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Genetic Parameters and Stress Tolerance Index for Quantitative Traits in Barley under Different Drought Stress Severities

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

To determine genetic parameters and drought resistance in barley, an experiment was conducted at Kafr El-Hamam Agricultural Research Station in Zagazig, El-Sharqiyah Governorate, Egypt. The fourteen and two checks genotypes were evaluated under a diverse set of conditions that ranged from non-stress condition to conditions with moderate to severe. The analysis of variance displayed that yield, and other studied traits were significantly affected by seasons and genotypes (p<0.01), while, the genotypes x seasons interaction showed significant or highly significant for most studied characteristics during non-stress, moderate stress and severe stress conditions. The highest values of the mean performance for most studied traits were recorded under non-stress, followed by mild pressure and then severe stress for all or most the studied genotypes. Most studied genotypes were better than the checks varieties during non-stress, moderate, severe stress conditions. The variance components and heritability showed significant or highly significant for most studied traits under non-stress, moderate and severe stress conditions. The maximum values of genetic variance were found for most studied traits under drought stress conditions followed by the environmental and genotypes

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× season variances. High heritability coupled with high genetic advance as percent of the mean was observed for most studied traits under non-stress, moderate and severe stress conditions. The differences between phenotypic coefficients of variation (PCV%) were higher than the values of genotypic coefficients of variation (GCV%) for all studied traits during non-stress, moderate and severe stress conditions. The highest values of GCV% and PCV% were recorded for most studied characteristics during severe stress condition. The values of the relative coefficient of variation were higher than the unity for most studied traits during non-stress and drought stress conditions. Hence, these genetic parameters can be used as direct selection criteria for barley improvement under drought stress conditions. The values of stress tolerance (STI) based on moderate stress were better than the benefits of STI based on severe stress. Cluster analysis classified the genotypes into three groups, i.e., tolerant, semi-tolerant and susceptible. Based on mean performances, stress tolerance and cluster analysis, 1, 4, 6 and ten genotypes recorded the best values and are identified as the best drought-tolerant genotypes for most studied traits and can be used in future barley breeding programme during moderate stress condition in Egypt.

Keywords: Genetic parameters; stress tolerance index; drought stress; barley.

1. INTRODUCTION

Barley ranked fourth in cereal crop after wheat, rice and maize [1]. It is mainly used as food, animal fodder and as a raw material for beer production [2]. Barley has been given the least importance in Egypt among the cereal crops and cultivation confined to marginal lands associated with drought and saline conditions. It is mainly grown in northern coastal regions where the average annual precipitation is about 135 mm in North West Coast and slightly higher in North Sinai [3]. Being drought tolerant and short growing season crop, barley is a key ingredient in the feeding of small ruminants.

The primary goal in plant breeding is looking for and selection of the genotypes with high seed yield and other traits. Seed yield is a complex trait that directly or indirectly associated with the other morphological and physiological characteristics. It is also strongly influenced by the environmental literature [4]. Selection based on seed yield and its components should be based on genotypic variance and the proportion of the genetic gain and heritability for each trait. However, before starting the breeding activities, it is necessary to know the genetic parameters of drought tolerance, because they allow getting knowledge on the possibilities for selecting superior genotypes.

Stresses of heat, drought, cold, diseases and pests are major factors limiting crop production and development [5]. Drought stress is the most critical factor limiting crops production in agricultural systems in arid and semi-arid regions [6]. Exploring the possibilities of drought-tolerant crops is the time required for all terrestrial crop species especially in the climate change scenario. Drought resistance can be defined as the relative yield of a genotype compared to other genotypes subjected to the same drought stress [7]. Drought susceptibility of a genotype is often measured as a function of the reduction in yield under drought stress [8]; while the values are confounded with differential yield potential of genotypes [9]. Drought is an important abiotic factor affecting the yield and yield stability of food cereals, and this stress affects simultaneously many traits leading to a decrease in yield [10]. Accordingly, drought tolerance is one of the leading components of yield stability. Reduction of crop yield under water deficit conditions is the primary concern of plant breeders [11]. The relative yield performance of genotypes in drought-stressed and favourable environments seems to be a common starting point in the identification of desirable genotypes for variable rainfed conditions. Some researchers believe in selection under favourable conditions [12] and some belief in selection under typical drought conditions [13,14]. Nevertheless, there exist numerous researchers that chose the midway and believe in choice under both favourable and stressed conditions [15,16].

Understanding plant responses to drought are of great importance and also a fundamental part of crops breeding tolerant to drought stress [17]. The reaction of plants to drought pressure depends on several factors such as developmental stage, severity and duration of importance, and genotype. Therefore, sufficient genetic information regarding the genotypic variance and the proportion of gene gain and heritability of yield traits of barley under drought is essential and vital to get progress in plant breeding program. In this context, barley germplasm serves as a valuable genetic resource of useful genes and can be used as rich sources of genetic variation in various crop improvement programs [11]. According to Mohammadi et al. [5] relative yield performance and yield stability are the two essential growth attributes which help in the identification of drought tolerant genotypes under variable rainfall conditions. Stress Tolerance Index (STI) was defined as a useful tool for determining high yield and stress tolerance potential of genotypes [16].

Drought stress tolerance is a complex trait that is obstructed by low heritability and deficiency of successful selection approaches [8]. Therefore, selection of barley genotypes should be adapted to drought stress. Besides, drought tolerance mechanism should be identified during the development of new cultivars to increase the productivity [18]. Heritability, a measure of the phenotypic variance attributable to genetic causes, has a predictive function of breeding crops [19]. It provides an estimation of gene advance a breeder can expect from selection applied to a population under specified environment. The higher the heritability estimates, the more straightforward are the selection procedures [20]. It has been emphasised that heritability alone is not enough to make sufficient improvement through selection in advance generations unless accompanied by a substantial amount of genetic advance. The utility of heritability, therefore, increases when it is used to calculate genetic progress, which indicates the degree of gain in character obtained under particular selection pressure. Thus, genetic advance is yet another essential selection parameter that aids breeder in a selection program [21].

In this study, the genetic studies on quantitative traits in barley were undertaken to: (1) estimate genetic parameters and stress tolerance index (2) identify drought tolerant genotypes and (3) determine whether to use optimum or moderate or severe drought stress to evaluate drought stress tolerance in Egypt.

2. MATERIALS AND METHODS

2.1 Genetic Material and Field Procedure

Sixteen genotypes including two varieties checks (Giza 123 and Giza 2000) of barley were chosen and tested under different drought stress severities (Table 1). The three separate experiments were carried out at Kafr El-Hamam Agricultural Research Station at Zagazig, El-Sharqiyah Governorate, Egypt during two successive seasons 2015/2016 and 2016/2017. In each experiment, the sixteen lines and varieties of barley (Table 1) were planted in a randomized complete block design with three replications. The non-stress experiment was irrigated with three irrigations i.e., sowing, after 30 days from sowing at tillering stage and 75 days after sowing at booting stage. The moderate stress experiment was irrigated with two irrigations i.e., time sowing and after 30 days

Table 1. List of 16 Genotypes of barley used for drought tolerance assessment

Code	Genotypes	Origin
1	Alanda//Lignee527//Arar/5/Ager//Api/CM67/3/Ce1/W12269//Ore/4/Hhammao1/ 6/Alanda-o1//Gerbe1/Hama/5/Chn o1/3/Arizona5908/Aths//Bgs/4/Lignee640/Bgs//Cel	ICARDA
2	M64-76/Bonn//Jo/York/3M5/Galt//As46/4/Hj34-80/Astrix/5/NK1272/6/Giza121	ICARDA
3	Alanda//Lignee527//Arar/3/Alanda-01	ICARDA
4	GiZa124/7/Man/Huiz /M69-69/3/Apm/R1//11272/4/CP/Bra/5/ Joso .S◌́ /6/Chn-o1/W12291	Egypt
5	CL10114/Attiki//NK1272/3/ Mzq/C1O3909- 2//Aths	ICARDA
6	Lignee527/NK1272//Alanda	ICARDA
7	Alanda- 02/4/ Arizona5908/Aths//Asse/3/F208- 74/5/Alanda/3/ C1o8887/C105761//lignee640	ICARDA
8	Alanda/3/C108887 /Clo5761//Lignee640/4/Alanda/Lossalka	ICARDA
9	Alanda/Harma//Alanda 01	ICARDA
10	Rihane/Giza123(1925)	Egypt
11	Aths/ lignee86//ACSAD410	ICARDA
12	Nigrate /5/w/2198 /4/ Attiki//Avt/Toi/82/Vt(sel.2.2)	ICARDA
13	80-5145 /Hma-01 /3/Arar/19-3//W12291	ICARDA
14	Malouk//aths/Lignee686	ICARDA
15	Giza 123	Egypt
16	Giza2000	Egypt

from time sowing. While, the severe stress experiment was irrigated with one irrigation only at the time of sowing. The stress experiments were not provided with any supplemental irrigation after drainage even if the stress was very severe. Each replication had contained sixteen plots (genotypes). Each genotype was sown in a plot size of 3m x 3.5m (10.5 m^2). Each plot comprised of 15 rows with 3.5m long, 20 cm between rows and 5 cm within rows. All the recommended cultural practices of barley production in the area were done as usually.

2.2 Traits Measurement

The data on plant height (cm), spike length (cm), peduncle length (cm), flag leaf area (cm^2), days to maturity (days), grain weight/spike (g), number of spikes/m^2, number of grains/spike, 1000-grain weight (g), grain yield (kg/fed.) and biology yield (ton/fed.) traits were recorded in this study.

2.3 Stress Tolerance Index

According to Fernandez [16], stress tolerance index (STI) for each genotype was calculated using the following formula:

$$STI = \frac{G_n x G_S}{(\bar{G_n})^2}$$

Where:

G_n= genotype under non-stress condition.
G_s= genotype under stress condition.
$\bar{G_n}$= mean of all genotypes under non-stress condition.

2.4 Statistical and Genetic Procedures

A combined analysis of variance was performed to determine the effect of genotype (G), season (S) and G × S interaction on phenotypic data from three trials in two years and computed according to the method of Gomez and Gomez [22]. The environmental (σ_E^2), genotypic (σ_G^2) and genotype x season interaction (σ_{GS}^2) variances were estimated with analysis of variance (ANOVA) by Searle et al. [23]. Heritability estimates were calculated in broad sense on entry (BSH_1) and plot mean (BSH_2) basis using the formula suggested by Fehr [24]. The extent of genetic advance to be expected by selecting ten percent of the superior progeny was calculated according to Robinson et al. [25]. Genotypic (GCV%), phenotypic (PCV%) and error (ECV%) coefficients of variation were calculated according to Burton [26]. The heritability and genetic advance estimates were categorized as suggested by Robinson et al. [25] and Johnson et.al. [27] (0-30% = low; 31-60% = moderate; above 60% = high) and (0-10% = low, 10-20% = moderate and above 20% = high), respectively. Standard errors (SE) of variance components and heritability were calculated according to Lothrop et al. [28]. Cluster analysis was done using a computer software program PAST version 2.17c.

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

According to statistical model of Gomez and Gomez [22], the data were analyzed independently to confirm the differences among studied genotypes over the two studied seasons in barley (Table 2). The combined analysis of variance during non-stress, moderate stress and severe stress conditions showed that all studied traits were significantly affected by seasons and genotypes at 1% probability level ($p<0.01$) except days to maturity which exhibited significance ($p<0.05$). The genotypes x seasons interaction (GEI) had significant or highly significant for number of spikes/m^2, 1000-grain weight and grain yield (kg/fed.) during non-stress, moderate stress and severe stress conditions, for plant height through non-stress, and moderate stress conditions, for peduncle length and biology yield (ton/fed.) under moderate and severe stress conditions, for flag leaf area under non-stress condition and for number of grains/spike under moderate stress condition. A large proportion of total variation were caused by the seasons and followed by genotypes, while the lowest proportion was due to the GEI. These indicate that there were substantial differences in genotypes responses across seasons for all studied traits during non-stress, moderate stress and severe stress conditions. These finding was in accordance with Nazari and Pakniyat [11], Singh et al. [29] and EL-Shawy et al. [30].

These results indicate the existence of a high degree of genetic variability (or diversity) for the studied genotypes to be exploited in breeding program of barley, and that also reflected the broad ranges observed for each trait. Also, the magnitude of differences between genotypes was sufficient to provide some scope for selecting genotypes to improve drought tolerance in barley. Higher magnitude of mean squares due to environments indicates considerable differences between environments for all studied traits during non-stress, moderate stress and severe stress conditions. Previous investigations reported that environmental conditions positively affected the yield of various barley genotypes [30].

The significance of the GEI suggests the existence of a differentiated performance of the genotypes during different seasons. Selections of genotype that interact less with the environment in which they are to be grown are known to reduce genotype and environment interaction to a considerable extent [31]. Benmehamad et al. [32] stated that a genotype × environment variance component was higher than the genotypic variance component for grain yield in barley under stress and non-stress conditions.

The values of experimental coefficient of variation (CV%) were higher than 10% for grains weight/spike through non-stress, moderate and severe stress conditions and peduncle length over non-stress condition (Table 2). While, the values of CV% were ranged from 20% to 8.93% for other remaining traits at the three studied conditions. These results displayed the

Table 2. Combined analysis of variance across normal and drought stress conditions for studied traits in barley

Traits	Irrigation conditions	Mean squares					CV%
		Seasons (S)	Replications within season	Genotypes (G)	G x S	Pooled error	
Degree of freedoms		**1**	**4**	**15**	**15**	**60**	
Plant height (cm)	Normal	3102.33**	653.00**	372.35**	0.84**	0.18	0.35
	Moderate stress	1997.04**	395.82**	261.92**	0.40**	0.08	0.24
	Severe stress	1314.99**	294.19**	351.40**	1.83	2.95	2.05
Spike length (cm)	Normal	18.69**	5.67**	3.60**	0.07	0.37	8.72
	Moderate stress	11.05**	0.69	3.75**	0.03	0.28	7.45
	Severe stress	16.16**	1.05**	3.71**	0.23	0.28	8.93
Peduncle length (cm)	Normal	46.26**	10.84**	13.98**	0.17	0.99	10.36
	Moderate stress	61.86**	9.91**	10.93**	4.35**	0.41	6.91
	Severe stress	9.36**	0.69**	6.93**	0.01**	0.001	0.47
Flag leaf area (cm^2)	Normal	44.09**	3.26**	8.23**	0.63**	0.11	3.17
	Moderate stress	49.70**	3.82**	8.50**	0.56	0.43	6.64
	Severe stress	26.89**	0.88*	11.68**	0.25	0.26	5.95
Days to maturity (days)	Normal	720.78**	0.76	13.47*	0.01	5.92	2.17
	Moderate stress	706.58**	0.75	13.20*	0.01	5.81	2.17
	Severe stress	979.62**	41.61**	12.20*	0.01	5.37	2.17
Grains weight/ spike	Normal	3.43**	0.30*	0.49**	0.00	0.11	11.35
	Moderate stress	3.43**	0.02	0.40**	0.00	0.09	10.25
	Severe stress	2.87**	0.15	0.47**	0.004	0.11	13.68
No. of spikes/m^2	Normal	49127.30**	5502.15**	9297.38**	848.07**	221.55	4.15
	Moderate stress	83905.40**	13081.15**	9496.81**	40.64**	6.34	0.56
	Severe stress	18037.29**	4567.74**	6743.93**	13.09**	3.31	0.59
No. of grains /spike	Normal	279.74**	131.17**	122.63**	3.54	4.60	3.27
	Moderate stress	212.86**	113.66**	49.14**	0.03*	0.02	0.20
	Severe stress	851.71**	25.31	110.03**	0.32ns	11.45	6.02
1000-grain weight (g)	Normal	808.67**	110.92**	202.96**	0.99**	0.14	0.88
	Moderate stress	462.59**	45.98**	104.51**	0.33**	0.03	0.47
	Severe stress	233.33**	98.19**	98.40**	0.19**	0.08	0.81
Grain yield (Kg/fed.)	Normal	2713985.38**	119925.83**	159324.70**	5611.78**	2691.55	2.46
	Moderate stress	2389770.62**	118712.12**	182844.00**	5860.12*	2813.07	2.60
	Severe stress	2810565.52**	117366.30**	344381.65**	11627.08*	5578.98	4.09
Biology yield (Ton/fed.)	Normal	11.64**	0.44**	1.61**	0.00	0.01	1.41
	Moderate stress	32.71**	1.13**	1.70**	0.06*	0.03	2.56
	Severe stress	40.08**	0.72**	3.25**	0.13**	0.05	3.98

** and **: significant at 5% and 1% levels of probability, respectively* environmental influence was large for grains weight/spike and peduncle length traits and its low for other remaining traits through different water stress severities. The magnitude of CV% indicated that the genotypes had exploitable genetic variability for the studied traits during moderate and severe stress conditions. Mohammadi et al. [33] stated that, the high CV% were recorded for extrude of spike, while for other traits, moderate to small CV% were observed in barley during drought stress.

3.2 Mean Performances

The mean performance of the studied traits was recorded the highest values under non-stress condition, followed by moderate stress condition and then severe stress conditions for most the studied genotypes as Table 3. The means values of studied traits reduced under drought stress conditions for all genotypes, suggesting genetic variability in these genotypes for drought tolerance. Most studied genotypes were better than the grand means and checks varieties during non-stress, moderate, severe stress conditions. The highest values were showed by check 15 for spike length, flag leaf area and 1000-grain weight traits under moderate and severe stress conditions, for peduncle under moderate stress condition and for plant height, grain weight/spike and number of grains/spike traits under severe stress condition. While the best values for other studied traits were recorded by check 16 under drought stress conditions.

The genotype 1 showed highest value for plant height and 1000 grain weight traits under non-stress (135.21 cm and 57.05 g, respectively), moderate (124.79 cm and 47.05 g, respectively) and severe (95.78 cm and 45 g, respectively) stress conditions, as well as for grain weight/spike (3.56 g) and number of spikes/m^2 (528.27) traits during non-stress and moderate stress conditions, respectively. In case spike length trait, the genotype 11 at non-stress (8.16 cm) and moderate stress (8.57 cm) and the genotype 15 through severe stress (6.64 cm) recorded the highest values. As for peduncle length and flag leaf area traits were showed no superior genotypes which were better than the checks varieties through normal and water stress conditions except the genotype 10 for peduncle length (8.29 cm) at severe stress condition. The smallest days to maturity were noticed for the genotype 4 with the values of 109.64, 108.56 and 103.98 under non-stress, moderate and severe stress conditions, respectively. The maximum values for grain weight/spike were registered for genotype 10 during moderate stress (3.24 g) and the two genotypes 8 and 11 meanwhile severe stress with value of 2.81 g. The genotypes 2 and 13 for number of spikes/m^2 at normal and severe stress conditions (415.53 and 393.51, respectively) and the genotype 6 for number of grains/spike at normal (75.99), moderate (66.09) and severe (64.21) stress conditions were displayed the highest values of mean performances. The highest values were recorded for grain yield by the genotype 10 (2328.62, 2234.54 and 2212.73 kg/fed.) under normal, moderate and severe stress conditions, respectively, as well as for biology yield by the genotype 11 (7.29 ton/fed.) through non-stress condition and by the genotype 10 (6.82 and 6.80 ton/fed.) at moderate and severe stress conditions, respectively.

Based on the results of each trait the response of genotypes at each condition was different. The studied traits of all studied genotypes have been observed to be affected by drought stress to a considerable extent. These genotypes produced the best values of the studied traits during the normal conditions but some genotypes could perform well under drought stress conditions. Using mean performance as an indicator of adaptation, the genotypes 1, 4, 6 and 10 appears to be broadly adapted and relatively drought tolerant under moderate and severe stress conditions, although their yield potential may be less than that of genotypes adapted to the non-stress condition. These results suggest that differences in the expression of yield potential under drought have a genetic basis. Due to its resistance to lodging, genotype 10 had the better than other genotypes for grain and most studied traits under moderate and severe stress conditions. However, the yield potential of the genotype at moderate stress condition was higher than at severe stress condition and could be cultivated under moderate stress condition. The genotypes 4 and 12 showed the smallest days to maturity during drought stress conditions and could be used as a source of early maturity cultivar in breeding program.

The ranking of genotypes according to grain yield in each year was different indicating different responses of genotypes to different levels of drought. This finding justified the utilization of stress tolerance index to describe the behavior of genotypes under stress and non-stress conditions [32]. Selection based on just yield cannot be effective but selection through yield and its components is more efficiency. The possibility of selecting individual genetically different from the mean of a segregating population is obviously of great interest to the plant breeder. To evaluate such a possibility, heritability is considered together with genetic advance.

3.3 Genetic Parameters

Genetic parameters for studied traits under normal, moderate and severe stress conditions in barley genotypes are presented in Table 4. The error (σ^2_E) and genetic (σ^2_G) variances showed highly significant for all studied traits under non-stress, moderate and severe stress conditions except the error variance had significant for grain yield (kg/fed.) during severe stress condition. The genotypes × season variances (σ^2_{GS}) were exhibited significant or highly significant for number of spikes/m^2, 1000-grain weight and grain yield through non-stress, moderate and severe stress conditions, for plant height at normal and moderate stress conditions, for peduncle length and biology yield at moderate and severe stress conditions as well as for flag leaf area at normal condition. Significant is because the values of variances were higher than the standard error values, while, highly significant indicates that the variances values were double the standard error values.

The highest values of the genetic variance were registered for all studied traits over non-stress, moderate and severe stress conditions except days to maturity and grains weight/spike traits, followed by the σ^2_E and σ^2_{GS} for most studied traits under all studied conditions. The σ^2_{GS} was equal zero for spike length, days to maturity, grains weight/spike and number of grains/spike traits under non-stress, moderate and severe stress conditions, for plant height and flag leaf area traits at severe stress and for peduncle length and biology yield traits at normal condition, because their values were negative. These results provided the evidence that yield and yield related traits are influenced much under normal and drought condition. While, the maximum values of genotypic variance recorded for most studied traits under drought stress conditions. This result convinced that most of studied traits were activated and pronounced their effects when plants faced the drought stress condition. Greater differences between genotypic and experimental variances gave evidence that these traits were greatly influenced by the environment under drought stress.

Heritability plays a predictive role in breeding programme, showing the reliability of phenotypes as a guide to its breeding value. The broad sense heritability across two years on entry mean basis (BSH_1) and plot mean basis (BSH_2) estimates were showed highly significant for all studied traits during non-stress, moderate and severe stress conditions except peduncle length over moderate stress condition which was significant. The significant is due to the heritability values were higher than the standard error values, while, highly significant because that the values of heritability were twice the values of standard error.

During non-stress and stress conditions, the values of BSH_1 were higher or very higher than BSH_2 for all studied traits except plant height and number of grains/spike under moderate stress condition as well as peduncle length at severe stress condition, which were equal. According to Robinson et al., (1949), the BSH_1 were recorded the highest values ($BSH_1 \geq 0.60$) for all studied traits through the non-stress and stress conditions. While, the greatest values were found by BSH_2 for all studied traits at the non-stress and stress conditions ($BSH_2 > 0.60$) except days of maturity and grains weight/spike traits over the non-stress and stress conditions and peduncle length at moderate stress condition, which were low ($BSH_2 < 0.30$) or moderate ($BSH_2 > 0.30$). The highest values of broad sense heritability revealed that greater proportion of the entire variance was due to the greater genotypic variance influenced less by environmental factors and the less contribution of the experimental error in the total phenotypic variability, therefore having high heritable variations. Superior heritability values indicates the greater effectiveness of selection and improvement to be expected for these studied traits in future breeding programmes as the genetic variance is mostly due to the additive gene action under drought stress conditions. From previous investigations by Singh et al. [29], Mohammadi et al. [33] and Pal et al. [34] the highest values of heritability in broad sense for most studied traits were found during normal and drought stress conditions, indicating that these traits are controlled by additive effects.

It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program. High genetic advance values coupled with high heritability were recorded for grain yield, number of spikes/m^2 and plant height traits under normal and drought stress conditions. This indicated the additive nature of genetic variation was transmitted from the parents to the progeny. Also, these traits can easily be fixed in the genotypes by progeny selection or any modified selection procedures aiming to exploit the additive gene effects in early generations during drought stress conditions. The genetic advance will be less when the BSH had mainly due to non-additive affects (dominance and / or epistasis) and which need to be improved by cyclic hybridization, heterosis breeding, diallel selective mating system and biparental mating system duly adopting standard selection procedures. High heritability coupled with high or moderate genetic advance as percent of mean (GAM%) were noticed for most studied traits meantime non-stress and drought stress conditions indicating the preponderance of additive gene action. The highest values of GAM% were registered for two yields and most studied traits during severe stress condition. High heritability coupled with high genetic advance as percent of mean were observed for most studied traits in barley through non-stress and drought stress conditions [29,33,35].

The values for phenotypic coefficients of variation (PCV%) were greater than the values of genotypic coefficients of variation (GCV%) for all studied traits during non-stress and drought stress conditions except plant height and number of grains/spike during moderate stress condition. These differences were few and which indicate that the phenotype was close to the genotype, and environmental influence was less on these traits. Since the broad sense heritability was high for this trait, hence this also means that greater proportion of variability was due to genetic factor. The highest values of GCV% and PCV% were recorded for most studied traits during severe stress condition. These results indicate that the least variability for GCV% and PCV% corresponded to high heritability in drought stress conditions. Hence, these traits can be used as indirect selection criteria under drought stress conditions. The highest values of error coefficients of variation (ECV%) were observed for peduncle length, number of spikes/m^2 and 1000-grain weight traits at non-stress; for flag leaf area and grain yield traits at moderate stress as well as for the other studied traits at severe stress. From previously results, the values of the relative coefficient of variation (RCV= GCV%/ECV%) were higher than the unity for all studied traits during non-stress and drought stress conditions except days to maturity and grains weight/spike traits under all water conditions. The highest values of RCV (RCV >1) indicate that environmental variation among the genotypes was lower than the genetic variation from the average during drought stress conditions for the studied traits. From these results the differences between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments. These genetic parameters can be used for defining which direct selection criteria, breeding methods, and experimental designs are more suitable to obtain barley genetic gains for drought tolerance. Singh et al. [29] reported that the highest estimate of GCV% and PCV% were noted for peduncle length, grain yield/plant, and number of grains/ear during both irrigated and rainfed environments in barley.

3.4 Stress Tolerance Index (STI)

Fernandez [16] suggested STI, as stress tolerance index to use for identification of high tolerance genotypes based on the ratio of means under non-stress to the moderate and severe stress indexes. In the case of stress tolerance index (STI_1) based on non-stress to the moderate stress index, one (number of grains/spike), four (days to maturity, grains weight/spike and number of spikes/m^2), five (plant height), seven (1000-grain weight), eight (grain yield) and nine (spike length and biology yield) genotypes were better than the one or two checks as presented in Table 5. As for stress tolerance index (STI_2) under non-stress to the severe stress index, one (flag leaf area), four (days to maturity), five (spike length and number of spikes/m_2), six (grain weight/spike and 1000-grain weight), eight (biology yield), nine (grain yield), ten (plant height) and eleven (number of grains/spike) genotypes were better than the one or two checks (Table 5). On the other hand, no superior genotypes were better than the checks for peduncle length and flag leaf area traits during STI_1 and STI_2. This implies that STI may be useful in identifying stress-tolerant genotypes under non-stress and drought stress conditions. Several investigators reported that water stress reduced ion uptake, nutrient metabolism, photosynthesis and translocation rates and increased respiration, which reduced available assimilates for grain filling and finally decreased grain yield [36]. The genotype 1 for plant height,

Table 3. Mean values of studied traits of barley genotypes under normal and drought stress conditions over the two seasons

Genotypes	Irrigation regimes	Traits										
		PH	SL	PL	FLA	DM	GW/S	No.S/m^2	No.G/S	1000 GW	GY	BY
1	Normal	135.21	7.43	9.49	10.10	112.87	3.56	403.29	60.86	57.05	2072.28	6.16
	Moderate	124.79	7.82	8.26	9.56	111.75	2.98	528.27	59.39	47.05	2009.18	6.14
	Severe	95.78	6.14	6.69	7.42	107.05	2.55	344.32	48.55	45.00	1448.71	4.45
2	Normal	122.96	6.67	10.20	11.27	112.87	2.83	415.53	64.44	39.22	2107.25	5.82
	Moderate	120.48	7.12	9.29	10.89	111.75	2.73	476.55	62.26	37.64	2159.46	6.60
	Severe	91.56	5.88	7.31	9.48	107.04	2.39	304.97	59.20	35.63	1708.47	5.25
3	Normal	118.61	7.22	7.59	8.47	111.26	2.41	316.93	62.43	35.14	2153.60	6.36
	Moderate	116.47	7.64	7.70	7.89	110.15	2.42	405.58	60.92	33.98	2056.81	6.28
	Severe	84.28	6.23	6.96	6.50	105.49	2.20	275.46	58.02	30.00	1877.87	5.77
4	Normal	117.03	7.55	10.38	7.82	109.64	2.44	364.53	64.45	31.07	1663.04	5.62
	Moderate	115.00	7.95	10.17	7.34	108.56	2.64	456.28	61.30	29.82	1621.24	4.95
	Severe	90.71	6.05	7.85	6.02	103.98	2.46	334.48	56.84	28.13	1410.04	4.33
5	Normal	124.64	5.67	6.38	10.95	112.87	2.95	410.50	68.26	42.28	1956.78	6.47
	Moderate	122.93	5.91	7.77	10.41	111.75	2.81	476.55	63.22	41.21	1867.69	5.70
	Severe	93.62	6.61	4.90	9.58	107.05	2.75	295.13	59.20	38.91	1683.25	5.17
6	Normal	121.57	7.30	9.80	10.59	113.51	3.17	344.58	75.99	39.22	2157.81	7.31
	Moderate	119.02	6.99	8.33	10.09	112.39	3.13	415.72	66.09	38.04	2110.61	6.44
	Severe	79.08	4.34	7.13	9.19	107.66	2.67	309.89	64.21	36.56	1747.97	5.37
7	Normal	116.83	7.24	8.82	9.15	112.22	2.95	325.03	64.58	44.01	1926.40	6.40
	Moderate	113.34	7.49	8.81	8.59	111.11	3.02	395.44	58.43	43.09	1774.07	5.42
	Severe	87.80	5.45	5.62	6.92	106.44	2.46	300.25	59.72	35.63	1583.78	4.87
8	Normal	127.50	7.81	7.94	10.35	112.87	2.86	327.45	63.85	47.06	2199.36	6.15
	Moderate	121.37	7.68	7.95	9.71	111.75	3.08	405.58	59.39	41.60	2169.49	6.62
	Severe	84.03	7.80	5.35	8.40	107.04	2.81	295.13	59.20	39.38	1955.94	6.01
9	Normal	120.68	7.11	9.73	11.42	112.87	2.92	377.88	67.38	43.80	2225.18	6.74
	Moderate	116.47	7.76	9.20	10.92	111.75	2.93	415.72	60.35	42.59	2141.67	6.54
	Severe	77.71	6.30	7.31	9.72	107.05	2.05	324.65	53.48	35.63	2001.51	6.15
10	Normal	123.65	7.68	10.98	11.88	110.61	3.02	406.31	69.60	35.65	2328.62	7.11
	Moderate	119.60	6.79	9.44	11.50	109.52	3.24	506.97	63.22	33.18	2234.54	6.82
	Severe	87.94	6.20	8.29	10.52	104.88	2.27	354.16	56.84	30.94	2212.73	6.80
11	Normal	110.21	8.16	10.20	9.67	112.55	3.17	325.32	60.90	44.82	2265.44	7.29
	Moderate	107.86	8.57	10.26	9.13	111.43	2.86	466.41	58.62	40.61	2160.69	6.60
	Severe	70.50	5.58	8.11	7.85	106.73	2.81	265.62	56.52	35.72	2059.34	6.33

Genotypes	Irrigation regimes	Traits										
		PH	SL	PL	FLA	DM	GW/S	No.S/m^2	No.G/S	1000 GW	GY	BY
12	Normal	118.80	7.05	11.12	10.38	109.97	2.76	324.81	69.08	38.71	2229.16	7.13
	Moderate	116.96	7.17	10.31	9.82	108.88	2.79	425.86	64.18	36.75	2195.49	6.70
	Severe	87.96	6.26	7.67	8.49	104.31	2.14	295.13	58.02	31.88	2079.07	6.39
13	Normal	100.03	5.78	10.15	11.13	113.51	2.67	284.06	64.48	42.78	2150.57	7.09
	Moderate	99.25	5.91	10.29	10.50	112.39	2.25	425.86	57.47	38.24	2092.85	6.39
	Severe	69.75	5.41	6.42	9.15	107.66	2.33	393.51	55.55	32.81	1948.39	5.99
14	Normal	121.67	5.84	7.84	10.24	115.77	2.60	360.67	64.44	43.80	2247.59	6.98
	Moderate	122.34	6.22	7.27	9.61	114.62	2.89	471.48	58.43	38.73	2217.36	6.77
	Severe	83.81	4.91	5.35	8.66	109.81	1.95	265.62	53.28	34.88	2102.81	6.62
15	Normal	110.90	6.69	11.47	12.16	112.55	2.98	365.56	57.86	41.26	2025.71	6.69
	Moderate	108.64	6.86	12.42	11.60	111.43	2.70	471.48	57.47	39.82	1902.19	5.81
	Severe	79.97	6.64	7.13	10.94	106.72	2.39	314.81	52.89	36.85	1655.51	5.09
16	Normal	119.79	5.96	11.76	10.47	111.58	2.92	385.93	71.64	39.73	2083.26	6.55
	Moderate	119.41	6.09	10.21	10.03	110.47	3.07	486.69	66.09	38.14	1976.23	6.04
	Severe	78.16	5.54	8.03	9.29	105.82	2.01	304.97	47.36	34.03	1739.18	5.34
Grand mean	Normal	119.38	6.95	9.61	10.38	112.34	2.89	358.65	65.64	41.60	2112.00	6.62
	Moderate	116.50	7.12	9.23	9.85	111.23	2.85	451.90	61.05	38.78	2043.10	6.24
	Severe	83.92	5.96	6.88	8.63	106.55	2.39	311.13	56.18	35.12	1825.91	5.61

PH., plant height; SL., spike length; PL., peduncle length; FLA., flag leaf area; DM., days to maturity; GW/S., grain weight/spike; No.S/m^2., number of spikes/m^2; No.G/S ., number of grains/spike; 1000-GW., 1000-grain weight; GY., grain yield (kg/fed.); BY., biology yield (ton/fed.)

Table 4. Genetic variability parameters for studied traits in barley genotypes under normal and drought stress conditions

Traits	Irrigation regimes	Genetic parameters										
		Variance components			Heritability		GA	GAM %	GCV %	PCV %	ECV %	RCV
		σ^2_E	σ^2_G	σ^2_{GS}	BSH_1	BSH_2						
Plant height (cm)	Normal	0.18±0.03	61.92±22.66	0.22±0.10	1.00±0.37	0.99±0.36	13.83	11.59	6.59	6.60	0.35	18.83
	Moderate	0.08±0.01	43.59±15.94	0.11±0.05	1.00±0.37	1.00±0.36	11.61	9.97	5.67	5.67	0.24	23.63
	Severe	2.95±0.53	58.26±21.39	0.00±0.29	0.99±0.36	0.95±0.35	13.38	15.94	9.10	9.13	2.05	4.44
Spike length (cm)	Normal	0.37±0.07	0.59±0.22	0.00±0.02	0.91±0.34	0.62±0.23	1.28	18.50	11.04	11.60	8.72	1.27
	Moderate	0.28±0.05	0.62±0.23	0.00±0.02	0.93±0.34	0.69±0.25	1.34	18.81	11.09	11.50	7.45	1.49
	Severe	0.28±0.05	0.58±0.23	0.00±0.03	0.92±0.36	0.67±0.26	1.29	21.61	12.77	13.28	8.93	1.43
Peduncle length (cm)	Normal	0.99±0.18	2.30±0.85	0.00±0.06	0.93±0.34	0.70±0.26	2.58	26.82	15.78	16.33	10.36	1.52
	Moderate	0.41±0.07	1.10±0.72	1.32±0.53	0.60±0.39	0.39±0.25	1.43	15.48	11.34	14.62	6.91	1.64
	Severe	0.001±0.000	1.15±0.42	0.004±0.002	1.00±0.37	1.00±0.36	1.89	27.42	15.60	15.61	0.47	33.19

Traits	Irrigation regimes	Genetic parameters										
		Variance components			Heritability		GA	GAM %	GCV %	PCV %	ECV %	RCV
		σ_E^2	σ_G^2	σ_{GS}^2	BSH_1	BSH_2						
Flag leaf area	Normal	0.11±0.02	1.27±0.50	0.17±0.08	0.99±0.37	0.82±0.32	1.97	18.95	10.84	10.92	3.17	3.42
	Moderate	0.43±0.08	1.32±0.52	0.04±0.07	0.93±0.37	0.74±0.29	1.96	19.87	11.68	12.09	6.64	1.76
	Severe	0.26±0.05	1.91±0.71	0.00±0.03	0.98±0.36	0.88±0.33	2.40	27.82	15.99	16.17	5.95	2.69
Days to maturity	Normal	5.92±1.06	2.24±0.82	0.00±0.36	0.69±0.25	0.27±0.10	2.20	1.96	1.33	1.60	2.17	0.61
	Moderate	5.81±1.04	2.20±0.80	0.00±0.35	0.69±0.25	0.27±0.10	2.17	1.96	1.33	1.60	2.17	0.61
	Severe	5.37±0.96	2.03±0.74	0.00±0.33	0.69±0.25	0.27±0.10	2.09	1.96	1.34	1.61	2.17	0.62
Grains weight/ spike	Normal	0.11±0.02	0.08±0.03	0.00±0.01	0.82±0.30	0.43±0.16	0.45	15.68	9.85	10.88	11.35	0.87
	Moderate	0.09±0.02	0.07±0.02	0.00±0.01	0.82±0.30	0.44±0.16	0.41	14.47	9.06	9.98	10.25	0.88
	Severe	0.11±0.02	0.08±0.03	0.00±0.01	0.81±0.30	0.42±0.15	0.44	18.45	11.63	12.90	13.68	0.85
No. of spikes/m^2	Normal	221.55±39.79	1408.22±568.17	208.84±104.10	0.91±0.37	0.77±0.31	62.96	17.56	10.46	10.98	4.15	2.52
	Moderate	6.34±1.14	1576.03±577.96	11.44±4.96	1.00±0.37	0.99±0.36	69.72	15.43	8.78	8.80	0.56	15.68
	Severe	3.31±0.60	1121.81±410.42	3.26±1.61	1.00±0.37	0.99±0.36	58.89	18.93	10.77	10.78	0.59	18.25
No. of grains /spike	Normal	4.60±0.83	19.85±7.47	0.00±0.51	0.96±0.36	0.81±0.31	7.69	11.72	6.79	6.92	3.27	2.08
	Moderate	0.02±0.00	8.19±2.99	0.00±0.00	1.00±0.37	1.00±0.36	5.03	8.25	4.69	4.69	0.20	23.45
	Severe	11.45±2.06	18.28±6.70	0.00±0.70	0.91±0.33	0.61±0.23	7.16	12.75	7.61	8.00	6.02	1.26
1000-grain weight	Normal	0.14±0.02	33.66±12.35	0.28±0.12	1.00±0.37	0.99±0.36	10.19	24.49	13.95	13.98	0.88	15.85
	Moderate	0.03±0.01	17.36±6.36	0.10±0.04	1.00±0.37	0.99±0.36	7.32	18.88	10.74	10.76	0.47	22.85
	Severe	0.08±0.01	16.37±5.99	0.04±0.02	1.00±0.37	0.99±0.36	7.11	20.25	11.52	11.53	0.81	14.22
Grain yield (kg/fed.)	Normal	2691.55±483.42	25618.82±9702.21	973.41±702.41	0.96±0.37	0.87±0.33	276.70	13.10	7.58	7.72	2.46	3.08
	Moderate	2813.07±505.24	29497.31±11133.25	1015.68±733.53	0.97±0.37	0.89±0.33	297.39	14.56	8.41	8.54	2.60	3.23
	Severe	1265.0±1002.01	55459.09±20970.34	2016.03±1455.36	0.98±0.37	0.94±0.36	409.99	22.45	12.90	13.04	1.95	6.62
Biology yield (ton/fed.)	Normal	0.01±0.00	0.27±0.10	0.00±0.00	1.00±0.37	0.97±0.36	0.91	13.72	7.81	7.82	1.41	5.54
	Moderate	0.03±0.00	0.27±0.10	0.01±0.01	0.97±0.37	0.88±0.33	0.91	14.51	8.39	8.54	2.56	3.28
	Severe	0.05±0.01	0.52±0.20	0.03±0.02	0.96±0.37	0.87±0.33	1.25	22.20	12.87	13.13	3.98	3.23

σ_E^2, σ_G^2 and σ_{GS}^2: Error, genetic and genotypes × season variances, respectively.
BSH_1 and BSH2: Heritability in broad sense on entry and plot mean, respectively.
GCV%, PCV% and ECV%: Genotypic, phenotypic and error coefficients of variation, respectively.
RCV: Relative coefficient of variation

Table 5. Estimates of stress tolerance index from studied traits of barley genotypes under moderate (STI_1) and severe (STI_2) stress conditions over the two seasons

Genotypes	Stress tolerance index	Traits										
		PH	SL	PL	FLA	DM	GW/S	No. S/m^2	No.G/S	1000 GW	GY	BY
1	STI_1	1.18(1)	1.20(3)	0.85(10)	0.90(12)	1.00(7)	1.27(1)	1.66(1)	0.84(12)	1.55(1)	0.93(8)	0.86(13)
	STI_2	0.91(1)	0.95(3)	0.69(10)	0.70(11)	0.96(7)	1.09(1)	1.08(2)	0.69(14)	1.48(1)	0.67(14)	0.63(14)
2	STI_1	1.04(4)	0.98(9)	1.02(7)	1.14(4)	1.00(7)	0.93(10)	1.54(3)	0.93(7)	0.85(11)	1.02(5)	0.88(12)
	STI_2	0.79(3)	0.81(9)	0.81(6)	0.99(4)	0.96(7)	0.81(9)	0.99(3)	0.89(6)	0.81(9)	0.81(10)	0.70(13)
3	STI_1	0.97(9)	1.14(4)	0.63(13)	0.62(15)	0.97(4)	0.70(15)	1.00(14)	0.88(9)	0.69(13)	0.99(7)	0.91(9)
	STI_2	0.70(9)	0.93(5)	0.57(11)	0.51(13)	0.93(4)	0.64(14)	0.68(13)	0.84(9)	0.61(13)	0.91(8)	0.84(8)
4	STI_1	0.94(10)	1.24(2)	1.14(4)	0.53(16)	0.94(1)	0.77(13)	1.29(8)	0.92(8)	0.54(15)	0.60(13)	0.64(16)
	STI_2	0.74(6)	0.95(3)	0.88(5)	0.44(14)	0.90(1)	0.72(11)	0.95(4)	0.85(8)	0.51(14)	0.53(15)	0.56(15)
5	STI_1	1.08(3)	0.69(13)	0.54(15)	1.06(6)	1.00(7)	0.99(8)	1.52(4)	1.00(5)	1.01(6)	0.82(11)	0.84(14)
	STI_2	0.82(2)	0.78(10)	0.34(15)	0.97(5)	0.96(7)	0.97(4)	0.94(5)	0.94(2)	0.95(3)	0.74(12)	0.76(11)
6	STI_1	1.02(5)	1.06(7)	0.88(9)	0.99(7)	1.01(8)	1.19(2)	1.11(11)	1.17(1)	0.86(10)	1.02(5)	1.08(5)
	STI_2	0.67(10)	0.66(12)	0.76(8)	0.90(7)	0.97(8)	1.01(3)	0.83(9)	1.13(1)	0.83(8)	0.85(9)	0.90(7)
7	STI_1	0.93(11)	1.12(5)	0.84(11)	0.73(14)	0.99(6)	1.07(5)	1.00(14)	0.88(9)	1.10(3)	0.77(12)	0.79(15)
	STI_2	0.72(8)	0.82(8)	0.54(12)	0.59(12)	0.95(6)	0.87(6)	0.76(10)	0.90(5)	0.91(5)	0.68(13)	0.71(12)
8	STI_1	1.09(2)	1.24(2)	0.68(12)	0.93(10)	1.00(7)	1.06(6)	1.03(13)	0.88(9)	1.13(2)	1.07(4)	0.93(8)
	STI_2	0.75(5)	1.26(1)	0.46(13)	0.81(10)	0.96(7)	0.96(5)	0.75(11)	0.88(7)	1.07(2)	0.96(6)	0.84(8)
9	STI_1	0.99(7)	1.14(4)	0.97(8)	1.16(3)	1.00(7)	1.03(7)	1.22(9)	0.94(6)	1.08(4)	1.07(4)	1.01(7)
	STI_2	0.66(11)	0.93(5)	0.77(7)	1.03(3)	0.96(7)	0.72(11)	0.95(4)	0.84(9)	0.90(6)	1.00(5)	0.95(6)
10	STI_1	1.04(4)	1.08(6)	1.12(6)	1.27(2)	0.96(3)	1.17(3)	1.60(2)	1.02(4)	0.68(14)	1.17(1)	1.11(1)
	STI_2	0.76(4)	0.99(2)	0.98(2)	1.16(2)	0.92(3)	0.82(8)	1.12(1)	0.92(4)	0.64(12)	1.16(1)	1.10(1)
11	STI_1	0.83(13)	1.45(1)	1.13(5)	0.82(13)	0.99(6)	1.09(4)	1.18(10)	0.83(13)	1.05(5)	1.10(3)	1.10(3)
	STI_2	0.55(13)	0.94(4)	0.89(4)	0.70(11)	0.95(6)	1.07(2)	0.67(14)	0.80(11)	0.93(4)	1.05(3)	1.05(3)
12	STI_1	0.98(8)	1.05(8)	1.24(3)	0.95(9)	0.95(2)	0.92(11)	1.08(12)	1.03(3)	0.82(12)	1.10(3)	1.09(4)
	STI_2	0.73(7)	0.91(7)	0.92(3)	0.82(9)	0.91(2)	0.71(12)	0.75(11)	0.93(3)	0.71(11)	1.04(4)	1.04(4)
13	STI_1	0.70(14)	0.71(12)	1.13(5)	1.09(5)	1.01(8)	0.72(14)	0.94(15)	0.86(11)	0.95(8)	1.01(6)	1.03(6)
	STI_2	0.49(14)	0.65(13)	0.70(9)	0.95(6)	0.97(8)	0.75(10)	0.87(8)	0.83(10)	0.81(9)	0.94(7)	0.97(5)
14	STI_1	1.04(4)	0.75(11)	0.62(14)	0.91(11)	1.05(9)	0.90(12)	1.32(7)	0.87(10)	0.98(7)	1.12(2)	1.08(2)
	STI_2	0.72(8)	0.59(14)	0.45(14)	0.82(9)	1.01(9)	0.61(15)	0.74(12)	0.80(11)	0.88(7)	1.06(2)	1.06(2)
15	STI_1	0.85(12)	0.95(10)	1.54(1)	1.31(1)	0.99(6)	0.96(9)	1.34(6)	0.77(14)	0.95(8)	0.86(10)	0.89(11)
	STI_2	0.62(12)	0.92(6)	0.88(5)	1.24(1)	0.95(6)	0.85(7)	0.89(7)	0.71(13)	0.88(7)	0.75(11)	0.78(10)
16	STI_1	1.00(6)	0.75(11)	1.30(2)	0.98(8)	0.98(5)	1.07(5)	1.46(5)	1.10(2)	0.88(9)	0.92(9)	0.90(10)
	STI_2	0.66(11)	0.68(11)	1.02(1)	0.90(8)	0.94(5)	0.70(13)	0.92(6)	0.79(12)	0.78(10)	0.81(10)	0.80(9)

PH., plant height; SL., spike length; PL., peduncle length; FLA., flag leaf area; DM., days to maturity; GW/S., grain weight/spike; No.S/m^2., number of spikes/m^2; No.G/S ., number of grains/spike; 1000-GW., 1000-grain weight; GY., grain yield (kg/fed.); BY., biology yield (ton/fed.)

grains weight/spike and 1000-grain weight traits; the genotype 6 for number of grains/spike; the genotype 4 for days to maturity and the genotype 10 for grain and biology yields traits were recorded the highest or best values of STI_1 and STI_2. The highest values of STI_1 and STI_2 were observed by the genotypes 1 and 10 for number of spikes/m^2 and by the genotypes 11 and 8 for spike length, respectively.

The results revealed these previously genotypes were the drought tolerant genotypes based on STI, which their high quantity is indicating tolerant genotypes for most studied traits. Other studied genotypes were identified as semi-tolerance or semi-sensitive to drought stress. In this study the all studied genotypes showed that, the values of STI_1 were better than the values of STI_2 for all studied traits. In this study, we recommend using moderate drought stress condition to identify drought tolerant genotypes. Therefore, the genotypes 1, 4, 6 and 10 were considered the most drought tolerant under moderate drought stress conditions for most studied traits. Stress Tolerance Index (STI) was considered to be the best parameters for selection of drought-tolerant genotypes under irrigated and water-stressed conditions in barley [37]. EL-Shawy et al. [30] reported that, the high values for STI indicate suitability of the studied genotypes for drought tolerance and desirability for both water deficit and non-deficit conditions.

3.5 Cluster Analysis

Separate cluster analysis has been used for description of genetic diversity and grouping based on all studied traits under STI_1 and STI_2. The dendrogram based on STI_1 and STI_2 showed that the genotypes tended to divided into six clusters and are presented in Fig. 1. During STI_1, the first (I), third (III) and sixth (VI) clusters comprised of three genotypes i.e. (16, 2 and 10), (1, 5 and 14) and (8, 7 and 3), respectively. The second cluster (II) including tow genotypes (13 and 15). The fourth cluster (IV) consisted of the genotype 4. The fifth cluster (V) included of four genotypes (11, 12, 6 and 9). Regarding of STI_2, the first (I), second (II), third (III), fifth (V) and sixth (VI) clusters consisted of three genotypes i.e., (15, 2 and 16), (9, 13 and 6), (10, 12 and 11), (14, 5 and 8) and (4, 3 and 7), respectively, however, the fourth cluster (IV) comprised of one genotype (1).

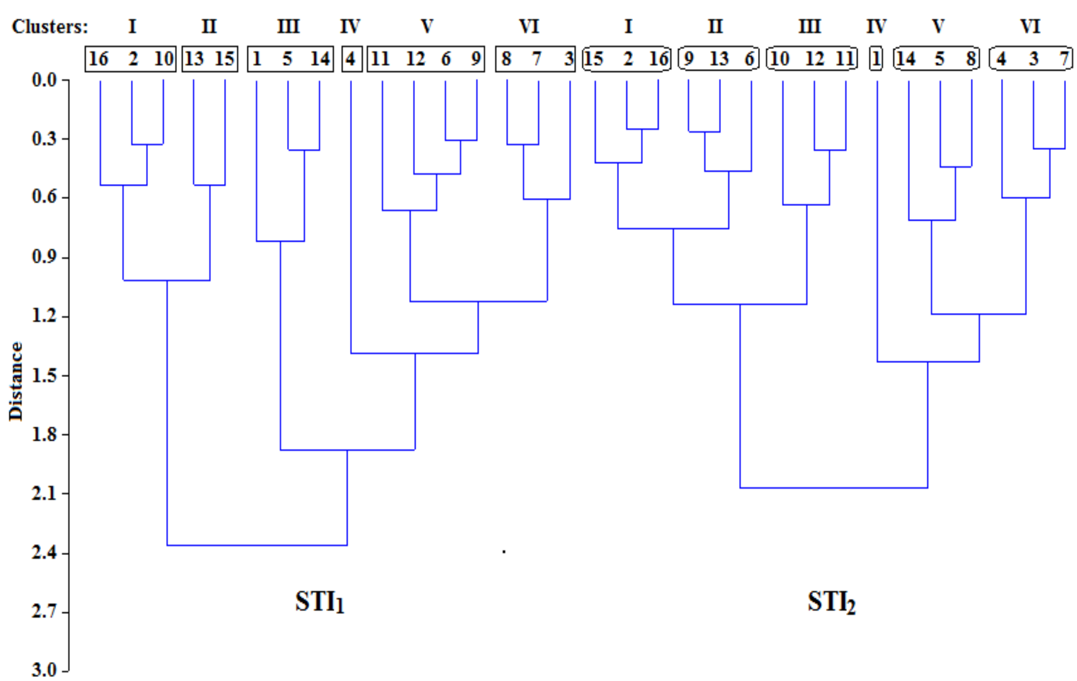

Fig. 1. Dendrogram of cluster analysis of sixteen genotypes based on stress tolerance index during under non-stress to the moderate (STI_1) and severe (STI_2) stress indexes

The highest clusters based on STI_1 and STI_2 were the third and fourth clusters, respectively. These clusters exhibited a desirable resistance to drought and highest values for most studied traits during non-stress and drought stress conditions. On the other hand, the lowest clusters were the second and first clusters through STI_1 and STI_2, respectively. These clusters were a lowest resistance to drought and lowest values for most studied traits during non-stress and drought stress conditions. The other clusters in STI_1 and STI_2 were moderate and desirable resistance to drought for most studied traits meantime normal, moderate and severe stress conditions.

The results obtained of stress tolerance index had confirmed by cluster analysis based on STI_1 and STI_2. Cluster analysis discriminated genotypes 1, 4, 6 and 10 as the most droughts tolerant. Therefore they are recommended to be used as parents for improvement of drought tolerance in future genotypes of barley. Subhani et al. [38] and Yousefi [39] mentioned that, the results of cluster analysis showed that the some genotypes were the most resistant to drought and the highest seed yield; on the other side, the other genotypes were the lowest resistant to drought and seed yield.

4. CONCLUSIONS

The analysis of variance and genetic parameters indicated the existence of extensive genetic variability in materials used during non-stress, moderate stress and severe stress conditions. This indicates that the size of differences in genotypes was enough to select from them against drought. More significant differences between genotypic and experimental variances gave evidence that the environment significantly influenced these traits under drought stress. During screening drought tolerant genotypes using mean performances, stress tolerance index and cluster analysis, the genotypes 1, 4, 6 and 10 were recorded the highest values for yield and most studied traits under non-stress, moderate stress and severe stress conditions. During drought stress, the moderate stress was better than the severe stress. Therefore, emphasis should be placed on these genotypes as reliable candidates when developing promising barley varieties under moderate stress condition in Egypt.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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