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Estimation of Combining Ability and Genetic Components for Yield Contributing Traits in Spring Barley under Normal and Salinity Conditions

E. Mansour[#] and E. S. A. Moustafa[*]
Crop Science Department, Faculty of Agriculture, Zagazig University, Zagazig 44519 and [*]Genetic Resources Department, Desert Research Center, Cairo 11753, Egypt.

HALF diallel analysis among diverse eight six-rowed hulled spring barley genotypes was performed to provide information on general and specific combining ability, gene action and heritability for different agronomic traits under normal and salinity conditions. The genotypes used were four commercially cultivars (Giza 123, Giza 126, Giza 132 and Giza 2000) and the other four were introduced from ICARDA (Australian, CHK 38, CHK 2 and CHK 53). The parents were grown and crossed during 2014-2015 in the Experimental Farm of Faculty of Agriculture (Ghazala), Zagazig University, Egypt. In the second season 36 genotypes *i.e.* 28 hybrid combination and eight parents were sown at two distinct locations. The first was in Ghazala as normal condition and the other was under salinity condition in the Experimental Farm of Desert Research Center, Ras-Sudr Research Station, South Sinai, Egypt, with salinity in irrigation water and soil containing 4500 ppm and 5535 ppm, respectively. All field experiments lay out in a randomized complete block design with three replications. The measured traits were; plant height (cm), spike length (cm), number of spikes per plant, number of grains per spike, grain weight per spike (g), 100 grain weight (g) and grain yield per plant (g). Analysis of variance indicated that there were highly significant differences between parental genotypes and theirs F1 crosses for all studied traits. General (GCA) and specific (SCA) combining ability effects were highly significant under both conditions for all traits. The parental genotypes; P3 (Australian) and P6 (CHK 53) showed good performance as well as good GCA effects under salinity condition, while P4 (CHK 38) and P8 (Giza 2000) under normal one and P2 (Giza 126), P5 (CHK 2) and P7 (Giza 132) under both conditions. The cross combinations; P3×P5, P3×P8 and P5×P8 exhibited good performance and significant positive SCA effects for grain yield and its attributes under salinity, while P2×P7, P3×P4, P4×P7, P5×P7 P6×P7 and P7×P8 under both conditions. The variance due to SCA was higher than that of GCA for all the traits except plant height and number of spikes per plant under salinity condition and 100 grain weight under normal condition. The components of genetic variance suggested more contribution of the dominance effects in the inheritance of the studied traits compared to

[#]Corresponding author e-mail address: sayed_mansour_84@yahoo.es

additive ones. Narrow sense heritability values changed from environment to another, it ranged from low to moderate (4.62% to 31.96). Wr-Vr graphs showed high degree of genetic diversity for parents with different degrees of dominance and different distribution of dominant and recessive alleles in the parental material for all traits under both conditions.

Barley (*Hordeum vulgare* L.) is one of the main cereal crops in the world, ranking fourth in terms of planted area and total production after maize, wheat and rice (FAOSTAT, 2016). It has very broad ecological adaptation and it is grown in regions with climates unfavorable for production of other cereals. It is commonly grown under dry conditions, poor and even saline soils. Due to these characteristics, it has been the principal grain produced in numerous stress-prone areas (Poehlman, 1985). The major uses of barley today are; mainly for livestock feed, malt, a component in a variety of foods, and has minor uses in the pharmaceutical industry (Biel and Jacyno, 2013). The barley cultivation area in the world in 2014 was 49.7 million hectares produced 8.5 million tons (FAOSTAT, 2016). While Egypt was involved in these values with low cultivation area which was 82500 hectares produced 5100 tons, therefore, it is needed to increase both; cultivated area and productivity.

Salinity in irrigation water and in soil is one of the major limiting factors for agricultural productivity. Large proportion of the total land area in the world is salt-affected. Egypt faces salinity problem and exploiting these areas is necessary to increase the production and reduce the gap between production and consumption of important crops (El‑Hendawy *et al*., 2009). Therefore, using salt tolerant genotypes present an important solution for this economic problem (Kulshreshtha & Singh, 2011).

Developing high yielding-varieties and tolerant to biotic or abiotic stresses is the main objective of breeding programs. It is necessary to have suitable information about the nature of genetic variability in the available breeding materials to achieve efficient selection (Zecevic *et al*., 2010). The selection mainly depends on additive genetic variance, effect of the environment and genotype by environment interaction (Eshghi & Akhundova, 2009).

Diallel cross analysis is a useful mating system used by plant breeders and geneticists to estimate the genetic nature of qualitative and quantitative traits (Hallauer & Miranda, 1988). It is an effective analysis to compute general (GCA) and specific combining ability (SCA) in a set of genotypes and compare their performance in different crosses combinations, and also to investigate the action of genes and heritability of important traits (Walejkl & Rusell, 1977; Salgotra *et al*., 2009 and Zhang *et al*., 2015). It leads to identify suitable parents with high combining ability, which is very useful for producing hybrids with greater

heterosis in barley breeding programs (Zhang *et al*., 2015). The genotypes which present high GCA indicate that they have ability to combine well with others and could be used to produce improved lines in breeding programs as well as indicate to additive gene effects for the studied traits (Madić *et al*., 2014). On the other hand the genotypes which present high values of SCA indicate to combine well only in certain crosses also indicate to dominance gene effects for the studied traits (Qu *et al*., 2012). The combining ability can be analyzed using the Griffing (1956) method, whereas to study gene action, genetic components and heritability, the Hayman (1954) method can be used. Griffing and Hayman analyses are often used together for completing data interpretation (Syukur *et al*., 2010). This provides an opportunity to obtain a rapid and general picture of genetic control for a set of genotypes in early generations. Also the regression graph of covariance (Wr) and variance (Vr) of arrays in diallel crosses provided useful information for the average degree of dominance of genes affecting the studied traits and the distribution of dominant and recessive alleles in the used parents (Jinks & Hayman, 1953 and Jana, 1975).

The aim of this work was to determine general and specific combining ability in a half diallel cross involving eight spring barley genotypes and their F1 crosses. And also to study the gene action and heritability of different agronomic traits under normal and salinity conditions, which provide useful information for barley breeding programs.

Materials and Methods

Field experiments and plant materials

The plant materials used in this study included four commercial cultivars and the others were introduced from ICARDA (Table 1). In the first season 2014-2015, parents were grown in the Experimental Farm of Faculty of Agriculture (Ghazala), Zagazig University, Egypt (30° 34′ N, 31° 34′ E). 8×8 half diallel mating system was used to produce 28 F1 hybrids. In the second season 2015-2016 the derived hybrid seeds from 28 crosses and their parents were sown at two distinct locations. The first was in Ghazala as normal condition and the other was under salinity condition in the Experimental Farm of Desert Research Center, Ras-Sudr Research Station, South Sinai, Egypt (29° 35′ N, 32° 41′ E) with salinity in irrigation water and soil containing 4500 ppm and 5535 ppm, respectively (Table 2). Both experiments were layout in the field of a randomized complete block design (RCBD) with three replications. Each of 36 entries was planted in a single row, 2 meter long with 20 cm between rows and 10 cm within rows spacing's. All recommended agronomic practices from sowing until harvesting including irrigation, nitrogen, potassium and phosphate fertilizers and pest, disease and weed control were applied for barley in each region.

Studied traits

Ten plants were selected randomly from each replication for parents and F1s to record observations of; plant height (cm), spike length (cm), number of spikes

per plant, number of grains per spike, grain weight per spike (g), 100 grain weight (g) and grain yield per plant (g).

TABLE 1. Name, origin and pedigree of eight barley genotypes.

Codes	Genotype	Origin	Year of release	Pedigree
P1	Giza 123	Egypt	1988	Giza 117 / FAO 86
P2	Giza 126	Egypt	1995	Baladi Bahteem/S D729-Por12762-BC
P3	Australian	ICARDA	-	SALIAN/4/DEIRALLA106/CEL/3/ BCOMR/MZG//APM/5106
P4	CHK 38	ICARDA	-	BARBATA/4/BACA(S)/3/AE253// EI08887/CIO5761/5/DAT00CRA
P5	CHK 2	ICARDA	-	MARI/ATHS*2//AVT/ATTIKI/3/ ATHS /LIGNEE686/5/AGER//API/ CM67 /3/CEL/WI2269//ORE/4/ALANDA
P6	CHK 53	ICARDA	-	Atahualpa//Alanda-01/Hamra/3/Keel ICB03-0170-26AP-0AP
P7	Giza 132	ICARDA	2006	Rihane-O5 // AS 46 / Aths*2" Aths / Lignee 686
P8	Giza 2000	Egypt	2000	Giza 117 / Bahtim 52 // Giza 118 / FAO 86/3/ Baladi 16/ Gem. (Giza 121)

TABLE 2 Soil properties of the experimental sites Ghazala and Ras-Sudr.

	Ghazalah (Soil)	Ras-Sudr (Soil)	Ras-Sudr (Irrigation water)
Sand%	20.61	86.08	
Silt%	31.82	8.05	
Clay%	47.57	10.67	
Textural class	Clay	Sandy loam	
CaCO3 (g kg^{-1})	6.14	56.99	
Organic matter (g kg^{-1})	10.34	2.20	
pH	8.02	7.78	8.62
EC(dSm^{-1})	1.94	8.65	7.03
Soluble cations and anions (mmolc L^{-1})			
Ca^{++}	5.22	38.22	
Mg^{++}	4.37	27.44	
Na^{+}	4.52	58.83	40.05
K^{+}	5.39	2.01	0.12
HCO3^{-}	6.08	3.43	4.54
Cl^{-}	6.58	64.14	48.94
SO4$^{=}$	6.84	58.93	29.23
Available nutrient (mg kg^{-1}soil)			
N	57.32	20.20	
P	8.15	4.10	
K	149.3	50.80	

Statistical analysis

Data obtained from barley Diallel crosses was statistically were performed according to (Griffing, 1956) method 2, model 1, the analysis was applied for each environment separately. Also, the components of genetic variance and Wr-Vr graphs were estimated by Hayman (1954a), Hayman (1954b) and Mather & Jinks (1982).

Results and Discussion

For generating useful information on general and specific combining ability, gene action and heritability for important agronomic traits, diallel analysis for eight diverse spring barley genotypes was performed. This could help in the selection process in breeding programs under normal and salinity conditions.

Analysis of variance

Analysis of variance for studied traits is presented in Table 3. It was found highly significant differences between genotypes at both locations for all studied traits. This result provides evidence for presence of genetic variability in the used materials, which could be exploited in barley breeding programs for improving yield and its contributing traits. Dividing the genotypic variance into parents, crosses and parent vs. crosses, indicated that the variance due to parents as well as crosses were highly significant for all studied traits. Also it was found highly significant differences among parents and their F1 crosses for all traits except plant height and 100 grain weight under normal condition (Ghazala). Similar differences between parents and crosses were found by other researchers as Eshghi & Akhundova (2009), Saad *et al*. (2013), Zhang *et al*. (2015), Ahmadi *et al*. (2016), Patial *et al*. (2016) and Pesaraklu *et al*. (2016).

The variance due to general (GCA) and specific combining ability (SCA) are showed in Table 3. It was found that the variance of GCA and SCA was highly significant under both conditions for all studied traits. This indicated that both additive and non-additive gene actions contributed significantly in the inheritance of these traits, and it reveals the importance of both types of gene action in selecting transgressive genotypes through barley breeding programs. However, the variance due to SCA was higher than that of GCA for all traits except plant height and number of spikes per plant under salinity condition and 100 grain weight under normal condition. This result suggested the importance of non-additive gene action in the inheritance of these traits. Furthermore the ratio of GCA/SCA was less than one supporting the forgoing result. Hence, selection for these traits should be in later generation within the segregating populations. The importance of additive and non-additive gene action in the inheritance of the studied traits was confirmed previously by different authors Yilmaz & Konak (2000), Ali *et al*. (2007), Potla *et al*. (2013), Saad *et al*. (2013), Madić *et al*. (2014), Tofiq *et al*. (2015) and Patial *et al*. (2016).

Mean performance of parents and F1 crosses

Mean performance of barley genotypes and their F1 crosses for studied traits under both conditions are showed in Table 4. Wide significant differences were noticed among the parents and the crosses for all studied traits under both conditions. Also, it was observed considerable differences between the two locations of study for all traits. The mean values of traits reduced at Ras-Sudr (salinity condition) compared with their respective at Ghazala (normal condition). This reduction was caused by the salinity stress effect. The highest reduction was assigned for grain yield per plant (37.8%) followed by number of spikes per plant (28.2%) and plant height (14.5%). Otherwise the lowest reduction was assigned for Spike length (8.1%) followed by 100 grain weight (10.1%), number of grains per spike (12.3%) and grain weight per spike (12.6%).

TABLE 3. Mean squares of agronomic traits for the eight barley genotypes and their 28 F1 crosses under normal (Gh.) and salinity (Rs.) conditions.

Source of variance	df	Plant height (cm)		No. of spikes/plant		Spike length (cm)		No. of grains/spike	
		Gh.	Ras.	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
Genotypes	35	149.41**	249.59**	23.53**	38.24**	2.58**	3.07**	205.10**	271.04**
Parents	7	158.78**	134.62**	6.14**	2.85**	1.20**	2.57**	111.76**	154.68**
Crosses	27	152.41**	115.56**	21.01**	31.62**	1.82**	2.37**	83.92**	137.40**
P. vs. C.	1	2.70 ns	4673.42**	213.38**	464.72**	32.83**	25.48**	4130.40**	4693.83**
Error	70	2.74	1.03	0.23	0.38	0.02	0.03	1.15	1.04
GCA	7	47.87**	304.79**	13.15**	50.88**	2.52**	2.91**	155.78**	67.59**
SCA	28	174.80**	246.68**	26.13**	36.89**	2.60**	3.21**	217.43**	324.32**
σ^2GCA/σ^2SCA		0.27	1.24	0.50	1.38	0.97	0.91	0.72	0.21

n.s.: non-significant, * $P < 0.05$, ** $P < 0.01$

TABLE 3. Cont.

Source of variance	Grain weight/spike (g)		100 grain weight (g)		Grain yield/plant (g)	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
Genotypes	1.34**	1.45**	0.75**	0.86**	572.54**	667.12**
Parents	0.58**	0.95**	0.57**	0.21**	79.51**	19.13**
Crosses	0.98**	0.96**	0.82**	0.91**	497.92**	517.28**
P. vs. C.	16.60**	18.42**	0.01 ns	4.11**	6038.55**	9248.68**
Error	0.01	0.01	0.02	0.01	0.64	0.79
GCA	0.92**	0.78**	1.14**	0.24**	522.92**	583.81**
SCA	1.45**	1.65**	0.65**	1.03**	584.95**	708.79**
σ^2GCA/σ^2SCA	0.64	0.47	1.76	0.24	0.89	0.82

n.s.: non-significant, * $P < 0.05$, ** $P < 0.01$

TABLE 4. Mean performances of the agronomic traits for eight barley genotypes and their 28 F1 crosses under normal (Gh.) and salinity (Rs.) conditions.

Genotypes	Plant height (cm)		No. of spikes/plant		Spike length (cm)	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
P1	81.0	66.2	11.4	5.6	6.6	6.6
P2	93.9	68.9	10.9	6.0	6.7	6.2
P3	100.8	51.1	11.9	6.6	7.7	7.6
P4	95.6	65.4	8.4	6.2	6.1	4.8
P5	96.1	73.9	9.4	6.9	6.3	5.4
P6	81.4	65.9	10.4	7.1	6.4	6.2
P7	86.1	67.2	11.4	5.2	7.5	7.0
P8	93.1	60.6	13.0	4.2	6.0	5.4
P1 × P2	91.1	79.8	12.4	8.6	8.5	7.4
P1 × P3	104.0	74.3	14.9	10.1	7.8	7.4
P1 × P4	91.0	76.9	13.4	6.1	7.9	7.8
P1 × P5	95.7	77.4	13.4	8.4	7.9	7.5
P1 × P6	80.5	79.7	13.9	6.7	7.8	7.5
P1 × P7	90.4	84.7	11.7	11.7	8.6	5.8
P1 × P8	85.2	84.3	13.4	6.7	7.7	7.4
P2 × P3	80.2	80.1	14.7	14.6	7.7	7.1
P2 × P4	85.2	73.7	12.4	10.4	7.3	7.2
P2 × P5	75.9	71.8	11.3	9.8	6.3	6.1
P2 × P6	95.2	68.2	14.4	9.2	8.4	6.2
P2 × P7	99.8	76.2	12.4	9.8	9.2	8.6
P2 × P8	84.3	81.8	12.9	7.2	7.6	6.5
P3 × P4	95.6	79.8	18.4	9.8	8.3	7.6
P3 × P5	91.0	80.3	14.7	14.6	8.1	7.7
P3 × P6	87.9	74.8	11.7	11.6	7.8	7.4
P3 × P7	80.4	73.2	13.3	12.8	6.6	5.9
P3 × P8	83.4	79.2	11.3	10.2	8.7	8.4
P4 × P5	91.0	87.8	16.3	7.6	6.5	6.3
P4 × P6	93.6	79.9	14.4	12.8	7.6	6.2
P4 × P7	90.2	84.9	17.3	9.7	9.0	8.5
P4 × P8	90.7	82.3	19.3	9.8	7.6	7.4
P5 × P6	90.1	89.9	15.1	15.0	7.9	7.1
P5 × P7	98.7	94.3	19.3	16.2	9.5	9.3
P5 × P8	99.0	87.2	18.9	18.8	8.1	7.4
P6 × P7	95.7	88.8	19.3	15.3	8.7	8.2
P6 × P8	103.7	78.6	11.3	9.2	7.4	6.6
P7 × P8	90.1	89.9	14.6	14.4	8.9	8.5
L.S.D $_{0.05}$	**2.69**	**1.66**	**0.78**	**1.00**	**0.20**	**0.30**

It was noticed that the parent Giza 126 (P2) showed the highest values for number of grains per spike, 100 grain weight, grain weight per spike and grain yield under both conditions. Also, Australian (P3) exhibited highest values for spike length under both conditions, as well as presented highest plant height under normal condition; while CHK 2 (P5) surpassed the other genotypes under salinity condition. The shortest plant height was assigned for CHK 53 (P6) under normal condition and Australian (P3) under salinity condition. CHK 53(P6) gave the highest number of spikes per plant under salinity condition. Otherwise, Giza 2000 (P8) was the highest one under normal condition. Thus, these genotypes could be considered as good genotypes for increasing grain yield and its attributes under the target environment.

Also it was observed that the F1 crosses showed performance better than the parents in all studied traits (Table 4). The cross, P5×P7 presented the tallest plant height under salinity condition, and spike length under both conditions and highest

grain yield per plant under normal condition. Barley cross P6×P7 produced the highest number of spikes per plant under normal condition and number of grains per spike under salinity condition. Otherwise P5×P8 surpassed the other crosses in number of spikes per plant and grain yield per plant under salinity condition. P2×P7 produced the greatest number of grains per spike under normal condition and 100 grain weight under salinity one. Furthermore P7×P8 exhibited the highest grain weight per spike under both conditions. Similar genetic differences for studied traits were previously found by Ahmed *et al.* (1998), Sharma *et al.* (2002), Ali *et al.* (2007), Eshghi & Akhundova (2009), Aghamiri *et al.* (2012), Saad *et al.* (2013), Zhang *et al.* (2015), Patial *et al.* (2016) and Pesaraklu *et al.* (2016).

TABLE 4. Cont.

Genotypes	No. of grains/spike		Grain weight/spike (g)		100 grain weight (g)		Grain yield/plant (g)	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
P1	48.1	45.2	2.9	2.7	5.7	4.8	29.9	10.6
P2	57.3	52.2	3.5	3.3	6.6	5.3	34.0	13.7
P3	43.7	33.1	2.5	1.9	5.7	4.4	28.5	8.3
P4	40.7	30.7	2.3	1.5	5.8	5.0	18.9	8.5
P5	47.4	36.9	2.6	2.3	6.2	4.8	28.1	10.5
P6	41.0	40.7	2.3	2.1	5.3	4.6	21.5	10.5
P7	51.9	33.9	3.1	2.3	6.1	4.8	32.2	7.0
P8	40.1	35.3	2.3	1.8	5.9	5.0	29.8	5.6
P1 × P2	70.8	54.7	3.8	2.9	5.1	4.9	42.6	21.7
P1 × P3	54.2	51.0	4.0	3.5	6.0	5.6	44.0	29.3
P1 × P4	56.7	55.2	3.2	3.2	7.0	5.4	51.0	18.4
P1 × P5	67.0	55.7	4.2	4.0	5.6	5.3	48.5	25.7
P1 × P6	57.6	53.3	3.4	3.1	6.2	5.7	24.7	20.4
P1 × P7	55.2	36.6	2.7	2.5	6.2	5.6	29.7	22.1
P1 × P8	55.6	53.3	3.6	3.4	5.4	5.3	34.9	16.2
P2 × P3	55.5	47.8	3.0	2.3	5.4	5.1	35.4	34.1
P2 × P4	61.1	60.3	3.8	3.4	5.6	5.2	34.2	31.9
P2 × P5	59.9	57.4	3.6	3.2	5.1	5.1	32.8	29.5
P2 × P6	66.6	47.9	2.8	2.6	5.2	4.9	47.1	21.0
P2 × P7	71.2	51.7	4.1	3.8	6.5	6.4	55.7	29.8
P2 × P8	56.7	55.2	3.0	2.4	6.0	5.6	31.0	21.4
P3 × P4	61.5	59.4	4.3	4.1	5.8	5.4	62.8	35.6
P3 × P5	64.1	61.2	4.2	3.6	6.4	6.2	54.3	52.8
P3 × P6	64.0	62.2	3.5	3.3	5.5	5.3	44.0	40.7
P3 × P7	56.6	53.3	3.5	3.0	5.4	3.7	38.2	24.7
P3 × P8	67.2	64.6	3.5	3.3	5.2	5.0	37.2	35.4
P4 × P5	60.5	57.7	4.0	3.3	5.2	4.6	44.5	14.6
P4 × P6	60.2	53.1	3.0	2.6	5.7	5.5	44.1	41.0
P4 × P7	62.1	52.4	3.5	3.1	6.4	5.6	65.8	26.6
P4 × P8	58.6	50.9	3.4	3.3	5.4	4.4	57.4	17.7
P5 × P6	59.2	54.7	3.5	3.0	5.8	5.5	42.3	40.7
P5 × P7	67.4	60.8	4.0	3.8	6.3	5.2	78.5	51.6
P5 × P8	56.1	50.7	4.2	3.6	6.3	6.1	63.4	59.9
P6 × P7	69.9	66.9	4.6	4.0	5.3	5.1	57.1	55.1
P6 × P8	53.2	37.6	2.4	2.0	5.5	5.0	29.5	15.7
P7 × P8	63.7	56.1	4.7	4.2	6.5	6.0	53.7	50.8
L.S.D $_{0.05}$	**1.75**	**1.66**	**0.15**	**0.18**	**0.22**	**0.16**	**1.31**	**1.45**

General and specific combining ability effects

　　　The GCA effect was estimated of the parental genotypes for studied traits to identify the best parents and good combiners for producing transgressive phenotypes (Table 5). Negative GCA effect is desirable for plant height to avoid plant lodging, while for other traits positive effects are desirable to increase grain yield and its components. It was found that Giza 123 (P1) presented good combining ability for reducing plant height, furthermore it was a good combiner for increasing 100 grain weight under both conditions. Giza126 (P2) was a good combiner for reducing plant height and increasing number of grains per spike under both conditions. Australian (P3) was a good combiner for reducing plant height and increasing number of spikes plant, spike length, number of grains per spike and grain yield per plant under salinity condition. CHK 38 (P4) was a good combiner for number of spikes per plant and grain yield per plant under normal condition, otherwise, CHK 53 (P6) exhibited good combination for the same traits under salinity condition. CHK 2 (P5) and Giza 132 (P7) showed good combinations for grain yield and its components under both conditions. Giza 2000 (P8) was a good combiner for number of spikes per plant under normal condition and for 100 grain weight under salinity one. Hence, these genotypes can be further used in developing segregating populations in barley breeding programs, especially P3 and P6 under salinity condition, P4 and P8 under normal condition, and P5 and P7 under both conditions. Similar results in respect to GCA effects have been reported by Ali *et al*. (2007), Potla *et al*. (2013), Saad *et al*. (2013), Madić *et al*. (2014), Patial *et al*. (2016) and Pesaraklu *et al*. (2016).

TABLE 5. Estimates of general combining ability (GCA) effects of eight barley genotypes for the studied traits under normal (Gh.) and salinity (Rs.) conditions.

Parents	Plant height (cm)		No. of spikes/plant		Spike length (cm)		No. of grains/spike	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
P1	-1.64 **	-0.53 *	-0.57 **	-1.93 **	0.03 ns	0.03 ns	-0.74 **	-0.73 **
P2	-1.69 **	-2.53 **	-0.94 **	-0.72 **	-0.09 **	-0.20 **	3.58 **	2.20 **
P3	0.77 *	-5.07 **	-0.12 ns	0.84 **	0.11 **	0.32 **	-1.01 **	0.84 **
P4	1.20 **	0.12 ns	0.71 **	-1.02 **	-0.29 **	-0.31 **	-1.85 **	-0.69 **
P5	1.72 **	4.17 **	0.00 ns	1.54 **	-0.22 **	-0.12 **	0.83 **	1.46 **
P6	-0.68 ns	-0.33 ns	-0.50 **	0.54 **	-0.08 *	-0.21 **	-0.80 **	-0.04 ns
P7	-0.10 ns	3.18 **	0.92 **	1.16 **	0.64 **	0.53 **	2.93 **	-1.19 **
P8	0.41 ns	0.98 **	0.50 **	-0.41 **	-0.11 **	-0.05 ns	-2.94 **	-1.85 **
S.E.(gi-gj)	0.282	0.174	0.082	0.105	0.021	0.031	0.183	0.174

n.s.: non-significant, * $P < 0.05$, ** $P < 0.01$

TABLE 5. Cont.

Parents	Grain weight/spike (g)		100 grain weight (g)		Grain yield/plant (g)	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
P1	-0.01 [ns]	0.09 [**]	0.09 [*]	0.05 [**]	-4.16 [**]	-6.46 [**]
P2	0.04 [*]	0.02 [ns]	-0.26 [**]	0.04 [*]	-3.35 [**]	-2.29 [**]
P3	0.02 [ns]	-0.02 [ns]	-0.11 [**]	-0.18 [**]	-0.39 [*]	2.94 [**]
P4	-0.09 [**]	-0.11 [**]	0.05 [ns]	-0.02 [ns]	2.08 [**]	-3.71 [**]
P5	0.21 [**]	0.19 [**]	0.19 [**]	0.06 [**]	4.36 [**]	5.60 [**]
P6	-0.29 [**]	-0.22 [**]	-0.24 [**]	-0.06 [*]	-4.51 [**]	1.58 [**]
P7	0.25 [**]	0.18 [**]	0.29 [**]	0.04 [*]	6.97 [**]	3.49 [**]
P8	-0.12 [**]	-0.12 [**]	0.00 [ns]	0.06 [*]	-1.01 [**]	-1.15 [**]
S.E.(gi-gj)	0.015	0.018	0.023	0.017	0.137	0.152

N.S.: non-significant, * $P < 0.05$, ** $P < 0.01$

SCA effect is used for determining the best cross combinations for exploiting the heterosis. It was found significant effects for several crosses in each trait, indicates to presence of non-additive (dominance and epitasis) gene action (Table 6). The crosses; P2×P5, P3×P7 and P2×P6 exhibited the highest significant negative SCA effects for plant height under both conditions. Highest significant SCA values for number of spikes per plant and grain weight per spike were recorded by cross P6×P7 under normal condition as well as high values under salinity one. While under salinity condition the highest SCA for number of spikes per plant was recorded by P5×P8 and for grain weight per spike was recorded by P3×P4. Also P6×P7 presented the highest significant SCA for number of grains per spike under salinity condition as high value under normal condition. Otherwise, the highest one under normal condition was assigned for P3×P8 which exhibited also high value under salinity condition. The cross P5×P7 showed the highest SCA for spike length under both conditions. The highest SCA value of 100 grain weight was recorded by P1×P4 under normal condition while the highest one under salinity condition was P2×P7. Highest SCA value of grain yield per plant was assigned for P5×P7 under normal condition while the highest one under salinity condition was P5×P8. These cross combinations participated in at least one of good general combiner parent. Different crosses registered desirable SCA effects when studied by other authors (Ali *et al.*, 2007; Potla *et al., 2013*; Saad *et al.*, 2013; Madić *et al.*, 2014; Patial *et al.*, 2016 and Pesaraklu *et al.,* 2016).

TABLE 6. Estimates of specific combining ability (SCA) effects of the 28 crosses for the studied traits under normal (Gh.) and salinity (Rs.) conditions .

Crosses	Plant height (cm)		No. of spike/plant		Spike length (cm)		No. of grains/spike	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
P1 × P2	3.73 **	5.63 **	0.45 ns	1.34 **	0.90 **	0.52 **	10.08 **	2.37 **
P1 × P3	14.17 **	2.72 **	2.07 **	1.33 **	0.00 ns	-0.04 ns	-1.93 **	0.07 ns
P1 × P4	0.73 ns	0.09 ns	-0.21 ns	-0.80 *	0.42 **	0.99 **	1.43 *	5.82 **
P1 × P5	4.88 **	-3.41 **	0.50 ns	-1.03 **	0.41 **	0.55 **	9.07 **	4.12 **
P1 × P6	-7.86 **	3.32 **	1.45 **	-1.81 **	0.17 *	0.57 **	1.24 ns	3.28 **
P1 × P7	1.48 ns	4.81 **	-2.41 **	2.58 **	0.27 **	-1.84 **	-4.82 **	-12.35 **
P1 × P8	-4.26 **	6.68 **	0.01 ns	-0.85 *	0.11 ns	0.32 *	1.46 *	5.09 **
P2 × P3	-9.68 **	10.72 **	1.89 **	4.68 **	-0.03 ns	-0.07 ns	-4.89 **	-6.08 **
P2 × P4	-5.00 **	-1.13 ns	-0.83 **	2.32 **	-0.04 ns	0.61 **	1.53 *	8.01 **
P2 × P5	-14.85 **	-7.07 **	-1.23 **	-0.91 *	-1.10 **	-0.61 **	-2.31 **	2.96 **
P2 × P6	6.88 **	-6.13 **	2.38 **	-0.50 ns	0.83 **	-0.43 **	5.97 **	-5.09 **
P2 × P7	10.86 **	-1.63 *	-1.04 **	-0.53 ns	0.96 **	1.20 **	6.84 **	-0.16 ns
P2 × P8	-5.09 **	6.12 **	-0.17 ns	-1.51 **	0.13 ns	-0.29 *	-1.82 *	4.05 **
P3 × P4	2.88 *	7.51 **	4.35 **	0.09 ns	0.74 **	0.54 **	6.48 **	8.48 **
P3 × P5	-2.19 *	4.02 **	-0.05 ns	2.42 **	0.50 **	0.48 **	6.41 **	8.10 **
P3 × P6	-2.90 *	2.96 **	-2.00 **	0.47 ns	0.05 ns	0.26 *	7.96 **	10.60 **
P3 × P7	-10.92 **	-2.10 **	-0.97 **	0.91 ns	-1.86 **	-1.97 **	-3.13 **	2.86 **
P3 × P8	-8.44 **	6.10 **	-2.55 **	-0.07 ns	1.05 **	1.03 **	13.30 **	14.75 **
P4 × P5	-2.63 *	6.27 **	2.11 **	-2.83 **	-0.65 **	-0.36 **	3.67 **	6.08 **
P4 × P6	2.37 *	2.89 **	0.73 *	3.39 **	0.25 **	-0.36 **	4.98 **	3.02 **
P4 × P7	-1.59 ns	4.38 **	2.20 **	-0.33 ns	0.97 **	1.21 **	3.21 **	3.50 **
P4 × P8	-1.65 ns	4.02 **	4.62 **	1.35 **	0.31 **	0.74 **	5.57 **	2.61 **
P5 × P6	-1.64 ns	8.89 **	-1.67 **	3.05 **	0.55 **	0.39 **	1.30 ns	2.42 **
P5 × P7	6.34 **	9.77 **	4.91 **	3.66 **	1.42 **	1.80 **	5.80 **	9.68 **
P5 × P8	6.16 **	4.86 **	3.55 **	7.79 **	0.78 **	0.52 **	0.33 ns	0.23 ns
P6 × P7	5.74 **	8.72 **	5.41 **	3.77 **	0.48 **	0.78 **	9.91 **	17.29 **
P6 × P8	13.23 **	0.70 ns	-2.17 **	-0.77 ns	-0.06 ns	-0.26 *	-0.92 ns	-11.38 **
P7 × P8	-3.13 *	8.74 **	-0.31 ns	3.84 **	0.68 **	0.99 **	5.86 **	8.33 **
S.E.(sij - sji)	1.05	0.64	0.30	0.39	0.08	0.12	0.68	0.64

n.s.: non-significant, * P < 0.05, ** P < 0.01

TABLE 6. Cont.

Crosses	Grain weight/spike (g)				100 grain weight (g)				Grain yield/plant (g)			
	Gh.		Ras.		Gh.		Ras.		Gh.		Ras.	
P1 × P2	0.34	**	-0.19	*	-0.55	**	-0.40	**	8.28	**	3.85	**
P1 × P3	0.57	**	0.41	**	0.26	*	0.51	**	6.69	**	6.20	**
P1 × P4	-0.10	ns	0.21	**	1.10	**	0.17	*	11.20	**	1.96	**
P1 × P5	0.58	**	0.69	**	-0.48	**	-0.03	ns	6.43	**	-0.04	ns
P1 × P6	0.27	**	0.22	**	0.53	**	0.47	**	-8.55	**	-1.35	*
P1 × P7	-0.97	**	-0.81	**	0.07	ns	0.31	**	-14.96	**	-1.53	*
P1 × P8	0.34	**	0.41	**	-0.46	**	-0.03	ns	-1.79	ns	-2.85	**
P2 × P3	-0.46	**	-0.70	**	-0.05	ns	0.02	ns	-2.69	*	6.86	**
P2 × P4	0.40	**	0.53	**	0.00	ns	-0.05	ns	-6.37	**	11.24	**
P2 × P5	-0.05	ns	-0.02	ns	-0.58	**	-0.20	**	-10.12	**	-0.45	ns
P2 × P6	-0.35	**	-0.16	*	-0.11	ns	-0.24	**	13.10	**	-4.95	**
P2 × P7	0.39	**	0.58	**	0.73	**	1.11	**	10.18	**	1.91	**
P2 × P8	-0.30	**	-0.53	**	0.48	**	0.35	**	-6.49	**	-1.78	**
P3 × P4	0.99	**	1.26	**	0.03	ns	0.37	**	19.24	**	9.73	**
P3 × P5	0.60	**	0.40	**	0.52	**	1.08	**	8.45	**	17.62	**
P3 × P6	0.35	**	0.57	**	0.06	ns	0.38	**	6.99	**	9.52	**
P3 × P7	-0.22	**	-0.21	**	-0.58	**	-1.39	**	-10.28	**	-8.41	**
P3 × P8	0.16	*	0.45	**	-0.46	**	-0.07	ns	-3.26	**	6.95	**
P4 × P5	0.49	**	0.20	*	-0.78	**	-0.67	**	-3.80	**	-13.92	**
P4 × P6	-0.03	ns	-0.10	ns	0.07	ns	0.36	**	4.70	**	16.45	**
P4 × P7	-0.13	*	-0.01	ns	0.29	**	0.35	**	14.84	**	0.17	ns
P4 × P8	0.24	**	0.51	**	-0.46	**	-0.80	**	14.44	**	-4.08	**
P5 × P6	0.11	ns	-0.01	ns	0.02	ns	0.27	**	0.54	ns	6.93	**
P5 × P7	0.14	*	0.37	**	0.04	ns	-0.14	*	25.29	**	15.87	**
P5 × P8	0.66	**	0.55	**	0.32	**	0.79	**	18.20	**	28.76	**
P6 × P7	1.23	**	1.07	**	-0.50	**	-0.04	ns	12.72	**	23.42	**
P6 × P8	-0.56	**	-0.63	**	-0.04	ns	-0.23	**	-6.86	**	-11.38	**
P7 × P8	1.16	**	1.11	**	0.43	**	0.67	**	5.82	**	21.82	**
S.E.(sij - sji)	0.06		0.07		0.09		0.06		0.51		0.56	

n.s.: non-significant, $^*P < 0.05$, $^{**}P < 0.01$

Components of genetic variance

The components of genetic variance for studied traits are given in Table 7. The additive component (D) was not significant for all traits except plant height under salinity condition and number of grains per spike under normal condition which was positive and significant. On the other hand, the dominance components (H_1 and H_2) were positive and significant for all studied traits. Furthermore, the value of H_1 was higher than D, proposing more contribution of the over-dominance effects in the inheritance of these traits compared to additive ones. This was confirmed by the net dominance component (h^2) which was positive and significant for all traits under both conditions except plant height and 100 grain weight under normal condition which was not significant. Average degree of dominance $(H_1/D)^{1/2}$ was higher than unity for all studied traits under both conditions which underline the presence of over-dominance gene effects for these traits. The dominance effects for these traits suggesting that selection in early generations may not be useful and it should be delayed to late generations. The importance of both additive and non-additive components in the inheritance of studied traits, with more presence for dominance components is in accordance with the results of Sharma *et al*. (2002), Ali *et al*. (2007), Eshghi & Akhundova (2009), El-Seidy *et al*. (2010), Aghamiri *et al*. (2012), Tofiq *et al*. (2015), Patial *et al*. (2016) and Pesaraklu *et al*. (2016).

TABLE 7. Components of genetic variance for different traits under normal (Gh.) and salinity (Rs.) conditions.

Components	Plant height (cm)		No. of spikes/plant		Spike length (cm)		No. of grains/spike	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
D	51.94 [ns]	44.49 [**]	1.96 [ns]	0.80 [ns]	0.39 [ns]	0.84 [ns]	36.84 [**]	51.17 [ns]
H1	263.90 [**]	251.94 [**]	33.93 [**]	43.91 [**]	2.91 [**]	4.03 [**]	208.53 [**]	370.27 [**]
H2	208.63 [**]	216.47 [**]	27.70 [**]	36.02 [**]	2.66 [**]	3.51 [**]	199.15 [**]	309.38 [**]
F	101.51 [ns]	40.58 [ns]	5.27 [ns]	0.10 [ns]	0.27 [ns]	1.07 [ns]	27.73 [ns]	103.15 [ns]
h²	0.01 [ns]	766.56 [**]	34.97 [**]	76.18 [**]	5.38 [**]	4.17 [**]	677.46 [**]	769.91 [**]
E	0.98	0.39	0.09	0.15	0.01	0.01	0.41	0.39
$(H1/D)^{1/2}$	2.25	2.38	4.16	7.40	2.72	2.19	2.38	2.69
H2/4H1	0.20	0.21	0.20	0.21	0.23	0.22	0.24	0.21
KD/KR	2.53	1.47	1.96	1.02	1.29	1.81	1.38	2.20
h2/H2	0.00	3.54	1.26	2.12	2.02	1.19	3.40	2.49
h(n.s)	5.09	26.54	17.22	31.96	21.45	14.63	15.55	5.42

n.s.: non-significant, [*] P < 0.05, [**] P < 0.01

TABLE 7. Cont.

Components	Grain weight/spike (g)		100 grain weight (g)		Grain yield/plant (g)	
	Gh.	Ras.	Gh.	Ras.	Gh.	Ras.
D	0.19 ns	0.31 ns	0.18 ns	0.07 ns	26.17 ns	6.05 ns
H1	1.72 **	2.04 **	0.89 **	1.32 **	728.17 **	827.35 **
H2	1.48 **	1.65 **	0.82 **	1.24 **	603.46 **	701.13 **
F	0.27 ns	0.59 ns	0.10 ns	0.11 ns	45.44 ns	25.25 ns
h^2	2.72 **	3.02 **	0.00 ns	0.67 **	990.55 **	1517.22 **
E	0.00	0.00	0.01	0.00	0.34	0.33
$(H1/D)^{1/2}$	3.00	2.56	2.22	4.41	5.28	11.70
H2/4H1	0.22	0.20	0.23	0.24	0.21	0.21
KD/KR	1.62	2.19	1.29	1.44	1.39	1.43
h2/H2	1.83	1.83	0.00	0.54	1.64	2.16
h(n.s)	16.76	11.64	27.17	4.62	25.85	23.35

n.s.: non-significant, * $P < 0.05$, ** $P < 0.01$

The relative frequency of dominant to recessive alleles in the genotypes (F) was positive and insignificant for all studied traits, revealing to abundance of dominant alleles than recessive ones in the parents, as well as the important role of dominant genes for the studied traits (Table 7). This is corresponding with the proportion of dominance and recessive genes (KD/KR) in the parents which was more than the unity, implying that the dominant genes were more frequent than recessive ones for all studied traits under both conditions. Also this result is supported by the estimates of the ratio $H_2/4H_1$ which were less than 0.25 for all traits under both conditions, confirming the unequal distribution of positive and negative alleles among the parents. The environmental component (E) was high for plant height, number of spikes per plant, number of grains per spike and grain yield per plant under both conditions revealing the importance of environmental factors in expression of these traits, while low value was assigned for other traits. These results are in agreement with the finding of Rohman *et al.* (2006), Eshghi & Akhundova (2009), Aghamiri *et al.* (2012), Metwali *et al.* (2014) and Pesaraklu *et al.* (2016).

Phenotypic selection efficiency depends on the proportion of narrow sense heritability, where it is directly relative to additive genetic variance (Falconer *et al.*, 1996). Narrow sense heritability values were detected for all studied traits and changed from environment to another, it ranged from low to moderate (4.62% to 31.96). Especially under salinity condition the values were lower than normal one for grain yield and its components (Table 7). The low values due to excess of dominance effect as well as great effect of the environmental factors in the genetic control of these traits. Similar low narrow sense heritability was reported by Rohman *et al.* (2006) for number of spikes per plant, Eshghi & Akhundova (2009) for number of grains per spike, Pesaraklu *et al.* (2016) for plant height, spike length , grain weight per

spike and 100 grain weight and Tofiq *et al*. (2015) and Ahmadi *et al*. (2016) for grain yield per plant.

Wr-Vr Graph

The regression graphs of covariance (Wr) and variance (Vr) were constructed for further understanding the genetic nature of parental variation. The graphs for studied traits under normal condition (Ghazala) are shown in Fig. 1, and under salinity condition (Ras-Sudr) are shown in Fig. 2. Under normal condition, the regression line passed below the origin in all studied traits except plant height and 100 grain weight, the line passed through and above the origin, respectively. This indicated to presence of complete dominance genes effects in the inheritance of plant height, partial dominance for 100 grain weight and over dominance for the remaining traits. While under salinity condition, the regression line passed below the origin in plant height, grain weight per spike and 100 grain weight revealing to presence of over dominance in the inheritance of these traits. In number of spikes per plant, spike length and grain yield, the line passed over the origin revealing the presence of partial dominance. While in number of grains per spike, the line passed through the origin revealing the presence of complete dominance.

Under normal condition the distribution of parents along the regression line revealed that P4 possess maximum number of dominant alleles for plant height (Fig. 1). Also P1 and P2 carry dominant alleles for number of spikes per plant, grain weight per spike and grain yield per plant, P1 and P3 for spike length, P2 and P5 for number of grains per spike, and P3 and P6 for 100 grain weight. Otherwise P3 carries maximum number of recessive alleles for plant height, P4 and P5 carry recessive alleles for number of spikes per plant, P5 for spike length, P6 for number of grains per spike, P8 for grain weight per spike, P1 and P4 for 100 grain weight and P4, P5 and P7 for grain yield per plant.

While under salinity condition P2 possesses maximum number of dominant alleles for plant height and number of grains per spike (Fig. 2). Also P1 and P4 carry dominant alleles for number of spikes per plant, P1 and P3 for spike length, P1 for grain weight per spike and 100 grain weight, and P1 and P2 for grain yield per plant. While P3 carries maximum number of recessive alleles for plant height, as well as P8 carry recessive alleles for number of spikes per plant and grain weight per spike, P7 for spike length, number of grains per spike and 100 grain weight, and P5 and P8 for grain yield per plant. These results reveal to genetic diversity of parents, therefore, it could be expected that the combination of these genotypes lead to high degree of heterosis and production high values of the traits. Similar finding was reported by Jana (1975), Abdel-Sabour *et al*. (1990), Madić *et al*. (2005), Rohman *et al*. (2006), Eshghi & Akhundova (2009), Aghamiri *et al*. (2012) and Ciulca *et al*. (2012).
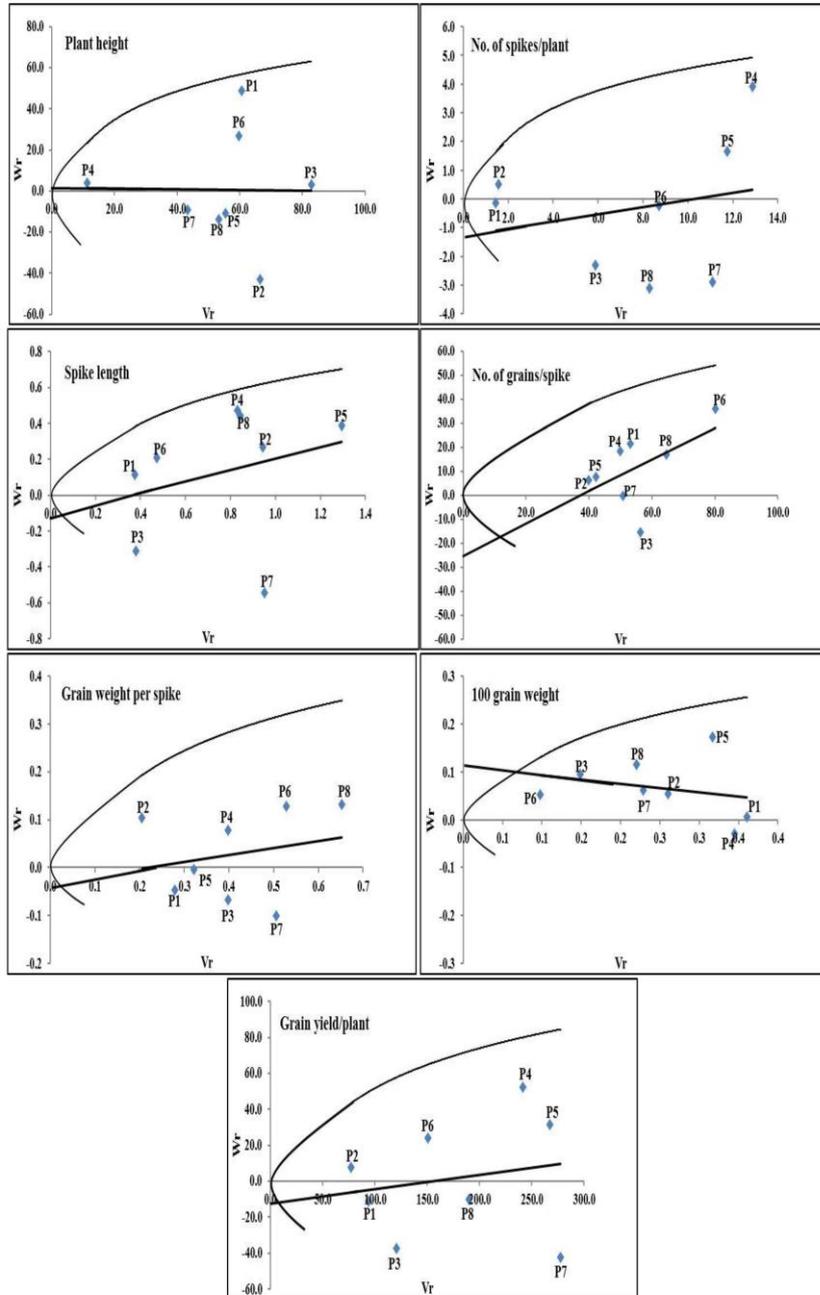
Fig. 1. Wr-Vr graph for different agronomic traits of parental barley genotypes under normal condition.
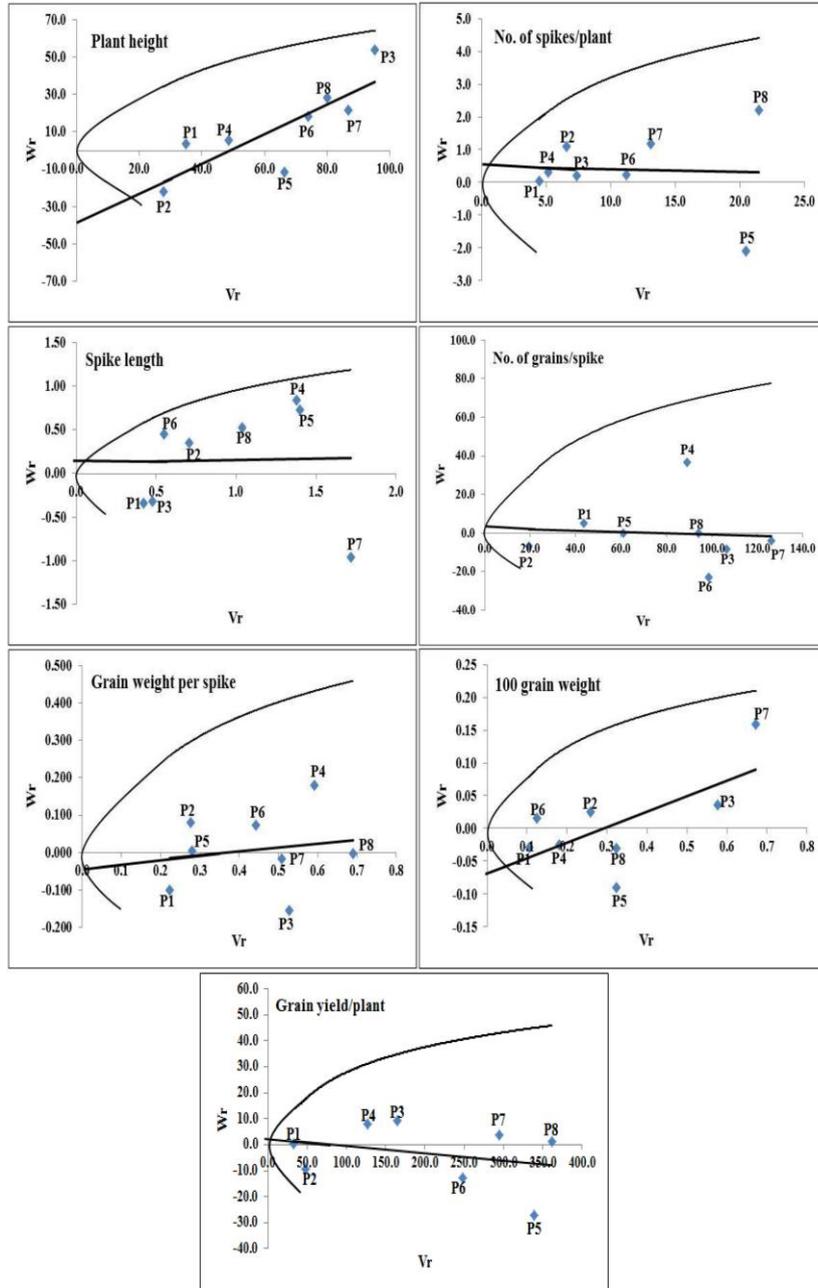
Fig. 2. Wr-Vr graph for agronomic different traits of parental barley genotypes under salinity condition.

Conclusion

This work focused on eight six-rowed hulled spring barley genotypes and their crosses which could be exploited further in barley breeding to improve production under normal and salinity conditions. Most of used genotypes exhibited good performance and combining ability for different traits. Especially P3 and P6 under salinity condition, P4 and P8 under normal one and P2, P5 and P7 under both conditions. At least one of these genotypes participated in the cross combinations which presented high performance and SCA values for studied traits. The best specific crosses were, P3×P5, P3×P8 and P5×P8 under salinity, and P2×P7, P3×P4, P4×P7, P5×P7 P6×P7 and P7×P8 under both conditions. Thus; these parental genotypes and their crosses could be further used in developing segregating populations in barley breeding programs, to improve grain yield and contributing traits under both conditions.

The obtained results by using Griffing and Hayman approach illustrated the importance of both additive and non-additive genetic components in the inheritance of studied traits, with more presence for dominance components. Also Wr-Vr graphs supported this result, where, the dominance effect was excess for all studied traits. On the other hand, the distribution of dominant and recessive alleles in the parental material for all traits reveals to genetic diversity of parents.

From all forgoing results, it could be concluded that the above mentioned cross combinations lead to high degree of heterosis and higher production for improving yield and its components when exploited it in future barley breeding programs. Otherwise, the presence of dominance effect as well as great effect of the environmental factors in the genetic control of studied traits reflected moderately low narrow sense heritability estimates. Which reveals that selection should be delayed to later generation.

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تقدير القدره على التآلف ومكونات التباين الوراثي للصفات المحصولية في الشعير الربيعي تحت الظروف الطبيعية والملحية

السيد منصور السيد و إيهاب سعودى عبدالحميد مصطفى*

قسم المحاصيل ـ كلية الزراعة ـ جامعة الزقازيق – الزقازيق و
* قسم الأصول الوراثية ـ مركز بحوث الصحراء-القاهرة- مصر.

أجريت هذه الدراسة باستخدام ثمانية تراكيب وراثية مختلفة من الشعير الربيعي المغطى تم التهجين بينها بنظام الهجن التبادلية في اتجاه واحد (half diallel cross) لدراسة القدره العامة والخاصة على التآلف (بطريقة جرفنج ١٩٥٦) ، وتقدير مكونات التباين الوراثي (بطريقة هايمن ١٩٥٤) ، وكفاءة التوريث لصفات المحصول ومكوناته تحت الظروف الطبيعية والملحية. التراكيب الوراثية الثمانية المستخدمة كانت عباره أربعة أصناف محلية (جيزه ١٢٣، جيزه ١٢٦، جيزه ١٣٢ وجيزه ٢٠٠٠) وأربعة تراكيب مستورده من الإيكاردا (,Australian, CHK 38 CHK 2 and CHK 53). تم زراعة الأباء والتهجين بينهم خلال موسم ٢٠١٤ - ٢٠١٥ بمزرعة كلية الزراعة ، جامعة الزقازيق. وفى الموسم التالى تم زراعة بذور هجن الجيل الأول والأباء فى موقعين مختلفيين. الموقع الأول كان فى مزرعة غزالة بمحافظة الشرقية ممثل الظروف الطبيعية، والموقع الثانى كان فى (مزرعة مركز بحوث الصحراء، بمحطة بحوث راس سدر، محافظة جنوب سيناء) ممثل لظروف الاجهاد البيئي تحت تأثير ملوحة مياه الري والتربه بتركيز ٤٥٠٠ و ٥٥٣٥ جزء فى المليون، على التوالى. تم استخدام تصميم القطاعات كاملة العشوائية فى ثلاث مكررات فى كلا التجربتين. تم دراسة صفات إرتفاع النبات (سم)، طول السنبله (سم)، عدد السنابل على النبات، عدد حبوب السنبله، وزن حبوب السنبله (جم)، وزن المائة حبه (جم) و محصول حبوب النبات الفردي (جم).

إشار تحليل التباين إلى وجود فروق عالية المعنوية بين الأباء وكذلك بين هجن الجيل الأول فى جميع الصفات تحت الدراسة. وكانت القدره العامة والخاصة على التآلف عالية المعنوية فى جميع الصفات تحت ظروف البيئتين. أظهر الأب الثالث (Australian) والأب السادس (CHK 53) محصول جيد وقدره عامة على التآلف عالية تحت ظروف الملوحة، بينما تفوق كل من الأب الرابع (CHK 38) والثامن (جيزه ٢٠٠٠) تحت الظروف الطبيعية، والأب الثانى (جيزه ١٢٦) والخامس (CHK 2) والسابع (جيزه ١٣٢) تحت ظروف كلا البيئتين. وكذلك اظهرت الهجن الثلاثة P5×P8 ،P3×P8 ،P3×P5 محصول جيد وقدره خاصة على التآلف معنويه وموجبه لصفة المحصول والصفات المساهمه تحت ظروف الملوحة، وخمسة هجن هي P2×P7, P3×P4, P4×P7, P5×P7 P6×P7, P7×P8 تحت كلا البيئتين. كان تباين القدره الخاصة أعلى من تباين القدره العامة على التآلف لجميع الصفات تحت الدراسة ماعدا صفة إرتفاع النبات تحت ظروف الملوحة ووزن المائة حبه تحت الظروف الطبيعية.

أظهرت نتائج مكونات التباين الوراثى (Hayman 1954) مساهمة كبيره للفعل الجينى السيادى فى وراثة الصفات تحت الدراسة مقارنة بالفعل الجينى المضيف. تغيرت قيم كفاءة التوريث المقدرة بالمعنى الخاص من بيئة لأخرى وتراوحت من متوسطة الى منخفضة (٤٫٦٢ – ٣١٫٩٦%). كذلك أظهر التحليل البيانى (Wr-Vr graph) درجة عالية من التنوع الوراثى للأباء بدرجات مختلفة من السيادة وتوزيع الأليلات السائدة والمتنحية لكل الصفات تحت الدراسة فى كلا البيئتين.