree of dominance showed over-dominant gene action having value greater than 1 for this character which is the compatible into the findings of Rabbani et al. (2009) they also reported over-dominant gene action for this trait. Negative intercepts of Wr/Vr regression line indicated over dominance gene action (Figure 1a). Similar findings of over-dominance gene action for this trait have been reported by Ahmad et al. (2011), Farooq et al. (2014) and Rashid et al. (2012) have reported partial dominance for days to heading using different wheat genotypes. High broad sense (88.7%) and moderate narrow sense (41.8%) heritability was estimated for days to heading (Table 4) which indicated dominant nature of greater proportion of the heritable variation. Similar findings have been reported by Eid (2009) for days to heading while studied different wheat genotypes. Array points displayed that PS-13, PJ-11, AH and Lal-13 were near to the origin having more dominant genes for heading while genotypes

KW and JB were far away from the origin with less numbers of dominant genes (Figure 1a).

Spike length (cm)
Highly significant dominant (b) and additive (a) genetic effects were observed for spike length (Table 3) additive effects were however observed greater than dominant gene effects. Significant 'b3' showed role of specific genes while non-significant item 'b1', 'd' and 'c' showed absence of dominance deviations, reciprocal and maternal effect. Both scaling tests showed fully adequacy of the model (Table 2). Highly significant 'b2' and 'b3' showed symmetrical gene distribution and role of specific genes while significant item b1 indicated directional dominance deviation of genes. Non-significant (c) showed the absence of maternal effects while reciprocal effects (d) was observed significant and retesting changed only b1 from significant to non-significant. Non-significant b1 indicated suppression of dominance deviation of gene action by maternal effect (Table 3) while Fida et al. (2008) reported non-significant maternal effects for spike length using wheat genotypes.

Genetic component of variation showed significant dominant (H) and additive (D) gene effects (Table 4). Unequal proportion of positive and negative alleles were confirmed by the presence of unequal magnitude of H_1 and H_2. The ratio of $H_2/4H_1$ further confirmed unequal genes distribution having value 0.136 which was less than 0.25. Significant and positive F value suggested the presence of dominant genes for spike length which was further confirmed by dominant to recessive genes ratio having value (4.04). Ratio > 1 suggests proportion of more dominant genes (Farshadfar and Amiri (2015)). Significant E indicate role of environmental effects while average degrees of dominance suggested partial dominance gene action and non-significant h^2 indicate absence of dominance effects due to heterozygous loci. Fida et al. (2008) reported similar findings of over-dominance gene action for spike length in bread wheat genotypes.

Positive intercept of regression line for spike length showed partial dominance gene action (Figure 1b). Similar results of partial dominance gene action have been reported by Zare-Kohan and Heidari (2014) while over-dominant gene action has been published by Ullah et al. (2006) and Rabbani et al. (2009). Several researchers reported both dominant and additive gene action for spike length under different wheat

Table 3: *Analysis of variance for various traits in wheat 8 × 8 diallel crosses at Peshawar during 2015–16.*

SOV	d.f.	Days to heading MS	Retested against d	Spike length MS	Spikelets spike⁻¹ MS	Retested against c	d	Grain yield plant⁻¹ MS	Retested against d
a	7	28.85**		6.36**	11.66**	13.33**		161.21**	
b	28	8.76**	5.51**	0.97**	2.85 ns		3.26**	35.21**	7.54**
b₁	1	8.05 ns	5.06 ns	0.00 ns	3.11 ns		3.55 ns	9.02 ns	1.93 ns
b₂	7	8.46**	5.32**	1.82**	2.63 ns		3.00*	24.27**	5.20**
b₃	20	8.90**	5.60**	0.73*	2.91 ns		3.33**	40.35**	8.64**
c	7	1.25 ns		0.15 ns	1.30*			3.88 ns	
d	21	1.59**		0.10 ns	0.87**			4.67**	
Total	63	7.77		1.19	3.01			35.55	

*: significant; **: highly significant and **ns**: non-significant; **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 and **d**: reciprocal effect.

Table 4: *Estimates of genetic components of variation for various traits in wheat 8 × 8 diallel crosses at Peshawar during 2015–16.*

Genetic components	Days to heading	Std. Errors	Spike length	Std. Errors	Spikelets spike⁻¹	Std. Errors	Grain yield plant⁻¹	Std. Errors
D	5.75*	0.788	1.46*	0.086	1.84*	0.296	25.06*	2.389
H₁	7.10*	1.811	0.84*	0.198	1.34*	0.68	27.59*	5.493
H₂	5.22*	1.576	0.46*	0.173	1.01ns	0.592	22.06*	4.779
F	5.30*	1.862	1.34*	0.204	1.30ns	0.699	17.33*	5.646
h²	1.04ns	1.057	-0.04ns	0.116	0.26ns	0.397	1.01ns	3.205
E	0.31ns	0.262	0.095*	0.028	0.442*	0.098	0.71ns	0.796
(H₁/D)¹ᐟ²	1.11		0.759		0.854		1.05	
(H₂/4H₁	0.18		0.136		0.189		0.2	
(4DH₁)¹ᐟ² +F/(4DH₁)¹ᐟ²-F	2.42		4.046		2.42		1.98	
h²(ns)	41.85		54.69		38.23		51.57	
h²(bs)	88.77		79.48		60.76		94.47	

*: significant; **ns**: non-significant; **D**: additive effect; **H₁** and **H₂**: dominance effect; **F**: frequencies of dominant to recessive alleles; **h²**: overall dominance effect due to heterozygous loci; **E**: shows environmental effect.

genotypes. High broad sense (79.4%) and moderate narrow sense (54.6%) heritability was computed for spike length (Table 4). Such findings of high heritability for spike length were also estimated by Rabbani et al. (2009). Genotypes PJ-11, PS-13 and PS-05 were located near to the origin with maximum number of dominant genes while cultivar KW was far away from the origin having less dominant genes (Figure 1b). The remaining genotypes were located more towards the origin. Ullah et al. (2006) also reported the presence of dominant and recessive genes for controlling the inheritance of this trait.

Spikelets spike⁻¹

Diallel analysis indicated highly significant, additive gene effect (a) for spikelets spike⁻¹ (Table 3). Non-significant item b3, b2, b1 and b showed the absence of specific genes effect, symmetrical gene distribution, directional dominance deviation and dominant genes effect, respectively. Significant 'd' and 'c' showed the presence of reciprocal and maternal effects. Retesting of 'a' against 'c' remain unchanged. The significance of 'a' and 'b' against 'd' changed b2, b3 and b from non-significant to significant level which indicate role of reciprocal effect on this trait whereas b1 remained unchanged. Both scaling test confirmed fully adequacy of the model (Table 2). For adequacy of the model such findings for spikelets spike⁻¹ in wheat genotypes were also reported by Akram et al. (2009).

Diallel analysis revealed significant dominant (H) and additive (D) genes effects (Table 4). Unequal proportion of positive and negative alleles were confirmed by unequal magnitude of H₁ and H₂. The ratio

of $H_2/4H_1$ (0.18) also depicted unequal genes distribution. Non-significant F and h^2 indicate the absence of dominance effect and overall effects due to heterozygous loci. The ratios of dominant to recessive genes were 2.42. Significant E indicated influence of environment in the expression of this trait. Average degrees of dominance (0.854) suggested partial dominance gene action. In graphical representation positive intercept of regression line showed partial-dominance gene action (Figure 2a). These findings are strongly supported by the findings of Ullah et al. (2010). They also reported additive with partial dominance gene action while Akram et al. (2009) reported over-dominance gene action for spikelets spike^{-1}. High (60.7%) broad sense and moderate (38.2%) narrow sense heritabilities were recorded for spikelets spike^{-1} (Table 4). High broad sense heritability for spikelets spike^{-1} have also been observed by Ullah et al. (2006). In graphical representation cultivar PS-13 and PJ-11 were located nearest to the origin having more dominant genes while cultivar PS-05 was far away with less dominant genes for spikelets spike^{-1} (Figure 2a).
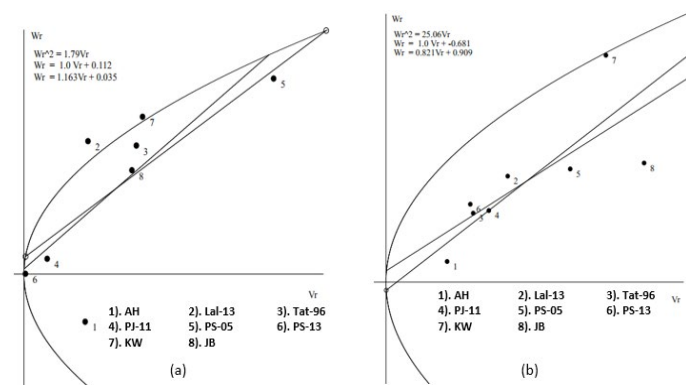

Figure 2: *Wr/Vr graphs,* **a)** *Spikelets spike^{-1} and* **b)** *Grain yield plant^{-1}.*

Grain yield plant^{-1} (g)

Diallel analysis showed significant dominant (b) and additive (a) gene effects for grain yield plant-1 (Table 3). Highly significant b3 and b2 components showed presence of specific genes and asymmetrical gene distribution among the parents while non-significant b1 showed the absence of dominance deviation. Reciprocal effect 'd' was observed significant and required retesting while maternal effect (c) was observed non-significant. After re-testing of 'b' component against 'd', significance of b_1, b_2 and b_3 components were not changed. Such consistency revealed the absence of reciprocal effects on dominance, role of specific genes and directional dominance, respectively for grain yield. Both the adequacy tests validated the model for grain yield (Table 2). Yield is in agreement with the findings of Ahmad et al. (2017b).

Dominant (H) and additive (D) components of variation were observed significant (Table 4). However, dominance variation was greater in magnitude than additive. Unequal values of H_1 and H_2 showed unequal distribution of positive and negative alleles which was further confirmed by ratio of $H_2/4H_1$ (0.20), which was less than 0.25. Significant and positive F value revealed the presence of more dominant genes. Ratio of dominant to recessive genes having value 1.98 indicated the presence of more dominant genes for grain yield. Non-significant h^2 showed the absence of dominance effects due to heterozygous loci while significant (E) indicated influence of environment on grain yield. Average degrees of dominance value were 1.05 which indicate over-dominant gene action for grain yield. The value of average degree of dominance > 1 implied the presence of over-dominant gene action (Ullah et al., 2006).

Negative intercepts of regression line in Wr/Vr graph showed over-dominance type of gene action for grain yield (Figure 2b). Over-dominance type of gene action for this trait has previously been reported by Chowdhry et al. (2002). Khan et al. (2000) and Ahmad et al. (2017b) reported additive gene action with partial dominance for this trait. Heritability serves as selection criteria for various traits. Moderate (51.5%) narrow and high (94.4%) broad sense heritabilities were estimated which showed the preponderance of non-additive gene (Table 4). High broad sense heritability was also computed by Ahmed et al. (2016) while moderate narrow sense heritability was reported by Farshadfar et al. (2014) for grain yield in bread wheat.

Location of array points indicated that cultivar AH was nearest to the origin with maximum numbers of dominant genes while land race KW was far away having more recessive genes (Figure 2b). The remaining parents were located closer to the origin having preponderance of dominant genes for grain yield. Similar findings of dominant genes in wheat genotypes have been reported by Ullah et al. (2010). Rabbani et al. (2009) however reported both dominant and recessive genes for this trait were published by for different wheat genotypes. Overall the study showed that both dominant and additive gene action were involved for controlling inheritance of the desired traits

and improvement is possible through selection in segregating generations.

Conclusions and Recommendations

This study revealed the involvement of dominant and additive gene action in controlling the inheritance of yield and yield associated traits. Improvement for the desired traits is possible through efficient selection in the succeeding segregating generations to develop high yielding cultivar(s).

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Author's Contribution

Sher Nawab Khan: Conducted the experiment, compiled and analysed the results and wrote the paper.
Ghulam Hassan: Designed the experiment, proof read and revised the manuscript.

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