

An Investigation of Gene Action on Different Traits of Barley (*Hordeum Vulgare* L.) Using Partial Diallel Crosses System

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Abstract: The present study was carried out to investigate the genetic structure of 10 hybrids generated by crossing five cultivars of barley with their first (F₁) and Second (F₂) progeny in growing season 2011-2012 to evaluate these genotypes under normal (0.0 g l⁻¹ sea salt) and salinity stress (7 g l⁻¹ sea salt) conditions in form of randomized complete block design with three replications in a half diallel fashion. The studied traits included spike length (cm), no. of kernels/spike, no. of spikelets/spike, no. of spikes/plants, chlorophyll a, b contents, calcium and magnesium content. The analysis of variance revealed significant differences among genotypes (5 parents + 10 F₁'s + 10 F₂'s) and for all the studied traits, except chlorophyll b. The results showed that components additive and dominance effects of genes were significant for all studied traits. The estimated value of average degree of dominance (H₁/D)^{0.5} revealed that non-additive genetic effects was more pronounced in the inheritance of the chlorophyll a, b contents, calcium and magnesium in all the two generations (F₁ and F₂ crosses) and spike length (cm), no. of kernels/spike, no. of spikelets/spike and no. of spikes/plants for F₁ crosses. On contrary, additive genetic effects was evident for spike length (cm), no. of kernels/spike, no. of spikelets/spike and no. of spikes/plants for F₂ crosses. The traits including, chlorophyll a, b and calcium were controlled by over dominance in all the two generations (F₁ and F₂ crosses). The traits including spike length (cm), no. of kernels/spike, no. of spikelets/spike and no. of spikes/plants controlled by over dominance in F₁ crosses and partial dominance in F₂. While, magnesium were controlled by partial dominance effects of genes. The genetic component (H₂) was recorded with low magnitude than (H₁) for all traits in both F₁ and F₂ under 0.0 and 7 g l⁻¹ sea salt. The f value was positive for most traits of F₁ and F₂ generations, while it was negative for magnesium in both of F₁ and F₂ generations in all cases of sea salt treatments. The narrow sense heritability was high to moderate for most the studied traits. Moreover, the lowest value was also detected in some cases.

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1-Introduction

Barely is crop with a great adaptation potential in many regions of the world, ranking the forth in terms of planting area only after wheat, rice and maize (FAO, 2005) growers can obtain a harvest in areas with low precipitations, mainly because this crop has advantages in aspects such as tolerance, drought tolerance, frost tolerance, and the early period of development. Abiotic stress (mainly cold, salinity, heat and water stress) is the principal cause of the crop failure world wide, dipping average yields for most major crops by more than 50% (Jaleel *et al.*, 2007a and 2007b).

Barely is an autogamous plant and one of the oldest members of family Poaseae, its use in human's and animal's food, barely has attracted big attentions (Manli, 1985). The study of genetic conditions of different agricultural plants is one of the essential

factors for the success of inbreeding plans. Therefore it is required that precise and comprehensive information of the genetic parameters controlling the components of yield is collected and used for making decisions on the selection of an appropriate breeding method (Aghamiri *et al.*, 2012). Moreover, among all the mating designs, diallel mating, especially half diallel provided a simple and convenient method for estimating genetic parameters (Ghannadha *et al.*, 1995; Pal and Kumar, 2009).

The diallel analysis advocated by (Hayman, 1954; Mather and Jinks, 1982) provides reliable method particularly in autogamous crops to review the genetic system and gene action involved in the expression of plant attributes, right in the First generation (F₁) and second generation (F₂). Diallel cross is used to study the genetic diversity and polygenic systems of quantitative traits. As the most

important traits are inherited in a quantitative manner (Xing-Yang and Yang, 2006), therefore the results of such crosses are valuable for the improvement of the traits inside and among populations, as well as the production of cultivars (Yates, 1947; Viana and Cardoso, 1999). Koroleva (1985) studied in a diallel project the seed weight per plant, weight of 1000 barley seeds in F_1 and F_2 , and in both studied traits gene over dominance was observed. Moreover, the genes had positive effects. Chowdhry *et al.* (2002) studied five cultivars of barley using diallel cross method. The variance analysis of generations showed that the traits plant height, number of seeds per spike, weight of 1000 seeds, and seed yield in plant are controlled mainly in form of over dominance. In the control of spike length inheritance, incomplete dominance and additive effects were observed.

Genetic information about the nature of various relationships between different gene alleles, and genetic behavior of most growth characters in barley under saline stress would be an efficient to help the breeder in revealing the genetic potentialities of recommendable genotypes and organize an effective genetic improvement program (Farhad and Mohammad, 2008; Naqib, 2009). Zang *et al.* (2002) proposed that if plant responses to salinity were dissected into components, then breeding would be more efficient. Assessment of plant performance in field situations is a reliable method for evaluating plan performance in saline environments (Aslam *et al.*, 2001). The success of a barley breeding program for

the development of abiotic stress tolerant varieties depends on precise estimates of genetic variation components of traits of interest and their dominant, additive and non-allelic interaction effects (Ezatallah *et al.*, 2013).

The objective of this investigation was made to estimate the genetic components of variance and heritability of some yield and biochemical traits assess some selection criteria for identifying salt tolerance in barley genotypes which can be recommended for subsequent plant breeding projects.

2. Materials and methods

Five barley (*Hordeum vulgare* L.) genotypes differing in tolerance to salinity were obtained from the Barley Department, Agriculture Research Center, Giza, Egypt, for use in this study. The origin and pedigree of these genotypes are presented in Table 1. One set of diallel crosses was made during the growing season 2009-2010, by crossing the five parents in all possible combination to obtain a total of 10 F_1 hybrids and in growing season 2010-2011 the F_1 seeds were sowing to obtain seeds of second generation F_2 . During season 2011-2012 (P_1 , F_1 and F_2) were used to evaluate these genotypes under control (0.0 g l⁻¹ sea salt) and salinity stress (7.0 g l⁻¹ sea salt) conditions by diallel cross designs (excluding reciprocals) in a randomized block design with three replications at Biological Science Department, Faculty of Science-North Jeddah, King Abdul-Aziz University, Saudi Arabia.

Table 1 Pedigree, origin and degree of tolerance to salinity of the parental line and varieties

Code	Genotype name's	Pedigree	Origin	Degree of salt tolerance
1	Giza 123	Giza117/FAO 86(Giza117 = Baladi 16/Palestine 100	Egypt	Tolerant
2	Giza 124	Giza 117/Bahteem52/Giza118/FAO86	Egypt	Tolerant
3	Arar	Perga/Sektorisai	Syria	Mid-Tolerant
4	Mari	Bouns X Ray-mutant	Syria	Moderate
5	Beecher	Atlas/Vaughan	Syria	Sensitive

2.1. Data recorded

2.1.1. Yield parameters

At mature stage, spike length (cm), no. of kernels/spike, no. of spikelets/spike and no. of spikes/plants were recorded.

2.1.2. Biochemical parameters

The content of chlorophyll a and b in leaves were measured spectrophotometrically at 662 nm and 644 nm according to Sukran *et al.* (1998). The formulae for samples dissolved in acetone are as follows: $C_a = 11.75 A_{662.6} - 2.35 A_{645.6}$ and $C_b = 18.61 A_{645.6} - 3.96 A_{662.6}$ where C_a and C_b are the concentrations of chlorophyll a and b, respectively.

Calcium and magnesium content were measured by dried shoots of each treatment (control and 7 g l⁻¹ sea salt) for three days to obtain dried samples. 2.5 ml of nitric acid (HNO₃ conc.) was added to 0.07 g of dry sample and the mixture boiled for 60 – 90 min, then transferred to a beaker and the volume adjusted to about 40 ml with distilled water and boiled for 10 minutes. This was cooled and then filtered through glass wool into a flask and beaker rinsed with distilled water into a 50 ml volumetric flask. The concentration of Ca and Mg concentration were determined by flame absorption spectrophotometer.

2.2. Statistical analysis

Estimating the components of variation and determining the nature of gene action in the studied characters were carried out using the diallel biometric approach as outlined by (Hayman, 1954). The development of an effective plant breeding program and the efficiency of selection largely depend upon the magnitude of genetic variability existing in the plant material under study, therefore analysis of variance and components of variation were applied.

3. Results and discussions

The analysis of variance revealed significant differences among 15 genotypes (5 parents + 10 F_1 's) for all the studied traits, except Chlorophyll b under 7.0 g l⁻¹ and this suggests that high genetic variability for these traits in the genotypes studied (Table 2). While, The analysis of variance revealed significant differences among 15 genotypes (5 parents + 10 F_2 's) for all the traits, indicating the presence of considerable amount of genetic diversity in the material (Table 3).

Components of genetic variation and other genetic statistics for spike length and no. of kernels/spike under different treatments of sea salt in F_1 and F_2 hybrids are presented in Table (4). For spike length, and no. of kernels/spike, the additive genetic variance (D) was greater than dominance genetic variance (H_1 and H_2) under control and 7.0 g l⁻¹ sea salt for F_2 indicating preponderance of additive genetic variance. While, the dominance was greater than additive in F_1 for two traits under all levels of sea salt except for spike length under 7.0 g l⁻¹ of sea salt. The H_1 and H_2 were positive in all cases. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the traits, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents (Table 4). The f value was positive except for Spike length in F_1 and F_2 for the control treatment and no. of kernels/spike in F_1 for the control and 7.0 g l⁻¹ sea salt. The positive significant of the f value indicated that dominance alleles were more than recessive alleles. The average degree of dominance (H_1/D)^{1/2}, was less than unity for Spike length at 7.0 g l⁻¹ sea salt while, the average degree of dominance was more than unity for all the other cases. If the average degree of dominance is less than one it indicated partial dominance and greater than one indicated over dominance is present. Similar results were obtained by (Barati, 2003; Rezaie *et al.*, 2004; Mostafavi *et al.*, 2005). The proportion of dominant genes with positive or negative effects in the parents can be judged from the ratio of $H_2/4H_1$ with maximum 0.25 value. The positive and negative alleles ($H_2/4H_1$) as shown by values were less than 0.25 in all cases. This

suggests inequality of distribution of increasing and decreasing alleles. Similar results were reported by (Bouzerzour and Djakoune, 1998) in barley. However, the gene frequency seemed to be nearly symmetrical as the range of this component ($H_2/4H_1$) were less than 0.25 for these traits. The estimates of the consistency of expression of the degree of dominance across all segregating loci (KD/KR) were between zero and one, except for spike length under 7.0 g l⁻¹ sea salt for F_1 and F_2 and no. of kernels/spike under 0.0 g l⁻¹ and 7.0 g l⁻¹ sea salt for F_2 which was more than unity. The absolute value of the statistic varies from zero to one, where 1 indicates a constant dominance level over all loci. This finding is in agreement with earlier reports of (Ciulca *et al.*, 2000; Bhatnagar *et al.*, 2001; Dharam and Kumar, 2009). The narrow sense heritability was high for spike length under 7.0 g l⁻¹ sea salt for F_2 and no. of kernels/spike for F_2 under all salt levels and moderate for spike length for F_1 under 7.0 g l⁻¹ Sea Salt and no. of kernels/spike, for F_1 under all salt levels indicating that selection for improvement of these traits would be effective.

Components of genetic variation and other genetic statistics for no. of spikelets/spike and no. of spikes/plant under different treatments of sea salt in F_1 and F_2 hybrids are presented in Table (5). The diallel analysis revealed significant role of additive genetic component (D) for the inheritance of no. of spikelets/spike and no. of spikes/plants. The non-additive component (H_1) was found to be important for the genetic control of all cases. Additive and non-additive genetic components were significant for no. of spikelets/spike and no. of spikes/plants. However, the relative magnitude of dominant component (H_2) was higher as compared to additive component (D) in F_1 for no. of spikelets/spike in all cases of sea salt and no. of spikes/plants in F_1 under control treatment, indicating the preponderance of dominant gene effects in controlling the inheritance of these traits. While, the additive genetic variance (D) was greater than dominance genetic variance for, no. of spikes/plants under 0.0 g l⁻¹ and 7.0 g l⁻¹ sea salt for F_2 and F_1 in case of 7.0 g l⁻¹ sea salt, indicating preponderance of additive genetic variance. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the cases, except no. of spikes/plants at F_2 under control treatment indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents (Table 5). The estimates of f component were positive for no. of spikelets/spike and no. of spikes/plants. in F_2 under control treatment, indicating unequal distribution of dominant and recessive gene frequencies in the parents. The average degree of dominance (H_1/D)^{1/2}, was greater than unity for no. of spikelets/spike for F_1 under 0.0 g l⁻¹ and 7.0

$g\ l^{-1}$ sea salt while, no. of spikes/ plants reported greater than unity for F_1 under control treatment. If the average degree of dominance was greater than one indicates over dominance is present. Similar results were obtained by (Barati, 2003; Rezaie *et al.*, 2004). The average degree of dominance was less than unity for all the other cases. If the average degree of dominance is less than one it indicated partial dominance is present. The proportion of dominant genes with positive or negative effects in the parents can be judged from the ratio of $H_2/4H_1$ with maximum 0.25 value. The positive and negative alleles ($H_2/4H_1$) as shown by values were less than 0.25 in all cases except for no. of spikes/ plants under control. This suggests inequality of distribution of increasing and decreasing alleles. Similar results were reported by (Bouzerzour and Djakoune, 1998; Roy, 2000). However, the gene frequency seemed to be nearly symmetrical as the range of this component ($H_2/4H_1$) were less than 0.25 for these traits. The estimates of the consistency of expression of the degree of dominance across all segregating loci(KD/KR) were between zero and one, except for no. of spikes/ spike and no. of spikes/plants in F_1 under control and F_2 under $7.0\ g\ l^{-1}$ sea salt, which was more than unity. The absolute value of the statistic varies from zero to one, where 1 indicates a constant dominance level over all loci. This finding is in agreement with earlier reports of (Ciulca *et al.*, 2000; Bhatnagar *et al.*, 2001 and Dharam and Kumar, 2009). The calculation of heritability is important because it can provide us with the information required for the transfer of traits from parents to their progeny, accelerates the evaluation of genetic and environmental effects on phenotype diversity, and helps selection. The narrow sense heritability was high for no. of spikes/ spike and, no. of spikes/plants for F_2 all cases and F_1 under $7.0\ g\ l^{-1}$ sea salt, moderate for no. of spikes/ spike and, no. of spikes/plants for F_1 under control treatment indicating that selection for improvement of these traits would be effective. The highest value of narrow-sense heritability was reported by Seyed *et al.* (2012).

Components of genetic variation and other genetic statistics for Chlorophyll a and Chlorophyll b under different treatments of sea salt in F_1 and F_2 hybrids are presented in Table (6). Additive and non-additive genetic components were significant for Chlorophyll a and Chlorophyll b. The non-additive component (H_1) was found to be important for the genetic control for Chlorophyll a and Chlorophyll b in F_1 and F_2 generations in all cases of sea salt., indicating the preponderance of dominant gene effects in controlling the inheritance of these traits.. The H_1 and H_2 were positive in all cases. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the cases, indicating that positive and

negative alleles were not in equal frequencies in the material under study and beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents (Table 6). The f value was positive in F_1 and F_2 for chlorophyll a under the control in both of F_1 and F_2 generations, and chlorophyll b under the control in F_1 . The positive significant of the f value indicated that dominance alleles were more than recessive alleles. The average degree of dominance $(H_1/D)^{1/2}$ was greater than unity for all traits in all cases while, the average degree of dominance was less than unity for Chlorophyll b under $7.0\ g\ l^{-1}$ sea salt in F_2 generation. If the average degree of dominance is less than one it indicated partial dominance and greater than one indicated over dominance is present and this finding is in agreement with earlier reports of (Medicil *et al.*, 2004; Mohmood *et al.*, 2004). The proportion of dominant genes with positive or negative effects in the parents can be judged from the ratio of $H_2/4H_1$ with maximum 0.25 value. The positive and negative alleles ($H_2/4H_1$) as shown by values were less than 0.25 in all cases. This suggests inequality of distribution of increasing and decreasing alleles. The estimates of the consistency of expression of the degree of dominance across all segregating loci(KD/KR) were between zero and one, except for chlorophyll a under the control in both F_1 and F_2 generations, and chlorophyll b under control for F_1 which was more than unity. This finding is in agreement with earlier reports of Mohmood *et al.* (2004). The narrow sense heritability was high for chlorophyll a and b under $7.0\ g\ l^{-1}$ sea salt for F_1 and moderate for chlorophyll b for F_2 under $7.0\ g\ l^{-1}$ sea salt indicating that selection for improvement of these traits would be effective.

Components of genetic variation and other genetic statistics for calcium and magnesium under different treatments of sea salt in F_1 and F_2 hybrids are presented in Table (7). Additive and non-additive genetic components were significant for calcium and magnesium. The non-additive component (H_1) was found to be important for the genetic control for calcium of F_1 and F_2 in all cases of treatments of sea salt.. The non-additive component (H_1) was found to be important for the genetic control for magnesium in both F_1 and F_2 generations under control treatment. While, additive genetic components were significant for magnesium under $7.0\ g\ l^{-1}$ sea salt in both F_1 and F_2 generations. The H_1 and H_2 were positive in all cases. The genetic component (H_2) was recorded with low magnitude than (H_1) for all the cases, indicating that positive and negative alleles were not in equal frequencies in the material under study and beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents (Table 7). Similar results were reported by (Spehar,

1995; Sirohiand and Yayasani, 2001). The f value was positive for calcium in both of F₁ and F₂ generations in all cases of treatments of sea salt. While it was negative for magnesium in both of F₁ and F₂ generations in all cases of sea salt treatments. The positive significant of the f value indicated that dominance alleles were more than recessive alleles. The average degree of dominance $(H_1/D)^{1/2}$, was greater than unity for calcium in both of F₁ and F₂ generations in all cases except for F₂ under the control, while the average degree of dominance was less than unity for magnesium in both of F₁ and F₂ generations in all cases except for F₁ under control treatment. These results are in the same line with Muhammad *et al.* (1995). The proportion of dominant genes with positive or negative effects in the parents can be judged from the ratio of H₂/4H₁ with maximum 0.25 value. The positive and negative alleles (H₂/4H₁) as shown by values were less than 0.25 in all cases for

calcium and magnesium. This suggests inequality of distribution of increasing and decreasing alleles. The estimates of the consistency of expression of the degree of dominance across all segregating loci(KD/KR) was more than unity for calcium in both F₁ and F₂ generations in all cases of treatments of sea salt. While, magnesium varies from zero and one in both of F₁ and F₂ generations in all cases of treatments of sea salt. These results are in harmony with those obtained by (Muhammad *et al.*, 1995; Sirohiand and Yayasani, 2001). The narrow sense heritability was high for magnesium under 7.0 g l⁻¹ sea salt for in both of F₁ and F₂ generations under 7.0 g l⁻¹ sea salt, moderate for Calcium under control treatment of F₁, indicating that selection for improvement of these traits would be effective. While, the narrow sense heritability was low for the other cases. Similar results were obtained by (Muhammad *et al.*, 1995; Sirohiand and Yayasani, 2001).

Table 2 Analysis of variances and tested of validity for some yield and biochemical traits in F₁ diallel crosses of the five parents under control (tape water) and 7.0 g l⁻¹ of sea salt.

Source of variation	df	Spike Length		No. of kernels/spike		No. of spikelets/spike		No. of spikes/plants		Chlorophyll a		Chlorophyll b		Calcium		Magnesium	
		0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹
Replication	2	0.92*	0.533	9.872	7.0474	1.484	0.0083	0.197	0.241	0.264	0.005	0.0049	0.030	7.787	6.084*	2.66	3.322**
Genotypes	14	2.61**	3.42**	184.75**	52.37**	16.15**	25.87**	0.95**	1.21**	55.25**	57.39**	38.18**	6.623	33.06**	34.90**	8.55**	7.36**
Error	28	0.229	0.4493	5.485	3.7994	0.813	0.583	0.102	0.089	0.212	0.067	0.026	0.015	1.394	1.855	2.151	0.621
t ²		3.572	0.0093	10.233*	0.6462	0.5965	1.6875	0.825	2.64	0.636	1.654	39.30**	2.729	0.799	3.369	1.019	4.942
b		0.228	1.046	0.2884	0.5663	0.8088	0.6832	1.123	0.696	-0.392	0.343	0.6033	0.439	0.0813	-0.120	-0.077	0.3690
± SE (b)		0.239	0.3033	0.0451	0.2919	0.1688	0.2553	0.361	0.146	0.859	0.379	0.051	0.206	0.3499	0.226	0.330	0.1738
H ₀ :b = 0		0.951	3.449*	6.4056**	1.9399	4.793*	2.6761	3.109	4.77**	-0.456	0.905	11.86**	2.134	0.232	-0.531	-0.236	2.1224
H ₀ :b = 1		3.25*	-0.151	15.806**	1.4862	1.133	1.2410	-0.339	2.084	1.62	1.735	1.619	2.722	2.625	4.945*	3.263*	3.628*

Table 3 Analysis of variances and tested of validity for some yield and biochemical traits in F₂ diallel crosses of the five parents under control (tape water) and 7.0 g l⁻¹ of sea salt.

Source of variation	df	Spike Length		No. of kernels/spike		No. of spikelets/spike		No. of spikes/plants		Chlorophyll a		Chlorophyll b		Calcium		Magnesium	
		0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹	0.0 g l ⁻¹	7.0 g l ⁻¹
Replication	2	0.5836	0.0831	3.276	2.184	3.852	0.404	0.006	0.94**	2.707	1.014	1.207	0.009	7.78**	6.08**	0.266	3.32**
Genotypes	14	1.89*	2.36**	47.82**	17.27**	14.24**	17.96**	0.738**	0.94**	39.69**	95.43**	8.96**	0.888**	33.06**	34.90**	8.55**	7.36**
Error	28	0.760	0.1978	4.697	0.928	1.675	0.431	0.1373	0.0512	6.199	1.946	0.954	0.037	1.394	1.855	2.150	0.620
t ²		1.4697	0.0493	3.195	0.3196	1.704	0.141	1.059	0.149	0.147	2.325	2.969	14.5**	11.72**	26.75**	1.203	2.625
b		0.074	0.835	1.173	1.052	0.688	1.022	1.150	0.939	0.627	0.751	0.780	0.847	0.0812	-0.120	-0.077	0.369
± SE (b)		0.2990	0.4001	0.116	0.187	0.1689	0.097	0.441	0.108	0.339	0.127	0.104	0.036	0.349	0.226	0.330	0.173
H ₀ :b = 0		0.247	2.086	10.05**	5.614	4.073*	10.48**	2.607	8.70**	1.84	5.90**	7.50**	23.24**	0.232	-0.530	-0.235	2.12**
H ₀ :b = 1		3.0969	0.4127	-1.484	-0.2767	1.247	-0.225	-0.341	0.566	1.098	1.96	2.11*	4.18**	2.62*	4.94**	3.26*	3.63**

Table 4 The components of variation and their relative proportions for Spike length and No. of kernels/spike under different treatments of sea salt in F₁ and F₂ hybrids.

Components of variation and parameters	Spike length				No. of kernels/spike			
	0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt		0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D ± SE (D)	0.223±0.339	0.066±0.444	1.524**±0.119	1.613±0.090	31.364±18.82	31.75**±1.12	10.52**±2.71	11.526**±0.424
F ± SE (F)	-0.28±0.84	-0.139±1.11	0.095±0.299	0.176±0.225	-47.50±47.01	5.882*±2.80	-12.08±6.78	0.960±1.060
H ₁ ± SE (H ₁)	2.696±0.915	0.394±1.200	1.426**±0.323	0.099±0.243	132.5**±50.8	3.186±3.035	33.59**±7.33	0.498±1.1466
H ₂ ± SE (H ₂)	2.539±0.830	0.318±1.088	1.253**±0.293	0.063±0.220	113.4*±46.10	1.810±2.753	28.67**±6.64	0.348±1.040
h ² ± SE (h ²)	2.897±0.560	-0.0355±0.73	0.668**±0.198	-0.0009±0.14	15.20±31.12	-0.1223±1.859	2.86±4.489	-0.050±0.702
E ± SE (E)	0.091±0.138	0.249±0.181	0.151**±0.048	0.0633±0.036	1.925±7.68	1.53**±0.459	1.338±1.108	0.337±0.1733
(H ₁ /D) ^{1/2}	3.469	1.217	0.967	0.1243	2.055	0.1583	1.7866	0.1039
H ₂ /4H ₁	0.235	0.202	0.219	0.1590	0.213	0.1420	0.2133	0.1745
KD/KR	0.686	0.396	1.066	1.563	0.461	1.826	0.5137	1.501
h ² (ns)	0.315	0.299	0.632	0.9028	0.618	0.872	0.61811	0.9266

Table 5 The components of variation and their relative proportions for No. of spikelets/spike and No. of spikes/plants under different treatments of sea salt in F₁ and F₂ hybrids.

Components of variation and parameters	No. of spikelets/spike				No. of spikes/plants			
	0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt		0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D ± SE (D)	5.92**±1.479	5.59**±0.973	10.92**±1.450	10.96**±0.240	0.36**±0.075	0.35**±0.027	0.563**±0.030	0.559**±0.003
F ± SE (F)	2.676±3.695	-1.015±2.430	-0.826±3.624	-0.0918±0.600	0.204±0.188	-0.007±0.068	-0.147±0.0771	-0.032**±0.008
H ₁ ± SE (H ₁)	16.45**±3.99	0.998±2.628	12.74**±3.918	0.4632±0.6495	0.888**±0.20	0.051**±0.04	0.177**±0.083	-0.0151±0.009
H ₂ ± SE (H ₂)	15.60**±3.62	0.848±2.383	10.460±3.554	0.4465±0.5891	0.733**±0.19	0.0556±0.067	0.1663*±0.075	-0.010±0.008
h ² ± SE (h ²)	2.697±2.446	-0.0066±1.60	1.538±2.399	-0.0002±0.397	0.0119±0.125	0.0177±0.045	0.305**±0.051	0.0011±0.0056
E ± SE (E)	0.285±0.603	0.6068±0.397	0.181±0.592	0.1429±0.0981	0.0363±0.030	0.043**±0.01	0.033**±0.012	0.0368**±0.001
(H ₁ /D) ^{1/2}	1.668	0.2112	1.0800	0.1027	1.574	0.1905	0.5608	0.082
H ₂ /4H ₁	0.2369	0.2125	0.2051	0.2409	0.2064	0.2721	0.2345	0.170
KD/KR	1.313	0.6463	0.9322	0.9600	1.442	0.9435	0.6209	2.216
h ² (ns)	0.328	0.8048	0.7151	0.9560	0.4125	0.7577	0.8284	0.895

Table 6 The components of variation and their relative proportions for chlorophyll a and chlorophyll b under different treatments of sea salt in F₁ and F₂ hybrids

Components of variation and parameters	Chlorophyll a				Chlorophyll b			
	0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt		0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D ± SE (D)	12.56±8.523	11.67±4.26	11.67**± 3.0	30.72**±3.69	4.72±1.870	2.700**±0.399	1.59**±0.40	0.320**±0.017
F ± SE (F)	12.08±21.29	29.10**±10.66	-10.57±7.72	-42.92**±9.3	3.45±4.67	-2.07*±0.998	-1.20±1.01	-0.423**±0.04
H ₁ ± SE (H ₁)	84.83**±23.01	182.75**±11.53	37.56**±8.35	131.5**±9.98	43.99**±5.05	15.99**±1.079	4.22**±1.081	0.813**±0.04
H ₂ ± SE (H ₂)	77.84**±20.87	148**±10.45	31.80**±7.57	107.80**±9.1	40.88**±4.58	14.816**±0.97	3.59**±0.98	0.679**±0.043
h ² ± SE (h ²)	0.079±14.09	72.10**±7.06	47.54**±5.11	123.5**±6.11	85.51**±3.09	14.77**±0.660	3.08**±0.66	0.529**±0.029
E ± SE (E)	0.0717±3.47	1.99±1.74	0.0211±1.26	0.628±1.509	0.008±0.763	0.323*±0.163	0.005±0.163	0.011±0.007
(H ₁ /D) ^{1/2}	2.598	1.978	1.793	1.034	3.0500	1.216	1.6290	0.7966
H ₂ /4H ₁	0.2294	0.202	0.2117	0.204	0.2323	0.231	0.2128	0.2088
KD/KR	1.454	4.407	0.5967	0.1938	1.272	0.5203	0.623	0.0933
h ² (ns)	0.1605	0.229	0.6371	0.3508	0.1762	0.2990	0.6544	0.4094

Table 7 The components of variation and their relative proportions for magnesium and calcium under different treatments of sea salt in F₁ and F₂ hybrids

Components of variation and parameters	Calcium				Magnesium			
	0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt		0.0 g l ⁻¹ (Control)		7.0 g l ⁻¹ Sea Salt	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
D ± SE (D)	6.424±5.65	6.42±5.65	1.66±6.249	1.66±6.249	0.915±2.03	0.9155±2.034	3.411**±0.27	3.411**±0.270
F ± SE (F)	5.69±14.12	2.84±14.12	4.105±15.61	2.052±15.61	-0.155±5.08	-0.077±5.082	-0.996±0.675	-0.498±0.675
H ₁ ± SE (H ₁)	47.66**±15.26	11.91±15.26	50.44**±16.87	12.61±16.87	10.32**±5.49	2.582±5.494	0.89±0.73	0.224±0.730
H ₂ ± SE (H ₂)	42.71**±13.84	10.67±13.84	41.55**±15.30	10.388±15.31	10.08*±4.98	2.521±4.983	0.678±0.663	0.1696±0.662
h ² ± SE (h ²)	1.22±9.34	0.305±9.348	32.18**±10.33	8.04±10.334	0.041±3.36	0.010±3.364	0.421±0.447	0.105±0.447
E ± SE (E)	0.60±2.30	0.606±2.30	0.712±2.55	0.712±2.551	0.675±0.830	0.675±0.830	0.2669*±0.110	0.266±0.110
(H ₁ /D) ^{1/2}	2.724	0.6809	5.500	1.3750	3.359	0.839	0.513	0.1281
H ₂ /4H ₁	0.224	0.2239	0.21	0.206	0.245	0.244	0.190	0.1892
KD/KR	1.390	1.38	1.58	1.5767	0.951	0.9509	0.56	0.556
h ² (ns)	0.2009	0.4234	0.225	0.2171	0.170	0.287	0.8412	0.864

D: additive genetic variance, H₁ and H₂: dominance genetic variance and corrected dominance genetic variance, F₁: product of additive by dominance, E: expected environmental variance, (H₁/D)^{1/2}: average of degree dominance, KD/KR: proportion of dominance genes, h² (ns): heritability for diallel in a narrow sense.

Conclusion

The analysis of variance revealed significant differences among genotypes (5 parents, 10 F₁'s and 10 F₂'s) for all the studied traits, except Chlorophyll b. The genetic system that controls in the inheritance of most traits in both generations is mainly dominance; hybridization can play a great role in breeding method of these traits. On contrary, additive genetic effects was evident in some cases. Over dominance was predominant and partial dominance was also, observed in some cases. The genetic component (H₂) was recorded with low magnitude than (H₁) for all traits in all the two crosses, indicating that beneficial positive alleles are not proportional to that of deleterious negative alleles at all loci among parents. The f value was positive for most traits of F₁ and F₂ generations. The positive significant of the f value indicated that dominance alleles were more than recessive alleles. The positive and negative alleles (H₂/4H₁) as shown by values were less than 0.25 in all cases. This suggests inequality of distribution of increasing and decreasing alleles. The estimates of the consistency of expression of the degree of dominance across all segregating loci (KD/KR) was more than unity for calcium and less than unity for magnesium all the two crosses (F₁ and F₂) under the two sea salt treatments while, it was different directions in other traits. The absolute value of the statistic varies from zero to one, where 1 indicates a constant dominance level over all loci. The narrow sense heritability was high to moderate for most the studied traits. Moreover, the lowest value was also, observed in some cases. Additive gene effects and high heritability estimates for most traits suggested that these traits could be improved effectively through early generation selection, while the dominance gene effects and low heritability estimates for some cases favor delayed stage plant selection.

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