


Genetic analysis of yield and its components in four barley (*Hordeum vulgare* L.) crosses under water stress condition.

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ABSTRACT

The present study was carried out at Gemmeiza Agricultural Research Station, El-Gharbia Governorate, Egypt, during the three growing seasons of 2019/20, 2020/21, and 2021/22 to determine the genetic variance components and type of gene action controlling yield and its components by using the means of the six populations (P1, P2, F1, F2, BC1, and BC2) of the four barley crosses. The base generation of the four crosses was sown under normal (1636.06 m³ fed⁻¹) and water stress conditions (601.06 m³ fed⁻¹). Mean effects (m) varied for all attributes in all crosses and were highly significant. Additionally, under both scenarios, the relative significance of additive-dominance effects changed with characters and crosses. Results generally showed that non-allelic interactions existed in all crosses for all the examined characteristics. In most of the examined traits, dominance was stronger than additive and additive dominance among the epistatic components, showing that these traits were significantly influenced by dominance and associated non-allelic interactions. For the majority of the examined qualities under both circumstances, positive heterotic effects compared to the mid parent and better parent were discovered. For the majority of the studied traits, the highest predicted genetic advance values were paired with high and moderate narrow-sense heritability values in all crosses. These findings suggested that early generations could be used for selection to obtain high-yielding genotypes under either normal or stressful conditions. Finally, the most promising crosses were the two crosses 2 and 3 under water stress conditions (601.06 m³ fed⁻¹), which had high genetic advances associated with high heritability and would be of interest in breeding programs for improving the most studied traits in barley.

Keywords: Barley, water stress, yield, generation mean analysis, six populations, heterosis, heritability, genetic advance.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important cereals ranked the fourth in world cereal production. It is the main crop grown in a large scale in rainfed areas of Egypt and is adapted to grow under adverse conditions, such as drought, low soil fertility, saline soil and high or low temperature under rainfed conditions on the border governments of Egypt (Kumar *et al.*, 2014; Idehen *et al.*, 2017; Byrne *et al.*, 2018; Ahmed and Hassan, 2019). It is also considered as the most suitable crop that can be grown over a wide range of soil variability and under many adverse conditions. The major use of barley in Egypt as well as in the developed countries, is as food and feed. There is renewed interest in using the crop as a human food in North Africa and in the malting industry (Idehen *et al.*, 2017; Kumar *et al.*, 2020). Also, the increased use for animal feeding, especially for sheep and goats had resulted in a sharp demand for barley.

Barley is the dominant cereal grown in Northwest Coast and North Sinai of Egypt, as well as newly reclaimed lands. Most of these soils suffer from water shortage and low soil fertility (Hassanein, 2019; Zainab Sharkawy El-khalifa *et al.*, 2022). The development of barley cultivars that have the ability to grow under drought and other environmental stresses is needed.

An additional avenue is the cultivation of the early maturing barley cultivars before cotton, to support wheat production in Egypt for bread making and to overcome the gap between wheat consumption and production. Since barley production areas located in different environments, developing well adapted barley cultivars is one of the main objectives for barley breeders. In this respect, (Katta *et al.*, 2009; Amer, 2010; El-Refaey *et al.*, 2015;

Mansour 2017; Madakemohekar *et al.*, 2018; Kumar *et al.*, 2020) reported the possibility of developing some barley genotypes that combine high yield potential under a wide range of environmental stresses.

A fundamental experimental breeding generation, generation mean analyses are quantitative biometric techniques based on assessments of the phenotypic performance of specific quantitative features on as many plants as possible (parental, filial, backcrosses and first segregating generation). Gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance, dominance x dominance) interactions responsible for the inheritance of quantitative traits are estimated using generation mean analysis in plant breeding, as described by Kearsey and Pooni (1996). It aids in comprehending the effectiveness of the parents utilized in crossings and the potential for crosses to be used for pedigree selection or the exploitation of heterosis. However, the degree of heritability and genetic progress are correlated with the selection efficiency (Singh and Narayanan, 1993).

As a result, the major goal of this study was to investigate new, promising barley genotypes that may provide high yields and are more resistant to water stress by 1) Researching the effects of inbreeding depression and heterosis on yield and yield components. 2. Researching the inheritance of yield and its elements.

MATERIALS AND METHODS

The experimental material comprised of five parental varieties/lines of barley that were variable in their response under normal and drought conditions to obtain four crosses: cross 1 (Giza-134 × Line-3); cross 2 (Line-3 × Line-10); cross 3 (Line-10 × Giza -138) and cross 4 (Line-10 × Giza-137). Pedigree of parental genotypes is given in Table (1).

The current study was carried out on the experimental farm of Gemmeiza Agricultural Research Station in El-Gharbia Governorate, Egypt, throughout the course of three growing seasons: 2019–2020, 2020–21, and 2021/22. To create the hybrid seeds for the 2019–20 growing season, the parental genotypes were crossed. In order to simultaneously create F1 plants, the hybrid seeds from the four crosses were sown throughout the 2020–2021 growth season. These plants were selfed to produce F2, and a portion of the F1 plants from each cross were backcrossed to the two parents to produce the two backcrosses (BC1 and BC2). The crossings were duplicated simultaneously to create enough F1 seed. During the growing season of 2022–2022, the base generation of the four crosses (P1, P2, F1, F2, BC1 and BC2) were sown in three replications under normal (three irrigation after sowing; irrigation at tillering, at elongation, and at heading stage (favorable condition)) and water stress circumstances (sowing irrigation only). There were three rows for the P1, P2, and F1 generations, respectively. Each of the three generations, BC1, BC2, and F2, had seven rows. In the 1.5 m-long row, the seeds were spaced 15 cm and 30 cm apart. For each cross, data were gathered on 30, 30, 300, and 75 randomly selected parent, F1, F2, and backcross plants.

Table 1: Name and pedigree of the five parental barley genotypes used in this study.

No.	Genotypes	Pedigree	Response to normal and drought conditions
1	Giza-134	Alanda-01/4/WI2291/3Api/CM67//L2966-69	MT
2	Giza-137	Giza 118 /4/Rhn-03/3/Mr25-//Att//Mari/Aths*3-02	MT
3	Giza-138	Acsad1164/3/Mari/Aths*2//M-Att-73-337-1/5/Aths/ lignee686 /3/Deir Alla 106//Sv.Asa/ Attiki /4/Cen/Bglo."S")	T
4	Line-3	EgSK07/08no.1751-1-1-2	MT
5	Line-10	CBSSO5M00677T-E-2M-OM-OAP_OTR	T

Tolerant (T), Moderately Tolerant (MT)

Table 2. Amount of irrigation water supplied and total rainfall in m³fed⁻¹ for the two treatments.

Treatments	water applied (m ³ fed ⁻¹) at				Total irrigation, (m ³ fed ⁻¹)	Rainfall, (m ³ fed ⁻¹)	Total water (m ³ fed ⁻¹)
	Sowing	II	III	VI			
T 1 (Normal)	520	360	345	330	1555	81.06	1636.06
T 2 (stress)	520	-	-	-	520	81.06	601.06

* Fadden (fad.) = 4200 m²

Table 3. Monthly mean air temperature (°C), mean relative humidity (RH %) and rainfall (mm month⁻¹) in winter season of 2021/22 at Gemmeiza site.

Month	Temperature (°C)		RH%	Wind speed (ms ⁻¹)	Rainfall (mm)
	maximum	minimum			
December	19.37	7.15	60.63	6.43	0.34
January	16.76	3.73	59.04	5.07	1.08
February	19.48	5.22	61.52	5.58	0.39
March	21.82	2.91	62.38	4.88	0.06
April	32.22	4.10	50.20	5.50	0.02
May	33.80	7.38	36.64	6.70	0.04

* Source: Water Requirement and Field irrigation Res., Dept., SWERI, ARC. Egypt.

Table 4: Mechanical analysis of experimental soils.

season				2021/2022				
Particle size distribution (%)				Tex. class	HC	IR	WSG	WHC
Corease sand	Fine sand	Silt	Clay					
10.05	14.12	29.45	46.38	Clayey	1.05	3.05	65.85	50.28

Hc= hydraulic conductivity, IR= infiltration ratio, WSG=water stable aggregates, WHC= water holding capacity.

Table 5. Bulk density and some hydrodynamic constants of the studied soil.

depth	season 2021/2022			
	FC	WP	AW	Bd
0-15 cm	45.55	24.01	21.54	1.18
15-30 cm	43.05	23.03	20.02	1.20
30-45 cm	41.88	21.12	20.76	1.25
45-60cm	39.02	19.89	19.13	1.36
Average	42.38	22.01	20.36	1.25

FC= Field capacity, wp= water point, Aw= available water, Bd= bulk density.

The data were collected on the basis of individual plant for number of spikes per plant, number of grains per spike, grains weight per spike, 100-grain weight, biological yield per plant and grain yield per plant. The growing conditions were identical for all generations since they followed the standard practices.

Statistical and genetic analysis:

According to Mather (1949), the scaling test was used to determine if non-allelic interactions existed or not. To determine whether the additive-dominance model was appropriate in each situation, the quantities A, B, C, and D along with their variances were determined. By using the square root of the corresponding variances of the mean, the standard errors for A, B, C, and D were calculated. The effects of A, B, C, and D were divided by their respective standard errors to determine the t-values. In each test, the estimated t-values were contrasted with the tabulated value of t at the 5% and 1% levels of probability. The sum of the degrees of freedom for each generation included is known as the degrees of freedom (df). All different kinds of non-allelic interactions are present, according to the relevance of the A and B scales. The relevance of the C scale points to (dd) epistasis kinds. Gene interactions of the type (aa) are revealed by the significance of D scale, while those of the type (aa) and (dd) are revealed by the significance of C and D scales (Singh and Narayanan, 1993). An analysis of variance for all traits was performed, and then a generation mean analysis was used according to the method of Mather and Jinks (1982). Genetic analysis of generation means to give estimates of the types of gene effects were obtained using the relationships given by Gamble (1962). Heritability estimates were computed in both broad (H) and narrow senses (h^2) for F₂ generation according to Allard (1960) and Mather (1949). The expected genetic advance from selection (G_a) was calculated using the formulae proposed by Johnson *et al.* (1955), with a selection differential (k) equal 2.06 for 5% selection intensity and heritability in the narrow sense. The predicted genetic advance where the expected genetic gain upon selection was expressed as percentage of F₂ mean ($G_a\%$) was calculated following Miller *et al.* (1958).

Drought susceptibility index (SI): It was applied to gauge how well each genotype tolerated drought in general. Emphasis must be placed on the fact that SI, rather than yield level under dry conditions per se, provides a measure of drought tolerance based on minimization of yield loss under stress compared to moist conditions. Using the generalized formula described by Fisher and Maurer (1978), this index was generated from genotype means for grain yield (SI). $SI = (1 - Y_d / Y_p) / D$.

Where: Y_d = Performance of a genotype under drought stress, Y_p = Performance of a genotype under normal irrigation, D = drought stress intensity = $1 - (\text{mean } Y_d \text{ of all genotypes} / \text{mean } Y_p \text{ of all genotypes})$.

Crop-water relationships:

1 -Water Consumptive use (CU):

Soil samples were gathered before, after, and during harvest time (15–60 cm higher from the shape of the soil) in order to establish the crop (CU). The equation provided by Israelsen and Hansen (1962) was used to compute the amount of crop water used between two subsequent irrigations.

$$CU (cm) = \frac{Q2 - Q1}{100} \times Bd \times ERZ$$

Where:

Cu = Water Consumptive use (cm).

Q2 = Soil moisture content (% wt/wt) 48 hrs after irrigation.

Q1 = Soil moisture content (% wt/wt) just before the next irrigation.

Bd = Bulk density of soil layer ($g\ cm^{-3}$).

ERZ = Effective root zone depth (cm).

2-Water use efficiency (WUE):

Water use efficiency was calculated accordance with Jensen (1983) as follows:

$$WUE = \frac{Y}{CU}$$

Where:

WUE = Kg grain m^{-3} water consumed. Y = grain yield ($Kg\ ha^{-1}$).

CU = water consumptive use ($m^3\ Fed^{-1}$).

3-water applied

The amount of applied irrigation water was determined by James (1988):

The rate of discharge from a single orifice can be calculated using the Equation

$$Q = CA(2gH)^{0.5}$$

Where:

Q = Orifice flow discharge C = Discharge coefficient t = 0.6 Range (0.6 & 0.8)
 A = Cross-sectional area of orifice or pipe (ft²) g = Acceleration due to gravity (32.2 ft/s²)
 H = Effective head on the orifice (measured from center of orifice to water surface).

4-Water Productivity (WP) was calculated according to Ali *et al.* (2007) as kg grains/m³ water applied .

WP = Gy/l

Where: Gy = Grain yield (kg Fed⁻¹) and I = Irrigation water applied m³ Fed⁻¹.

RESULTS

Mean and variance of mean:

Means and mean variance of the studied traits for the four crosses and the six populations P₁, P₂, F₁, F₂, BC₁ and BC₂ under two conditions of irrigation were presented in Table 6. The findings showed that generation means varied for all examined features in all crosses and were considerably lower under stress than under normal irrigation. For most of the examined attributes in the four crosses under both circumstances, the F₁ mean values were higher than the mid parental means. For grain yield and its components under both normal and water-stress circumstances, F₂ population mean values were in the middle of the two parents and lower than F₁ mean values. However, under the two irrigation treatments, BC₁ and BC₂ mean performance values changed and were connected to the recurrent parent mean.

Estimation of type of gene action:

Six parameters and the scalability test were computed using these data (Gamble ,1962). In the four crossings for all attributes under consideration under both conditions, at least one of the scales (A, B, C, and D) was significant Table 7. For all examined traits in all crossings, the estimated mean effects (m), which represent the contribution resulting from the overall mean plus the locus effects and interaction of the fixed loci, were found to be significant. Data in Table 7 pointed out that, the values of dominance gene effects were higher in magnitude than those of the additive gene actions in all traits of the studied crosses, except for grain yield/plant in the crosses 1 and 4 under water stress condition.

From the results in Table 7 it can be concluded that significant and positive additive (a) and dominant (d) genetic variances were observed in crosses 3 and 4 for No. of spikes/plant, No. of grains/spike for cross 4, the grains weight/spike for crosses 3 and 4, the cross 4 for 100-grain weight and the crosses 1 and 4 for grain yield/plant under normal irrigation treatment. While, under stress condition, the same was obtained in the cross 4 for No. of spikes/plant, the cross 1 for No. of grains/plant, the cross 3 for grains weight/spike and the cross 2 for grain yield/plant under stress condition, indicating that both additive and dominance were important for the inheritance of these traits.

For non- allelic interactions i.e., additive x additive (aa), additive x dominance (ad) and dominance x dominance (dd), data were shown in Tables 7 indicated that, (aa) epistatic effect was more important and higher in magnitude than (dd) epistatic effects in the inheritance of No. of spikes/plant in the crosses 1 and 3, biological yield/plant in the crosses 2 and 3 and grain yield/plant in the crosses 2, 3 and 4 under normal irrigation condition. While under stress condition, the same case were observed for No. of spikes/plant in the crosses 1 and 2, 100-grain weight in the cross 2, biological yield/plant in the crosses 1 and 4 and grain yield /plant in the cross 3.

The signs of dominance and dominance x dominance were similar for No. of spikes/plant in the cross 4 and biological yield/plant in the crosses 1 and 4 under normal irrigation condition. Meanwhile, under stress condition, the same was observed for number of spikes/plant in the crosses 3 and 4, 100-grain weight in the crosses 1 and 3; biological and grain yields/plant in the cross 4. In such cases, the complementary epistasis seems to operating. On the other side, the signs of [d] and [aa] type of epistasis were similar in all crosses for all the studied traits; except for cross 1 for biological yield/plant under normal condition.

Table 6. Mean (\bar{X}) and variance mean ($S^2_{\bar{X}}$) of the studied traits in the four crosses for six populations P₁, P₂, F₁, F₂, BC₁ and BC₂ under normal and water stress conditions

	Crosses	Statistical	Normal						Stress					
		Parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
Number of spikes / plant (spike)	1	\bar{X}	16.63	17.63	18.30	16.47	17.55	17.19	13.20	14.25	16.40	13.11	14.43	14.96
		$S^2_{\bar{X}}$	0.023	0.030	0.021	0.045	0.109	0.137	0.020	0.026	0.028	0.039	0.124	0.095
	2	\bar{X}	17.65	18.22	18.85	16.58	18.90	18.80	14.30	14.65	15.90	14.20	15.39	14.75
		$S^2_{\bar{X}}$	0.023	0.028	0.023	0.044	0.122	0.109	0.023	0.023	0.020	0.045	0.081	0.143
	3	\bar{X}	18.22	17.40	18.98	16.95	18.74	17.57	14.60	14.70	15.76	13.93	14.49	13.94
		$S^2_{\bar{X}}$	0.018	0.023	0.028	0.041	0.110	0.130	0.025	0.019	0.024	0.047	0.115	0.130
	4	\bar{X}	18.22	16.20	18.9	16.51	17.95	15.65	14.60	13.56	15.85	13.06	13.97	12.85
		$S^2_{\bar{X}}$	0.020	0.021	0.025	0.048	0.112	0.156	0.022	0.025	0.019	0.053	0.158	0.152
Number of grains / spike (grain)	1	\bar{X}	70.30	72.32	74.60	70.07	76.12	74.34	62.88	64.65	67.88	65.30	68.57	65.50
		$S^2_{\bar{X}}$	0.34	0.56	1.01	0.33	1.22	1.18	0.42	0.56	0.50	0.26	0.89	0.92
	2	\bar{X}	72.30	73.62	75.56	74.63	77.20	74.78	64.60	65.20	68.33	66.71	69.34	67.77
		$S^2_{\bar{X}}$	0.41	0.63	0.91	0.34	0.93	1.22	0.41	0.45	0.59	0.37	1.29	1.06
	3	\bar{X}	73.62	71.20	75.13	71.70	75.09	73.59	65.20	64.73	68.59	67.08	69.20	66.63
		$S^2_{\bar{X}}$	0.35	0.48	0.74	0.29	1.18	1.08	0.34	0.40	0.56	0.35	1.07	1.08
	4	\bar{X}	73.62	70.36	74.90	70.23	75.40	72.15	65.20	61.60	68.44	67.14	69.60	64.90
		$S^2_{\bar{X}}$	0.32	0.54	0.66	0.29	0.97	1.19	0.44	0.35	0.41	0.38	1.33	1.19
grains weight/ spike (gm)	1	\bar{X}	3.28	3.55	3.65	3.50	3.70	3.65	3.05	3.25	3.36	3.25	3.47	3.48
		$S^2_{\bar{X}}$	0.001	0.001	0.001	0.002	0.007	0.006	0.001	0.001	0.001	0.002	0.004	0.010
	2	\bar{X}	3.56	3.72	3.74	3.60	3.76	3.96	3.240	3.300	3.400	3.300	3.500	3.490
		$S^2_{\bar{X}}$	0.001	0.001	0.002	0.002	0.006	0.005	0.001	0.002	0.001	0.002	0.005	0.004
	3	\bar{X}	3.75	3.53	3.66	3.58	3.90	3.65	3.33	3.51	3.57	3.41	3.60	3.40
		$S^2_{\bar{X}}$	0.001	0.002	0.001	0.002	0.005	0.006	0.002	0.001	0.002	0.002	0.004	0.005
	4	\bar{X}	3.76	3.49	3.80	3.39	3.88	3.57	3.31	3.36	3.38	3.22	3.40	3.28
		$S^2_{\bar{X}}$	0.001	0.001	0.002	0.002	0.007	0.005	0.001	0.002	0.002	0.001	0.005	0.004

Table 6 cont.

Traits	Crosses	Statistical	Normal						Stress					
		Parameter	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
100-grain weight (g)	1	X ⁻	4.37	4.50	5.03	4.55	4.94	5.08	4.00	4.12	4.49	4.08	4.06	4.18
		S ² X ⁻	0.002	0.001	0.001	0.002	0.007	0.007	0.002	0.002	0.001	0.002	0.005	0.007
	2	X ⁻	4.50	5.00	5.15	4.90	5.08	5.33	4.00	4.12	4.49	4.08	4.06	4.18
		S ² X ⁻	0.001	0.002	0.002	0.002	0.005	0.005	0.002	0.002	0.001	0.002	0.005	0.007
	3	X ⁻	5.00	4.55	5.59	5.06	5.40	5.28	4.12	4.32	4.89	4.18	4.32	4.74
		S ² X ⁻	0.001	0.002	0.002	0.002	0.006	0.005	0.001	0.001	0.002	0.002	0.006	0.006
	4	X ⁻	5.00	4.50	5.30	4.85	5.25	5.03	4.32	4.41	4.53	4.20	4.60	4.79
		S ² X ⁻	0.001	0.001	0.002	0.002	0.005	0.006	0.001	0.002	0.001	0.001	0.004	0.004
Biological yield / plant (g)	1	X ⁻	83.70	87.46	88.70	84.90	82.70	86.20	78.65	79.20	80.40	78.45	76.89	81.47
		S ² X ⁻	0.38	0.41	0.31	0.29	0.78	0.93	0.39	0.41	0.28	0.28	0.72	0.93
	2	X ⁻	87.50	88.40	89.60	85.60	86.34	88.79	79.10	81.60	81.56	80.20	82.60	83.53
		S ² X ⁻	0.35	0.41	0.29	0.28	0.85	0.90	0.40	0.36	0.33	0.27	0.77	0.83
	3	X ⁻	88.45	88.90	90.40	86.40	88.20	87.92	81.56	83.30	82.30	81.50	84.55	84.20
		S ² X ⁻	0.36	0.40	0.31	0.29	0.83	0.81	0.40	0.40	0.26	0.25	0.76	0.72
	4	X ⁻	88.44	90.82	91.13	87.50	86.90	89.50	81.55	83.70	83.40	80.14	81.30	81.27
		S ² X ⁻	0.36	0.43	0.32	0.27	0.74	0.82	0.38	0.41	0.33	0.26	0.76	0.69
Grain yield / plant (g)	1	X ⁻	31.75	30.73	33.18	31.20	34.32	32.03	27.30	28.50	30.10	30.21	30.70	27.25
		S ² X ⁻	0.15	0.19	0.17	0.25	0.68	0.72	0.22	0.23	0.30	0.22	0.82	0.53
	2	X ⁻	30.73	34.10	35.58	30.39	34.89	32.88	28.50	29.60	31.90	29.30	32.10	28.90
		S ² X ⁻	0.15	0.25	0.21	0.23	0.61	0.56	0.24	0.23	0.35	0.26	0.62	0.78
	3	X ⁻	34.06	34.42	35.76	32.72	35.46	33.58	29.60	30.19	32.62	27.25	31.76	29.54
		S ² X ⁻	0.25	0.14	0.17	0.21	0.65	0.58	0.25	0.18	0.33	0.24	0.75	0.64
	4	X ⁻	34.06	33.33	34.12	30.28	35.11	31.90	29.60	29.88	31.40	28.25	30.32	26.23
		S ² X ⁻	0.15	0.15	0.22	0.24	0.75	0.65	0.16	0.20	0.29	0.25	0.80	0.68

Table 7. Estimates of scaling test and type of gene action of four barley crosses for all studied trait

Traits	Normal										
	Crosses	Scaling test				Gamble procedures					
		A	B	C	D	(m)	(a)	(d)	(aa)	(ad)	(dd)
Number of spikes / plant	1	0.17	-1.55**	-4.98**	-1.80**	16.47**	0.36	4.77**	3.60**	0.86	-2.22
	2	1.30	0.53	-7.25**	-4.54**	16.58**	0.10	10.00**	9.08**	0.38	-10.91**
	3	0.28	-1.24	-5.78**	-2.41**	16.95**	1.17**	5.99**	4.82**	0.76	-3.86
	4	-1.22	-3.80**	-6.18**	-0.58	16.51**	2.30**	2.85*	1.16	1.29*	3.86
Number of grains / spike	1	7.34**	1.76	-11.54**	-10.32**	70.07**	1.78	23.93**	20.64**	2.79	-29.74**
	2	6.54**	0.38	1.48	-2.72	74.63**	2.42	8.04*	5.44	3.08*	-12.36
	3	1.43	0.84	-8.28**	-5.28**	71.70**	1.50	13.27**	10.55**	0.29	-12.83
	4	2.28	-0.96	-12.87**	-7.09**	70.23**	3.25*	17.10**	14.19**	1.62	-15.51**
Grains weight/ spike	1	0.47**	0.10	-0.12	-0.35**	3.50**	0.05	0.94**	0.70*	0.19	-1.28**
	2	0.22	0.46**	-0.36**	-0.52**	3.60**	-0.20*	1.14**	1.04**	-0.12	-1.72**
	3	0.39**	0.11	-0.28	-0.39**	3.58**	0.25*	0.80**	0.78**	0.14	-1.28**
	4	0.20	-0.15	-1.29**	-0.67**	3.39**	0.31**	1.51**	1.34**	0.18	-1.39**
100-grain weight	1	0.473**	0.636**	-0.743**	-0.926**	4.55**	-0.14	2.45**	1.85**	-0.08	-2.96**
	2	0.515**	0.504**	-0.174	-0.596**	4.90**	-0.25*	1.59**	1.19**	0.01	-2.21**
	3	0.207	0.416**	-0.504*	-0.563**	5.06**	0.12	1.94**	1.13**	-0.10	-1.75**
	4	0.199	0.252	-0.703**	-0.577**	4.85**	0.22*	1.70**	1.15**	-0.03	-1.61**
Biological yield/ plant	1	-7.00**	-3.76	-8.96**	0.90	84.90**	-3.50**	1.32	-1.80	-1.62	12.56*
	2	-4.42*	-0.42	-12.70**	-3.93*	85.60**	-2.45	9.51**	7.86*	-2.00	-3.02
	3	-2.45	-3.46	-12.55**	-3.32*	86.40**	0.28	8.37**	6.64*	0.51	-0.73
	4	-5.77**	-2.95	-11.52**	-1.40	87.50**	-2.60*	4.30	2.80	-1.41	5.92
Grain yield / plant	1	3.71*	0.15	-4.04	-3.95**	31.20**	2.29*	9.84**	7.90**	1.78	-11.76**
	2	3.47*	-3.92**	-14.45**	-7.00**	30.39**	2.01	17.17**	14.00**	3.70**	-13.55**
	3	1.10	-3.02	-9.13**	-3.61**	32.72**	1.88	8.73**	7.21**	2.06	-5.29
	4	2.04	-3.66*	-14.52**	-6.45**	30.28**	3.21*	13.33**	12.90**	2.85**	-11.28**

(*) and (**) significant at 0.05 and 0.01 levels probability, respectively.

Table (7) cont.

Traits	Stress										
	Crosses	Scaling test				Gamble procedures					
		A	B	C	D	(m)	(a)	(d)	(aa)	(ad)	(dd)
Number of spikes / plant	1	-0.74	-0.73	-7.81**	-3.17**	13.11**	-0.53	9.02**	6.34**	-0.01	-4.87**
	2	0.58	-1.05	-3.95**	-1.74**	14.20**	0.64	4.91**	3.48**	0.82	-3.01
	3	-1.38*	-2.58**	-5.10**	-0.57	13.93**	0.55	2.25	1.14	0.60	2.82
	4	-2.51**	-3.71**	-7.62**	-0.70	13.06**	1.12*	3.17*	1.40	0.60	4.82**
Number of grains / spike	1	6.38**	-1.53	-2.09	-3.47**	65.30**	3.07*	11.06**	6.94*	3.96**	-11.79
	2	5.75**	2.01	0.38	-3.69**	66.71**	1.57	10.81**	7.38	1.87	-15.14*
	3	4.61*	-0.06	1.21	-1.67	67.08**	2.57	6.97	3.34	2.34	-7.89
	4	5.56*	-0.24	4.88	-0.22	67.14**	4.70**	5.48	0.44	2.90	-5.76
Grains weight/ spike	1	0.53**	0.35*	-0.02	-0.45**	3.25**	-0.01	1.11**	0.90**	0.09	-1.78**
	2	0.36*	0.28*	-0.14	-0.39**	3.30**	0.01	0.91**	0.78**	0.04	-1.42**
	3	0.30*	-0.28	-0.34	-0.18	3.41**	0.20*	0.51*	0.36	0.29**	-0.38
	4	0.11	-0.18	-0.55**	-0.24	3.22**	0.12	0.52*	0.48	0.15	-0.41
100-grain weight	1	-0.369**	-0.241	-0.796**	-0.093	4.08**	-0.12	0.62*	0.19	-0.06	0.42
	2	-0.368**	0.262	-1.509**	-0.701**	4.18**	-0.42**	2.07**	1.40**	-0.32**	-1.30**
	3	-0.319*	-0.528**	-0.891**	-0.022	4.26**	0.01	0.16	0.04	0.10	0.80
	4	0.344**	0.644**	-0.996**	-0.992**	4.20**	-0.19*	2.14**	1.98**	-0.15	-2.97**
Biological yield/ plant	1	-5.27**	3.34	-4.85	-1.46	78.45**	-4.58**	4.39	2.92	-4.31	-0.99
	2	4.54*	3.90	-3.02	-5.73**	80.20**	-0.93	12.67**	11.46**	0.32	-19.90**
	3	5.24**	2.80	-3.46	-5.75**	81.50**	0.35	11.37**	11.50**	1.22	-19.54**
	4	-2.35	-4.56*	-11.49**	-2.29	80.14**	0.03	5.35	4.58	1.11	2.33
Grain yield / plant	1	4.00*	-4.10**	4.84*	2.47	30.21**	3.45**	-2.74	-4.94	4.05**	5.04
	2	3.80*	-3.70	-4.70*	-2.40	29.30**	3.20**	7.65*	4.80	3.75**	-4.90
	3	1.30	-3.73*	-16.02**	-6.80**	27.25**	2.22	16.32**	13.59**	2.52*	-11.16*
	4	-0.36	-8.82**	-9.29**	-0.05	28.25**	4.09**	1.77	0.11	4.23**	9.07

(*) and (**) significant at 0.05 and 0.01 levels probability, respectively.

Heterosis, potency ratio and inbreeding depression:

Table 8 showed heterosis over mid-parent and better parent, potency ratio, and inbreeding depression. For the number of grains/spikes, biological yield/plant, and grain yield/plant in nearly all crossings under both conditions, considerable and highly significant desired percentages of heterosis relative mid and better parents with low inbreeding depression were demonstrated. There were a few cases, such as the number of spikes per plant, grain weight per spike, and 100-grain weight, where the inbreeding depression was highly significant in a positive direction in all crosses under both conditions. Results revealed overdominance for all studied traits in all crosses except for biological yield per plant in crosses 2, 3, and 4 under water stress conditions.

Heritability in broad and narrow-senses and genetic advance:

Heritability in broad and narrow-senses and genetic advance, are presented in Table 9. Broad sense heritability values (H^2) were generally higher than the corresponding narrow-sense heritability (h^2), indicating the presence of non-additive of gene action. Broad sense heritability values were high in all cross for all studied traits and ranged from 77.75% in cross 1 for number of grains/spike to 95.31% in cross 4 for number of spikes/plant under normal condition and 80.90.18% in cross 1 for number of grains/spike to 95.93% in cross 4 for number of spikes/plant under water stress condition.

Narrow- sense heritability was generally estimated to be lower than corresponding broad sense heritability, indicating the presence of non-additive gene action. The low h^2 estimated, ranging from 7.24% in cross 3 for number of grains/spike to 71.86% in cross 2 for grain yield/plant under normal condition and from 24.71 in cross 1 for number of grains/spike to 75.37% in cross 2 for number of spikes/plant under water stress conditions, suggested that the inheritance is complex.

Drought susceptibility index (SI):

The means performance of the drought susceptibility index (SI) of all crosses for six populations P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 , which were calculated for grain yield are presented in, Table 10. Results indicated that, all of the crosses were tolerant to drought stress in most cases and might be used to improve the most studied traits in barley under water stress conditions.

Crop -water relationships:

Table 11 presented the values for water applied (WA), water consumptive use (WCU), water productivity (WP) and water use efficiency (WUE) values of barley yield under water stress conditions. The results showed that the amount of water applied and water consumptive use increased in case of frequent irrigation normal than irrigation under stress, but, water productivity (WP) and water use efficiency (WUE) were dressed. The data indicated that the CU was reduced by 64.08%, while water applied was the same for all crosses under both normal ($1636.06 \text{ m}^3 \text{ fed}^{-1}$) and stress ($601.06 \text{ m}^3 \text{ fed}^{-1}$) conditions. Furthermore, water stress caused an increase in Water productivity (kg m^{-3}) WP with average (58.55%). The results showed that the highest average WUE occurred under stress treatment (5.75 kg m^{-3}) followed by normal treatment (2.31 kg m^{-3}).

Table 8. Heterosis, potence ratio and inbreeding depression in four crosses for all studied traits.

Traits	Crosses	Normal				Stress			
		<u>Heterosis</u>		<u>Heterosis</u>		<u>Heterosis</u>		<u>Heterosis</u>	
		MP	PR	BP	ID%	MP	PR	BP	ID%
Number of spikes / plant	1	6.83**	2.34	3.80**	10.00**	19.49**	5.10	15.09**	20.06**
	2	5.10**	3.21	3.46**	12.04**	9.84**	8.14	8.53**	10.69**
	3	6.57**	2.85	4.17**	10.70**	7.58**	22.20	7.21**	11.61**
	4	9.82**	1.67	3.73**	12.65**	12.57**	3.40	8.56**	17.60**
Number of grains / spike	1	4.61**	3.26	3.15**	6.07	6.45**	4.65	5.00**	3.80
	2	3.56**	3.94	2.64**	1.23	5.29**	11.43	4.80**	2.37
	3	3.76**	2.25	2.05*	4.57	5.58**	15.43	5.20**	2.20
	4	4.04**	1.79	1.74*	6.24	7.95**	2.80	4.97**	1.90
Grains weight/spike	1	7.00**	4.11	2.91**	4.11**	6.68**	3.27	3.38**	3.27**
	2	2.73**	3.74	0.54**	3.74**	3.98**	2.94	3.03**	2.94**
	3	0.50**	2.19	-2.40**	2.19**	4.43**	4.48	1.79**	4.48**
	4	4.82**	10.79	1.06**	10.79**	1.29**	4.73	0.49**	4.73**
100-grain weight	1	13.57**	9.47	11.96**	9.66**	10.60**	7.21	9.00**	9.22**
	2	8.37**	1.57	2.89**	4.70**	15.83**	6.60	13.12**	14.55**
	3	17.10**	3.64	11.84**	9.55**	2.59**	1.16	0.34	6.17**
	4	11.55**	2.20	5.99**	8.49**	3.69**	3.69	2.67**	7.28**
Biological yield/plant	1	3.65**	1.66	1.42*	4.28	1.87**	5.36	1.52**	2.43
	2	1.88**	3.67	1.36*	4.46	1.51*	0.97	-0.05	1.67
	3	1.95**	7.67	1.69**	4.42	-0.16	0.15	-1.20*	0.97
	4	1.67*	1.26	0.34	3.98	0.94	0.72	-0.36	3.91
Grain yield / plant	1	6.21**	3.78	4.49**	5.97	7.89**	3.67	5.61**	-0.37
	2	9.77**	1.88	4.34**	14.60	9.81**	5.18	7.77**	8.15
	3	4.44**	8.44	3.89**	8.51	9.12**	9.24	8.05**	16.45
	4	1.27*	1.17	0.19	11.26	5.58**	11.86	5.09**	10.04

(*) and (**) significant at 0.05 and 0.01 levels probability.

Table 9. Heritability percentage in broad (H) and narrow (h²) senses and expected and predicted Genetic advance from selection (Ga and Ga %) from selection in four crosses for all studied traits.

Traits	Crosses	Normal				Stress			
		Heritability		Genetic advance		Heritability		Genetic advance	
		H	h ²	Ga	Ga %	H	h ²	Ga	Ga %
Number of spikes / plant	1	94.63	62.51	4.71	28.62	93.47	59.60	4.20	32.01
	2	94.48	69.20	5.18	31.27	95.14	75.37	5.70	40.13
	3	94.05	52.32	3.76	22.16	95.03	68.85	5.31	38.09
	4	95.31	60.41	4.73	28.65	95.93	52.80	4.32	33.10
Number of grains / spike	1	77.75	17.22	3.52	5.02	80.90	24.71	4.48	6.85
	2	79.12	42.38	8.84	11.84	86.18	41.01	8.91	13.35
	3	80.26	7.24	1.40	1.95	86.87	48.68	10.34	15.41
	4	81.22	13.79	2.65	3.77	89.35	33.30	7.30	10.87
Grains weight/spike	1	93.88	28.21	0.44	12.45	94.84	24.98	0.40	12.26
	2	91.60	36.06	0.51	14.20	91.93	58.23	0.83	25.18
	3	92.22	18.43	0.26	7.27	89.61	59.96	0.86	25.10
	4	91.39	28.85	0.43	12.64	89.39	35.16	0.48	14.85
100-grain weight	1	93.75	16.67	0.27	5.85	94.12	63.24	1.07	26.36
	2	91.09	67.86	1.05	21.33	91.67	38.60	0.60	14.37
	3	90.83	61.67	0.98	19.45	90.90	62.26	0.93	21.94
	4	91.65	34.69	0.50	10.32	90.63	50.00	0.65	15.52
Biological yield/plant	1	87.81	53.20	10.25	12.07	87.88	53.36	10.08	12.85
	2	87.97	42.82	8.06	9.42	86.72	49.75	9.15	11.42
	3	88.10	58.70	11.28	13.05	86.72	51.47	9.16	11.24
	4	86.72	53.59	9.88	11.29	86.20	61.37	11.17	13.94
Grain yield / plant	1	93.22	61.96	11.11	35.61	88.15	48.91	8.23	27.25
	2	90.88	71.86	12.22	40.20	88.93	67.61	12.39	42.30
	3	91.46	56.14	9.23	28.22	88.79	57.81	10.17	37.33
	4	92.17	54.37	9.52	31.43	90.73	54.58	9.81	34.72

Table 10. Mean Value of drought tolerance for grain yield (g/plant) for the six populations under normal and water stress conditions.

Crosse	parameters	Normal	Stress	Reduction
		Grain yield g/plant	Grain yield g/plant	SI
Cross 1	P1	31.75	27.30	1.305
	P2	30.73	28.50	0.675
	F1	33.18	30.10	0.864
	F2	31.20	30.21	0.295
	BC1	34.32	30.70	0.982
	BC2	32.03	27.25	1.389
Cross 2	P1	30.73	28.50	0.675
	P2	34.10	29.60	1.228
	F1	35.58	31.90	0.963
	F2	30.39	29.30	0.334
	BC1	34.89	32.10	0.744
	BC2	32.88	28.90	1.127
Cross 3	P1	34.06	29.60	1.219
	P2	34.42	30.19	1.144
	F1	35.76	32.62	0.817
	F2	32.72	27.25	1.556
	BC1	35.46	31.76	0.971
	BC2	33.58	29.54	1.120
Cross 4	P1	34.06	29.60	1.219
	P2	33.33	29.88	0.963
	F1	34.12	31.40	0.742
	F2	30.28	28.25	0.624
	BC1	35.11	30.32	1.270
	BC2	31.90	26.23	1.654

Table 11. Displayed the values for water applied ($m^3 fed^{-1}$), grain yield($kg fed^{-1}$), water consumptive use ($m^3 Fed^{-1}$), water productivity ($kg Fed^{-1}$) and water use efficiency ($Kg m^{-3}$) for six populations P₁, P₂, F₁, F₂, BC₁ and BC₂ in the four crosses under normal and water stress conditions.

Crosses	Six parameters	Normal		Stress		Normal			Stress		
		Grain yield $kg fed^{-1}$	Water applied $m^3 fed^{-1}$	Grain yield $kg fed^{-1}$	Water applied $m^3 fad^{-1}$	CU $m^3 Fed^{-1}$	WUE $kg m^{-3}$	Wp $kg Fed^{-1}$	CU $m^3 Fed^{-1}$	WUE $kg m^{-3}$	Wp $kg Fed^{-1}$
Cross 1	P1	2963.33	1636.06	2548	601.06	1350.40	2.19	1.81	510.20	4.99	4.24
	P2	2868.13	1636.06	2660	601.06	1410.25	2.03	1.75	498.50	5.34	4.43
	F1	3096.8	1636.06	2809.33	601.06	1380.30	2.24	1.89	485.50	5.79	4.67
	F2	2912	1636.06	2819.6	601.06	1355.30	2.15	1.78	488.30	5.77	4.69
	BC1	3203.2	1636.06	2865.33	601.06	1380.30	2.32	1.96	510.30	5.61	4.77
	BC2	2989.47	1636.06	2543.33	601.06	1356.15	2.20	1.83	475.30	5.35	4.23
Cross 2	P1	2868.13	1636.06	2660	601.06	1385.10	2.07	1.75	465.80	5.71	4.43
	P2	3182.67	1636.06	2762.67	601.06	1350.13	2.36	1.95	480.15	5.75	4.60
	F1	3320.8	1636.06	2977.33	601.06	1310.20	2.53	2.03	469.85	6.34	4.95
	F2	2836.4	1636.06	2734.67	601.06	1290.45	2.20	1.73	475.65	5.75	4.55
	BC1	3256.4	1636.06	2996	601.06	1305.30	2.49	1.99	470.45	6.37	4.98
	BC2	3068.8	1636.06	2697.33	601.06	1345.20	2.28	1.88	475.65	5.67	4.49
Cross 3	P1	3178.93	1636.06	2762.67	601.06	1310.28	2.43	1.94	490.13	5.64	4.60
	P2	3212.53	1636.06	2817.73	601.06	1329.20	2.42	1.96	495.30	5.69	4.69
	F1	3337.6	1636.06	3044.53	601.06	1324.15	2.52	2.04	470.35	6.47	5.07
	F2	3053.87	1636.06	2543.33	601.06	1325.90	2.30	1.87	475.85	5.34	4.23
	BC1	3309.6	1636.06	2964.27	601.06	1309.50	2.53	2.02	490.13	6.05	4.93
	BC2	3134.13	1636.06	2757.07	601.06	1380.20	2.27	1.92	465.70	5.92	4.59
Cross 4	P1	3178.93	1636.06	2762.67	601.06	1305.20	2.44	1.94	470.30	5.87	4.60
	P2	3110.8	1636.06	2788.8	601.06	1320.95	2.35	1.90	490.40	5.69	4.64
	F1	3184.53	1636.06	2930.67	601.06	1340.20	2.38	1.95	455.50	6.43	4.88
	F2	2826.13	1636.06	2636.67	601.06	1335.20	2.12	1.73	480.65	5.49	4.39
	BC1	3276.93	1636.06	2829.87	601.06	1340.20	2.45	2.00	490.40	5.77	4.71
	BC2	2977.33	1636.06	2448.13	601.06	1315.15	2.26	1.82	468.70	5.22	4.07

Water applied (WA), water consumptive use (WCU), water productivity (WP) and water use efficiency (WUE).

DISCUSSION

Generation mean analysis helps plant breeders determine the relative importance of each type in genetic variation in the inheritance of different quantitative characters and understand the performance of the parent, used in the hybrid combinations. However, the significance of any one of the scale reveals the presence of non-allelic interaction.

The significance of mean effect (m) indicated that these traits were quantitatively inherited. The values of dominance gene effects were higher in magnitude than those of the additive gene actions. However, in quantitative inherited traits, gene action is described as additive, dominance and epistatic effects. Additive effect is defined as the average effect of genes; dominance as the interaction of allelic genes and epistasis as interaction of non-allelic genes that influence a particular trait.

Regarding the negative values observed in most cases with either main effects; [a] and [d] or the non-allelic interactions; [aa], [ad] and [dd], it might indicate that, the alleles responsible for less value traits were over-dominant over the alleles controlling high value. However, it could be detected that, the effects of additive and dominant genes were in the opposite direction, where their signs were not similar. This was true for all crosses in most studied traits.

It might be concluded that dominance effects were larger than the additive in most cases, which might indicate that dominance gene effects play the major role in controlling the genetic variation of most studied traits. When additive effects were larger than non-additive ones, it is suggested that selection in early segregating generations would be effective, while if the non-additive portion was larger than additive one, the improvement of the characters needs intensive selection through later generations. These conclusions are in the same line with those found by Zeng *et al* (2001); Eid (2006); Munir *et al.*, (2007); Khattab *et al.*, (2010); Mansour (2012); Amin (2013); Ljaz *et al.*, (2013); El-Refaey *et al.*, (2015); Mansour (2017); Madakemohekar *et al.*, (2018); Habouh (2019) and Sharshar and Genedy (2020).

The epistatic effect (aa) was more important and higher in magnitude than (dd) epistatic effects in this study in most cases. These results are in good agreement with those reported by Khattab *et al.*, (2010), El-Akhdar (2011), Aykutunok *et al.* (2011); Mansour (2012); Amin (2013) El-Refaey and Abd El-Razek (2013); El-Refaey *et al.*, (2015) and Mansour (2017) and Mohamed and Eissa (2022).

Exceptionally, the other traits in other crosses had significant and greater magnitude of dominance x dominance epistatic gene interaction than additive x additive gene effects. Thus, those traits were mainly controlled by the dominance x dominance type of epistasis. Therefore, selection for these traits would be fruitful if delayed until dominance and epistatic effects are reduced to minimum. These results are in the same line with those obtained by Abd-El-Haleem *et al.*, (2010); El-Refaey and Abd El-Razek (2013); Raikwar (2015); Abaas *et al.*, (2016); Madakemohekar *et al.*, (2018); Habouh (2019); Sharshar and Genedy (2020) and Mohamed and Eissa (2022).

The parameter additive x dominance epistatic gene interaction was significant and positive or negative, (Tables 7), indicating that dominance was increasing and decreasing for the studied traits respectively. However, Ramalingam and Sivasamy (2002) stated that the preponderance of additive x dominance epistatic effect was higher in magnitude for the number of spikes/plant in cross 4 under normal irrigation, besides, grain yield/plant in the cross 4 at stress condition. This might suggest delayed selection and inter-mating followed by pedigree selection for improvement for this trait. On the other side, the negative sign of additive x dominance interaction in some crosses for some traits may suggest dispersion of genes in the parents.

In the crosses where the sign of dominance and dominance x dominance were similar, suggesting complementary type of epistasis, this might suggest the possibility of considerable amount of heterosis in these crosses for these traits. On the other hand, in the rest of traits which were represented in most cases, the signs of dominance and dominance x dominance were opposite, suggesting duplicated type of non-allelic interaction in these traits. However, duplicate epistasis considered unfavorable in breeder's point of view, because the presence of duplicate epistasis often leads to a decrease in the expression of the trait. Conversely, it is probable that crossing differed in the parental lines would lead to complementary epistasis that would increase the trait in view.

Mahmoud (2006), Mansour (2012), El- Refaey *et al.*, (2015); Raikwar (2015); Mansour (2017); Madakemohekar *et al.* (2018); Habouh (2019) and Sharshar and Genedy (2020). came to the similar conclusions.

However, when epistatic effects were significant for a trait, the possibility of obtaining desirable segregates through inter-mating in early segregations by breaking undesirable linkage could be available or it is suggested to adopt recurrent selection for handling the above crosses for rapid improvement. Khattab *et al.*,(2010), El-Akhdar (2011), Aykutunok *et al.*,(2011); Amin (2013) ; El- Refaey *et al.*,(2015); Madakemohekar *et al.*, (2018); Habouh (2019) and Sharshar and Genedy (2020) came to the same conclusion.

Heterosis is expressed as the percentage deviation of F1 mean performance from the better parent or mid parent of the trait. High positive values of heterosis would be of interest for most traits under investigation. The low values of inbreeding depressions reflect the low reduction in the mean of F₂ generation due to the direct effect of homozygosity. This low reduction might be attributed to the low sensitivity of the present materials to the inbreeding processes. However, the heterotic effects in most cases pointed out were attributed to over dominance, where potence ratio exceeded the unity. These results were in general agreement with those reported by Khattab *et al.*, (2010); and El-Akhdar (2011); Amin (2013), El-Refaeey and Abd El-Razek (2013); El- Refaey *et al.*,(2015) ; Mansour (2017) ;Madakemohekar *et al.*, (2018) and Habouh (2019) and Mohamed and Eissa (2022).

The highest values of predicted genetic advance were coupled with high and moderate narrow- sense heritability values in all crosses for most studied traits. These results indicated the possibility of practicing selection in early generations and obtaining high -yielding genotypes either at normal or at stress condition. These results agree with the findings of (El- Akhdar (2011) Aykutunok *et al.*,(2011);Mansour (2012);Amin (2013); El-Refaeey and Abd El-Razek (2013);El-Refaeey *et al.*, (2015); Abaas *et al.*, (2016) ;Mansour (2017); Madakemohekar *et al.*, (2018);Habouh (2019); Sharshar and Genedy (2020) and Mohamed and Eissa (2022).

For the drought susceptibility index (SI), which provides a measure of stress resistance based on minimization of yield loss under stress as compared to optimum conditions, rather than on yield level under stress, it has been used to characterize the relative drought tolerance of wheat genotypes (Fisher and Maurer, 1978). This index was used to estimate the relative stress injury because it had accounted for variation in yield potential and stress intensity. This index might be estimated based on many traits. Lower stress susceptibility index than unity (SI<1) is synonymous with high stress tolerance, while high stress susceptibility index (SI >1) means higher stress sensitivity.

For water applied (WA), water consumptive use (WCU), water productivity (WP) and water use efficiency (WUE) values of barley yield as affected by water stress condition, similar results were early reported by Shirazi *et al.*, (2014) and Said *et al.*, (2015) who reported that water stress reduced the PWA and WP and explained that the genotype which use water more efficiently could produce maximum biomass. This finding is confirming the fact that if the crop performance under soil water stress is acceptable, it will be better under available soil moisture conditions. The same results were obtained by Kamel *et al.*, (2008) and Ali (2009).

CONCLUSION

Crosses 2 (Line 3 x Line 10) and 3 (Line 10 x Giza 138) were considered very important crosses for the development of promising genotypes under water stress conditions through selection at successive generations and might be useful in the barley breeding program to improve barley genotypes that had a high genetic advance associated with high heritability.

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التحليل الوراثي لصفات المحصول ومكوناته لأربع هجن من الشعير تحت ظروف الاجهاد المائي

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أجريت هذه الدراسة بمزرعة محطة البحوث الزراعيه بالجميزه - محافظة الغربية - مصر خلال ثلاث مواسم زراعية 2020/2019، 2021/2020 و2022/2021 لتقدير مكونات التباين الوراثي ودراسة تأثير الفعل الجيني لصفات المحصول ومكوناته باستخدام نظام العشائر الستة (الأب الأول، الأب الثاني، الجيل الأول، الجيل الثاني، الهجين الرجعي الأول و الهجين الرجعي الثاني) لأربعة هجن من الشعير. تم زراعة العشائر الستة لهذه الهجن تحت ظروف الري العادية (1636.06م³ فدان⁻¹) والإجهاد المائي (601.06 م³ فدان⁻¹). أظهرت النتائج أن متوسطات الأجيال كانت عالية المعنوية بالنسبة لكل الصفات في كل الهجن. تشير النتائج إلى أهمية تأثيرات كل من الفعل الوراثي المضيف والسيادي والتي اختلفت تبعاً للصفات والهجن تحت كل من البيئتين ، كما أشارت النتائج بصورة عامة إلى وجود تفاعل بين العوامل غير الأليلية بالنسبة لكل الصفات في كل الهجن. أما بالنسبة لمكونات التفاعل فان التفاعل السيادي x السيادي كان ذو تأثير أكبر من تأثير الفعل الوراثي المضيف x المضيف و المضيف x السيادي في معظم الصفات المدروسة. تقديرات عالية المعنوية موجبة لقوة الهجين بالمقارنة بمتوسط الأبوين والأب أفضل تم الحصول عليها في معظم الصفات المدروسة تحت كل من البيئتين. كانت أعلى القيم للتقدم الوراثي المتنبأ به مرتبطة بالقيم العاليه والمتوسطه للمكافئ الوراثي بمعناه المحدود بالنسبة لمعظم الصفات المدروسة في كل الهجن. تشير هذه النتائج إلى إمكانية الإنتخاب في الأجيال الأنعزاليه المبكره والحصول علي تراكيب وراثيه عالية المحصول. بصورة عامة فان أفضل الهجن المبشرة هما الهجينان الثاني والثالث حيث أعطيا أعلى القيم بالنسبة للمكافئ الوراثي بمعناه المحدود وكذلك التقدم الوراثي المتوقع والمتنباً به نتيجة للانتخاب لذلك يمكن التوصية بإدخال تلك الهجن في برنامج إنتخابي للإستفادة منها في تحسين هذه الصفات في الشعير تحت ظروف الإجهاد المائي (601.06 م³ فدان⁻¹).

الكلمات المفتاحية: الشعير، الإجهاد المائي، المحصول، تحليل متوسط الأجيال، الست عشائر، قوة الهجين، المكافئ الوراثي ، التقدم الوراثي.