

## INHERENT PATTERN OF SOME YIELD CONTRIBUTING TRAITS IN SPRING WHEAT (*TRITICUM AESTIVUM* L.)

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### Keywords:

Diallel analysis, gene action, regression, bread wheat

### ABSTRACT

**Background** Estimation of various kinds of gene actions to understand inheritance mechanism of different quantitative traits is helpful to improve grain yield of any crop.

**Methodology** To accomplish genetic study for eight parameters of spring wheat, twenty cross combinations from five parents were developed by full diallel method.

**Results** Analysis of variance indicated that significant differences were present among wheat genotypes for all plant traits under study. The graphical presentation demonstrated that the assessed plant traits of five wheat varieties were ruled by additive gene action with partial-dominance. This publicized that simple selection for these characters were effective in early segregating generations to improve grain yield in spring wheat. Non-allelic interaction was found absent as the unit line did not deviate significantly from unit slope of any trait. Distribution of array points along regression line showed that variety SA-42 had maximum dominant genes for number of spikelets spike<sup>-1</sup>, number of grains spike<sup>-1</sup> and grain yield mother spike<sup>-1</sup> while Lassani-2008 had maximum dominant genes for grain yield mother plant<sup>-1</sup>, spike length, number of spikelets spike<sup>-1</sup>, 1000-grain weight and grain yield plant<sup>-1</sup>. Iqbal-2000 had maximum recessive genes for different studied traits.

**Conclusion** Based on the results, it is concluded that selection of studied plant traits for wheat yield improvement would be effective in early generations and might be helpful for wheat breeders trying to develop new high yielding wheat varieties.

### INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the leading cereal crops in Pakistan as well as many countries of the world. Wheat is the major staple food of Pakistan's people and it occupies a prominent position in the cropping pattern of the country. It covers around 9.180 million hectares with annual production of 25.478 million tons (Government of Pakistan, 2015). Although, Pakistan has made an impressive improvement in wheat production and has attained self-sufficiency in wheat yield but still continuous efforts are required to improve more grain yield with better quality. To achieve this purpose, it is essential to explore the ways and means to increase per unit area production of wheat. Having the limited land and water resources, production of wheat can only be increased through the development of high yielding wheat varieties. Thus, the augment in yield potential has been fundamental concern for wheat breeders. The improvement in crop plants depends upon the extent

of genetic variability present within the population or it may be induced through mutation, hybridization and other methods. As the new variability for the quantitative traits is generated, it is likely to alter the pattern of variability of its component traits as well. Therefore, to develop high yield wheat varieties, it is important to know the type of gene action and its manipulation for various plant characters in a particular set of a cross. This genetic information provides a guideline for selecting elite parents and desirable cross combinations which could be taken forward to later segregating generations for the development of new wheat genotypes. Diallel technique (Hayman 1954; Jinks 1954) provides very imperative information about the genetic mechanism in the segregating generations.

Genetic analysis of quantitative traits exhibited different patterns of inheritance in plants. Different researchers did work on wheat by using diallel analysis (Khan et al. 2000; Chowdhry et al. 2001; Khan and Habib 2003; Malik et al. 2005; Sharma

Cite As: Akhtar N, M Shabir, T Mahmood, F Hussain, I Haq (2016) Inherent pattern of some yield contributing traits in spring wheat (*Triticum aestivum* L.). J. Environ. Agric., 1(1): 42-49

et al. 2005; Xiuli et al. 2009; Yao et al. 2011; Irshad et al. 2012; Kaukab et al. 2013). Brahim and Mohamed (2014) studied different plant traits in wheat and reported that these were controlled by partial dominance with additive type of gene action but still more research work is required on this aspect to improve grain yield by using diallel methods and other techniques to fully understand the mechanism of inheritance of different quantitative traits and their impact on grain yield in different varieties of wheat. The present study was planned to extend this diallel approach in wheat by estimating various kinds of gene action in locally adopted wheat varieties to understand the mechanism of inheritance of different quantitative traits which will be helpful to improve the grain yield of wheat. Knowledge obtained from this experiment might be effective to develop appropriate strategies for continued genetic improvement in grain yield and some important yield contributing traits of spring wheat.

## MATERIALS AND METHODS

The present study was conducted in the experimental area of University College of Agriculture, University of Sargodha, Sargodha. The experimental material comprised of five wheat varieties viz., Lasani-2008, Yakora-73, SA-42, Chakwal-50, and Iqbal-2000 was sown in the field and developed direct and reciprocal crosses by using 5x5 full diallel method. Next year, parents and their  $F_1$  generations were sown in the field in triplicate randomized complete block design by keeping plant to plant and row to row distances of 15 and 30 cm, respectively. Normal cultural practices like irrigation, hoeing and fertilizers (NPK) were given equally to each treatment. At maturity 10 random plants from each treatment (parents as well as direct and reciprocal crosses) were selected and data were recorded for plant height, number of tillers plant<sup>-1</sup>, spike length, number of spikelets spike<sup>-1</sup>, number of grains spike<sup>-1</sup>, grain yield per mother spike<sup>-1</sup>, 1000-grain weight and grain yield plant<sup>-1</sup>. The data were subjected to analysis of variance technique (Steel et al. 1997) to calculate the differences among studied wheat genotypes. Genetic effects were investigated by using diallel analysis technique developed by Hayman (1954) and Jinks (1954). The information about gene action was obtained by plotting covariance ( $W_r$ ) of each array against the respective variance ( $V_r$ ). Regression coefficients were calculated for all studied plant parameters. The position and slope of regression line fitted to array points within parabola limits exploited the degree of dominance and presence or absence of gene interaction. The intercepts provide a measure of average degree of dominance as:

- **Complete dominance:** when the regression line passes through origin (zero intercept)

- **Partial dominance:** when the regression line passes through above origin (positive intercept)
- **Over dominance:** when the regression line passes through below origin (negative intercept)
- **No dominance:** when regression line touches parabola limits

## RESULTS AND DISCUSSION

Analysis of variance exhibited that highly significant difference were present among wheat genotypes for all the studied plant parameters indicating a wide range of genetic diversity among parental materials used in this experiment (Table 1).

Plant height is an essential morphological trait of wheat plant. Wheat varieties genetically vary in plant height from short stature to medium and tall. Tall cultivars are more vulnerable to lodging than medium or short stature cultivars. So in wheat breeding, plant height should be considered as an important trait due to its direct effect on grain yield. The plant material used in this experiment was varied from short to tall stature. The parents showed a wide range of variation (69.50 to 107.90 cm) for plant height and array means indicated that variety SA-42 was the best general combiner having the array means 98.90 cm while variety Yakora-73 was the poorest performer with array means of 76.89 cm (Table 2). The graphical analysis (Figure 1A) showed that plant height was controlled by additive with partial dominance type of gene action as regression line intercepted the  $W_r$ -axis above the point of origin. Non-allelic interaction was absent as regression line did not deviate from the unit slope. The additive gene action with partial dominance is suggested that selection based on plant height in early generations would be effective than late generations to develop high yielding new wheat genotypes. The distribution of array points on regression line indicated that the variety Yakora-73 possessed maximum dominant genes for plant height as closest to the point of origin whereas variety Iqbal-2000 had maximum recessive genes. Our results are in accordance with the findings of Kashif and Khaliq (2003); Bukhsh et al. (2003); Farooq et al. (2010); Yao et al. (2011) and Irshad et al. (2012). They also reported additive gene action with partial dominance for plant height in wheat. But the results are contrary with Kaukab et al. (2013) who reported that plant height in wheat was controlled by over- dominance type of gene action.

Number of tillers plant<sup>-1</sup> is a vital yield contributing trait in wheat as more the number of fertile tillers plant<sup>-1</sup> ensure higher grain yield in wheat. In our study the array means for number of tillers plant<sup>-1</sup> were ranged from 7.50 to 10.04 which indicated that the genetic variation was present among parents (Table 3). The variety Yakora-73 showed good general combining ability with other wheat varieties for this trait and had good specific

combining ability with Lasani-2008. Graphical presentation for number of tillers plant<sup>-1</sup> revealed that additive types of gene action with partial dominance controlled this trait as indicated by Wr/Vr graph in which regression line intercepted the

Wr-axis above the point of origin. As regression line followed the unit slope showed no epistasis (Figure1B). The results indicated that early generation selection for this trait to improve wheat grain yield would be effective. The arrangement

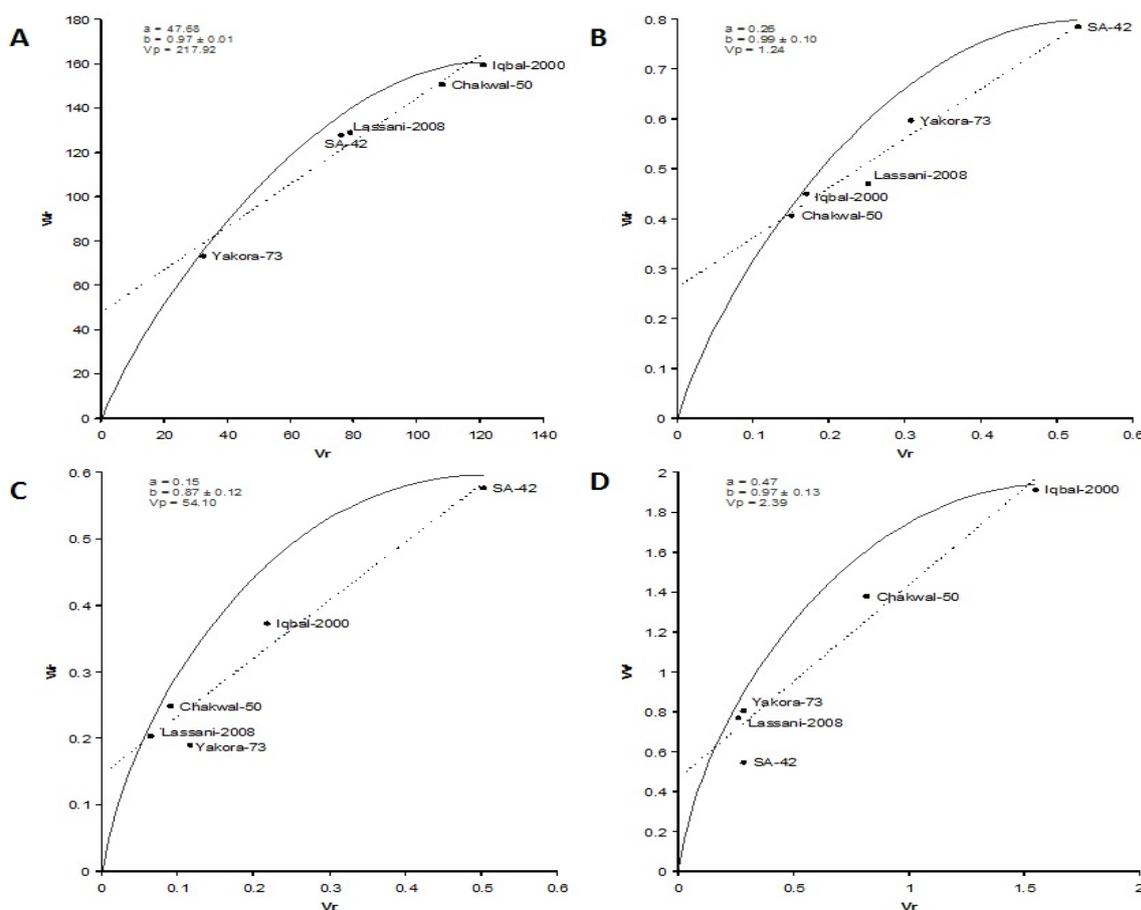
**Table1** Mean squares of five wheat genotypes and their all possible F<sub>1</sub> progenies for various plant traits

SOV	df	PH	NTP	SL	NSS	NGS	GYMS	TGW	GYP
Replication	2	39.84 <sup>NS</sup>	0.359 <sup>NS</sup>	0.053 <sup>NS</sup>	1.012 <sup>NS</sup>	5.136 <sup>NS</sup>	0.203 <sup>NS</sup>	2.653 <sup>NS</sup>	0.114 <sup>NS</sup>
Genotypes	24	56.43 <sup>**</sup>	1.767 <sup>**</sup>	0.946 <sup>**</sup>	3.835 <sup>**</sup>	41.334 <sup>**</sup>	0.421 <sup>**</sup>	9.381 <sup>**</sup>	23.68 <sup>**</sup>
Error	48	20.88	0.217	0.228	0.611	7.476	0.168	3.500	7.131

NS: Non-significant, \*Significant, \*\*Highly significant, PH: Plant height, NTP: Number of tillers plant<sup>-1</sup>, SL: Spike length, NSS: Number of spikelets spike<sup>-1</sup>, NGS: Number of grains spike<sup>-1</sup>, GYMS: Grain yield mother spike<sup>-1</sup>, TGW: 1000-grain weight, GYP: Grain yield plant<sup>-1</sup>

**Table 2** Array means from 5×5 diallel cross in spring wheat for plant height

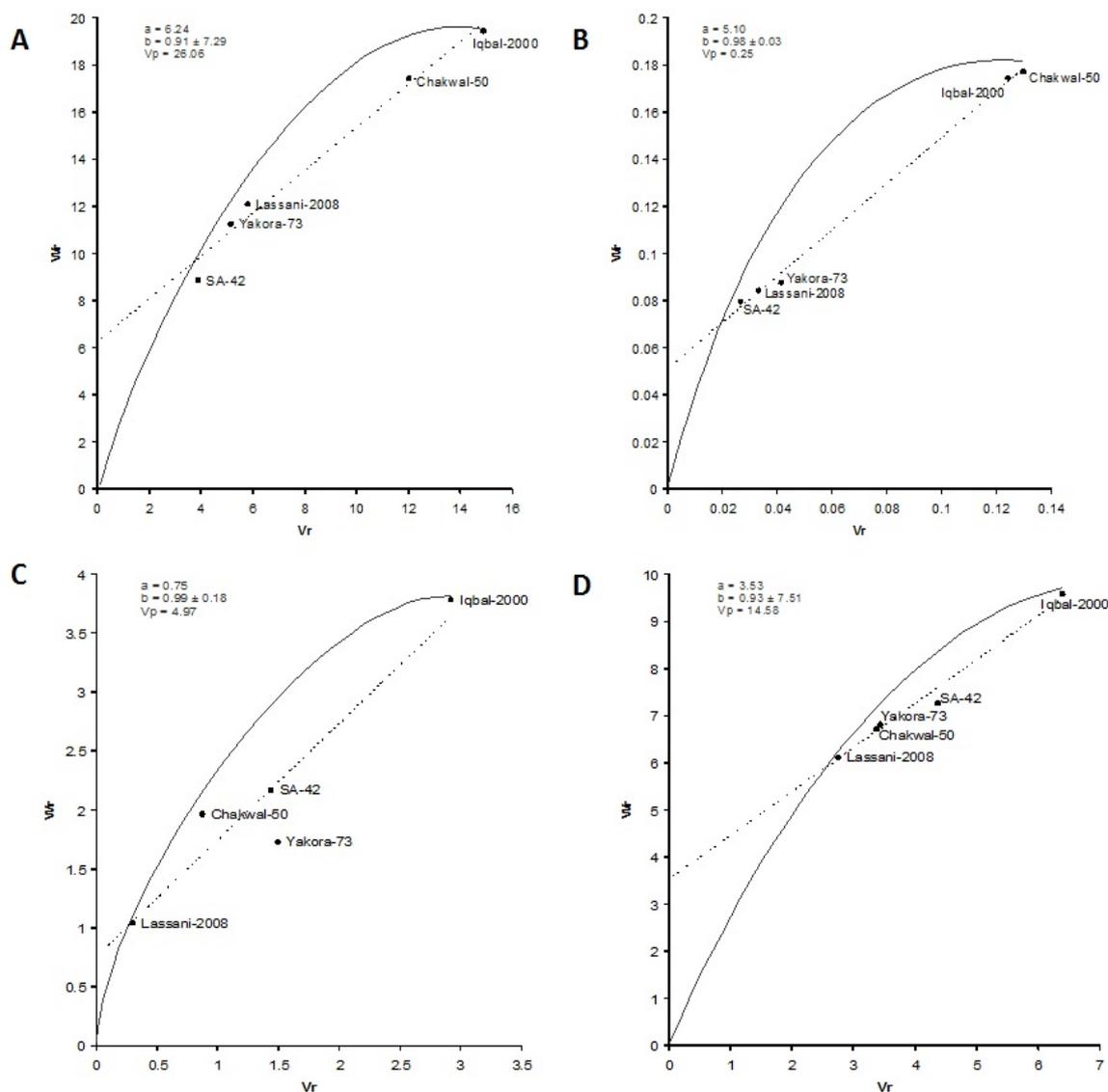
Genotypes	Lassani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lasani--2008	<b>100.63</b>	80.30	101.40	99.52	98.37
Yakora-73	80.30	<b>69.50</b>	84.35	76.13	74.15
SA-42	101.40	84.35	<b>107.90</b>	100.57	100.29
Chakwal-50	99.52	76.13	100.57	<b>98.93</b>	98.08
Iqbal-2000	98.37	74.15	100.29	98.08	<b>97.80</b>
Total	480.22	384.15	494.51	473.23	468.69
Array Mean	96.04	76.89	98.90	94.65	93.74



**Figure 1** Vr/Wr graphs for (A) Plant height, (B) Number of tillers plant<sup>-1</sup>, (C) Spike length and (D) Number of spikelets spike<sup>-1</sup>

**Table 3** Array means from 5×5 diallel cross in spring wheat for number of tillers plant<sup>-1</sup>

Genotypes	Lasani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lasani-2008	<b>9.83</b>	9.92	9.23	9.53	8.68
Yakora-73	9.92	<b>10.04</b>	8.92	9.42	8.83
SA-42	9.23	8.92	<b>7.50</b>	8.78	7.93
Chakwal-50	9.53	9.42	8.78	<b>9.20</b>	8.65
Iqbal-2000	8.68	8.83	7.93	8.65	<b>8.03</b>
Total	47.19	47.13	42.36	45.58	42.12
Array Mean	9.44	9.43	8.47	9.12	8.43



**Figure 2** Vr/Wr graphs for (A) Number of grains per spike<sup>-1</sup>, (B) Grain yield mother spike<sup>-1</sup>, (C) 1000-grain weight and (D) Grain yield per plant<sup>-1</sup>

of array points on regression line exhibited that Chakwal-50 had maximum dominant genes being closest to the point of origin while SA-42 had maximum recessive genes being farther from the origin. These results get conformity with the findings of Khan and Habib (2003); Nazeer et al. (2004); Khan et al. (2007); Farooq et al. (2010);

Irshad et al. (2012); Adel and Ali (2013); Kaukab et al. (2013).

Spike length is an important yield related trait of wheat. It directly contributes to the grain yield. The array means (Table 4) showed that the parental values ranged from 9.53 to 11.70 cm for spike length indicating the presence of genetic variability among

**Table 4** Array means from 5×5 diallel cross in spring wheat for spike length

Genotypes	Lasani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lasani-2008	<b>11.33</b>	11.47	10.87	11.18	10.95
Yakora-73	11.47	<b>11.70</b>	11.18	11.27	10.78
SA-42	10.87	11.18	<b>9.53</b>	10.57	9.77
Chakwal-50	11.18	11.27	10.57	<b>11.07</b>	10.73
Iqbal-2000	10.95	10.78	9.77	10.73	<b>10.47</b>
Total	55.8	56.4	51.92	54.82	52.70
Array Mean	11.16	11.28	10.38	10.96	10.54

parents. The variety Yakora-73 had good general combining ability having an array mean value of 11.28 and showed good specific combining ability when it was crossed with Lasani-2008. While, variety SA-42 was found the poorest performer in this experiment. The graphical presentation (Figure 1C) indicated that spike length was also governed by additive type of gene action with partial dominance as exhibited by regression line which intercepted the  $W_r$ -axis above the point of origin. The non-allelic interaction was not present as the unit line did not deviate significantly from unit slope. The positions of array points on regression line showed that the variety Lasani-2008 had maximum dominant genes for spike length while SA-42 had maximum recessive genes. Our results are in accordance with the finding of Subhani and Chowdhry (2000), Kashif and Khaliq (2003) and Yao et al. (2011) who also reported that additive type of gene action with partial dominance was prominent for spike length in wheat but contrary with Kaukab et al. (2013) who found over-dominance gene action.

Number of spikelets spike<sup>-1</sup> is the key trait in wheat breeding as more spikelets per spike results in more grains per spike. So, this trait should be given due consideration while selecting genotypes for high yield. In the present study, the expression of the parents for number of spikelets spike<sup>-1</sup> was ranged from 18.80 to 22.70 having ample diversity (Table 5). The variety Iqbal-2000 had good general combining ability (21.39) for this trait and had developed good specific combination with Chakwal-50.  $W_r/V_r$  graph (Figure 1D) exhibited that number of spikelets spike<sup>-1</sup> was governed by partial-dominance type of gene action as the regression line intercepted  $W_r$ -axis above the point of origin. The distribution of array points indicated that the variety SA-42 had the more dominant genes being closest to the point of origin while Iqbal-2000 had the more recessive genes being farther from the origin. Our results get support from the findings of Kashif and Khaliq (2003); Nazan (2008); Akram et al. (2009), Irshad et al. (2012), Adel and Ali (2013). They observed similar type of gene action in different wheat genotypes for spikelets per spike.

Number of grains spike<sup>-1</sup> is one of the most important yield contributing traits in wheat. It directly correlates with grain yield production. The expression of parent values were ranged from 57.30

to 70.67 which indicated that ample genetic variation was present for this trait among studied wheat genotypes and simple selection in early segregating generations would be effective to improve the grain yield in wheat (Table 6). The variety Chakwal-50 had good general combining ability for this trait and had found good specific combiner in cross with Iqbal-2000. Graphical analysis (Figure 2A) indicated that regression line intercepted the  $W_r$ -axis above the point of origin, thus revealing partial-dominance with additive gene action. Non-allelic interaction was missing as regression line did not deviate from the unit slope. The distribution of array points on regression line indicated that genotype SA-42 had the more dominant genes being closest to the point of origin whereas genotype Iqbal-2000 had the more recessive genes due to farther from the origin. Current results are in accordance with the findings of Nazeer et al. (2004); Sharma et al. (2005); Nazan (2008); Akram et al. (2009); Brahim and Mohamed (2014). They also reported that the plant trait number of grains per spike in wheat was controlled by additive with partial dominant genes while, Farooq et al. (2010) reported over-dominance type of gene action controlled this trait.

Regarding grain yield mother spike<sup>-1</sup>, the appearance of the parental values in array means (Table 7) showed a good range of differences (2.60-3.70 g) for this trait. The variety Chakwal-50 had good general combining ability with other varieties while the cross between Chakwal-50 x Iqbal-2000 had good specific combining ability whereas SA-42 proved the poorest performer for this trait. The graphical presentation (Figure 2B) indicated the partial-dominance type of gene action as regression line intercepted the  $W_r$ -axis above the point of origin with no epistasis. The distribution of array points represented that wheat variety SA-42 had more dominant genes for grain weight mother spike<sup>-1</sup> being nearest to the point of origin while Chakwal-50 had more recessive genes as its distance from the point of origin was maximum. These results are in agreement with the findings of Satyavart et al. (1999); Subhani and Chowdhry (2000); Kashif and Khaliq (2003); Khan and Habib (2003); Nazeer et al. (2004) and Farooq et al. (2010) who reported that grain yield mother spike<sup>-1</sup> was controlled by additive with partial dominant genes in wheat.

1000-grain weight is a fundamental yield component and is more or less stable character of wheat cultivars. The array means (Table 8) expressed the parental values which were ranged from 22.97 to 28.53 indicating ample genetic diversity for thousand grain weight (TGW). The variety Iqbal-2000 was found the best general combiner having array mean value of 26.45 and had a good specific combination in cross Iqbal-2000 x Lassani-2008 while Yakora-73 was found 1000-grain weight is a fundamental yield component and is more or less stable character of wheat varieties. The array means (Table 8) expressed the parental values which were ranged from 22.97 to 28.53 indicating ample genetic diversity for 1000-grain weight (TGW). The variety Iqbal-2000 was found the best general combiner having array mean value of 26.45 and had a good specific combination in cross Iqbal-2000 x Lasani-2008 while Yakora-73 was found the weakest general combiner (24.29) for this trait. The values of  $W_r/V_r$  graphical presentation (Figure 2C) indicated that additive type of gene action with partial dominance as intercepted point on  $W_r$ -axis is positive. Non-allelic interactions were also absent as regression line did not deviate from the unit slope. The array point's arrangement on regression line revealed that wheat variety Lasani-2008 had more dominant genes while variety Iqbal-2000 had more the recessive

genes for the expression of this trait. Based on the present findings it is suggested that selection in early segregating generations is effective to improve this trait in wheat. These results get support from the findings of Subhani and Chowdhry (2000); Khan and Habib (2003); Nazeer et al. (2004); Farooq et al. (2010); Brahim and Mohamed (2014).

The ultimate goal of wheat breeding is to get maximum grain yield with good quality. It is a complex polygenic trait which is developed with the combination of different morphological traits. The existence of highly significant differences among parental wheat varieties (ANOVA) and the expression of parental values by array means exhibited a wide range of (27.03 to 35.67) genetic variation for grain yield per plant (Table 9). The variety Lasani-2008 showed the maximum grain yield plant<sup>-1</sup> having the array means 33.58 while variety SA-42 had the lowest grain yield per plant having the array means 29.17). Graphical expression indicated that regression line intercepted the  $W_r$ -axis just above the point of origin, thus revealing partial-dominance type of gene action. Non-allelic differences are absent as regression line did not deviate from the unit slope. It was observed that variety Lasani-2008 had maximum number of dominant genes for grain yield plant<sup>-1</sup> while Iqbal-2000 carried maximum recessive genes for controlling this trait (Figure 2D). These results are

**Table 5** Array means from 5×5 diallel cross in spring wheat for number of spikelets plant<sup>-1</sup>

Genotypes	Lasani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lasani-2008	<b>20.83</b>	20.62	19.93	21.07	21.25
Yakora-73	20.62	<b>20.33</b>	19.83	21.12	21.05
SA-42	19.93	19.83	<b>18.80</b>	20.18	19.57
Chakwal-50	21.07	21.12	20.18	<b>22.17</b>	22.40
Iqbal-2000	21.25	21.05	19.57	22.40	<b>22.70</b>
Total	103.7	102.95	98.31	106.94	106.97
Array Mean	20.74	20.59	19.66	21.39	21.39

**Table 6** Array means from 5×5 diallel cross in spring wheat for number of grains spike<sup>-1</sup>

Genotypes	Lassani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lassani-2008	<b>63.80</b>	61.42	60.45	66.52	64.23
Yakora-73	61.42	<b>60.90</b>	58.28	64.13	63.23
SA-42	60.45	58.28	<b>57.30</b>	62.32	58.85
Chakwal-50	66.52	64.13	62.32	<b>70.67</b>	69.27
Iqbal-2000	64.23	63.23	58.85	69.27	<b>66.33</b>
Total	316.42	307.96	297.2	332.91	321.91
Array Mean	63.28	61.59	59.44	66.58	64.38

**Table 7** Array means from 5×5 diallel cross in spring wheat for grain yield mother spike<sup>-1</sup>

Genotypes	Lassani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lassani-2008	<b>3.00</b>	2.90	2.70	3.51	3.12
Yakora-73	2.90	<b>2.60</b>	2.57	3.05	2.75
SA-42	2.70	2.57	<b>2.53</b>	2.87	2.88
Chakwal-50	3.15	3.05	2.87	<b>3.70</b>	3.60
Iqbal-2000	3.12	2.75	2.88	3.60	<b>3.40</b>
Total	14.87	13.87	13.55	16.73	15.75
Array Mean	2.97	2.77	2.71	3.27	3.15

**Table 8:** Array means from 5×5 diallel cross in spring wheat for 1000- grain weight

Genotypes	Lassani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lassani-2008	<b>27.17</b>	26.28	26.87	26.45	27.62
Yakora-73	26.28	<b>22.97</b>	23.83	24.18	24.18
SA-42	26.87	23.83	<b>24.20</b>	25.18	25.55
Chakwal-50	26.45	24.18	25.18	<b>25.70</b>	26.35
Iqbal-2000	27.62	24.18	25.55	26.35	<b>28.53</b>
Total	134.39	121.44	125.63	127.86	132.23
Array Mean	26.88	24.29	25.13	25.57	26.45

**Table 9:** Array means from 5×5 diallel cross in spring wheat for grain yield plant<sup>-1</sup>

Genotypes	Lassani-2008	Yakora-73	SA-42	Chakwal-50	Iqbal-2000
Lassani-2008	<b>35.67</b>	31.95	32.15	33.22	34.92
Yakora-73	31.95	<b>27.73</b>	27.40	29.12	30.08
SA-42	32.15	27.40	<b>27.03</b>	30.10	29.15
Chakwal-50	33.22	29.12	30.10	<b>32.00</b>	33.12
Iqbal-2000	34.92	30.08	29.15	33.12	<b>34.10</b>
Total	167.91	146.28	145.83	157.56	161.37
Array Mean	33.58	29.26	29.17	31.51	32.27

in agreement with the findings of Khan et al. (2000); Kashif and Khaliq (2003); Nazeer et al. (2004); Sharma et al. (2005); Khan et al. (2007); Akram et al. (2009); Farooq et al. (2010); Irshad et al. (2012). But Adel and Ali (2013) and Kaukab et al. (2013) reported over dominance type of gene action for this trait.

## CONCLUSION

Based on the present research findings, it is concluded that additive gene action with partial dominance is prominent in most of the studied plant parameters which suggesting that selection in early segregating generations using these traits may lead to develop high yielding wheat varieties through modified pedigree selection method.

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