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An estimation of the combining ability of barley genotypes and heterosis for some quantitative traits

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ARTICLE INFO

Article history:

Received 27 July 2012015

Accepted 8 March 2016

Available online 11 April 2016

Keywords:

Genetic analysis
Diallel cross
Heritability
Combining ability

ABSTRACT- Barley (*Hordeum vulgare* L.) is one of the most important cereals in the world which is used as human and cattle feed and for malt production. One of the most important steps in a hybrid and selection breeding program of barley is the selection of suitable parents with high general (GCA) and specific combining ability (SCA) for grain yield. In order to estimate the combining ability and heterosis in barley for a number of qualitative traits, seven genotypes were crossed in one-way diallel crosses using Griffing (Method II). Grain number per spike, grain weight per spike, spike weight, 1000-grain weight, number of spikelet, plant height, spike length, peduncle length, days to physiological maturity, and spikelet density were measured. Results of variance analysis showed that there were very significant differences between genotypes for all the measured traits. General combining ability (GCA) effect was significant for all traits, 166.352 genotype had the highest value of GCA for grain number per spike (4.757), grain weight per spike (0.245), spike weight (0.378) traits, whereas Specific combining ability (SCA) effect was significant for all traits except for plant height, days to physiologic maturity, and spikelet density. Three crosses 67.110×283.352, 95.110×216.352 and Sahra×216.352 showed the highest values of SCA for grain number per spike (7.704), grain weight per spike (0.371) and 1000-grain weight (8.619), respectively. Moreover, dominance variance was the most effective factor in genetic control of traits. Three crosses 216.352×283.352, 104.110×216.352 and Sahra×216.352 showed the highest values of heterosis for grain number per spike (4.95), grain weight per spike (44.13) and 1000-grain weight (31.6), respectively. Maximum and minimum broad sense heritability was obtained in the number of grains per spike (87.7%) and spike density (47.36%) respectively. Lowest and highest narrow sense heritability was obtained for peduncle length (15.72%) and weight of grains per spike (50.5%), respectively. Estimates of SCA showed that 95.110×216.352, such as 67.110×283.352 crosses could be used in breeding programs to release cultivar to increase yield-related traits.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important cereals in the world and the fourth cereal both in terms of quantity produced and area of cultivation. In Iran, 18% of 8.8 million ha cereal farms was used for barley. Barley yield in Iran has been estimated 2.9 million tons, 66.1% of which is in irrigated farms and the rest is in dry farms (Agriculture Statistics, 2013). In 2008, Iran ranked the fourteenth in barley production (FAO, 2008). Use of barley hybrid is a strategy to enhance yield level; for this aim, specification of suitable parents with high GCA is important to attain high yield and benefit heterosis of their progenies. Heterosis studies have a direct relationship with breeding methodology for improving diversity and providing useful information about parents in breeding programs (Singh et al., 2004). Combining ability is one of the most important parameters to specify hybrid value. Awareness of combining ability of parents during breeding practice leads to efficiency increase of

cultivars and results in single hybrids. Therefore, determination of combining ability is a vital stage in the production of a new hybrid (Stoskopf, 1999). Specific combining ability is important to achieve better results and heterosis (Ciulca, 2006).

Diallel cross is used in genetic studies to specify heritability of important traits in a set of genotypes in order to recognize the best parents in hybrid production and variety breeding (Dehghani et al., 2006). Therefore, diallel cross is a convenient method to obtain information about genetic traces to fixate mother line and estimate general and specific combining abilities.

According to combining ability test for different traits, high values of SCA indicate higher share of gene dominance while high levels of GCA denote higher share of additive effects of the genes controlling the traits in plants. If both GCA and SCA are insignificant, epistasis of genes has a profound influence in controlling the traits (Fehr, 1993).

In the study conducted by Nakhjavan et al. (2009) on barley, spike length, 1000-grain weight, harvest index, days to physiologic maturity, and plant height possessed relative dominance. Moreover, grain yield and days to heading had over-dominance effects and hybrid production and selection in following generations were effective to improve these traits. In their study, narrow sense heritability varied from 25% for spike length to maximum 53% for plant height. In another study by Nakhjavan et al. (2012) on barley, both additive and dominance gene effects played a role in controlling morphologic traits. As the GCA/SCA variance was significant for plant height, spike length, 1000-grain weight, harvest index, and days to heading both in normal and drought stress situations, additive effects were more influential than non-additive effects to control these traits. This ratio was insignificant for grain yield in both conditions (i.e. normal and drought stress) and non-additive gene effects (i.e. dominance and epistasis) were more effective than additive gene effects. Pal and Kumar (2009) also studied barley and found that forage yield traits, including days to 50% heading, and the number of spikelet per spike showed high GCA values.

Nevertheless, we need to know more about the importance of GCA and SCA. Additionally, to develop favorable genotypes and germplasm resources, Diallel analysis provides a unique opportunity to test mother lines in all possible combinations. Therefore, the present study aims at the recognition of the best parents and crosses based on their GCA and SCA values for different traits. Also, this study is designed to estimate the combining abilities of barley genotypes to better understand gene effects.

MATERIALS AND METHODS

Seven barley genotypes (including Sahra desert native variety) (Table 1) were randomly selected according to available information in Agricultural Research Center of Gorgan, Iran and were sown in the autumn, 2010. In order to estimate gene effects, heritability, and combining ability of the genotypes, they were crossed in

a one-way diallel mating design in the spring, 2011. In the autumn 2011, the seeds derived from crosses and parents were sown in randomized complete block design with three replications. Days to physiologic maturity (when grain dry weights did not increase) was first recorded. Then, plant height (cm), peduncle length (cm), spike length (cm), spike weight (g), number of spikelet per spike, number of grains per spike, grain weight in spike (g), spike density (length spike/number spikelet per spike), and 1000-grain weight were measured from the average of 10 plants in each replication. Variance analysis and diallel analysis were performed using the second method of Griffing (1956).

To measure the type of the gene action, F_s was calculated by dividing GCA variance to SCA variance and was then compared with F_t . If this ratio is significant, additive gene effects are high and if not, epistasis and dominance are high. Additive variance was obtained by doubling GCA variance ($\delta_A^2 = 2\delta_g^2$) while dominance variance was estimated by SCA variance ($\delta_D^2 = \delta_s^2$). According to Griffing (1956), GCA and SCA are derived as follows:

$$\delta_g^2 = \frac{1}{n+2} (Mg - Ms) \tag{1}$$

$$\delta_s^2 = MS - M\acute{E} \tag{2}$$

$$\delta_E^2 = M\acute{E} \tag{3}$$

$$\delta_{ns}^2 = \frac{\delta_A^2}{\delta_A^2 + \delta_D^2 + \delta_E^2} \tag{4}$$

$$\delta_{bs}^2 = \frac{\delta_A^2 + \delta_D^2}{\delta_A^2 + \delta_D^2 + \delta_E^2} \tag{5}$$

where δ_E^2 stands for mean square of the experimental error, δ_A^2 additive variance, δ_g^2 general combining ability variance, δ_D^2 dominance variance, δ_s^2 specific combining Variance, M_g mean squares general combining ability variance and M_s mean squares specific combining ability variance. Data analyses were performed in SAS (version 9.1) (SAS Institute, 2002) and D₂ software (Dick, 1998).

Table 1. Description of barley parents used in diallel crosses

Number	Genotype	Name	Pedigree	Origin
1	95/110 ICARDA	Moroc9-75//W12291/C101387/3/H.spont.41-1	ICB94-0342-24AP-0AP-18AP-DAP	ICARDA
2	104/110 ICARDA	Soufara-02/3/RM1508/Por//W12269/4/Hml-02/ArabiAbiad//ER/Apm	ICB92-0926-0AP-18AP-0AP-11TR-0AP	ICARDA
3	283/352	-	Petunia 1	Temperate regions
4	166/352	-	ICNB-105960/Torkman	Temperate regions
5	67/110 ICARDA	Mtn-01	-	ICARDA
6	Sahra	-	-	Native Golestan
7	216/352	-	Zabol	Temperate regions

RESULTS AND DISCUSSION

The results of variance analysis, according to the second method of Griffing (1956), are summarized in Tables 2 and

3. Genotype effect was significant for all the traits indicating the presence of genetic differences among barley genotypes and their hybrids for the studied traits. Variance of GCA (Table 3) was significant for all the traits ($p < 0.01$) which points to the wide range of general combining ability among parent genotypes. Insignificant and low SCA reveals higher additive effects to control such traits as spike weight, spike density, days to physiologic maturity, and plant height. As MS(GCA)/MS(SCA) (Table 3) was significant in controlling the number of grains per spike, spike weight, spikelet density, days to physiologic maturity, and plant height, additive variance was more effective whereas non-additive effects were more influential in controlling grain weight in spike, 1000-grain weight, number of spikelet, spike length, and peduncle length. Nakhjavan et al. (2009) found similar results for plant height, spike length, and grain yield of barley in normal and drought stress conditions. They stated that dominance variance exceeded additive variance and dominance average ratio < 1 denoted relative dominance of traits. However, in another study by Nakhjavan et al. (2012), non-additive effects were more pronounced in physiologic maturity of barley under drought stress indicating over-dominant of gene acts.

Tahmasebi et al. (2008), Mann and Sharma (1995), and Rohman et al. (2006) claimed that non-additive gene effects were more considerable for plant yield barley and 1000-grain weight. Ciulca (2009) reported additive and non-additive effects on the number of grain per spike. Baghizadeh et al. (2005) concluded that additive variance was lower than dominance variance in spike weight, spike length, number of spikelet, 1000-grain weight, and number of grains indicating that the selection in selfing was not stable for these traits; therefore, crosses and community management were more influential than the selection practice.

Table 4 shows additive and dominance variance values and percentage as well as narrow and broad sense of heritability. The results indicate that broad sense heritability in the traits ranged between 47.36% and 87.7% pointing to the high effect of genetic variance to control these traits. In the study done by Pal and Kumar (2009), SCA of barley plant height, spike length, and number of spikelet were 16%, 35%, and 90%, respectively. Also, the significance of MS(GCA)/MS(SCA) for the number of spikelet reveals the role of additive gene effects to control this trait. SCA for

1000-grain weight in diallel crosses was estimated 53% (Singh et al., 2006). Jalata et al. (2011) observed high phenotypic and genotypic diversity coefficients on barley for grain yield, number of grain per spike, 1000-grain weight, and spike weight as well as high heritability for spike length (86.8%), 1000-grain weight (85.6%), number of grains per spike (75.5%), and grain yield in plant (71.4%). Sirohi et al. (2012) found similar results for heritability of grain yield (99.97%), harvest index (99.86%), days to heading (99.86%), plant height (97.63%), number of grains per spike (98.79%), and 1000-grain weight (95.11%) which is indicative of the fact that additive gene effects were more considerable to control these traits. PratapSingh (2011) found that general heritability for days to physiologic maturity, peduncle length, and grain yield were 71.64%, 97.58%, and 84.28%, respectively. High heritability led to genetic progress of grain yield in spike and plant, peduncle length, flag leaf length, and leaf width which are the most important traits for crop selection and improvement in barley production. Kumar et al. (2013) evaluated 15 barley lines by line \times tester method and observed high phenotypic and genotypic diversity coefficients for grain yield in spike and the number of grains, high heritability and average genetic progress for plant height, harvest index, and 1000-grain weight. These traits were influenced by additive gene effect while it is easy to improve them by selection practice.

In all the traits, the favorable genotypes were the ones with higher and positive values of the traits except for days to physiologic maturity, plant height and peduncle length. Therefore, positive values of GCA, SCA, and heterosis are beneficial. The 166/352 genotype had the highest positive and significant GCA (Table 5) among genotypes to increase the number of grains in spike (4.757), grain weight in spike (0.245), and spike weight (0.378). In addition, the parent 104.110 ICARDA had the highest negative GCA for these traits. The parents 166.352 and 283.352 had the highest positive and significant GCA for the number of grains in spike (43.2 and 29.4, respectively). The genotypes 95.110 ICARDA, 283.352, 216.352, and Sahra had the highest positive and significant GCA values to increase the number of spikelet, 1000-grain weight, spike length, and spikelet density, respectively. 67.110 ICARDA and 104.110 ICARDA genotypes had the highest negative and significant values to increase plant height, peduncle length, and days to physiologic maturity.

Table 2. Mean squares of source of variation for the measured traits on barley genotypes

S.O.V	DF	1000 grain weight	Grain weight per spike	Grain per spike	Spike weight	Spikelets per spike
Block	2	177.61*	0.49**	82.42*	0.74*	159.33**
Genotype	27	125.32**	0.27**	136.99**	0.6**	18.99*
Error	54	23.44	0.057	16.73	0.17	7.16
C.V		8.9	19.58	17.92	21.52	15.21
S.O.V	DF	Spike density	Date to physiological maturity	Spike length	Peduncle length	Plant height
Block	2	0.14*	0.065*	20.77**	24.69*	1.55**
Genotype	27	0.17*	0.044**	3.01**	14.95**	0.32*
Error	54	0.088	0.015	0.7	4.86	0.17
C.V		12.96	1.1	10.94	10.73	5.73

*, **: Significant at the 0.05 and 0.01 levels of probability, respectively

Table 3. Mean squares of general/specific combining abilities and their ratio, and heritability morphological traits

S.O.V	1000 grain weight	Grain weight per spike	Grains per spike	Spike weight	Spikelets per spike
GCA	72.16**	0.165**	96.62**	0.556**	11.94**
SCA	33.094**	0.072**	32.01**	0.099	5.058*
Error	7.81	0.019	5.7	0.057	2.386
2GCA/2GCA+SCA	0.813	0.82	0.857	0.918	0.825
$h^2_{N.S}$	21%	22%	31%	51%	23%
$h^2_{B.S}$	81%	79%	88%	71%	64%
S.O.V	Spikelet density	Date to physiological maturity	Spike length	Peduncle length	Plant height
GCA	0.117**	0.033**	1.74**	7.738**	0.232**
SCA	0.041 ^{n.s}	0.01 ^{n.s}	0.769**	4.202**	0.074 ^{n.s}
Error	0.03	0.005	0.239	1.631	0.057
2GCA/2GCA+SCA	0.85	0.868	0.82	0.786	0.862
$h^2_{N.S}$	33%	67%	22%	16%	36%
$h^2_{B.S}$	50%	67%	76%	67%	55%

*, **: Significant at the 0.05 and 0.01 levels of probability, respectively

Table 4. values and percentage of additive variance and dominance variance as well as general and specific heritability for the studied traits

Parameters	1000 grain weight	Grain weight per spike	Grains per spike	Spike weight	Spikelets per spike
Additive variance	8.67	0.02	14.34	0.101	1.52
Dominance variance	25.28	0.053	26.31	0.04	2.67
error	7.81	0.019	5.7	0.057	2.386
Add%	20.76	21.73	30.93	50.5	23.107
Dom%	60.53	57.6	56.76	21	40.62
Error%	18.7	20.65	12.29	28.5	36.27
$h^2_{N.S}$ %	20.76	21.73	30.93	50.5	23.107
$h^2_{B.S}$ %	81.29	79.34	87.7	71.5	63.72
Parameters	Spikelet density	Date to physiological maturity	Spike length	Peduncle length	Plant height
Additive variance	0.016	0.005	0.21	0.784	0.035
Dominance variance	0.011	0.005	0.53	2.57	0.017
error	0.03	0.005	0.239	1.631	0.057
Add%	28.07	33.33	21.45	15.72	32.11
Dom%	19.29	33.33	54.19	51.55	15.59
Error%	52.63	33.33	24.41	32.71	52.29
$h^2_{N.S}$ %	28.07	33.33	24.45	15.72	32.11
$h^2_{B.S}$ %	47.36	66.66	75.58	67.28	47.7

Add: Additive variance percentage, Dom: Dominance variance percentage

The best SCA values for attaining higher desirability of traits among the produced hybrids from seven genotypes were as follows: 283.352×67.110 for number of grains in spike (7.704), 166.352×Sahra for grain weight in spike (0.349), 216.352×Sahra for 1000-grain weight (8.619), 104.110×283.352 for number of spikelet (3.528), 104.110×283.352 for spike length (1.955), and 166.352×67.110 for peduncle length (-2.67). These crosses had the highest significant SCA to increase the traits. Diallel cross between the genotypes 283.352 and 67.110 had significant SCA for the traits related to yield such as the number of grains in spike, grain weight in spike, and the number of spikelet. The genotypes 95/110

and 104.110 had negative GCA in the number of grains in spike although their diallel cross with 216/352 had positive and significant SCA. Parents carry alleles to control and increase the number of grains in spike and to transfer them to the results of diallel cross. Transgressive segregation in the results of genotypes with lower grain number brought about the offspring with genes transferred from both parents and therefore, they were superior to their parents in that trait. This occurred for a number of spikelet where the offspring were superior to their parents whereas both parents had the lowest average values for this trait.

Table 5. General combining ability effects (diagonal values) and specific combining ability effects (above diagonal) for the studied traits

Grain per spike	95/110	104/110	283/352	166/352	67/110	Sahra	216/352
parent							
95/110	-2.28*	5.926**	-3.407 ^{n.s}	-10**	-5.185**	0.481 ^{n.s}	5.444**
104/110		-3.836**	-1.519 ^{n.s}	-8.444**	-3.963 ^{n.s}	-0.296 ^{n.s}	4.667*
283/352			3.164**	1.889 ^{n.s}	7.704**	0.27 ^{n.s}	0.667 ^{n.s}
166/352				4.757**	-0.556 ^{n.s}	4.778*	-9.592**
67/110					1.608 ^{n.s}	-0.407 ^{n.s}	-4.111 ^{n.s}
Sahra						-0.392 ^{n.s}	-0.778 ^{n.s}
216/352							-3.021**
Grain weight perspike							
95/110	-0.08 ^{n.s}	0.195 ^{n.s}	-0.105 ^{n.s}	-0.445**	-0.159 ^{n.s}	0.096 ^{n.s}	0.371**
104/110		-0.162**	0.06 ^{n.s}	-0.346**	-0.087 ^{n.s}	0.062 ^{n.s}	0.333**
283/352			0.068 ^{n.s}	0.177 ^{n.s}	0.276*	0.055 ^{n.s}	-0.037 ^{n.s}
166/352				0.245**	0.003 ^{n.s}	0.349**	-0.567**
67/110					0.053 ^{n.s}	-0.126 ^{n.s}	-0.031 ^{n.s}
Sahra						-0.03 ^{n.s}	-0.042 ^{n.s}
216/352							-0.094 ^{n.s}
Spike weight							
95/110	-0.177*	0.358 ^{n.s}	-0.168 ^{n.s}	-0.335 ^{n.s}	-0.215 ^{n.s}	-0.085 ^{n.s}	0.323 ^{n.s}
104/110		-0.371**	-0.07 ^{n.s}	-0.547**	-0.244 ^{n.s}	0.122 ^{n.s}	0.23 ^{n.s}
283/352			0.128 ^{n.s}	0.064 ^{n.s}	0.087 ^{n.s}	0.21 ^{n.s}	0.055 ^{n.s}
166/352				0.378**	-0.25 ^{n.s}	0.373 ^{n.s}	-0.519**
67/110					0.098 ^{n.s}	-0.19 ^{n.s}	0.311 ^{n.s}
Sahra						0.095 ^{n.s}	0.037 ^{n.s}
216/352							-0.152 ^{n.s}
1000 grain weight							
95/110	-5.21**	-5.493**	-8.867**	1.063 ^{n.s}	-1.322 ^{n.s}	-0.774 ^{n.s}	2.126 ^{n.s}
104/110		0.983 ^{n.s}	-4.426 ^{n.s}	8.137**	5.619*	2.1 ^{n.s}	3.567 ^{n.s}
283/352			3.357**	5.33*	3.744 ^{n.s}	7.893**	1.993 ^{n.s}
166/352				-1.172 ^{n.s}	-6.259**	-2.778 ^{n.s}	-6.478**
67/110					-0.754 ^{n.s}	1.704 ^{n.s}	-3.863 ^{n.s}
Sahra						0.198 ^{n.s}	8.619**
216/352							2.598*
Spikelets per spike							
95/110	1.735**	1.009 ^{n.s}	1.417 ^{n.s}	3.361**	-1.731 ^{n.s}	-1.657 ^{n.s}	1.861 ^{n.s}
104/110		0.291 ^{n.s}	3.528**	-0.25 ^{n.s}	-1.954 ^{n.s}	1.12 ^{n.s}	0.972 ^{n.s}
283/352			-0.116 ^{n.s}	1.157 ^{n.s}	3.12*	0.194 ^{n.s}	0.046 ^{n.s}
166/352				-0.672 ^{n.s}	-1.324 ^{n.s}	2.082 ^{n.s}	-1.731 ^{n.s}
67/110					-1.635**	-0.287 ^{n.s}	2.231 ^{n.s}
Sahra						-0.709 ^{n.s}	0.972 ^{n.s}
216/352							1.106 ^{n.s}
Plant height							
95/110	0.266**	0.001 ^{n.s}	0.078 ^{n.s}	0.022 ^{n.s}	-0.087 ^{n.s}	-0.02 ^{n.s}	0.15 ^{n.s}
104/110		-0.083 ^{n.s}	0.651**	-0.048 ^{n.s}	0.026 ^{n.s}	0.106 ^{n.s}	0.199 ^{n.s}
283/352			-0.054 ^{n.s}	0.099 ^{n.s}	0.07 ^{n.s}	-0.156 ^{n.s}	0.034 ^{n.s}
166/352				-0.032 ^{n.s}	-0.179 ^{n.s}	0.081 ^{n.s}	-0.329 ^{n.s}
67/110					-0.182*	-0.348 ^{n.s}	0.435*
Sahra						-0.129 ^{n.s}	0.142 ^{n.s}
216/352							0.151 ^{n.s}
Spike length							
95/110	0.492*	0.956*	-0.17 ^{n.s}	-0.524 ^{n.s}	-0.307 ^{n.s}	-0.692 ^{n.s}	1.662**
104/110		-0.263 ^{n.s}	1.955**	-0.242 ^{n.s}	-0.139 ^{n.s}	0.163 ^{n.s}	0.31 ^{n.s}
283/352			0.27 ^{n.s}	0.458 ^{n.s}	0.945*	-0.334 ^{n.s}	0.023 ^{n.s}
166/352				-0.553**	-0.239 ^{n.s}	0.743 ^{n.s}	-0.36 ^{n.s}
67/110					-0.356 ^{n.s}	-0.074 ^{n.s}	0.066 ^{n.s}
Sahra						-0.154 ^{n.s}	0.268 ^{n.s}
216/352							0.565**
Peduncle length							
95/110	0.136 ^{n.s}	-0.97 ^{n.s}	2.162 ^{n.s}	2.265 ^{n.s}	-0.942 ^{n.s}	0.055 ^{n.s}	-0.268 ^{n.s}
104/110		-1.664**	3.728**	0.518 ^{n.s}	0.375 ^{n.s}	1.618 ^{n.s}	0.799 ^{n.s}
283/352			-0.466 ^{n.s}	-1.064 ^{n.s}	-0.713 ^{n.s}	-1.674 ^{n.s}	1.287 ^{n.s}
166/352				0.691 ^{n.s}	-2.67**	1.616 ^{n.s}	-0.59 ^{n.s}
67/110					0.128 ^{n.s}	-1.534 ^{n.s}	3.944**
Sahra						-0.109 ^{n.s}	0.907 ^{n.s}
216/352							1.284*
Date to physiological maturity							
95/110	-0.043 ^{n.s}	0.116 ^{n.s}	0.083 ^{n.s}	0.09 ^{n.s}	-0.026 ^{n.s}	-0.006 ^{n.s}	0.009 ^{n.s}
104/110		-0.082**	0.035 ^{n.s}	-0.038 ^{n.s}	0.072 ^{n.s}	-0.028 ^{n.s}	0.047 ^{n.s}
283/352			0.041 ^{n.s}	0.0494 ^{n.s}	0.096 ^{n.s}	0.126 ^{n.s}	0.028 ^{n.s}
166/352				0.007 ^{n.s}	0.043 ^{n.s}	-0.013 ^{n.s}	0.122 ^{n.s}
67/110					0.004 ^{n.s}	0.034 ^{n.s}	0.022 ^{n.s}
Sahra						0.104**	-0.035 ^{n.s}
216/352							-0.031 ^{n.s}

*, ** : significant at the 0.05 and 0.01 levels of probability, respectively, and n.s: non-significant

Three out of twenty-one crosses showed positive mid-parent heterosis for addition number grain of spike trait; also, these characters showed four positive and significant crosses better than those of parent heterosis. Maximum increase over the mid-parent and also better parent heterosis were recorded between hybrids 283/352×216/352 and 283/352×67/110 on values 4.95% and 18.91%, respectively. Heterosis studies for grain weight on spike revealed that 12 crosses positive and significant mid-parent heterosis and ten crosses showed positive and significant better than those of parent heterosis. Between crosses, 104/110×216/352 had the highest heterosis and 95/110×216/352 the highest heterobiltiosis. The 1000 grain weight trait, thirteen out of twenty-one were being positive and significant mid-parent heterosis values, as if attached crosses 216/352×sahra were the most positive mid-parent heterosis. Ten out of twenty-one crosses were positive and better than those of parent heterosis for 1000 grain weight, as if attached cross 104/110×166/3562 being the highest, and so heterosis and heterobiltiosis amplitude variation was gained between (.56-31.6%) and (4.24-18-66%), respectively. Yin guang et al. (2009) studied heterosis and heterobiltiosis for 1000 grain weight on wheat and estimated 15.92 and 2.53, respectively.

After observing heterosis and transgressive segregation, Pal and Kumar (2009) recommended that diallel selective cross was the superior hybrid selection method followed by recurrent selection which increased favorable allele frequency in following generations to improve barley grain yield, green forage, and other correlated traits.

CONCLUSIONS

Significant variance among genotypes for the measured traits revealed genetic difference between the varieties.

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Besides, significant GCA and SCA indicated that most of the traits were controlled by additive and non-additive gene effects. However, additive gene effects were more considerable in controlling the number of grains in spike, spike weight, spikelet density, plant height, and days to physiologic maturity. Additive gene effects showed high yield of selection, additive and non-additive effects pointed to the methods based upon hybridization and selection in segregating generations, and non-additive effects represented efficiency of hybridization-based methods. As high values are suitable for some traits and low values are suitable for some others, the breeder will be able to select each parent according to the breeding aims. Among the studied genotypes, the 166/352 had the highest average values for the number of grains in spike, grain weight in spike, spike weight, and peduncle length. Therefore, this parent can be used in hybridization breeding programs to increase these traits. 95/110 genotypes had the best GCA for the number of spikelet and spike length; also, in the previous studies, there was a positive correlation between these two traits (Pesaraklu et al., 2012), and the parents with higher spike length had more spikelets. The genotype 104/110 had the highest GCA to increase peduncle length and days to physiologic maturity. The cross 67/110×283/352 had the highest SCA in the number of grains in spike, grain weight in spike, spike length, and number of spikelets. Also, the cross Sahra×216/352 had the highest SCA for 1000-grain weight.

ACKNOWLEDGEMENTS

Hereby we greatly appreciate the support of all the employees of Gorgan Agricultural Research Station who cooperated with us in this project.

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برآورد هتروزیس صفات کمی و قابلیت ترکیب پذیری برخی ژنوتیپ-های جو

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اطلاعات مقاله

تاریخچه مقاله:

تاریخ دریافت: ۱۳۹۴/۵/۵
تاریخ پذیرش: ۱۳۹۴/۱۲/۱۸
تاریخ دسترسی: ۱۳۹۵/۱/۲۲

واژه‌های کلیدی:

تجزیه ژنتیکی
تلاقی دای آلل
توارث پذیری
ترکیب پذیری

چکیده- جو (*Hordeum vulgare L.*) یکی از مهم‌ترین غلات جهان است که به‌عنوان غذای دام و انسان و تهیه جو مالت مورد استفاده قرار می‌گیرد. کاربرد هیبریداسیون در جو روشی برای بهبود بهره‌وری و گامی مهم در برنامه‌های به‌نژادی برای شناسایی والدین شایسته با GCA و SCA بالا برای عملکرد دانه و بهره‌برداری از هتروزیس است. به منظور برآورد قابلیت ترکیب‌پذیری و هتروزیس برای صفات کمی و تعیین قابلیت ترکیب‌پذیری در جو ۷ ژنوتیپ جو بصورت تلاقی دای آلل گریفینگ (روش ۲) داده شدند. صفات تعداد دانه در سنبله، وزن دانه در سنبله، وزن سنبله، وزن هزار دانه، تعداد سنبلچه، ارتفاع بوته، طول سنبله، طول پدانکل، روز تا رسیدگی فیزیولوژیک و تراکم سنبلچه اندازه-گیری گردید. نتایج تجزیه واریانس نشان داد تفاوت بسیار معنی‌داری بین ژنوتیپ‌ها از نظر کلیه صفات وجود دارد. اثرات ترکیب‌پذیری عمومی (GCA) برای همه صفات معنی‌دار بود، ژنوتیپ ۱۶۶/۳۵۲ بیشترین مقدار را در صفات تعداد دانه در سنبله (۴/۷۵۷)، وزن دانه در سنبله (۰/۳۴۵) و وزن سنبله (۰/۳۷۸) دارد، اثرات ترکیب‌پذیری خصوصی (SCA) نیز برای همه صفات بجز ارتفاع، رسیدگی فیزیولوژیک و تراکم سنبله‌چه معنی‌دار بود. سه تلاقی ۶۷/۱۱۰×۲۸۳/۳۵۲، ۹۵/۱۱۰×۲۱۶/۳۵۲ و ۲۱۶/۳۵۲×صحرای به ترتیب در صفات تعداد دانه در سنبله (۷/۷۰۴)، وزن دانه در سنبله (۰/۳۷۱) و وزن هزار دانه (۸/۶۱۹) بالاترین مقدار را نشان دادند. همچنین مشخص شد که واریانس غالبیت بیشترین نقش را در کنترل توارث صفات مورد بررسی به عهده دارد. سه تلاقی ۲۱۶/۳۵۲×۲۸۳/۳۵۲، ۲۱۶/۳۵۲×۱۰۴/۱۱۰ و ۱۰۴/۱۱۰×۲۱۶/۳۵۲×صحرای به ترتیب هتروزیس معنی‌دار در صفات تعداد دانه در سنبله (۴/۹۵)، وزن دانه در سنبله (۴۴/۱۳) و وزن هزار دانه (۳۱/۶) بالاترین مقدار را نشان دادند. بیشترین و کمترین وراثت‌پذیری عمومی به ترتیب در صفات تعداد دانه در سنبله (۸۷/۷) و تراکم سنبلچه (۴۷/۳۶) و کمترین و بیشترین وراثت‌پذیری خصوصی بترتیب برای صفات طول پدانکل (۱۵/۷۲) و وزن دانه در سنبله (۵۰/۵) بدست آمد. برآورد SCA نشان داد، می‌توان از تلاقی ۲۱۶/۳۵۲×۹۵/۱۱۰ همچنین تلاقی ۲۸۳/۳۵۲×۶۷/۱۱۰ در برنامه‌های اصلاحی جهت آزادسازی رقم برای افزایش صفات مرتبط با عملکرد استفاده نمود.