Research Article

Genetic Analysis of Important Morphological Traits Using Diallel Analysis in Wheat

Mian Ahmad Raza*, Ghulam Hassan and Naqib Ullah Khan

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

Abstract | This study was performed to investigate combining ability effects and gene actions for some important traits using diallel mating design in wheat at Peshawar Pakistan. Eight wheat genotypes viz. Janbaz (JNB), Fakhr-i-Sarhad (FS), Pirsabak 2005 (PS), AUP-5008 (AUP), Saleem 2000 (S2K), Tatara (TTR), Barsat (BST) and Siren (SRN) were crossed in all possible combinations during 2011-12 cropping season. The resultant F_1 hybrids were planted following a randomized complete block design using three replications in the subsequent wheat growing season of 2012-13. For days to maturity, F_1 cross combination PS × FS among the F_1 hybrids showed earliness (160.7) whereas F_1 cross combination BST × SRN and JNB × BST ranked first among the crosses for spike length (15.9 cm). Among the F_1 hybrids, FS × SRN and TTR × BST displayed maximum spikelets spike^{-1} (24.3) whereas for F_1 cross combinations, FS × SRN and TTR × BST had the highest number of grains spike^{-1} (58.9). The results of inheritance studies discovered that both additive and dominance type of inheritance mechanism was involved in the expression for maturity trait, plant stature, spike length, spikelet spike^{-1} and grains spike^{-1}. Negative intercept of regression line indicated the major role of over-dominance in the inheritance of plant height, spikelets spike^{-1} while for grains spike^{-1} the positive intercept of regression line indicated predominance of partial dominance in inheritance. F_1 cross combination FS × JNB were observed as good specific combiners for spike length, while hybrids FS × SRN and BST × S2K were revealed as good specific combiners for spikelets spike^{-1} and grains spike^{-1}, respectively. These F_1 cross combinations being good specific combiners for specific traits could be utilized in future breeding programs for the improvement of desired traits.

Introduction

Bread wheat (*Triticum aestivum* L.) is the staple food crop of the world. On global basis, about 218.46 million hectares were planted which produced about 713.2 million tons of wheat (FAOSTAT, 2014). It is also one of the major food crops of Pakistan. It occupied an area of 8.7 million hectares with a total production of 24.2 million tons (PBS, 2014). To meet the feed requirement of ever increasing population of Pakistan, there is a dire need to improve existing wheat cultivars with high yield potential. This could be accomplished by merging the appropriate characters from existing wheat germplasm through hybrid-

ization programs to develop desirable high yielding cultivars. In wheat improvement programs, knowledge of gene actions controlling the desired characters to be improved is desirable. The behavior and extent of gene action is an important factor for developing effective breeding program. Stuber, (1970) suggested that genetic models estimating additive, dominance and additive × additive interactions are realistic for the analysis of quantitative variation in most of the self-pollinated crops. Diallel crossing scheme could be used to understand the nature and magnitude of genetic variability among the group of genotypes. For the first time Schmidt, (1919) introduced a procedure which involved crossing a set of parental genotypes in such a way to produce all possible combinations including their reciprocals assessing genetic variation ascribable to the differences among the parental lines. Latter on diallel analysis proposed by Hayman, (1954a, 1954b, 1958), Jinks, (1954) and Jinks and Hayman, (1953) provided an efficient approach for the identification of desirable parents and crosses. It also and helps the plant breeders to identify the effective method of selection for isolation of superior genotypes among the hybrid populations.

Combining ability analysis is one of the authoritative method to estimate the general combining ability (GCA) and specific combining ability (SCA) effects which in turn helps to identify the desirable parents and crosses for utilization in breeding programs. The GCA helps in identification of superior parental genotypes whereas SCA identifies potential commercial hybrids for the desired traits. Selection of potential parents on the basis of GCA effects could produce superior recombinants through crossing with other counterparts. In this context combining ability analysis of the breeding material assumes vital importance for yield and yield associated traits. The concept of combining ability also helps the breeder to understand the nature of gene action. In view of importance of combining ability effects and nature of gene actions in controlling the expression of morphological traits in wheat breeding programs, the present study was conducted with the following broad objectives using F_1 diallel cross combinations and their parents.

I.   To determine the gene actions in controlling the expression of important morphological traits.

II.   To assess the general combining ability potential of parents and specific combining ability of F_1 crosses for various morphological traits.

Materials and Methods

The study was conducted at the Research Farm of The University of Agriculture Peshawar, Pakistan. During the first year of study (2011-12) the eight parental genotypes (Table 1) were planted under field conditions in a crossing block. At least 50 spikes for each of the 56 crosses (28 direct and 28 reciprocals) were manually emasculated and pollinated to have enough seed for the next planting season. All the 56 F_1's along with 8 parents were grown in next wheat growing season following randomized complete block design with three repeats. In each replication, each of the 64 genotypes (F_1's and parents) were planted in a single row while row-row and plant-plant distances of 25 cm and 10 cm respectively were maintained. Uniform cultural practices were used throughout the growing season for the experiment to reduce experimental error.

Table 1: *List of wheat genotypes used to develop F_1 crosses.*

Parent	Pedigree	Abbreviation used
Janbaz	Gen*2//Buc/Filk/3/Buchin	JNB
Fakhr-i-Sarhad	PFAU'S'/SERI//BOW'S'	FS
Pirsabak 2005	MUNIA/CHTO//AMSEL	PS
AUP-5008	OTUS/TOBA97	AUP
Saleem 2000	CHAM-6//KITE/PGO	S2K
Tatara	JUP/ALD "S" // KLT "S"/3VEE"S"	TTR
Barsat	FRET2	BST
Siren	PBW343*2/KUKU	SRN

Statistical analysis

The obtained data was analyzed following the analysis of variance (ANOVA) technique as narrated by Steel and Torrie, (1980) using MSTAT-C computer software. The null hypothesis was tested for no differences among various F_1 hybrid combinations and their parental genotypes. After significance of the afore mentioned test, Least Significant Difference (LSD) test was also used for separation and comparison of means. The significant data of all the studied parameters on 56 F_1 and eight parental genotypes attained after ANOVA was further analyzed following the combining ability analysis approach as according

to Griffing's, (1956) Method-I based on Eisenhart's Model-II (Singh and Chaudhary, 1979).

Result and Discussion

Days to maturity

The studied genotypes showed significant differences (p<0.05) for days to maturity (Table 2). Life duration of any plant is important to plane its rotation with other crops and overcome climatic hazards. According to Capristo et al. (2007) reproductive growth of wheat would occur under more favorable conditions in short-seasoned cultivars. Early maturing wheat genotypes are highly focused throughout the world. For the adaptability of wheat to different environments and geographical parts, maturity trait is considered as a critical parameter (Kohan and Heideri, 2012). Among the parental genotypes, FS and S2K took maximum (175.33) and minimum (163.7) number of days to maturity, respectively. Among the F_1 hybrids, the highest number of days to maturity was recorded for cross combination S2K×TTR (174.7) while the lowest (160.7) were observed for cross combination PS×FS (Table 3). Hayman analysis indicated the importance of both additive and dominance genetic effects of variance for days to maturity as both items 'a' and 'b' were found highly significant. Absence of maternal effects (c) and reciprocal effects (d) was also

Table 2: *Mean square values from ANOVA regarding various characters studied in 8 × 8 diallel crosses of wheat.*

Traits	Mean squares			
	Genotype (df= 63)	Replication (df =2)	Error (df =126)	CV %
Maturity Days	31.4*	19.3	11.8	2.0
Plant height	60.1 *	1286.0	42.4	7.7
Spike length	1.7**	7.3	0.57	6.3
Spikelets spike^{-1}	3.8**	8.6	1.6	6.1
Grains spike^{-1}	13.9**	41.6	7.9	5.1

*NS = Non-significant; ** = Highly significant at 0.01 level of probability; * = Significant at 0.05 level of probability*

Table 3: *Mean values of parents and their F_1 hybrids for various traits in 8 × 8 diallel crosses of wheat.*

Traits	Parental Means	Parental Ranges	F_1 Means	F_1 Ranges	Best F1's
Days to maturity	169.7	163.7 (S2K)-175.3 (FS)	169.5	160.7 (PS×FS) -174.7 (S2K×TTR)	PS×FS (160.7); AUP × PS (163.7); SRN × BST (164.3); AUP × SRN (165)
	Grand Mean	169.6	LSD $_{(0.05)}$ 5.5	CV 2.02	
Plant height (cm)	82.6	75.5 (S2K)-89.6(PS)	87.1	75.5 (AUP ×PS)- 95.9 (BST × PS; JNB × SRN)	AUP ×PS (75.5); S2K×TTR (76.9); AUP × BST (80); S2K × AUP (80.1) SRN × S2K (80.2)
	Grand Mean	86.5	LSD $_{(0.05)}$ 10.5	CV 7.5	
Spike length (cm)	11.7	10.9 (TTR)-12.7 (SRN)	12.0	10.9 (AUP × TTR) -15.9 (BST × SRN; JNB × BST)	BST × SRN (15.9); JNB × BST (15.9); PS × BST (13.5); JNB × FS (13.3)
	Grand Mean	12.0	LSD $_{(0.05)}$ 1.65	CV 8.5	
Spikelet spike^{-1}	20.0	18.3 (SRN) -22.1 (JNB)	20.9	17.6(S2K × SRN)- 24.3 (FS × SRN; TTR × BST)	FS × SRN (24.3); TTR × BST (24.3); JNB × PS (22.1); BST × S2K (22.1); AUP × JNB (22.1)
	Grand Mean	20.8	LSD $_{(0.05)}$ 2.0	CV 6.1	
Grains spike^{-1}	52.9	47.5 (TTR)-56.5 (JNB)	54.7	47.5 (AUP ×TTR)- 58.9 (FS × SRN; TTR × BST)	FS × SRN (58.9); TTR × BST (58.9); S2K × FS (58.3); BST × S2K (57.8); JNB × PS (57.8)
	Grand Mean	54.5	LSD $_{(0.05)}$ 4.5	CV 5.2	

revealed by non significant values of c and d items (Table 4). In a previous study Sami-Ullah et al. (2010) also described additive type of genetic mechanism coupled with partial dominance being responsible for the control of days to maturity trait in wheat.

Values regarding D, H_1 and H_2 were observed significant for days to maturity. Irregular dispersal of dominant genes among the parents was displayed by imbalanced values of H_1 and H_2. It was further supported by the ratio of $H_2/4H_1$, which was observed less than 0.25 implying the genes were equally distributed among the parents (Singh and Chaudhary, 1979). Non significant and negative value of 'F' indicated that the frequency of dominant genes was lower. Heterozygous loci effect for days to maturity was revealed by significant value of h^2. The environmental component 'E' was also observed significant indicating influence of environment. Complete dominance for studied trait was observed when value of $(H_1/D)^{1/2}$ the average degree of dominance was equal to 1.00. Low narrow and medium broad sense heritability estimates were estimated for trait under study (Table 5). Vr/Wr graph revealed that JNB had the most dominant genes as this genotype was nearer to the origin while F.S possessed the most recessive genes for days to maturity being placed far away from origin. Both S2K and AUP occupied intermediate position showing equal contribution of both dominant and recessive type of genes for days to maturity (Figure 1).

Results regarding all the three components of combining ability i.e. GCA, SCA and reciprocal effects were found highly significant for days to maturity (Table 6). It was also evident that additive, non-additive and maternal effects were involved in the ex pression of days to maturity. In previous studies conducted by Walton, (1971) and Kohan and Heidari, (2012) also observed similar results for controlling the expression
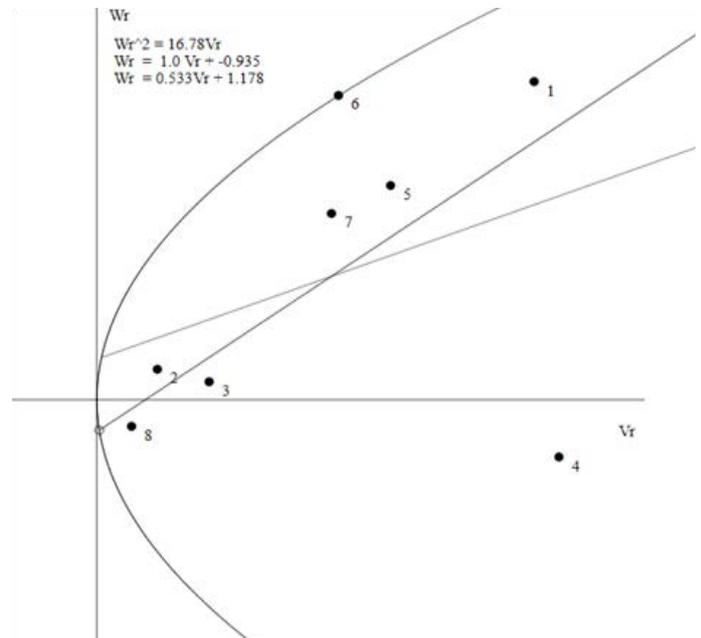

Figure 1: *The Vr/Wr graph regarding days to maturity explaining type of dominance and genotypes with dominant and recessive genes*
1=FS; 2= BST; 3= SRN; 4= PS; 5= S2K; 6= AUP; 7= TTR; 8= JNB

Table 4: *Mean squares using Hayman's analysis of variance for various traits in 8 × 8 diallel of wheat.*

Traits	a df=7	b df=28	b_1 df=1	b_2 df=7	b_3 df=20	c df=7	d df=21
Days to maturity	56.5**	27.6**	0.50 NS	32.7 NS	27.1**	31.0 NS	28.4 NS
Plant height	210.2**	57.6**	328.2 NS	12.5 NS	59.9**	78.6 NS	41.7 NS
Spike length	4.6**	1.1**	2.7 NS	0.51 NS	1.2**	1.5 NS	1.6 NS
Spikelet spike⁻¹	6.0**	4.1**	18.4 NS	2.5 NS	3.9**	2.3 NS	3.4 NS
Grains spike⁻¹	45.1**	11.1**	67.4 NS	9.7 NS	8.8**	14.9 NS	6.7 NS

Table 5: *Estimates of genetic components for various traits in in 8 × 8 diallel crosses of wheat.*

Traits	D	F	H_1	H_2	h^2	E	$(H_1/D)^{1/2}$	$H_2/4H_1$	$\frac{(4DH_1)^{1/2}+ F}{(4DH_1)^{1/2}- F}$	$h^2_{(ns)}$	$h^2_{(bs)}$
Days to maturity	15.4*	17.2 NS	15.7*	10.5*	-1.7*	3.9*	1.0	0.1	3.4	0.22	0.53
Plant height	-3.7*	-28.3 NS	-14.9*	-2.7*	38.9*	20.5*	2.0	0.04	-0.3	0.24	0.21
Spike length	-0.1 NS	-0.5 NS	-0.2 NS	-0.1 NS	0.2 NS	0.4*	1.7	0.07	-0.3	0.28	0.25
Spikelet spike⁻¹	0.9*	0.75 NS	1.8*	1.6*	2.4*	0.6*	1.4	0.22	1.8	0.16	0.50
Grains spike⁻¹	4.9*	2.25 NS	2.1 NS	1.8 NS	8.6*	2.8*	0.6	0.21	2.1	0.32	0.41

= value was significant when it exceeded 1.96 after dividing it with its standard error; D = additive genetic effect, F = frequencies of dominants to recessive alleles in parents, H_1 and H_2 = dominance effects, h^2=overall dominance effect due to heterozygous loci, E=environmental effect

Table 6: *Analysis of variance of combing ability for the studied traits.*

Characters	Mean squares			
	GCA (df= 7)	SCA (df= 28)	RCA (df= 28)	Error (df= 126)
Days to maturity	18.8**	9.2**	9.7**	3.9
Plant height	91.9**	17.7[NS]	4.2[NS]	14.1
Spike length	1.5**	0.3[NS]	0.5*	0.3
Spikelet spike^{-1}	2.0**	1.4**	1.0*	0.5
Grains spike^{-1}	15.0**	3.7[NS]	2.9[NS]	2.6

NS = Non significant ; ** = Highly significant at 0.01 level of probability; * = Significant at 0.05 level of probability

Table 7: *Values regarding general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for days to maturity.*

Parents	FS	BST	SRN	P/S	S2	AUP	TTR	JBZ
FS	0.22	0.22	1.09	-5.09	0.68	-1.26	1.32	-2.28
BST	3.17	-0.18	-1.84	3.80	1.74	-1.36	-0.95	-0.39
SRN	2.17	2.83	-0.39	2.51	0.78	0.34	-2.24	1.49
P/S	2.67	-2.17	2.67	-1.36	1.09	-1.18	-2.26	2.97
S2	-3.17	-1.83	2.00	-0.33	-1.30	-0.74	1.34	-1.59
AUP	2.33	-0.83	-2.83	-1.17	-1.67	0.14	1.57	0.80
TTR	-0.83	0.83	-2.50	-1.33	4.00	-1.33	1.05	-1.11
JBZ	0.00	-2.83	-3.00	0.33	3.83	-0.33	-0.67	1.82

of days to maturity on the basis of significant GCA and SCA effects. It was also noted that the GCA mean square was greater than SCA; therefore this reflects the major role of additive genes in the expression of days to maturity in the present set of genotypes. The highest negative SCA effects were displayed by FS×PS while the cross combination S2K×FS showed maximum negative reciprocal effects (Table 7).

Plant height
Significant differences (p<0.05) among the genotypes were observed for plant height (Table 2). Plant height especially in wheat assumes importance as pre-harvest falling of wheat crop leads to significant yield losses. Among parents, PS had tallest (89.6 cm) while S2K had shortest (75.5 cm) height. Among the F$_1$ crosses, BST × PS and JNB × SRN showed maximum (95.87 cm) plant height and AUP ×PS showed minimum (75.5 cm) plant height (Table 3). Hayman analysis indicated the significance of both items 'a' and 'b' implying the importance of both additive and dominance genetic effects of variance for plant height (Table 11). The non significant values of 'c' and 'd' items clarified the absence of maternal and reciprocal effects respectively for plant height trait. Additive type of gene action for the expression of plant height trait in wheat was also supported by the previous findings

of Sami-Ullah et al. (2010). Moreover, Rashid et al. (2012) reported that partial dominance with the absence of epistasis is responsible for controlling plant height in wheat (Table 4). Significant values of D, H (H$_1$, H2) and E were observed for plant height. Unequal values for both H$_1$ and H$_2$ components confirmed the irregular distribution of dominant genes among the parents. This was further supported by the low ratio of H$_2$/4H$_1$ (0.04) lesser than 0.25 (Table 5). Kohan and Heidari, (2012) also reported unequal distribution of dominant and recessive alleles for plant height in wheat. Non significant and negative values for 'F' indicated lower frequency of dominant genes and predominance of recessive alleles. These findings are also compatible with the findings of Kohan and Heidari, (2012). Heterozygous loci effects for this trait were manifested by significant value of h^2. The significant environmental component E displayed the influence of environment. Over dominance for this trait was observed as the value of (H$_1$/D)$^{1/2}$ which is the average degree of dominance was larger than 1.00. For plant height, both the heritability estimates i.e. narrow and broad sense were found lower (Table 5).

As evident from Vr/Wr graph, PS had the most dominant genes on account of its position being nearer to

Table 8: *Values regarding general combining ability (diagonal), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for plant height.*

Parents	FS	BST	SRN	P/S	S2	AUP	TTR	JBZ
FS	2.15	2.19	-1.49	-1.36	1.52	-2.05	3.32	2.73
BST	0.32	0.54	-1.82	4.71	1.86	3.44	-1.15	-5.21
SRN	-0.96	0.21	-1.63	1.91	1.23	0.08	2.46	0.69
P/S	1.75	0.48	-0.74	3.79	0.94	2.48	-2.81	-1.52
S2	1.05	0.54	-1.58	0.95	-4.15	-0.12	-4.52	1.63
AUP	-1.91	1.90	0.57	0.58	-2.28	0.35	2.74	-1.54
TTR	2.93	-1.53	-5.85	0.87	-0.67	0.57	-0.09	4.61
JBZ	1.28	3.32	0.19	2.42	-0.99	1.45	0.57	-0.96

Table 9: *Values regarding general combining ability (diagonal values), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for spike length.*

Parents	FS	BST	SRN	P/S	S2	AUP	TTR	JBZ
FS	0.10	0.45	-0.07	-0.25	0.20	-0.12	-0.19	0.69
BST	-0.22	0.57	0.81	0.48	0.30	-0.23	0.12	-1.08
SRN	0.30	2.32	0.24	-0.29	-0.21	0.04	-0.20	-0.25
P/S	0.10	-0.40	-0.27	0.05	0.35	0.02	0.20	-0.10
S2	0.02	0.12	0.15	0.22	-0.15	-0.04	-0.20	-0.06
AUP	-0.07	-0.47	0.28	0.37	0.07	-0.28	0.08	0.22
TTR	0.30	0.55	-0.22	-0.02	0.35	0.30	-0.34	0.61
JBZ	0.35	-0.05	-0.17	-0.42	0.15	-0.23	0.70	-0.20

the origin while, BST had the most recessive genes for the trait under investigation as this genotype is being placed far away from the origin. AUP has equal contribution of dominant and recessive genes as this genotype had the intermediate position (Figure 2). Significant GCA effect for plant height indicated the predominance of additive gene action. Non additive and maternal effects were considered unimportant in the inheritance of plant height. The GCA mean square was much greater than SCA mean square indicating the importance of additive genetic control for plant height (Table 6). Khan and Ali, (1998) also reported significant GCA effects for plant height. Combining ability effects depicted that three out of eight parents displayed desirable negative GCA effects. F_1 cross combination BST × JNB showed the highest negative SCA effects, while BST × PS displayed the highest positive SCA effects. The highest negative reciprocal effect was manifested y the hybrid TTR × SRN (Table 8).

Spike length
Results of the data revealed significant differences (p<0.05) among the genotypes for spike length (Table 2). Said et al. (2007) also reported significant dif-

ferences among wheat genotypes for spike length. Longer spikes will bear increased number of spikelets resulting in enhanced grain yield. Among the parents, SRN gave maximum (12.7 cm) spike length while
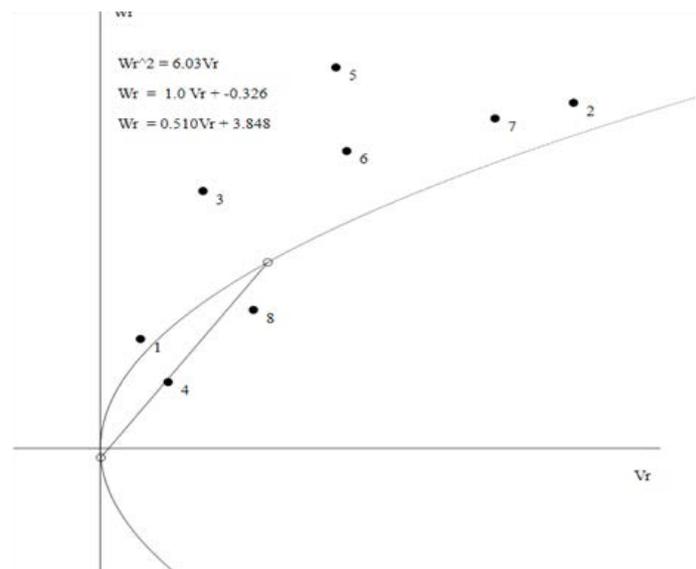
Figure 2: *The Vr/Wr graph regarding plant height explaining type of dominance and genotypes with dominant and recessive genes*
1=FS; 2= BST; 3= SRN; 4= PS; 5= S2K; 6= AUP; 7= TTR; 8= JNB

Table 10: *Values regarding general combining ability (diagonal values), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for spikelets spike⁻¹.*

Parents	FS	BST	SRN	P/S	S2	AUP	TTR	JBZ
FS	0.54	0.18	2.00	-1.07	-0.15	-0.53	-0.48	1.03
BST	-0.17	-0.11	-0.02	0.58	1.23	-0.24	-0.70	-1.02
SRN	1.07	0.80	-0.16	0.80	-1.25	0.65	0.28	-0.20
P/S	0.53	-0.40	-0.83	-0.16	0.15	0.40	0.48	0.30
S2	-0.47	0.27	1.73	0.27	-0.08	0.17	0.45	-0.18
AUP	0.08	-0.70	-0.07	-1.02	0.00	-0.38	0.47	-0.32
TTR	0.60	1.67	-0.23	-0.07	0.58	-0.03	-0.22	0.29
JBZ	-1.30	0.00	-0.07	-0.87	0.40	-0.50	-0.27	0.57

Table 11: *Values regarding general combining ability (diagonal values), specific combining ability (above diagonal) and reciprocal effects (below diagonal) for grain spike⁻¹.*

Parents	FS	BST	SRN	P/S	S2	AUP	TTR	JBZ
FS	1.01	0.68	0.80	-1.42	1.04	-0.77	0.49	1.05
BST	-0.37	-0.31	-1.53	-0.63	2.77	0.11	0.36	-2.13
SRN	2.05	1.77	0.56	0.60	-0.59	1.58	0.49	0.23
P/S	1.80	1.47	-1.63	-0.64	-0.56	-0.04	1.30	1.30
S2	-1.45	0.57	0.80	0.83	0.25	0.15	-0.40	-0.73
AUP	-0.10	-1.47	-0.63	-1.12	0.00	-1.25	1.01	-0.62
TTR	1.12	0.73	-0.63	0.10	0.40	0.23	-1.04	1.73
JBZ	-1.60	-1.03	-1.90	-2.93	1.00	-0.87	-1.30	1.42

TTR had the smallest (10.9 cm) spikes. Among the F_1 crosses, cross combination BST × SRN and JNB × BST had the longest spikes (15.9 cm) while AUP × TTR had the smallest (10.9 cm) spikes (Table 3). Hayman analysis indicated the importance of additive and dominance effects as both the components i.e. 'a' and 'b' were manifested highly significant (Table 4). Non significant values of 'c' and 'd' components demonstrated the absence of maternal effects and reciprocal effects respectively (Table 4). Gurmani et al. (2007) also reported additive genetic control with partial dominance for spike length as Wr-axis was touched by regression line above the point of origin. Unequal values of H_1 and H_2 were revealed which clarified the unbalanced dispersal of dominant genes among the parents and was further supported by the ratios of $H_2/4H_1$ (0.07) which was found lesser than 0.25. In addition to this, the non-significant negative 'F' value directed lower frequency of dominant genes and supported the presence of recessive alleles for the expression of spike length. Heterozygous loci effects for spike length were indicated by non significant vaue of h². Moreover, the values for 'E' component was also found significant thereby demonstrated the stimulus of environmental factors on expression of this trait. Over dominance for this trait was observed as the value of $(H_1/D)^{1/2}$ was found greater than 1.00.
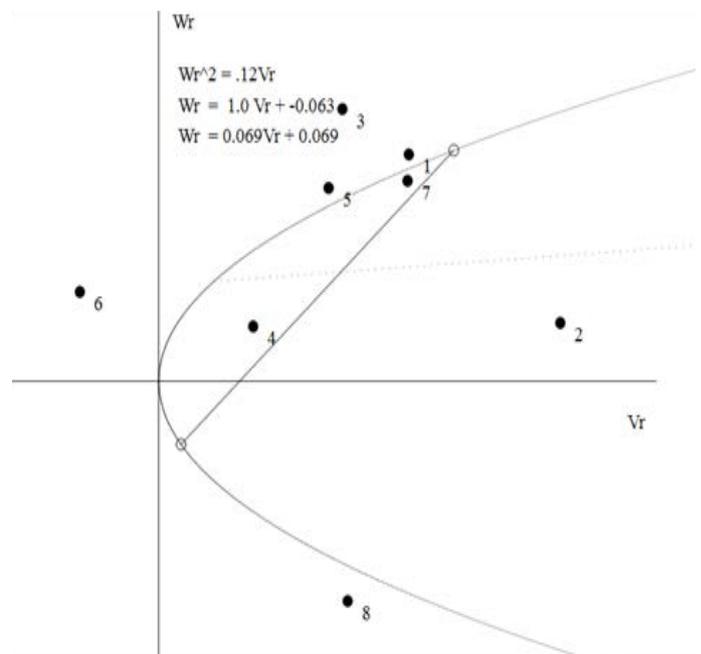
Figure 3: *The Vr/Wr graph regarding spike length explaining type of dominance and genotypes with dominant and recessive genes*
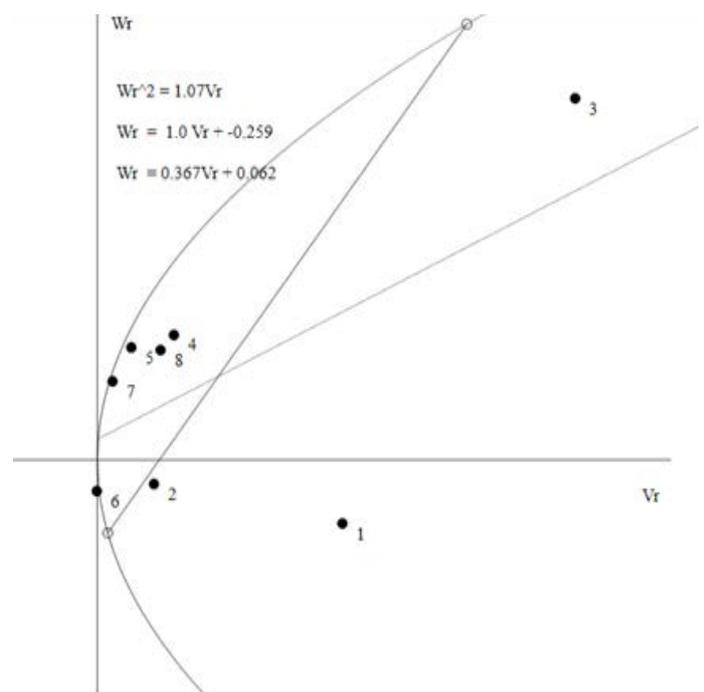*1=FS; 2= BST; 3= SRN; 4= PS; 5= S2K; 6= AUP; 7= TTR; 8= JNB*

For spike length low narrow and broad sense heritability estimates were recorded (Table 5).

Vr/Wr graph showed that AUP being closest to the origin possessed the most dominant genes whereas FS possessed the most recessive genes for the trait under investigation as it is placed far away from the origin. S2K has equal contribution of dominant and recessive genes due to its intermediate position (Figure 3). For spike length, the GCA and RCA effects were observed significant while SCA effect was displayed non significant (Table 6). Combining ability analysis of variance indicated the contribution of both additive and maternal effects in the inheritance of spike length. Malike et al. (2005) also reported significant GCA and non significant SCA effects for spike length. Combining ability effects showed the best performance of the parent BST for spike length with the highest GCA effects while F_1 hybrid FS × JNB displayed highest SCA effect for spike length (Table 9).

Spikelets spike^{-1}

Perusal of the data regarding spikelets spike^{-1} showed highly significant differences (p<0.01) among the genotypes (Table 2). Spikelets are the main part of spike comprising florets, each capable to produce single grain. The higher number of spikelets will result in increased number of florets, which in turn will enhance yield. Mean data revealed that JNB among the parental genotypes had the maximum (22.1) number of spikelets spike^{-1} while SRN had the minimum (18.7) number of spikelets spike^{-1}. Among the F_1 hybrids, FS × SRN and TTR × BST produced the highest (24.3) number of spikelets spike^{-1} while S2K × SRN showed the lowest (17.6) number of spikelets spike^{-1} (Table 3). Analysis of variance pertaining to Hayman approach indicated the importance of both additive and dominance effects as both the 'a' and 'b' components were found highly significant. Absence of maternal effects (c) and reciprocal effects (d) were also manifested for spikelets spike^{-1} (Table 4). Estimates of genetic components of variation showed significant D, H (H_1 and H_2) values which explained that both type of gene actions i.e. additive and dominance were involved in the expression of the trait under investigation. Unbalanced dispersal of dominant genes among the parents was demonstrated by imbalanced values of H_1 and H_2 and was further confirmed by $H_2/4H_1$ ratio (0.22), which was observed less than (0.25). Non significant 'F' value indicated high frequency of recessive alleles involved in controlling the inheritance of spikelets spike^{-1}. Heterozygous loci effects for spikelets spike^{-1} were indicated by significant value of h^2. The environmental component 'E' was also found significant which indicated the influence of environment on this trait. Since, the value of $(H_1/D)^{1/2}$ the average degree of dominance was greater than 1.00 thereby suggested over dominance type of gene action involved for this trait. For spikelets spike^{-1} low, narrow and medium broad sense heritability estimates were recorded (Table 5). Vr /Wr graph showed that AUP had the most dominant genes as these genotypes is having position nearer to the origin while PS had the most recessive genes for this trait as it is farthest from origin. TTR has equal contribution of dominant and recessive genes as it occupied intermediate position displaying for spikelets spike^{-1} (Figure 4). For spikelets spike^{-1}, the GCA, SCA and RCA were observed significant implying the involvement of additive, non-additive (epistatic and dominance) and maternal effects in the inheritance of spikelets spike^{-1} (Table 6). Combing ability analysis revealed that the parent JNB was the best general combiner while among the F_1 hybrids FS × SRN was the best specific combination (Table 10).

Figure 4: *The Vr/Wr graph regarding spikelets spike^{-1} explaining type of dominance and genotypes with dominant and recessive genes*
1=FS; 2= BST; 3= SRN; 4= PS; 5= S2K; 6= AUP; 7= TTR; 8= JNB

Grains spike^{-1}

Highly significant differences (p<0.01) among the

genotypes were observed for grains spike^{-1} (Table 2). Number of grains present spike^{-1} is one of the important yield contributing parameters in wheat. Among parents, JNB produced the highest number of grains spike^{-1} (56.5) while TTR had the lowest (47.8) number of grains spike^{-1}. Among the crosses, FS × SRN and TTR × BST had the highest (58.9) number of grains spike^{-1} while AUP ×TTR had the lowest (47.8) number of grains spike^{-1} (Table 3). Hayman analysis indicated the importance of additive and dominance effects as both 'a' and 'b' components were observed highly significant. The non-significant values of 'c' and 'd' components demonstrated the absence of maternal and reciprocal effects respectively (Table 4). Jadoon et al. (2012) also reported that both genetic components i.e. additive and non-additive were significant and actively involved in the control of this trait in a diallel set of F$_2$ generation. Estimates of genetic components of variation revealed the significance of D component while F, H (H$_1$, H$_2$) was observed as non-significant. Unequal values of H$_1$ and H$_2$ were found which confirmed that the distribution of dominant genes among the parents was not symmetrical and it was also supported by the lower ratio of H$_2$/4H$_1$ (0.21) than 0.25. Non-significant F value displayed the lower frequency of dominant genes. Heterozygous loci effects for grains spike^{-1} were indicated by significant value of h^2. The environmental component 'E' was also found significant thereby suggested the influence of environment on this trait. Since, the value for (H$_1$/D)$^{1/2}$ which is the average degree of dominance was observed lesser than 1.00 therefore partial dominance type of gene action was revealed for grain spike^{-1}. For grains spike^{-1}, medium narrow and broad sense heritability estimates were recorded (Table 5).

On the basis of Vr/Wr graph for grains spike^{-1}, PS is nearer to the point of origin and thus possessed the most dominant genes. However, the genotype S2K occupied farthest position from the point of origin thereby possessed the most recessive genes (Figure 5). Combining ability analysis for grains spike^{-1} revealed that mean square due to GCA was highly significant whereas both SCA and reciprocal effects were non-significant (Table 6). Additive type of gene action thus seemed to control the inheritance of grains spike^{-1}. Walton, (1971) and Khan et al. (1990) also observed significant GCA effects for grains spike^{-1} and reported the significance of additive genetic control mechanism for grains spike^{-1}. JNB seemed to be the best general combiner while F$_1$ cross combination

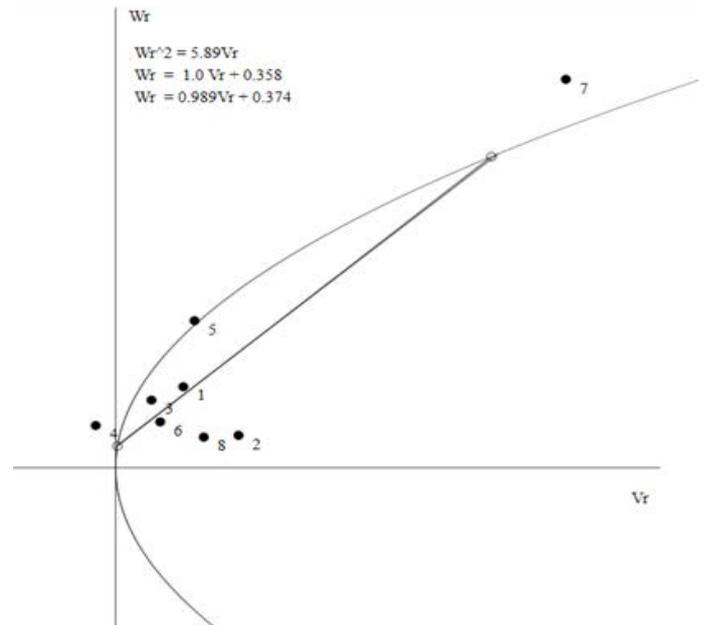BST × S2K showed the highest positive SCA effects for grains spike^{-1} (Table 11).

Figure 5: *The Vr/Wr graph regarding grains spike^{-1} explaining type of dominance and genotypes with dominant and recessive genes*
1=FS; 2= BST; 3= SRN; 4= PS; 5= S2K; 6= AUP; 7= TTR; 8= JNB

Author's Contribution

MAR presented the idea, planned experiments, analysed data and wrote the mansucirpt. GH supervised the researcha and improved the manuscript. NK co-supervised the researcha and helped in experimental work.

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