

## Research Article

# Partial Diallel Analysis of Genetic Behavior for Several polygenic Traits in Bread Wheat (*Triticum aestivum* L.)

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**Abstract**

A partial diallel-cross study involving nine bread wheat cultivars was carried out to determine the inheritance pattern of grain yield and related attributes. The results obtained in this study could provide valuable information to a breeding program developing high yielding wheat varieties under a rain-fed environment. The analysis of variance revealed significant differences among genotypes for all the studied traits. In the partial diallel analysis, the additive-dominant model adequately described most of the traits. Allelic interaction was over-dominant for biological yield/plant in group 1 and group 2, while partial dominance and over-dominance effects were found for other traits from both parental groups. The increases in the magnitude for the studied traits are generally determined by dominant genetic factors. The genitor Mahon-Demias (group 2) had the largest concentration of favorable alleles for biological yield/plant, number of spikes/plant and grain yield/plant. The parents Acsad<sub>9,01</sub> (group 1) and Rmada (group 2) had the most recessive genes for these characteristics.

**ABBREVIATIONS**

BY: Biological Yield per plant (g); SN: Number of Spikes per plant; GN: Number of Grains per spike; GY: Grain Yield per plant (g)

**INTRODUCTION**

Wheat (*Triticum aestivum* L.) occupies a prominent position in the cropping land scape of Algeria and ranks third among all the cereals after durum wheat and barley [1]. This crop is widely grown in the semiarid environments in which available moisture constitutes a primary constraint on its production. Improving drought resistance is therefore a major objective in plant breeding programs for rain-fed agriculture in Algeria [2]. To achieve this in an efficient manner, obtaining genetic information about abiotic stress related traits is of great importance for parent selection. Diallel cross designs are frequently used in plant breeding research to obtain information about genetic properties of parental lines and estimates of general and specific combining abilities and heritability [3]. Several methods have

been proposed for the genetic analysis of data from a diallel cross [4]. In general, Hayman's approach [5] appears to extract more genetic information than Griffing's method [6] from the same data set. Griffing's methodology includes only analysis of variance and estimation of general and specific combining abilities effects. Hayman's diallel analysis, on the other hand, may include statistical and graphical analyses of array variances and covariance, and estimate a number of genetic parameters [7,8]. It also provides information on the genetic mechanisms involved in the control of complex traits in early generations especially in self-fertilized crops like wheat. However, for the application of this method, certain assumptions must be met such as Mendelian inheritance, parental homozygosis, absence of reciprocal effect, absence of multiple allelism, gene distribution among parents, and absence of epistatic interactions [4,7,9]. The adaptation of Hayman's method to partial diallel crosses was developed by Viana et al [10]. This breeding methodology is based on a set of crosses made between two separate parent groups where crosses between parents belonging to the same group are not of

interest to the breeder [10]. The objectives of this investigation were to find out the patterns of inheritance for grain yield and its related traits in bread wheat material by means of Hayman's partial diallel approach as outlined by Viana et al [10]. The results obtained in this study could provide valuable information to a breeding program developing high yielding wheat varieties under a rain-fed environment.

## MATERIALS AND METHODS

### Plant materials

The experimental plant material was comprised of nine varieties/lines of bread wheat (Table 1). The parents were chosen based on their broad genetic background and large variations for grain yield and yield components (Table 1) [1,11]. These genotypes were divided into two divergent groups. Group 1 was composed of five varieties (female parents) and group 2 of four varieties (male parents). The crosses were made in a partial diallel fashion without reciprocals during May 2010 to produce 20F<sub>1</sub> hybrids.

### Experimental design

The seeds of 9 parents and 20 F<sub>1</sub> hybrids were sown in a randomized complete block design with three replications at the Agricultural Experimental Station (AES) of Setif, Algeria, during the crop season 2011/2012. Each experimental plot consisted of a single row 2.5 meters in length. The plant-to-plant and row-to-row distance was 15 and 30 cm, respectively. Standard agronomic practices such as fertilizer application and weed control were carried out. The amount of rainfall received during the

experimental period was 329.0 mm. At the time of maturity, ten guarded plants from each entry and each replication were taken at random and measurements were made of biological yield per plant (BY), number of spikes per plant (SN), number of grains per spike (GN), and grain yield per plant (GY).

### Statistical/Biometrical analysis

The data obtained were subjected to analysis of variance to test genotype effect according to Steel and Torrie [12]. The traits which showed significant difference among genotypes were further subjected to genetic analysis. The partial diallel model developed by Hayman [5] and modified by Viana et al [10] was used for genetic analysis.

## RESULTS AND DISCUSSION

### Analysis of variance

Analysis of diallel crosses to estimate genetic parameters can be carried out if there are significant differences between genotypes based on the *F*-test of different traits under study. The analysis of variance results revealed significant genotype effect for all the measured traits (Table 2). This suggests that high genetic variability exists for these traits and the estimation of genetic parameters can be applied to the wheat genotypes tested [13].

### Adequacy Tests for Additive-Dominance Model

The validity of the additive-dominance model for various plant traits and some of the underlying assumptions was tested by joint regression analysis. The regression coefficient (*b*) of all

**Table 1:** Genetic background and yield traits of the nine parents of bread wheat.

Genotypes	Group	Traits							
		DH	PH	SL	SN	TKW	NG	BY	GY
Acsad <sub>901</sub>	1	133.0	66.2	11.8	7.8	23.9	55.1	28.7	10.5
Acsad <sub>899</sub>	1	137.3	69.6	11.5	13.7	32.7	44.9	52.5	20.0
Acsad <sub>1135</sub>	1	132.7	80.9	13.5	15.0	32.8	44.4	58.1	21.7
Acsad <sub>1069</sub>	1	132.3	73.1	12.7	11.8	32.4	49.9	44.5	18.8
Ain Abid	1	137.7	71.6	14.0	8.8	26.1	60.0	38.7	13.7
Mahon-Demias	2	140.0	99.8	11.4	16.8	39.2	26.3	56.3	17.3
Rmada	2	132.7	76.0	13.6	14.1	29.5	47.6	49.7	20.4
Hidhab	2	137.3	63.2	12.2	12.4	27.3	55.0	48.5	18.8
El-Wifak	2	132.7	70.6	12.8	8.4	32.8	49.3	32.7	13.5

**Abbreviations:** DH: Number of days to heading, PH: Plant height (cm), SL: Spike length (cm), SN: Number of spikes per plant, TKW: Thousand-kernel weight (g), NG: Number of grains per spike, BY: Biological yield per plant (g), GY: Grain yield per plant (g).

**Table 2:** Analysis of variance of studied traits in partial diallel crosses of bread wheat.

Traits	Mean squares*		
	Replication	Genotypes	Error
Biological yield per plant (g)	212.8	238.7*	90.6
Number of grains per spike	52.3	152.8*	31.4
Number of spikes per plant	13.0	23.4*	3.4
Grain yield per plant (g)	62.0	39.7*	6.5

**Abbreviations:\*** P ≤ 0.05, Degrees of freedom for replication, genotypes and error mean squares are 2, 28 and 56, respectively.

**Table 3:** Scaling test for adequacy of additive-dominance model for various plant traits in bread wheat.

Traits	Groups	$b \pm se_b$	$b = 0$ vs $b \neq 0$	$b = 1$ vs $b \neq 1$
Biological yield per plant (g)	1	0.94±0.52	1.81 <sup>ns</sup>	0.12 <sup>ns</sup>
	2	0.99±0.39	2.53 <sup>ns</sup>	0.03 <sup>ns</sup>
Number of grains per spike	1	1.43±0.24	5.96*	1.79 <sup>ns</sup>
	2	0.77±0.14	5.50*	1.64 <sup>ns</sup>
Number of spikes per plant	1	1.11±0.42	2.64*	0.26 <sup>ns</sup>
	2	0.64±0.20	3.20*	1.80 <sup>ns</sup>
Grain yield per plant (g)	1	0.21±0.84	0.25 <sup>ns</sup>	0.94 <sup>ns</sup>
	2	1.08±0.36	3.00*	0.22 <sup>ns</sup>

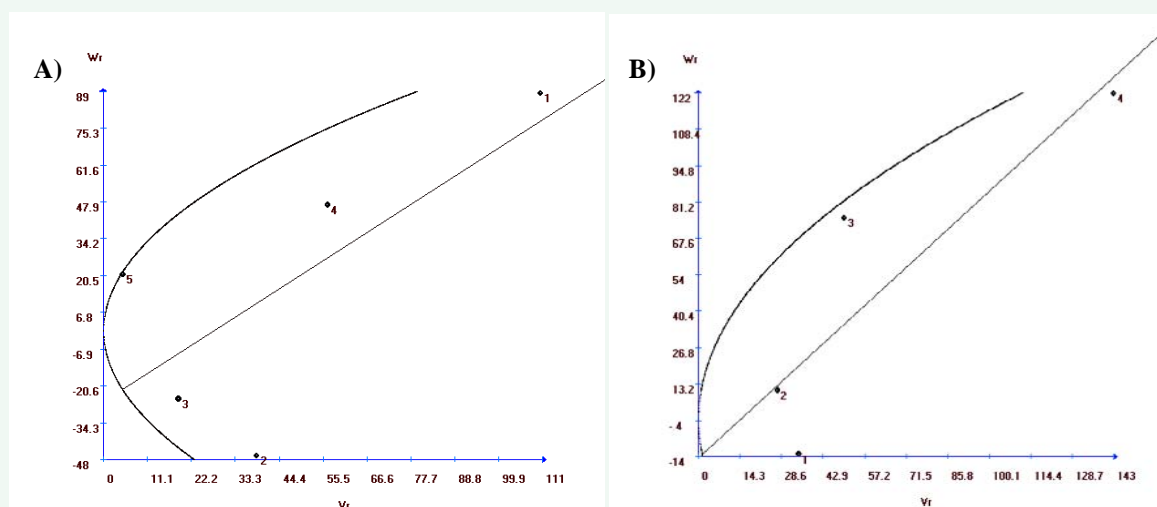
**Abbreviations:**  $b_0$ : coefficient of regression deviating from zero,  $b_1$ : coefficient of regression deviating from unity, ns: not significant, \*  $P \leq 0.05$ .

the traits deviated significantly from zero except for biological yield per plant in groups 1 and 2 and for grain yield in group 1 (Table 3). When the regression coefficient departs significantly from zero but not from one, this suggests the presence of intra-allelic gene interaction and independent distribution of genes among the parents for the traits. Thus, the results obtained suggested that additive-dominance model was adequate to determine genetic components of variation for the examined traits except for biological yield per plant in groups 1 and 2 and for grain yield in group 1 (Table 3). Hayman [14] indicated that even when a trait exhibits partial failure of the assumptions due to presence of non-allelic interactions, the analysis will still provide information about the genetic system controlling the trait though the estimates are certainly less reliable.

### Graphical analysis

A Hayman graphical analysis was conducted to evaluate the genetic relationships among parents. Graphic analysis was conducted with various modes of inheritance from additive to over-dominance, for the characters investigated. In the approach of diallel analysis, a Vr-Wr graph is drawn with the help of variances of arrays (Vr) and covariances between parents and their offspring (Wr). The slope and position of the regression line fitted to the array points within the limiting parabola indicates

the degree of dominance for a trait. The distance between the origin and the ordinate where the regression crosses the Wr axis provides a measure of average degree of dominance. The order of array points represented the distribution of dominant and recessive genes among the parents; those with most dominant genes are nearest the origin, while those having most recessive genes are the farthest. Graphics analysis indicated that in group 1 ( $G_1$ ), the variety A in Abid had more dominant genes for grains number per spike (GN) and grain yield per plant (GY), while Acsad<sub>1135</sub> had more dominant genes for biological yield per plant (BY) and spikes number per plant (SN). Acsad<sub>901</sub> had more recessive genes for BY, SN and GY, while Acsad<sub>899</sub> had more recessive genes for GN (Figures 1, 3, 5,7). In the second group 2 ( $G_2$ ), Mahon-Demias had the maximum number of dominant genes for BY, SN and GY, while Hidhab had more dominant genes for GN. Rmada had more recessive genes for BY, SN and GY while Mahon-Demias had more recessive genes for GN (Figures 1, 3, 5,7). Acsad<sub>1069</sub> from  $G_1$  and Hidhab from  $G_2$ , occupied central position along the regression line, is displaying an equal proportion of dominant and recessive genes for the four characters under study (Figures 1, 3, 5,7). These results suggest that combinations of these varieties will produce moderate BY, GN, SN and GY. The arrays of  $G_1$  and  $G_2$  groups were somewhat



**Figure 1** Vr on Vr graphs for biological yield per plant in  $G_1$  (a) and  $G_2$  (b) parental groups.

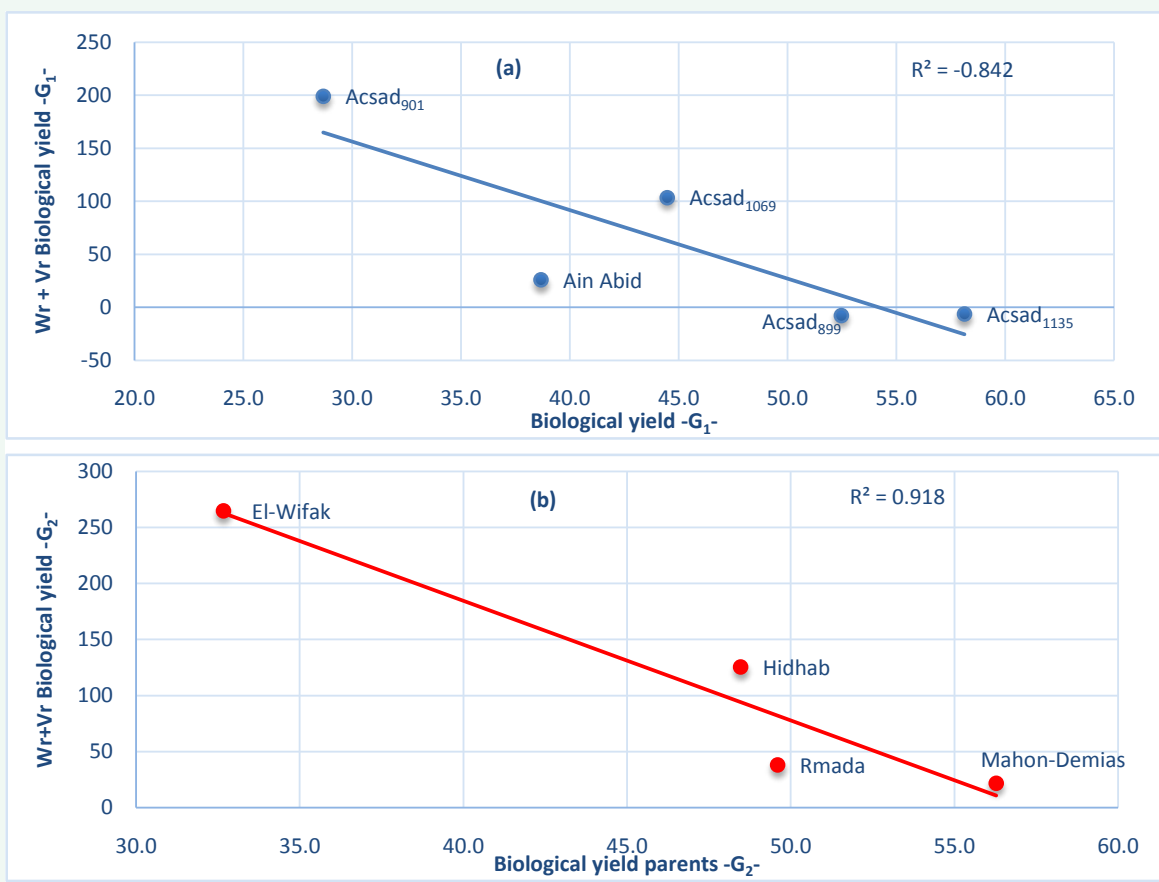


Figure 2 Wr + Vr on Parents values for biological yield per plant in G1 (a) and G2 (b) group of parents.

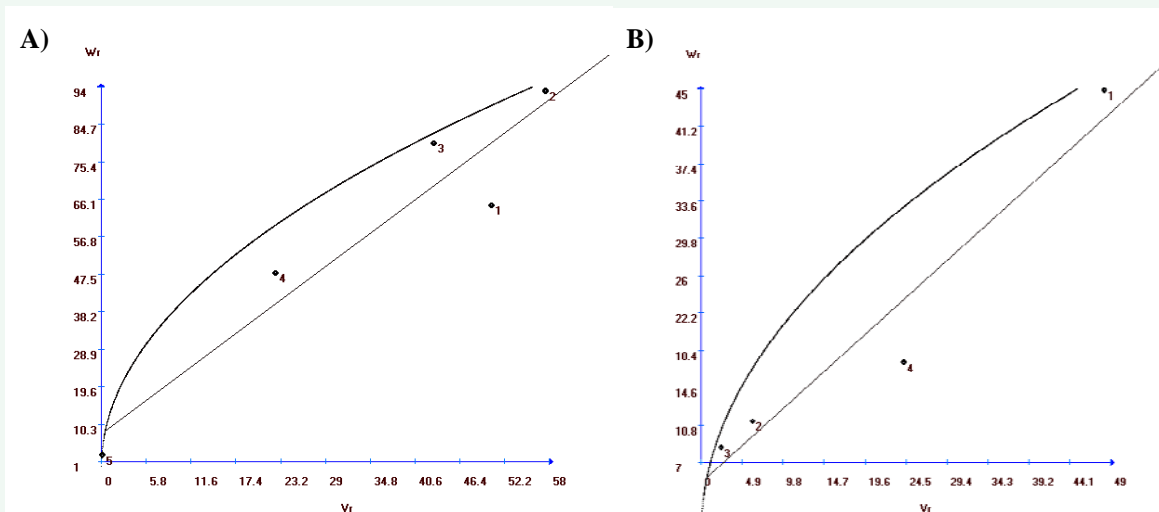
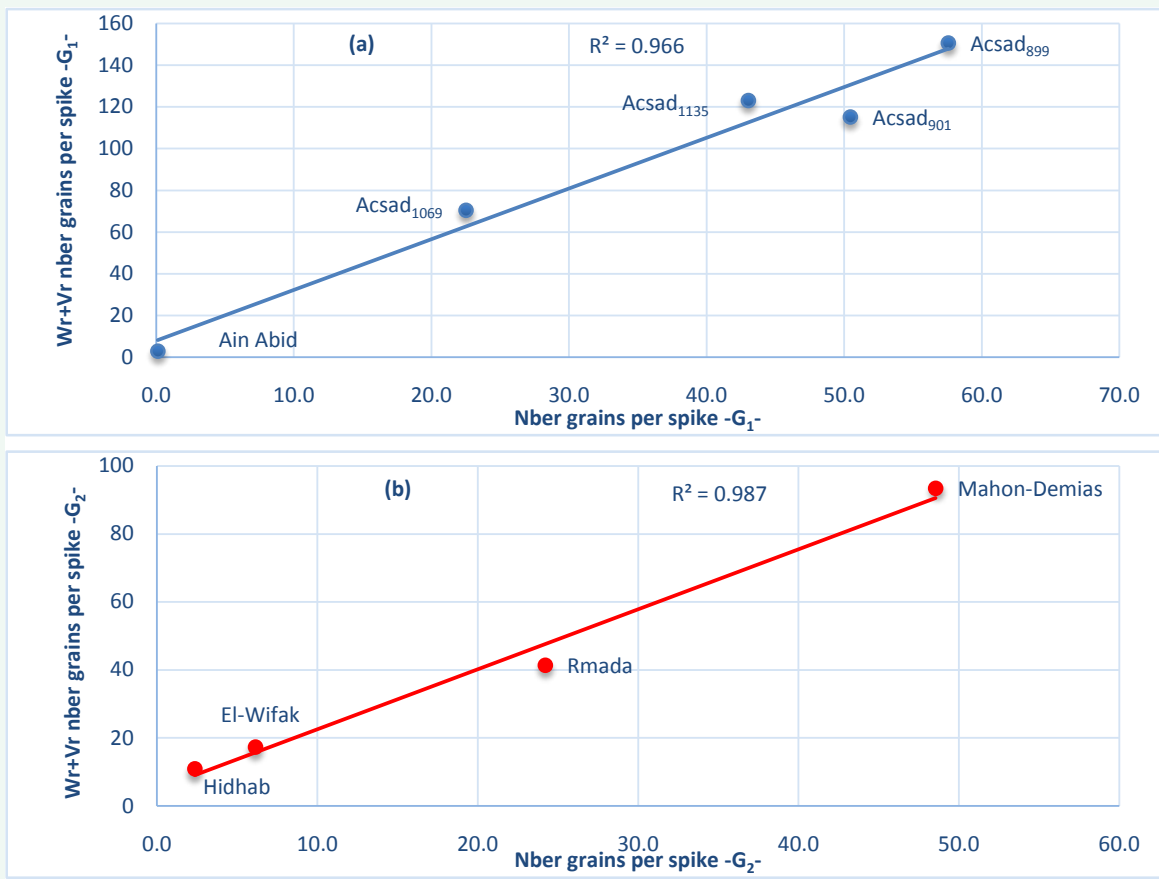


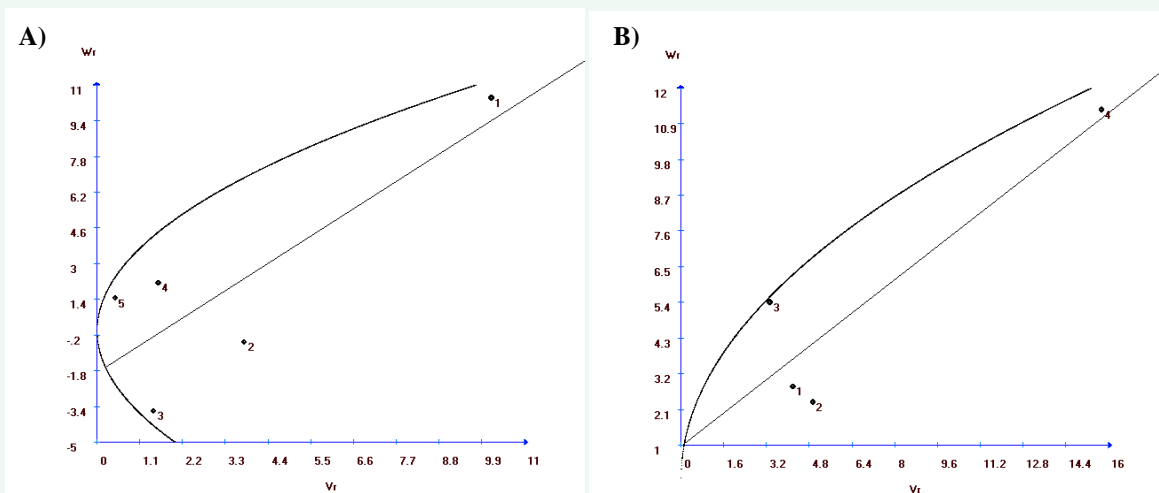
Figure 3 Wr on Vr graphs for number of grains per spike in G1 (a) and G2 (b) parental groups.

well distributed along the regression line, indicating that the parents were genetically divergent for BY, GN and GY. However, for SN there were more parents with an excess of dominant genes in both parental groups (Figures 1,3,5,7). The regression line crosses the Wr axis below the point of origin, suggesting over-dominant inheritance for BY and SN in G<sub>1</sub> and for BY and GY

in G<sub>2</sub>. The ordinate value of the regression line showed partial dominant inheritance for GN in both groups and for GY, in G<sub>1</sub> and SN, in G<sub>2</sub> (Figures 1,3,5,7). The results derived from the present study are in accordance with those of the earlier findings of Ali et al [15], Habib and Khan [16], Ullah et al [17], Irshad et al [18] and Ahmed et al [19] which reported additive gene action with partial



**Figure 4**  $W_r + V_r$  on Parents values for number of grains per spike in G1 (a) and G2 (b) group of parents.



**Figure 5**  $W_r$  on  $V_r$  graphs for number of spikes per plant in G1 (a) and G2 (b) parental groups.

dominance for number of grains per spike and grain yield. Asif et al [20] crossed five wheat varieties in all possible combinations and observed that economic yield per plant, biological yield and harvest index were controlled by over-dominance. Other authors, however, reported different gene action for the same traits studied [21-24]. This disagreement is due to the fact that

these traits behave differently for different set of genotypes and in different environments. To find the correlated response of the dominant genes with the phenotype of the common parent,  $W_r + V_r$  values of the arrays were plotted against the parental values. In the plant material studied, a negative correlation was observed for BY, SN and GY in both groups, indicating that

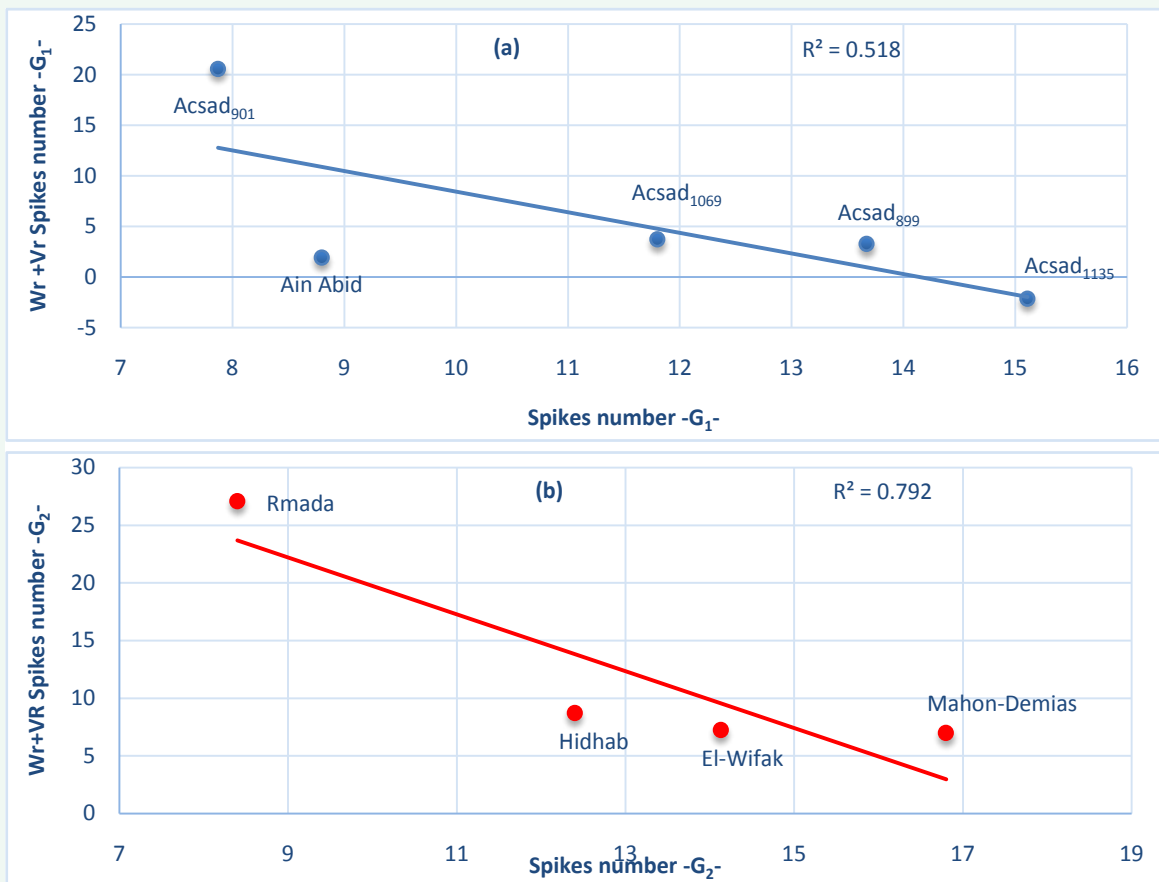


Figure 6 Wr + Vr on Parents values for number of spikes per plant in G1 (a) and G2 (b) parental groups.

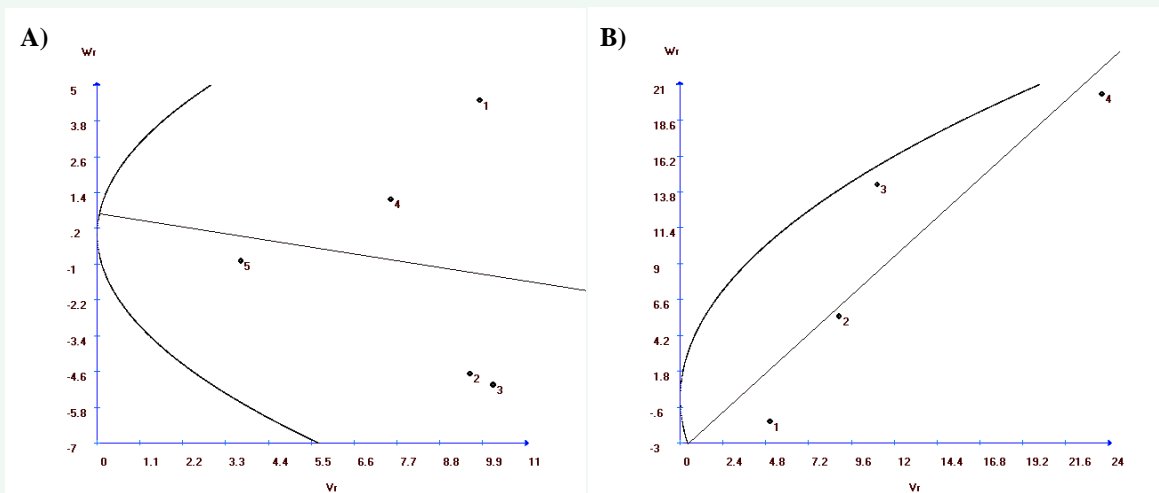


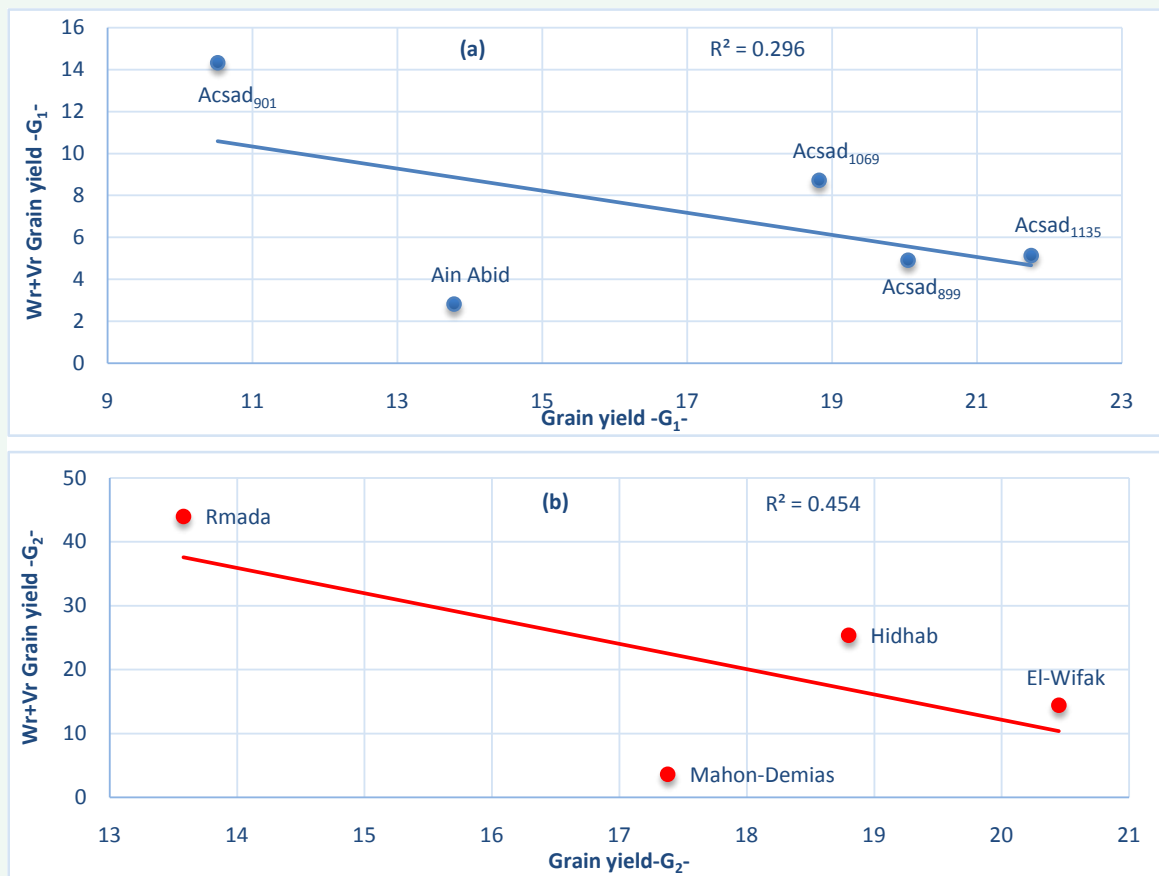
Figure 7 Wr on Vr graphs for grain yield per plant in G1 (a) and G2 (b) parental groups.

these traits are controlled by dominant alleles; while a positive correlation was observed for GN in both groups, indicating that these traits are controlled by recessive alleles (Figures 2-8).

### CONCLUSION

In order to fulfill the demands of rapidly increasing population, we need to increase the grain production per unit area

by using available resources. Therefore, it is necessary to utilize wheat cultivars having wider genetic base capable of producing better yield under a wide range of agro-climatic conditions. The present study analyzed two parental groups and found sufficient variability in both parental groups to sustain genetic improvement for BY, GN, SN and GY. Graphics analysis identified parents containing more dominant genes, those with more



**Figure 8**  $Wr + Vr$  on Parents values for grain yield per plant in  $G_1$  (a) and  $G_2$  (b) parental groups.

recessive genes and those which displayed equal proportion of dominant and recessive genes for the characteristics under study. The ordinate of the regression line suggested over-dominant inheritance for BY and SN in group 1 ( $G_1$ ) and for BY and GY in group 2 ( $G_2$ ); partial dominant inheritance for GN in both groups, for GY in group 1 and for SN in group 2. In both groups, BY, SN and GY are controlled by dominant alleles while GN is controlled by recessive alleles in both groups, as suggested by the sign of the correlation between  $Wr+Vr$  and parental values.

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