



GENETIC ANALYSIS IN SOME BARLEY VARIETIES AND THEIR HYBRIDS IN F₂ GENERATION

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ABSTRACT: Five two-rowed barely varieties were sown in full Diallel cross including reciprocals at Sulaimani – Qlyasan research station to produce 20 crosses. During the winter season of (2013-2014), 25 genotypes (20 F₂ crosses + 5 parents) were sown in a completely randomize block design CRBD with 3 replications. The most important results can be summarized as follow:

- The mean squares due to genotypes, gca, sca and rca, were highly significant for most characters.
- Parent 3 possess the highest value for most studied characters, while parent 1 recorded minimum values. The reciprocal cross 4x1 recorded the highest value for (grain weight / plant, biological weight / plant and weight of spikes / plant).
- The reciprocal cross 5x1 gave maximum positive Heterosis for (grain weight / plant) and most of its components.
- The average degree of dominance value was more than one for all characters due to Diallel crosses and for most characters due to reciprocal crosses, confirming the importance of non-additive gene effect in controlling the inheritance of these characters.

Key words: Genetic, barley, Hybrids, F₂ Generation

INTRODUCTION

Barley is a major cereal crop cultivated in the rain fed areas of the West Asia and North Africa (WANA) region, where drought is the most important abiotic factor limiting barely yield. Although barley shows a higher adaptability to drought than durum wheat and bread wheat, the probability of crop failure is high in marginal area suffering from unpredictable drought stress conditions. Heterozygosity has been demonstrated to be associated with drought tolerance in several crop species including barley. Considerable increases in barley grain yield have been reported because of increased heterozygosity of barley F₂-populations compared with genetically homozygous lines grown under drought conditions [1]. There is a long history of genetics research focused in trait inheritance and mapping in the conventional sense [2], also more recently on molecular and physical mapping and genetic analysis [3, 4, 5, 6, 7, 8, 9, 10, 11, 12]. The choice of an efficient breeding program depends to a large extent on the knowledge of gene action involved in the expression of the character. One of the most appropriate methods of genetic analysis is the generation mean analysis. In this method, epistatic effects as well as additive and dominance effects can be estimated. Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and what extent this variation is heritable. Because efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between the genotype and environment [13].

The main objective of the present study was to identify the best combining parents and their crosses on the basis of their general and specific combining ability for yield and its component traits for further amelioration of grain yield in barley.

MATERIALS AND METHODS

This study was carried out at Qlyasan Agricultural Research Station, Faculty of Agricultural Sciences, University of Sulaimani (Lat 35° 34' 307'' ; N, Long 45° 21' 992'' ; E, 765 masl), 2Km North West of Sulaimani city. Five varieties of two-rowed barely (*Hordeum distichum* L.) were used namely : (Local Barley, Zanbaka, ARTa/3/Avar, Roho/ Zanbaka and Avar/H/Sout).

All possible crosses (including reciprocals) were made in field conditions, 20 crosses were created. Seeds of 20 F₂ s crosses with their parents were sown during the September 2013 in a randomized complete block design with three replications. Each treatment was four rows of 2 meters long, 40cm apart rows and 15cm between plants with in row.

Evaluated characters

The data for this study were recorded for ten plants of each genotype from each replication:

(Plant height (cm), No. of spikes/plant, weight of spikes/plant (g), spike length (cm), No. of grains/spike, weight of grains / spike (g), 1000-grain weight (g), biological weight / plant (g) and grain weight/plant (g)).

Genetic Parameters:

-General Combining Ability effect (gca), Specific Combining Ability effect (sca), Heterosis %, Reciprocal Effect %, Heritability in broad sense, Heritability in narrow sense and Average degree of dominance (\bar{a}).

Analysis of Variance:

A range of statistical analysis was conducted for each character. A randomized complete block design (RCBD), with three replication was implemented. According to the following linear modeling [14].

$$Y_{ij} = \mu + T_i + R_j + e_{ij} \quad \left\{ \begin{array}{l} i = 1, 2, \dots, t \\ j = 1, 2, \dots, r \end{array} \right\}$$

Combining Ability Analysis:

The (gca) and (sca) were estimated using the general linear model for the analysis which take the formula of [15]:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + R_{ij} + r_k + e_{ijk}$$

The estimation of general and specific combining ability effect [15]:

$$\hat{g}_{ii} = 1/2p (Y_{i.} + Y_{.j}) - 1/p^2 Y_{...}$$

$$\hat{s}_{ij} = 1/2(Y_{ij} + Y_{ji}) - 1/2p (Y_{i.} + Y_{.i} + Y_{.j} + Y_{.j}) + 1/p^2 Y_{...}$$

$$\hat{r}_{ij} = 1/2 (Y_{ij} - Y_{ji})$$

Estimation of components of variance for both General and Specific Combining Abilities:

$$\sigma^2_{gii} = (g_{ii})^2 - \frac{MS_e}{p^2}$$

$$\sigma^2_{\hat{s}_{ij}} = \frac{1}{p-2} \sum (\hat{s}_{ij})^2 - \frac{MS'_e(p^2 - 2p + 2)}{2p^2}$$

$$\sigma^2_{\hat{r}_{ij}} = \frac{1}{p-2} \sum (\hat{r}_{ij})^2 - \frac{MS'_e}{2}$$

The estimation of standard error for the differences between the effects of the general combining ability of two parents:

$$S.E._{(g_i - g_j)} = \sqrt{\frac{MS'_e}{p}}$$

The estimation of standard error for the differences between the effects of two diallel crosses:

$$S.E._{(s_{ij} - s_{ik})} = \sqrt{\frac{(p-1)MS'_e}{p}}$$

The estimation of standard error for the differences between the effects of two reciprocal crosses:

$$S.E._{(R_{ij} - R_{ik})} = \sqrt{MS'_e}$$

The Estimation of Heterosis:

It was estimated as the percentage deviation of F2s hybrid from mid parental value (AGB301, 2004).

$$\text{Heterosis (H) \%} = \frac{F_2' - M.P}{M.P} \times 100$$

Where:

$$M.P = \frac{P_1 + P_2}{2}$$

Heritability:

Heritability in broad and narrow sense was estimated depending on the variance of general and specific combining abilities, and on the variance of experimental error according to Singh and Chaudhary, 1985 [15] and as follows:

$$h^2_{b.s} = \frac{\sigma^2 G}{\sigma^2 P} = \frac{\sigma^2 A + \sigma^2 D}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\sigma^2 gca + \sigma^2 sca}{2\sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

$$h^2_{n.s} = \frac{\sigma^2 A}{\sigma^2 P} = \frac{\sigma^2 A}{\sigma^2 A + \sigma^2 D + \sigma^2 e} = \frac{2\sigma^2 gca}{2\sigma^2 gca + \sigma^2 sca + \sigma^2 e}$$

The Average Degree of Dominance (\bar{a}):

The degree of dominance mean for all traits was estimated as follows:

$$\bar{a} = \sqrt{\frac{2\sigma^2 D}{\sigma^2 A}} = \sqrt{\frac{2\sigma^2 sca}{\sigma^2 gca}} = \sqrt{\frac{\sigma^2 sca}{\sigma^2 gca}} \quad \text{The estimation of reciprocal effects:}$$

$$\text{Reciprocal Effect (RE \%)} = \frac{(F_{2r}' - F_2')}{F_2'} \times 100$$

Analysis of Variance for Full Diallel Cross According to Griffing 1956 b, Method I, Model II (Parents + Diallel Crosses + Reciprocal Crosses):

S.O.V	d.f	SS	MS	EMS
Block	b-1= 2	$\frac{\sum Y^2 \cdot k}{p^2} - \frac{Y^2 \dots}{bp^2}$	MSb	
Genotype	P ² -1= 24	$\frac{\sum Y_{ij}^2}{b} - \frac{Y^2 \dots}{bp^2}$	MSg	
gca	p-1= 4	$\frac{1}{2p} \sum (Y_{i.} + Y_{.j})^2 - \frac{2}{p^2} Y^2 \dots$	MSgca	$\sigma^2 e + 2p \left(\frac{1}{p-1}\right) \sum g_i^2$
sca	$\frac{p(p-1)}{2} = 10$	$\frac{1}{2} \sum Y_{ij}(Y_{ij} + Y_{ji})^2 - \frac{1}{2p} \sum (Y_{.j} + Y_{j.})^2 + \frac{1}{p^2} Y^2 \dots$	MSsca	$\sigma^2 e + \frac{2}{p(p-1)kj} \sum_{i < j} S_{ij}^2$
rca	$\frac{p(p-1)}{2} = 10$	$\frac{1}{2} \sum (Y_{ij} - Y_{ji})^2$	MSrca	$\sigma^2 e + \left(\frac{2}{p(p-1)}\right) \sum_{i < j} r_{ij}^2$
Error	(b-1)(p ² -1)=48	SST-SSb-SSg	MSe	$\sigma^2 e$
Total	bp ² -1= 74	$\sum Y_{ijk}^2 - \frac{Y^2 \dots}{bp^2}$		

RESULTS AND DISCUSSION

The mean squares for genotypes, gca, sca, and rca represent in table-1, confirmed that the mean squares due to genotypes were highly significant for the characters (No. of spikes/plant, Weight of spikes / plant, Spike length, 1000-grain weight, Biological weight/plant and Grain weight/plant), while it was significant for the characters (Plant Height and No. of grains /spike), but it was not significant for (Weight of grains /spike). Respect to the mean squares due to gca , highly significant mean squares were estimated for the characters (No. of spikes/plant, Weight of spikes / plant, Spike length , No. of grains /spike, 1000-grain weight , Biological weight / plant and Grain weight/plant) , but it was significant for (plant height) and not significant for (Weight of grains /spike). The mean squares due to sca was highly significant for the characters (No. of spikes/plant, Weight of spikes / plant, Spike length, No. of grains/spike, Biological weight / plant and Grain weight/plant), while it was significant for (Plant Height and 1000-grain weight), and not significant for (No. of grains /spike and Weight of grains /spike). Respect to the mean squares due to rca , highly significant mean squares were estimated for the characters (No. of spikes / plant , Weight of spikes / plant , Spike length, 1000-grain weight, Biological weight/plant and Grain weight / plant) , and it was not significant for (Plant Height, No. of grains /spike and Weight of grains /spike) . Highly significant mean squares due to genotypes, gca and sca effects was found previously for (grain weight / plant) and almost all its components [16, 17].

Table 1: ANOVA Table (M.S) for Genotypes and Combining Abilities of Studied Characters

S.O.V	d.f	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant (g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	1000-grain weight (g)	Biological weight / plant (g)	Grain weight / plant (g)
Blocks	2	110.413 n.s	0.879 n.s	1.150 n.s	0.833 n.s	1.298 n.s	0.233 n.s	0.805 n.s	5.523 n.s	8.551 n.s
Genotypes	24	96.028 *	24.347 **	31.913 **	1.603 **	10.589 *	0.062 n.s	1.317 **	204.606 **	21.871 **
gca	4	49.717 *	7.389 **	6.068 **	0.530 **	10.636 **	0.039 n.s	1.093 **	50.181 **	6.558 **
sca	10	40.969 *	9.185 **	10.835 **	0.628 **	1.812 n.s	0.017 n.s	0.305 *	96.383 **	10.798 **
rca	10	15.967 n.s	7.337 **	12.268 **	0.442 **	2.405 n.s	0.016 n.s	0.311 **	47.230 **	4.076 **
Exp. Error	48	48.108	4.727	4.530	0.298	5.351	0.346	0.343	8.774	3.918

Table 2 explain the differences between genotypes due to studied characters. Parent 1 gave maximum value for (weight of grains / plant) with (0.993 g), while it produced minimum value for all studied characters expect (spike length). Respect to parent 2, which produced maximum value for the character (plant height) which was (85.333g), and exhibited the lowest value due to the characters (No. of spikes/plant, spike length and No. of grains/spike) with (12.148 spikes, 9.100cm and 21.067grains) respectively. Concerning to parent 3, table 2 confirm that this parent recorded maximum values for most characters (No. of spikes/plant, weight of spikes / plant, spike length, no. of grains / spike, biological weight / plant and grain weight / plant) with 18.251spike, 17.526g, 10.667cm, 25.067grain , 27.450g and 13.523g) respectively. As shown in the same table parent 4 recorded maximum value due to the character (1000 grain weight) with (11.587g) and showed the lowest value for the characters (No. of grains/spike) with (21.067grain). Parent 5 produced minimum value for the character (weight of grains / spike) with (0.785g). The average of Diallel and reciprocal crosses for studied characters where represent in the same table. The Diallel cross 1x3 gave minimum value for (No. of grains / spike) with (20.300 grains). The dialled cross 1x4 showed maximum value for (No. of spikes / plant) with (20.638) and minimum value for (weight of spikes / plant) with (9.432g). The Diallel cross 1x5 gave minimum value for (1000 grain weight) with (9.853g).

The Diallel cross 2x4 produced maximum value for (1000 grain weight) with (11.950g) and minimum value for (No. of spikes / plant) with (12.122). The Diallel cross 3x4 recorded minimum value for (plant height) with (77.333cm). The Diallel cross 3x5 showed minimum value for (grain weight / plant) with (8.664). The Diallel hybrid produced the highest value for (spike length and No. of grains/spike) with (12.267cm and 27.533) respectively. The reciprocal cross 4x1 recorded maximum value for (weight of spikes/plant , biological weight / plant and grain weight / plant) with (20.731,25.773 and 17.642g) respectively . The reciprocal cross 5x1 recorded maximum value for the character plant height and weight of grain/spike) with (98.333cm and 1.178g). The reciprocal crosses 5x2, 4x3 and 5x4 recorded minimum values for (biological weight /plant, spike length and weight of grains / spike) with (13.018 , 8.733 and 0.762g) respectively . Significant differences among barely genotypes for (plant height) were recorded previously by [18, 19]. Significant differences for (No. of spikes / plant, weight of spikes/plant and spike length) were recorded previously by [16, 17]. Significant differences between genotypes for all characters were recorded previously by [16, 17, 20].

Table 2: Means of Studied Characters for Genotypes (Parents and their F₂ Crosses)

crosses	Plant Height (cm)	No. of spikes / plant	Weigh t of spikes / plant (g)	Spike length (cm)	No. of grains /spike	Weigh t of grains /spike (g)	1000-grain weight (g)	Biologi cal weight / plant (g)	Grain weight / plant (g)
1 x 2	87.000	13.327	12.487	8.967	21.233	0.909	10.523	23.195	10.481
1 x 3	80.333	19.700	17.300	9.667	20.300	1.065	10.403	22.342	13.703
1 x 4	88.333	20.638	9.432	10.333	24.700	1.070	11.243	28.051	16.516
1 x 5	88.667	12.605	11.590	9.500	23.200	1.101	9.853	20.113	9.208
2 x 3	80.667	17.412	15.129	9.833	22.600	0.878	11.147	21.791	12.429
2 x 4	87.000	12.122	14.181	9.667	21.133	0.985	11.950	30.624	11.603
2 x 5	97.667	18.008	16.173	9.500	23.167	0.713	10.530	21.923	13.437
3 x 4	77.333	16.041	13.279	9.467	24.100	1.070	10.530	23.422	11.280
3 x 5	85.000	10.552	10.641	9.500	25.333	0.940	10.013	23.306	8.664
4 x 5	89.667	18.178	17.494	12.267	27.533	0.963	11.017	15.196	13.503
2 x 1	83.333	14.364	11.553	8.833	20.400	1.004	10.153	16.799	9.515
3 x 1	87.333	15.249	16.591	10.000	23.233	0.838	11.227	24.461	12.705
4 x 1	83.333	16.762	20.731	9.700	20.800	1.040	11.243	52.773	17.642
5 x 1	98.333	18.532	20.529	9.100	24.233	1.178	11.570	24.855	16.357
3 x 2	86.667	14.294	12.305	10.567	23.200	0.824	10.973	27.818	9.696
4 x 2	80.333	16.552	14.336	9.833	21.067	1.164	11.017	30.447	11.740
5 x 2	90.667	13.504	14.681	9.833	24.467	0.753	10.350	13.018	11.548
4 x 3	78.667	16.568	14.486	8.733	22.267	0.683	11.337	14.639	11.797
5 x 3	84.667	15.529	15.560	10.333	25.467	0.765	10.897	28.135	12.400
5 x 4	87.000	19.180	18.247	9.767	23.400	0.762	11.313	22.228	14.895
1	75.667	10.499	8.695	9.167	21.300	0.993	9.450	9.548	7.145
2	85.333	12.148	10.670	9.100	21.067	0.954	10.653	20.680	8.546
3	81.667	18.251	17.526	10.667	25.067	0.792	9.933	27.450	13.523
4	80.333	14.677	13.198	9.667	21.067	0.850	11.587	21.277	10.545
5	78.333	12.957	10.742	9.233	23.233	0.785	9.533	14.844	8.258
<i>Diallel Mean</i>	<i>86.167</i>	<i>15.858</i>	<i>13.771</i>	<i>9.870</i>	<i>23.330</i>	<i>0.969</i>	<i>10.721</i>	<i>22.996</i>	<i>12.082</i>
<i>Reciprocal Mean</i>	<i>86.033</i>	<i>16.053</i>	<i>15.902</i>	<i>9.670</i>	<i>22.853</i>	<i>0.901</i>	<i>11.008</i>	<i>25.517</i>	<i>12.830</i>
<i>General Mean</i>	<i>84.933</i>	<i>15.506</i>	<i>14.302</i>	<i>9.729</i>	<i>22.943</i>	<i>0.923</i>	<i>10.738</i>	<i>23.157</i>	<i>11.885</i>

The magnitude of Heterosis values estimated as the percentage of F₂s deviation from mid parental values for both Diallel and reciprocal crosses represented in table 3. Respect to Diallel crosses maximum desirable positive Heterosis values for the character (plant height) with (17.386%) produced by the cross 1x2 and for the characters (No. of spikes/ plant, biological weight / plant and grain weight) were (63.952 , 81.998, and 86.727%) produced by the cross 1x4. And for (1000 grain weight) it was (8.290%) showed by the cross 2x3, while for (weight of spikes / plant) was (51.062%) exhibited by the cross 2x5 and for the character (weight of grains/spike) was (30.369%) produced by hybrid 3x4, while the cross 4x5 produced maximum positive value for the character (spike length and No. of grains / spike) with (29.806 and 24.304%) respectively. Respect to reciprocal cross the highest positive Heterosis values for the character (biological weight/plant) was (242.394%) showed by the reciprocal cross 4x1, and for the characters (plant height, No. of spikes/plant, weight of spikes / plant , weight of grains / spike, 1000 grain weight and grain weight/plant) were (19.399, 58.016, 111.229, 32.471, 21.896 and 112.383%) respectively produced by the reciprocal cross 5x1, while for the characters (spike length and No. of grains/spike) there were (7.272 and 10.459%) respectively showed by the reciprocal cross 5x2 . The positive values indicated to the over-dominance gene effect due to the parent with the high value, while the negative Heterosis values confirm the partial-dominance gene effect due to the parent with low value. Positive and negative magnitude of Heterosis values were recorded previously for all studied characters by [16, 17].

Table 3: The percentage of heterosis values estimated for diallel and reciprocal crosses

crosses	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant (g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	Weight of spikes / plant (g)	1000-grain weight (g)	Biological weight / plant (g)	Grain weight / plant (g)
1 x 2	17.386	17.689	28.965	-1.825	0.236	-6.591	28.965	4.692	53.461	33.593
1 x 3	3.668	37.040	31.954	-2.521	-12.437	19.305	31.954	7.343	20.770	32.599
1 x 4	14.512	63.952	-13.832	9.735	16.601	16.058	-13.832	6.893	81.998	86.727
1 x 5	4.734	7.476	19.258	3.261	4.192	23.810	19.258	3.810	64.910	19.557
2 x 3	12.384	14.553	7.312	-0.506	-2.023	0.630	7.312	8.290	-9.451	12.642
2 x 4	14.933	-9.623	18.831	3.020	0.316	9.222	18.831	7.464	45.976	21.557
2 x 5	1.599	43.459	51.062	3.636	4.590	-18.006	51.062	4.326	23.424	59.929
3 x 4	-5.834	-2.571	-13.556	-6.885	4.480	30.369	-13.556	-2.138	-3.866	-6.266
3 x 5	-0.563	-32.377	-24.713	-4.523	4.900	19.281	-24.713	2.877	10.209	-20.443
4 x 5	15.973	31.562	46.149	29.806	24.304	17.822	46.149	4.324	-15.862	43.625
<i>S.E Diallel Crosses</i>	2.574	8.910	8.212	3.306	3.169	4.726	8.212	0.963	10.527	9.794
2 x 1	2.054	26.849	19.318	-3.285	-3.698	3.167	19.318	1.011	11.146	21.280
3 x 1	7.128	6.080	26.552	0.840	0.216	-6.124	26.552	15.838	32.228	22.945
4 x 1	10.877	33.156	89.382	3.009	-1.810	12.875	89.382	6.893	242.394	99.450
5 x 1	19.399	58.016	111.229	-1.087	8.832	32.471	111.229	21.896	103.791	112.383
3 x 2	6.616	-5.958	-12.715	6.914	0.578	-5.633	-12.715	6.606	15.594	-12.126
4 x 2	4.446	23.411	20.125	4.796	0.000	29.070	20.125	-0.929	45.132	22.996
5 x 2	8.927	7.578	37.127	7.273	10.459	-13.365	37.127	2.543	-26.710	37.449
4 x 3	-2.645	0.632	-5.701	-14.098	-3.468	-16.809	-5.701	5.359	-39.914	-1.972
5 x 3	1.739	-0.480	10.087	3.853	5.452	-3.002	10.087	11.952	33.041	13.862
5 x 4	4.030	38.814	52.435	3.351	5.643	-6.770	52.435	7.134	23.073	58.439
<i>S.E Reciprocal Crosses</i>	1.908	6.526	12.547	1.991	1.595	5.368	12.547	2.209	25.290	12.974

Data in table 4 explain the percentage of reciprocal effect which estimated as the F₂s Diallel crosses deviated from their reciprocal crosses. Positive and negative reciprocal effect values were recorded for all characters. The reciprocal cross 3x1 gave maximum positive reciprocal effect value for (No. of grains / spike) with (14.450%).

The reciprocal cross 4x1 recorded maximum positive effect value for the characters (weight of spikes/plant and biological weight /plant) with (119.783 and 88.131%) respectively , and also recorded maximum negative value for (No. of grains / spike) with (-15.789%) . The reciprocal cross 5x1 showed maximum positive value for the characters (plant height, 1000 grain weight and grain weight / plant) with (10.902, 17.422 and 77.672%) respectively . The reciprocal cross 3x2 showed maximum negative effect value for the characters (weight of spikes/plant and grain weight / plant) with (-18.662 and - 21.988%) respectively . The reciprocal cross 4x2 gave maximum negative effect value for (plant height and 1000 grain weight) with (-7.663 and -7.810%) respectively, and record maximum positive effect value for (weight of grain / spike) with (18.173%). The reciprocal cross 5x2 recorded the highest negative reciprocal effect value for the characters (No. of spikes /plant and biological weight/plant) with (-25.012 and -40.619%) respectively. Maximum negative effect value for (weight of grains / spike) recorded by the cross 4x3 with (-36.188%). The reciprocal cross 5x3 produced the highest positive effect values for the characters (No. of spikes/plant and spike length) with (47.170 and 8.772%) respectively. Finally the reciprocal cross 5x4 recorded maximum negative effect value for (spike length) with (-20.380%). The positive values for this effect indicate to the predominant of the reciprocal cross values, while the negative values indicate to the out yielding the Diallel cross values over their reciprocal cross values. Positive and negative effect due to reciprocal crosses were estimated previously by [16, 17].

Table 4: Estimation of reciprocal % effect for reciprocal crosses

Reciprocal crosses	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant (g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	1000-grain weight (g)	Biological weight / plant (g)	Grain weight / plant (g)
2 x 1	-4.215	7.784	-7.480	-1.487	-3.925	10.447	-3.516	-27.574	-9.217
3 x 1	8.714	-22.592	-4.094	3.448	14.450	-21.315	7.914	9.488	-7.281
4 x 1	-5.660	-18.784	119.783	-6.129	-15.789	-2.742	0.000	88.131	6.813
5 x 1	10.902	47.024	77.119	-4.211	4.454	6.996	17.422	23.577	77.642
3 x 2	7.438	-17.906	-18.662	7.458	2.655	-6.224	-1.555	27.658	-21.988
4 x 2	-7.663	36.552	1.088	1.724	-0.315	18.173	-7.810	-0.578	1.184
5 x 2	-7.167	-25.012	-9.225	3.509	5.612	5.659	-1.709	-40.619	-14.056
4 x 3	1.724	3.287	9.087	-7.746	-7.607	-36.188	7.661	-37.498	4.580
5 x 3	-0.392	47.170	46.224	8.772	0.526	-18.681	8.822	20.717	43.121
5 x 4	-2.974	5.512	4.300	-20.380	-15.012	-20.872	2.693	46.275	10.314
<i>S.E</i>	<i>2.165</i>	<i>9.240</i>	<i>16.000</i>	<i>2.774</i>	<i>3.010</i>	<i>5.883</i>	<i>2.557</i>	<i>13.151</i>	<i>9.934</i>

Table 5: Estimation of general combining ability effect for the parents (\hat{g}_{ii})

\hat{g}_{ii}	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant(g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	1000-grain weight(g)	Biological weight / plant (g)	Grain weight / plant (g)
1	-0.133	-0.288	-0.542	-0.286	-0.873	0.096	-0.226	0.011	0.156
2	1.467	-1.118	-1.084	-0.206	-1.003	-0.009	0.057	-0.460	-1.131
3	-2.533	0.679	0.732	0.214	0.721	-0.058	-0.099	0.924	0.087
4	-1.700	1.033	0.556	0.181	-0.229	0.021	0.544	2.836	1.121
5	2.900	-0.306	0.338	0.097	1.384	-0.049	-0.277	-3.311	-0.233
<i>S.E</i>	<i>1.791</i>	<i>0.561</i>	<i>0.550</i>	<i>0.141</i>	<i>0.597</i>	<i>0.152</i>	<i>0.151</i>	<i>0.765</i>	<i>0.511</i>

Data in table 5 represent the estimation of gca effect for the parents. Parent 1 gave maximum positive gca effect for (weight of grains / spike) with (0.096), and produced maximum negative gca effect for (spike length) with (-0.286). Parent 2 produced maximum negative gca effect values for the characters (No. of spikes/plant, weight of spikes / plant, No. of grains /spike , grain weight / plant) with (-1.118 , -1.084 , -1.003 and -1.131) respectively.

Parent 3 gave maximum positive gca effect for (weight of spikes / plant and spike length) with (0.732 and 0.214) respectively, and also gave maximum negative value for (plant height and weight of grains / spike) with (-2.533 and -0.058) respectively. Maximum gca of value for the characters (no. of spikes / plant , 1000 grain weight , biological weight / plant , and grain weight / plant) exhibited by parent 4 with (1.033 , 0.544 , 2.836 and 1.121) respectively . Parent 5 gave maximum positive gca effect value for (plant height and No. of grains / spike) with (2.900 and 1.384) respectively. And also gave maximum negative value for (1000 grain weight and biological weight/plant) with (-0.277 and -3.233) respectively. The positive gca effect value for these parents indicated to the high contribution of these parents toward the increasing the character values in their crosses , while the negative values due to gca effect indicated to the contribution of these parents to reduce the values of this character in their crosses. Significant gca reported previously by [21, 22, 23, 24].

Table 6: Estimation of specific combining ability effect for the diallel crosses (\hat{s}_{ij})

\hat{s}_{ij}	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant (g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	1000-grain weight(g)	Biological weight / plant (g)	Grain weight / plant (g)
1 x 2	-1.100	-0.254	-0.657	-0.337	-0.251	-0.053	-0.230	-2.712	-0.912
1 x 3	-0.033	1.612	2.717	0.503	0.233	-0.016	0.226	0.773	1.110
1 x 4	2.733	2.449	0.765	0.393	0.909	0.015	0.187	14.407	3.916
1 x 5	5.800	0.657	1.962	-0.241	0.263	0.169	0.477	2.627	0.973
2 x 3	-0.200	0.786	-0.233	0.463	0.239	-0.004	0.364	1.183	0.222
2 x 4	-1.033	-1.084	0.484	0.046	-0.611	0.140	0.144	5.002	-0.204
2 x 5	4.867	1.674	1.871	0.046	0.493	-0.132	-0.078	-1.916	1.971
3 x 4	-2.700	-0.914	-1.708	-1.024	-0.251	-0.009	-0.250	-7.887	-1.555
3 x 5	-0.467	-2.838	-2.272	-0.124	0.353	0.037	0.093	4.950	-1.207
4 x 5	2.200	2.445	2.675	1.009	1.369	-0.032	0.160	-3.970	1.425
<i>S.E</i>	3.582	1.123	1.099	0.282	1.195	0.304	0.302	1.530	1.022

Data in table 6 gave the estimation of sca effect for Diallel crosses. Maximum positive sca effect for (weight of spikes /plant) was (2.717) exhibited by the cross 1x3 , while for (No. of spikes / plant , biological weight / plant and grain weight / plant) showed by the cross 1x4 with (2.449 , 0.765 , 14.407 and 3.916) respectively. The cross 1x5 showed maximum sca effect for (plant height , weight of grains / spike and 1000 grain weight) with (5.800 , 0.169, 0.477 and 0.973) respectively , and the cross 4x5 gave maximum sca effect for the characters (spike length and no. of grains / spike) with (1.009 and 1.369) respectively. The maximum negative values due to sca effect for (weight of grains/spike) exhibited by the cross 1x2 with (-0.053) , while for (No. of grains / spike) it was (-0.611) produced by the cross 2x4 and for the characters (plant height , spike length , 1000 grain weight , biological weight / plant and grain weight /plant) were (-2.700, -1.024, -0.250, 7.887 and -1.555) respectively produced by the cross 3x4 , while for the characters (No. of spikes / plant and weight of spikes / plant) were (-2.838 and -2.772) exhibited by the cross 3x5. Significant sca reported previously by [21, 22, 23, 24].

Table 7: Estimation of specific combining ability effect for the reciprocal crosses (\hat{r}_{ij})

\hat{r}_{ij}	Plant Height (cm)	No. of spikes / plant	Weight of spikes / plant(g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike(g)	1000-grain weight (g)	Biological weight / plant (g)	Grain weight / plant (g)
2 x 1	1.833	-0.519	0.467	0.067	0.417	-0.048	0.185	3.198	0.483
3 x 1	-3.500	2.225	0.354	-0.167	-1.467	0.114	-0.412	-1.060	0.499
4 x 1	2.500	1.938	-5.649	0.317	1.950	0.015	0.000	-12.361	-0.563
5 x 1	-4.833	-2.964	-4.469	0.200	-0.517	-0.039	-0.858	-2.371	-3.575
3 x 2	-3.000	1.559	1.412	-0.367	-0.300	0.027	0.087	-3.014	1.367
4 x 2	3.333	-2.215	-0.077	-0.083	0.033	-0.090	0.467	0.088	-0.069
5 x 2	3.500	2.252	0.746	-0.167	-0.650	-0.020	0.090	4.453	0.944
4 x 3	-0.667	-0.264	-0.603	0.367	0.917	0.194	-0.403	4.391	-0.258
5 x 3	0.167	-2.489	-2.459	-0.417	-0.067	0.088	-0.442	-2.414	-1.868
5 x 4	1.333	-0.501	-0.376	1.250	2.067	0.101	-0.148	-3.516	-0.696
<i>S.E</i>	4.004	1.255	1.229	0.315	1.336	0.340	0.338	1.710	1.143

Respect to the estimation of sca effect for reciprocal crosses represent in table 7. The highest positive sca effect value for (plant height) was (1.833) recorded by the cross 2x1 and for weight of spikes/plant and grain weight / plant) was (1.412 and 1.367) respectively recorded by the cross 3x2, while for (1000 grain weight) it was (0.467) recorded by 4x2, and for (No. of spikes/plant and biological weight / plant) it was (2.252 and 4.453) respectively recorded by the cross 5x2. The highest sca effect value for the character (weight of grains / spike) was (0.194) recorded by the cross 4x3 and for (spike length and No. of grains / spike) which recorded by the cross 5x4 was (1.250 and 2.067). The highest positive values for sca effect ratified the ability of this parent to transfer this character to be improved in the cross by using parents possessing this type of character, while the negative values confirm the reduction of the characters value in these crosses when compared to the means of their parents.

Table 8: Estimation of some genetic parameters for the studied characters

Parameters	Plant Height (cm)	No. of spikes / plant	Weight of spikes/ plant(g)	Spike length (cm)	No. of grains /spike	Weight of grains /spike (g)	1000-grain weight(g)	Biological weight / plant (g)	Grain weight / plant (g)
Mse [^]	16.036	1.576	1.510	0.099	1.784	0.008	0.114	2.925	1.306
σ^2_{gca}	0.161	0.266	0.154	0.023	0.528	0.002	0.075	4.141	0.264
$\sigma^2_{sca} = \sigma^2_D$	40.969	9.185	10.835	0.628	1.812	0.018	0.305	96.383	10.798
$\sigma^2_{gca} / \sigma^2_{sca}$	0.004	0.029	0.014	0.037	0.292	0.098	0.246	0.043	0.024
σ^2_A	0.322	0.533	0.308	0.046	1.057	0.004	0.150	8.282	0.528
σ^2_{Dr}	0.035	2.881	5.379	0.172	0.311	0.004	0.098	22.153	1.385
\bar{a}	11.284	4.153	5.934	3.678	1.309	2.255	1.426	3.411	4.522
$b.s^2_h$	0.720	0.860	0.881	0.872	0.617	0.723	0.799	0.973	0.897
$n.s^2_h$	0.006	0.047	0.024	0.060	0.227	0.119	0.263	0.077	0.042
$\bar{a}r$	0.464	3.289	5.913	2.718	0.767	1.510	1.144	2.313	2.291
$b.s.r^2_h$	0.020	0.684	0.790	0.687	0.434	0.478	0.685	0.912	0.594
$n.s.r^2_h$	0.018	0.107	0.043	0.146	0.335	0.223	0.414	0.248	0.164

The estimation of same genetic parameters represent in table 8. It was indicated that the ($\sigma^2_{gca} / \sigma^2_{sca}$) was less than one for all studied characters confirming to the high contribution of non-additive gene effect in controlling the inheritance of these characters. The average degree of dominance was more than one for all characters except (weight of grain / spike). Heritability in broad sense for Diallel crosses was found to be high for almost all studied characters and it was ranged between (0.617 to 0.973) for the characters (No. of grains / spike and biological weight / plant) respectively. For reciprocal crosses heritability in broad sense was found to be low for the characters (plant height and No. of grain / spike) with (0.020 and 0.434) respectively, and it was moderate to high for other characters and reached to (0.912) for the character (biological weight / plant). Heritability in narrow sense for both Diallel and reciprocal crosses was low for all characters. Generally it was noticed the importance of non additive gene effect in controlling the inheritance of these characters. It was revealed previously that the non additive gene action were involved in the inheritance of most important characters with high estimates of broad sense heritability reported by [16, 1725, 26].

REFERENCES

[1] Abdel-Ghani, A. H. H. K. Parzies; S. Ceccarelli; S. Grando and H. H. Geiger 2005. Estimation of Quantitative Genetic Parameters for out crossing-Related Traits in Barley. Crop Science Society of America, 45:98-105.

[2] Smith, E. L. and J. W. Lambert 1968. Evaluation of Early Generation Testing in Spring Barley. Crop Science Society of America, 8:490-493.

[3] Graner, A, A. Jahoor, J. Schondelmaier; H. Siedler, K. Pillen; G. Fischbeck; G. Wenzel and R.G. Herrman. 1991. Construction of an RFLP map of barley. Theor Appl Genet 83:250-256.

[4] Hayes, P. M. B.H. Liu; S.J. Knapp; F. Chen; B. Jones; T. Blake and A. Kleinhofs. 1993. Quantitative trait locus effects and environmental interaction in a sample of North American barley germ plasm. Theoretical and Applied Genetics, 87(3), 392-401.

[5] Kleinhofs, A, A. Kilian; M.A. Saghai Maroof; R.M. Biyashev; P. Hayes; F.Q. Chen; N. Lapitan; A. Fenwick; T.K. Blake; V. Kanazin; E. Ananiev; L. Dahleen; D. Kudrna; J. Bollinger; S.J. Knapp; B. Liu; M. Sorrells; M. Heun; J.D.F ranckowiak; D. Hoffman; R. Skadsen and B.J. Steffenson. 1993. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare* L.) genome. The Appl Genet 86:705-712.

- [6] Y; J.P. Tomkins; R. Waugh; D.A. Frisch; D. Kudrna; A. Kleinhof; R.S. Brueggeman; G.I. Muehlbauer; R.P. Wise and R.A. Wing. 2000. A bacterial artificial chromosome library for barley (*Hordeum vulgare* L.) and the identification of clones containing putative resistance genes. *Theor Appl Genet* 101:1093-1099 .
- [7] Kleinhofs, A. and F. han. 2002. Molecular mapping of the barely genome , pp31-45, In G.A. Slafer, J.L. Moliniano, R. Savin, J. L. Araus and I. Romagosa (eds.) . *Barley Science:Recent Advance from Molecular Biology to Agronomy of Yield and Quality* . Food Products Press New York.
- [8] Caldwell, D. G. N. McCallum; P. Shaw; G. J. Muehlbauer; D. F. Marshall and R. Waugh. 2004. A structured mutant population for forward and reverse genetics in barley (*Hordeum vulgare* L.). *The Plant Journal*, 40(1), 143-150.
- [9] Druka, A;G. Muehlbauer; I. Druka; R. Caldo; U. Baumann; N. Rostoks; A. Schreiber; R. Wise; T. Close; A. Kleinhofs; A. Graner; A. Schulman; P. Langridge; K. Sato; P. Hayes; J. McNicol; D. Marshall and R. Waugh. 2006. An Atlas of Gene Expression from Seed to Seed through Barley Development. *Funct Integr Genomics*, 6:202-211.
- [10] Varshney, R.K.; P. Langridge and A. Graner. 2007. Application of genomics to molecular breeding of wheat and barley . *Advances in Genetics* 58: 121-155.
- [11] Hamblin M.T. T.J. Close P.R. Bhat; S. Chao J.G. Kling, K.J. Abraham; T. Blake; W.S. Brooks; B. Cooper; C.A. Griffey; P.M. Hayes; D.J. Hole; R.D. Horsley; D.E. Obert; K.P. Smith; S.E. Ullrich; G.J. Muehlbauer and J.L. Jannink. 2010. Population structure and linkage disequilibrium in U.S. barley germplasm: implications for association mapping . *Crop Sci*. 50:556-566.
- [12] Massman, J, B. Cooper; R. Horesley, S. Neate; R. Dill-Macky; S Chao; Y. Dong; P. Schwarz; G.J. Muehlbauer and K.P. Smith. 2011. Genome-wide association mapping of (*Fusarium*) head blight resistance in contemporary barley breeding germplasm. *Mol Breed* 27:439-454 .
- [13] Eshghi, R., and E. Akhundova. 2010. Genetic diversity in hulless barley based on agro morphological traits and RAPD markers and comparison with storage protein analysis . *African J. of Agriculture Research* Vol.5 (1), pp. 097-107.
- [14] Al-Mohammad, F., and M. A. AL-Yonis. 2000. *Agricultural Experimentation Design and Analysis*, Baghdad Univ. Ministry of Higher Education and Scientific Research part 1 and 2, pp 374 and 444 . (In Arabic).
- [15] Singh, R. K., and B. D. Chaudhary. 1985. *Biometrical Methods in Quantitive Genetic Analysis*. Rev.ed, pp318, Kalyani publishers, Ludhiana, New Dlhi. India.
- [16] Mohammad , L.F. 2012 .Genetic Analysis of Six-rowed Lines of Barely (*Hordeum vulgare* L.) Using Full Diallel Crosses. M.SC. Thesis College of Agricultural University of Sulaimani .
- [17] Khoshnaw , K.M.M. 2013. Diallel Crosses in Barely (*Hordeum distichum* L.), Path Coefficient and Stability Under Different Environmental Conditions in Kurdistan Region , Iraq . Dissertation submitted to the College of Agricultural University of Sulaimani .
- [18] Rohman, M.M., R. Sultana, R. Podder, A.T.M. Tanjimul, M.K. Islam and M.S. Islam. 2006. Nature of Gene Action in barley (*Hordeum vulgare* L.). *Asion Journal of Plant Sciences*. 5 (2): 170-173 .
- [19] Madic, M. ; D. Knezevic ; A. Paunovic and V. Zecevic. 2009. Inheritance of stem height and second-internode length in barley hybrids. *GENETIKA*, Vol. 41 , No. 3, 229-236 .
- [20] Riggs, I. and A. M. Hayter. 1973. Daillel analysis of the number of grains / ear in spring barley. *Herediij*, 31 (1), 95.105 .
- [21] Smith, L. 1951. Cytology and genetics of barley. *Bot. Rev.*, 17: 1-51; 133-202; 285-355 .
- [22] Chaudhary, B. D.; R. K. singh and S. N. kakar 1974. Estimation of Genetic Parameters in barley (*Hordeum vulgare* L.) I. Full, Half and Quarter Diallel Analysis . *Theoretical and Applied Genetics*, 45: 192-196.
- [23] Verma, A. K. S. R. Vishwakarma and P. K. Singh 2007. Line x Tester Analysis in barley (*Hordeum vulgare* L.) Across Environment. *Barley Genetics Newsletter*, 37:29-33.
- [24] Schittenhelm , S. J. A. Okeno and W. Friedt 2008. Prospects of Agronomic Improvement in Spring Barley Based on a Comparison of Old and New Germplasm. *Journal of Agronomy and Crop Science*, 176(5):295 – 303.
- [25] Chand, N. S. R. Vishwakarma, O.P. Verma, and M. Kumar. 2008. Worth of Genetic Parameter to Sort out New Elite Barley Lines over Heterogeneous Environments. *Barley Genetics Newsletter*. 38: 10-13 .
- [26] Reza, E., A. Mahmud, O.A. Islam, and B. Singh. 2009. Generation mean analysis for quantitative traits in barley under drought stress. *J. Plant Genet*. 23:8-16.

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