



Estimates of Variability, Genetic Parameters and Associated Relationships for Grain Yield and Its Components in Barley under Ras-Sudr Conditions

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ABSTRACT

Emerging of stress tolerant and high yielding crops has grown in importance, particularly in light of global population growth and environmental changes. In order to improve barley production under difficult conditions, high yielding genotypes should be chosen based on the performance and genetic variability of advanced cultivars produced in Ras-Sudr salinity water. Throughout three seasons (2016-2019), the F₂ generation of the cross CHK2 x Australia was planted in naturally saline soil (5000 ppm) and irrigated with naturally salty water at 6300 ppm. Genetic parameters, correlations, and path coefficient analyses have all been investigated for all traits. Variance analysis demonstrated the presence of highly significant variations across all genotypes for all variables, with both phenotypic and genotypic variation coefficients for grain/plant were high, indicating great variety for genetic improvement by selection. Using hierarchical clustering, breeding genotypes and their parents were divided into three groups according to their performance in salt conditions: highly, intermediately, and lowly. Furthermore, for all analysed parameters, broad sense heritability vary from 70.61% to 96.52%. The genetic advance, expressed as a percentage of mean estimates, varied from 4.82% for days to maturity to 45.14% for grain yield/plant. The number of spikes/plant, seed index, and grain yield/plant had high heritability and genetic advance. However, phenotypic correlation coefficients revealed positive significant relationships among grain yield/plant and plant height, spike length, number of grains/spike, and seed index. Furthermore, the number of spikes/plant, grains/spike, seed index, and days to maturity all had a positive and direct effect on grain yield, whereas plant height, days to heading, and spike length all had a negative and direct effect on yield, indicating the importance of these variables in improving production.

Keywords: Barley (*Hordeum vulgare*, L.), breeding lines, salinity, variability, genetic parameters, heritability, genetic advance, correlations, path analysis and cluster analysis.

1. Introduction

Barley (*Hordeum vulgare*, L.) has been known since ancient times and is assumed to have originated in the Fertile Crescent area of the East Mediterranean, where it was domesticated some 10,000 years ago. It is historically considered as a poor man's crop because to its low input needs and superior tolerance to difficult settings globally (Abdel-Ghani, 2013), ranking fourth in terms of planted area and total output behind wheat, rice, and maize (FAO, 2020). Barley is the main crop grown on a large scale in Egypt's North Coastal Region, as well as newly reclaimed lands; it is regarded as the best choice in the risky conditions of poor soils and newly reclaimed areas (El-Banna *et al.*, 2011), and it is typically cultivated in arid and semi-arid areas that are not suitable for other field crops (Naghii and Asgharipour, 2011). Furthermore, enhancing yield components may improve yield stability and/or yield potential in

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a number of environments, including specific stressors like salt (Zhu *et al.*, 2020).

The advanced rate of crop improvement is primarily determined by the amount of genetic variability present for various economic traits, whereas the study of statistical parameters such as variance, PCV, GCV, ECV, GA, and h^2 is not only useful in evaluating the genetic stability and performance of any particular genotype, but it is also a measure that determines the effectiveness of selection for a specific trait in that genotype (Azimi *et al.*, 2017). The link between grain yield and other agronomic characteristics offers a constant level of genetic variation among genotypes, affecting the efficacy of the selection approach (Abdel-Ghani, 2013). Simultaneous selection in barley cultivars based on related traits is the most desirable approach to improving traits such as grain yield, with the goal of determining the most valuable genotypes and the most suitable combination of traits with the goal of improving yield in different plants and identifying highly salt tolerant accessions (Eshghi *et al.*, 2011). Advanced breeding lines and germplasms of barley with improved agronomic performance, disease resistance, and abiotic stress tolerance, as well as grain quality features aimed at the malt and feed markets (Abdel-Ghani, 2013).

Correlation analysis measures aided in the development of a successful breeding strategy by identifying the best genotypes with the greatest features, notably the goal ones of grain and biological yields. When indirect selection of secondary characteristics was employed to increase the primary traits of interest, correlation coefficients were effective in determining the correlations between the variables and both yields (Jamshidi and Javanmard, 2018). The goal of cluster analysis is to discover superior genotypes under varied settings, therefore clustering existing genotypes based on morphological characteristics allows breeders to harness existing genetic resources for future breeding programmes (Enyew *et al.*, 2019). As a result, the effective goals of this current study are to determine; the efficiency of pedigree selection for grain yield in improving high yielding inbred lines after two cycles of selection of the F_2 -generation of CHK2 x Australia (*Hordeum vulgare*, L.); and revealed the effect of selection on the genetic variability, correlation, and path analysis between yield and its attributed characters; and finally to identify superior genotypes by clustering F_4 selected families based on their diversity in performance under salinity conditions (Ras-Sudr conditions).

2. Materials and Methods

2.1. Experimental Design and Plant Materials

This study was conducted throughout three growing seasons, 2016/17, 2017/18, and 2018/19, at the Desert Research Center's Experimental Farm, Ras-Sudr Research Station, South Sinai, Egypt (29° 35' N, 32° 41' E), with salt in irrigation water and soil having 6300 ppm and 5000 ppm, respectively. At the Central Laboratory, Desert Research Centre, Egypt, the physical and chemical parameters of the experimental site's soil were analysed using the technique specified by Piper (1950) and mechanically using Black *et al.*, (1965) (Table 1). Table. 2 exhibits the metrological data of the site obtained from Central Laboratory for Agricultural Climate, at Doki, Giza, Egypt.

Table 1: Mechanical and chemical analyses of the experimental site during 2018/19 growing season.

Depth (cm)	Mechanical analysis		Texture
	0-15	15-30	
Coarse sand %	22.61	35.2	calcareous saline
Fine sand %	45.49	28.4	
Silt %	16.48	18.96	
Clay %	15.33	17.1	
	Chemical analysis		
Ph		7.49	7.81
EC dsm-1		8.54	8.84
CaCO ₃		45.62	48.34
Soluble cations (mg/100g)	Na+	48.04	43.24
	Ca++	21.21	19.26
	Mg++	41.86	46.8
	K+	1.62	2.23
	HCO ₃ -	10.85	11.6
	Cl-	51.48	56.23
	SO ₄ --	27.35	20.24

Table 2: Meteorological data of the experimental site during 2018/19 growing season.

Month	Average Temperature (C°)	Relative Humidity (%)	Participants (mm)
Nov-18	19	58.6	6.4
Dec-18	14.05	65.3	8.5
Jan-19	12.25	52.6	0.7
Feb-19	13.5	54.8	7.4
Mar-19	15.15	52.9	8.2
Apr-19	18.8	44.5	1.1

The population used in the current study was the F₂ generation of the cross: CHK2 x Australia, such population was chosen as a promising population under saline conditions in a previous study for Mansour and Moustafa (2016).

In the first season 2016/17, the parents and F₂ seeds were sown individually in non-replicated trial; the highest grain yielding plants were selected to give F₃- seeds families that were sown in the second season. The parents and seeds of selected families were sown in a random complete blocks design (RCBD) with three replications in the second season 2017/18; the best 25 families in grain yield were chosen to supply the seeds of F₄-families. The parents and seeds of chosen F₄-families were seeded in a random complete blocks design (RCBD) with three replications during the third season 2018/19. In each replicate, each family and parents were sowed in a single row 3 m long, 30 cm apart, and 10 cm between hills. The highest ten grain yielding plants in each row have been selected and harvested. The highest 10 plants in grain yielding in each row were selected and harvested. Data were recorded for days to heading, days to maturity, plant height (cm), number of spikes/plant, spike length (cm), number of grains/spike, seed index and grain yield/plant (g).

Sowing and harvesting date in first, second and third seasons were 15th, 18th and 17th November; and in 25th, 28th, 26th of April, respectively. During the three growing seasons, the cultural practises recommended for barely production in the experiment region were followed. Grain sorghum (*Sorghum bicolor*, L.) was grown the previous summer.

2.2. Statistical Analysis

Data were properly analysed statistically, and differences between means were assessed at the 5% level of probability using Steel *et al.*, (1997) least significant difference (LSD) test.

The coefficients of genotypic and phenotypic variation (GCV and PCV) were categorised as Sivasubramanian and Madhavamenon (1973) recommended and broad sense heritability was determined as Walker (1960) suggested. The genetic advance is often given as a percentage of the mean, as determined by the Comstock and Robinson (1952) formula. The phenotypic correlation and the path analysis were made by (Singh and Choudhary (1985). Hierarchical cluster analysis was applied according to Melchinger *et al.*, (1991).

Using the UNIVARIATE and PROC CORR procedures, SAS software (SAS Institute Inc., 2003) was used to calculate all descriptive statistics (means, ranges, coefficients of variation, heritability, genetic progress, correlation and path analytic analyses) for each trait and among traits.

3. Results and Discussion

3.1. Analysis of variance and mean performance

Analysis of variances for 27 barley genotypes (2 parents and 25 F₄- families) on 8 quantitative traits were presented in Table. 3. The results for all traits investigated showed highly significant variances across genotypes, indicating that there was a large potential diversity among barley genotypes for various attributes, which would be useful for successful selection (Negash *et al.*, 2021). The same findings were achieved by Kumari *et al.*, (2019), Dido *et al.*, (2020) and Iannucci *et al.*, (2021).

The performance of the tested genotypes for yield and its related traits are shown in Table. 4. Results showed that means overall genotypes were 84.88 and 125.39 days for earliness traits. From all 27 genotypes 14 and 15 selected families exhibited earliness performance for days to heading and days to maturity, respectively. On the contrary hand, the three selected families; 81, 136, 76 were the latest performance in two earliness traits and 14, CHCK2, 82 and 192 families were the latest in maturity date. The genotypes exhibited range value of 80.44 days to 130.53 days for family No. 21 in day to heading and family No. 81 in days to maturity, respectively. This wide range indicates the variability in

genotypes. Earliness in heading and maturity in barley are considered as mechanism from plant for escape from unsuitable conditions such as salinity stress. Escape, therefore, is not considered to be stress resistance per se, but meantime the earliness barley genotype is desirable unfavorable conditions.

Table 3: Mean squares of the studied traits of the selected pedigree families in the F₄-generation in barley under Ras-Sudr conditions; season 2018/19.

S.O.V.	Rep.	Fam.	Error
d.f.	2	26	52
Traits			
Days to heading	0.32	49.68**	2.00
Days to maturity	0.88	31.67**	1.63
Plant height (cm)	0.55	140.33**	1.67
No. of spikes/plant	0.14	3.80**	0.45
Spike length (cm)	0.01	3.04**	0.37
No. of grains/spike	0.66	86.16**	2.44
Seed index	0.03	1.89**	0.09
Grain yield /plant (gm)	0.58	99.64**	3.02

*,** : Denote significance at P ≤0.05 and 0.01 probability level, respectively.

Table 4: Performance of the studied traits of the selected pedigree families in the F₄-generation in barley under Ras-Sudr conditions; season 2018/19.

Traits Fam. No.	Days to heading	Days to maturity	Plant height (cm)	No. of spikes /plant	Spike length (cm)	No. of grains /spike	Seed index	Grain yield /plant (gm)
CHK 2	88.34	130.02	69.26	6.10	7.37	69.27	4.14	19.53
Australian	83.92	123.08	73.12	5.00	7.35	68.67	4.29	14.54
2	81.86	122.98	72.61	7.12	9.87	82.54	5.67	28.28
4	81.04	122.07	86.90	9.08	10.21	88.32	6.64	33.45
7	86.82	127.98	74.31	6.65	8.22	81.16	5.52	19.68
8	81.33	122.64	83.33	7.95	10.01	84.04	6.51	21.76
10	82.84	123.75	73.28	6.86	9.11	82.13	5.59	29.12
11	81.11	122.09	85.31	8.44	10.16	85.27	6.64	33.22
12	81.49	122.71	81.83	7.64	9.94	90.32	6.60	29.81
13	81.24	122.37	84.36	8.18	10.02	83.38	6.61	30.64
14	88.84	130.34	69.32	6.14	8.04	80.09	5.49	25.69
19	84.34	123.94	72.91	6.76	9.06	81.98	5.59	28.86
20	86.15	127.94	74.27	6.65	8.94	81.35	5.56	20.18
21	80.44	122.06	87.31	10.29	10.54	92.25	6.68	34.58
28	90.24	128.10	73.89	6.00	7.98	79.08	4.78	18.28
30	85.24	127.69	73.60	6.67	9.04	81.37	5.56	27.88
81	93.60	130.53	62.45	5.89	7.91	76.46	4.58	15.46
82	88.19	129.97	69.33	6.14	8.11	81.07	5.50	26.59
83	81.53	122.76	80.96	7.41	9.94	83.23	6.48	24.86
84	81.37	122.67	82.01	7.80	10.01	91.16	6.60	30.52
76	91.47	128.37	71.37	6.00	7.93	78.31	4.73	17.87
77	81.73	122.88	71.88	7.21	9.88	83.22	5.73	22.60
136	92.12	130.37	62.52	5.92	7.93	77.39	4.68	16.95
138	81.73	122.77	80.13	7.24	9.89	83.22	6.43	24.53
190	82.00	123.26	71.39	7.10	9.80	82.27	5.65	22.32
191	82.53	123.34	72.64	6.99	9.46	82.15	5.64	22.01
192	90.20	128.94	69.52	6.00	7.99	79.20	4.83	29.43
Mean	84.88	125.39	75.18	7.01	9.06	81.81	5.66	24.76
Min	80.44	122.06	62.45	5.00	7.35	68.67	4.14	14.54
Max	93.60	130.53	87.31	10.29	10.54	92.25	6.68	34.58
LSD 0.05	2.32	2.09	2.12	1.10	1.00	2.56	0.49	2.85

Moreover, the agronomic traits viz; plant height (cm), No. of spikes/plant, spike length (cm), No. of grains/spike, seed index and grain yield/plant (g). The genotypes exhibited range value from 4.14 to 92.25 for seed index and No. of grains/spike, respectively. For the plant height the three selected families

21, 4, 11 were the tallest genotypes, while the two selected families 81 and 136 were the shortest. The selected family No. 21 was the highest in No. of spikes/plant (10.29), whereas 9 genotypes from 27 had low value ranged from 5 to 6.14 spikes/plant for the parental genotype Australia and the family No. 82, respectively. 13 selected families from 27 exhibited high values for spike length (cm) ranged from 10.54 cm for family No.21 to 9.46 cm for the family 191; and 10 selected families had low values ranged from 7.35 cm for the parental genotypes Australia to 8.22 cm for the family No. 7. The three selected families 21, 84, 12 revealed high No. of grains/spike (92.25, 91.16 and 90.32 grains, respectively), whereas the parental genotypes Australia (68.67) and CHK2 (69.27) showed lowest No. of grains/plant. The performance of seed index showed that 9 selected families had high value ranged from 6.68 for the family No. 21 to 6.43 for family 138 as well as the parental genotype Australia (4.29), the selected families 81 (4.58) and 136 (4.68) had lowest value. The three families No. 21, 4, 11 exhibited high grain yield/plant (34.58, 33.45, 33.22 g, respectively), while the parental genotype Australia and the two selected families No. 81 and 136 showed lowest grain yield/plant (14.54, 15.46, 16.95 g, respectively). From the previous results, it is clear that the selected families 21 then 4 and 11 exhibited the best performance for the most agronomic traits, so its families can be promising in breeding program for barley under salinity stress. Some of these results were agree with Dyulgerov and Dyulgerova (2020a), Al Lawati *et al.*, (2021) and Kaur *et al.*, (2022).

3.2. Variability and Genetic estimates

The variability was assessed via genotypic (GCV) and phenotypic (PCV) coefficients of variation, broad sense heritability (h^2), and genetic advance as a percentage of the mean (GAM%) among barley genotypes. Estimates of this genetic variability parameter are presented in Table 5.

Despite the low magnitude difference between phenotypic and genotypic coefficients of variation for all traits studied, the phenotypic coefficient of variation was clearly higher than the corresponding genotypic coefficient of variation for all traits studied, indicating very little environmental influence on the expression of the characters. According to Deshmukh *et al.*, (1986), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values are classified as low (10%), medium (10-20%), and high (>20%). In this study, the genotypes demonstrated low to moderate levels of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) for the studied traits, with the exception of grain yield/plant, which demonstrated a high level of both variations (>20%), indicating the presence of a wide range of both variations in all selected characters. The genotypic and phenotypic coefficients of variation varied from 2.52 for days to maturity to 22.92 for grain yield/plant, and from 2.72 to 23.97 for the same attributes. Grain yield/plant had the highest estimates of both variables (GCV and PCV) (22.92 and 23.97, respectively). In addition to PCV for spike length, moderate levels of genotypic and phenotypic coefficients of variation were found for the attributes; number of spikes/plant (15.08 and 17.88) and seed index (13.69 and 14.66) for GCV and PCV, respectively. Whereas the lowest values of both variations were recorded in traits; days to heading (4.70 and 4.98), days to maturity (2.52 and 2.72) and no. of grains/spike (6.46 and 6.73) in addition to GCV for spike length. Lodhi *et al.*, (2015), Kumar *et al.*, (2018) and Yadav and Singh (2021) found that the highest values of phenotypic and genotypic coefficients of variation were observed for grain yield/plant.

Heritability helps in estimating expected progress through selection (Yadav and Singh, 2021). According to Singh (2001), heritability levels are categorised as very high (80%), moderately high (60-79%), moderate (40-59%), and low (40%). The broad sense heritability (h^2) estimates in this study ranged from 70.61 for spike length to 96.52 for plant height. Estimates of broad sense heritability indicated moderately high to very high measures of all traits, due to the presence of large variances in the average values of those traits, which allow for effective selection among them to produce novel salt-tolerant genotypes (Moustafa, 2021). Two characters viz. No. of spikes/spike (71.07) and spike length (70.61) had moderately high estimates of heritability in the broad sense; other traits had very high heritability estimates viz. days to heading (88.81), days to maturity (86.00), plant height (96.52), No. of grains/spike (91.95), seed index (87.23) and grain yield/plant (91.43). Thus, if a character's heritability is very high, selection for these characteristics may be easier and more successful; they were mainly determined by additive gene effect and fixable by selection (Yadav and Singh, 2021). Marzougui and Chargui (2018) found that heritability ranging from 0.61 for plant height to 0.98 for No. of grains/spike. Moustafa (2021) found that broad sense heritability for all tested traits ranged from 71.1 to 89.47 in all

generations, while Ahmadi *et al.*, (2016) found that broad sense heritability ranged from 24% for grain yield/(t/ha) to 96% for the No. of grains/spike. Dinsa *et al.*, (2018) found that the broad sense heritability estimate varied from 22.26% to 70.50%. Dyulgerov and Dyulgerova (2020a) found that heritability in broad sense ranged from 10.10% for grain yield to 94.60% for spike length.

Estimates of genetic advance help in comprehending the type of gene action involved in the expression of different polygenic traits (Negash *et al.*, 2021). The genetic gain is determined by the amount of genetic diversity and the extent of the environment's masking impact (Segherloo *et al.*, 2016). According to Johnson *et al.*, (2010), expected genetic advance as a percentage of mean was classified as low (10%), moderate (10-20%), and high (>20%). Due to different scale of traits, genetic advance as a percentage of mean (GAM%) estimates ranged from 4.82 for days to maturity to 45.14 for grain yield/plant. GAM values expressed were highest for the traits; no. of spikes/spike (26.18), seed index (26.35) and grain yield/plant (45.14). However, moderate genetic advance in percentage of mean were recorded for plant height (18.30) and spike length (18.02) and No. of grains/spike (12.75). On the other hand, low genetic advance was shown for days to heading (9.12), days to maturity (4.82). Addisu and Shumet (2015) found that high genetic advance was observed for characters grain yield and No. of tillers/plant. Aynewa *et al.*, (2015) found that relatively high genetic advance was recorded for spike length, 1000 grain weight, No. of grains/spike, days to maturity, plant height and days to heading. Lodhi *et al.*, (2015) found that high genetic advance as percent of mean was observed for plant height and No. of grains/spike, while Ahmadi *et al.*, (2016) found that the highest and lowest expected genetic advance, observed for days to maturity and the No. of grains/spike, respectively.

High heritability coupled with high genetic advance is primarily due to the additive gene action. Moreover, high heritability with low genetic advance and moderate or low heritability with low genetic advance represent non additive gene action (Katiyar *et al.*, 2020). High heritability with high genetic advance was observed for No. of spikes/plant, seed index and grain yield/plant, emphasises the important role of these attributes in selection and improvement. On the other hand, high heritability with low genetic advance was shown in day to heading, days to maturity and No. of grain/spike, while high heritability with low genetic advance was shown in plant height and spike length. Kumar and Shekhawat (2013) found that plant height, spike length, No. of tillers/meter row length and grain yield showed high estimates of heritability along with high genetic advance (%of mean), while Kumari *et al.*, (2019) found that low heritability coupled with low genetic advance in percent of mean was recorded for days to heading.

Table 5: Variability, heritability and genetic advance for the studied traits of the selected families in the F₄-generation in barley under Ras-Sudr conditions; season 2018/19.

Parameters Traits	PV	GV	PCV (%)	GCV (%)	h ² (%)	GAM (%)
Days to heading	17.90	15.89	4.98	4.70	88.81	9.12
Days to maturity	11.64	10.01	2.72	2.52	86.00	4.82
Plant height (cm)	47.89	46.22	9.21	9.04	96.52	18.30
No. of spikes/plant	1.57	1.12	17.88	15.08	71.07	26.18
Spike length (cm)	1.26	0.89	12.39	10.41	70.61	18.02
No. of grain /spike	30.35	27.90	6.73	6.46	91.95	12.75
Seed index	0.69	0.60	14.66	13.69	87.23	26.35
Grain yield/plant (gm)	35.23	32.20	23.97	22.92	91.43	45.14

3.3. Phenotypic correlation and path coefficient analysis

Yield improvement as a complicated trait for which direct selection is ineffective (kumar *et al.*, 2013). The analysis of the phenotypic correlation coefficients was examined to determine the interrelationship between the characteristics evaluated. In this study, phenotypic correlation coefficient is displayed in Table 6. Days to heading and days to maturity had negative and highly significant correlation with all other studied traits, while it had positive and significant correlation together with each other. On the contrary, yield and other related traits viz. plant height, No. of spikes/plant, spike length, No. of grains/spike and seed index had positive and highly significant correlation with each other. The seed index, which is one of the main components of grain yield gave the highest magnitude of correlation associated with spike length followed by No. of grains/spike then No. of spikes/plant, which had large magnitude with each other. Moreover, moderate to high associated magnitude was

obtained in each pair of remaining correlations. Tofiq *et al.*, (2015) and Yadav *et al.*, (2019) found that highly significant and positive correlation were observed between grain yield/plant with No. of spikes/plant, while Kumar *et al.*, (2017) and Ghimire and Mahat (2019) found that with 1000 grain weight and spike length.

Although these correlations are helpful in determining the main components influencing grain yield, they provide an incomplete relationship of the relative importance of direct and indirect with other traits involved (Vinesh *et al.*, 2018). Path coefficient analyses are used to identify which characters contribute towards yield directly and indirectly. Data in Table 7 revealed path coefficient analysis for direct and indirect relationships between yield and its related characters.

No. of spikes/plant had the highest positive direct effect (0.69) on yield followed by no. of grains/spike (0.54), seed index (0.44) and days to maturity (0.11). These parameters were identified as direct selection. Vinesh *et al.*, (2018) found that spike length, plant height, No. of grains/spike, 1000-grain weight had positive direct effects on grain yield/plant, while Ahmadi *et al.*, (2016) found that thousand grain weight exhibited the highest direct effects on grain yield. Direct negative effect on yield was shown by plant height (-0.36), days to heading (-0.68) and spike length (-1.01). It was also supported by Matin *et al.*, (2019) and Aklilu *et al.*, (2020) found that direct negative effect on grain yield was shown by plant height. This was an indication of indirect selection. The direct negative effect on yield was also mentioned in a study of Yadav *et al.*, (2019) found that days to 50% flowering contributed considerable negative direct effect on grain yield/plant, which indicated the effectiveness of indirect selection. Kumar *et al.*, (2017) found that length spike and plant height exerted substantial positive indirect effects on grain yield/plant via 1000-grains weight.

Table 6: The phenotypic correlation coefficients among the studied traits of the selected families in the F₄-generation in barley under Ras-Sudr conditions; season 2018/2019.

Traits	X2	X3	X4	X5	X6	X7	X8
Day to heading..... X1	0.94**	-0.79**	-0.73**	-0.87**	-0.62**	-0.80**	-0.60**
Days to maturity..... X2		-0.77**	-0.69**	-0.84**	-0.58**	-0.73**	-0.51**
Plant height..... X3			0.85**	0.77**	0.70**	0.85**	0.65**
No. of spikes/plant.. X4				0.88**	0.83**	0.86**	0.74**
Spike lengthX5					0.85**	0.92**	0.68**
No. of grains/spike.. X6						0.89**	0.75**
Seed index..... X7							0.74**
Grain yield/plant.... X8							

*,** : Denote significance at P ≤0.05 and 0.01 probability level, respectively.

Table 7: Path analysis for direct effect (diagonal values) and indirect effect of 7 quantitative traits in grain yield/plant in the F₄-generation in barley under Ras-Sudr conditions; season 2018/2019.

Traits	Days to heading	Days to maturity	Plant height (cm)	No. of spikes /plant	Spike length (cm)	No. of grains /spike	Seed index
Days to heading	-0.678	-0.637	0.535	0.495	0.590	0.420	0.542
Days to maturity	0.104	0.111	-0.085	-0.077	-0.093	-0.064	-0.081
Plant height (cm)	0.288	0.280	-0.364	-0.309	-0.280	-0.255	-0.309
No. of spikes/plant	-0.506	-0.478	0.589	0.693	0.610	0.575	0.596
Spike length (cm)	0.882	0.851	-0.780	-0.892	-1.013	-0.861	-0.932
No. of grains/spike	-0.335	-0.314	0.378	0.449	0.459	0.541	0.481
Seed index	-0.355	-0.324	0.377	0.381	0.408	0.395	0.443
Grain yield/plant (g)	-0.600	-0.510	0.650	0.740	0.680	0.750	0.740

3.4. Cluster analysis

The objective of cluster analysis is to identify superior genotypes under Ras-Sudr conditions (salt stress conditions) after clustering them based on their diversity in performance under salt conditions. The genotypes were grouped into three clusters Figure 1., and there was a high degree of genetic divergence between the results obtained based on D2 values. The number of genotypes were included in Cluster I (12), cluster II (9) and cluster III (6). Based on the means calculated over the genotypes included in each cluster; cluster I showed the latest genotypes in earliness traits and lowest value of

other agronomic traits, followed by cluster II, cluster III exhibited earliness and highest other agronomic traits. This finding was agreement with Yadav *et al.*, (2018), Ghimire and Mahat (2019), Al Lawati *et al.*, (2021) and Moustafa (2021).

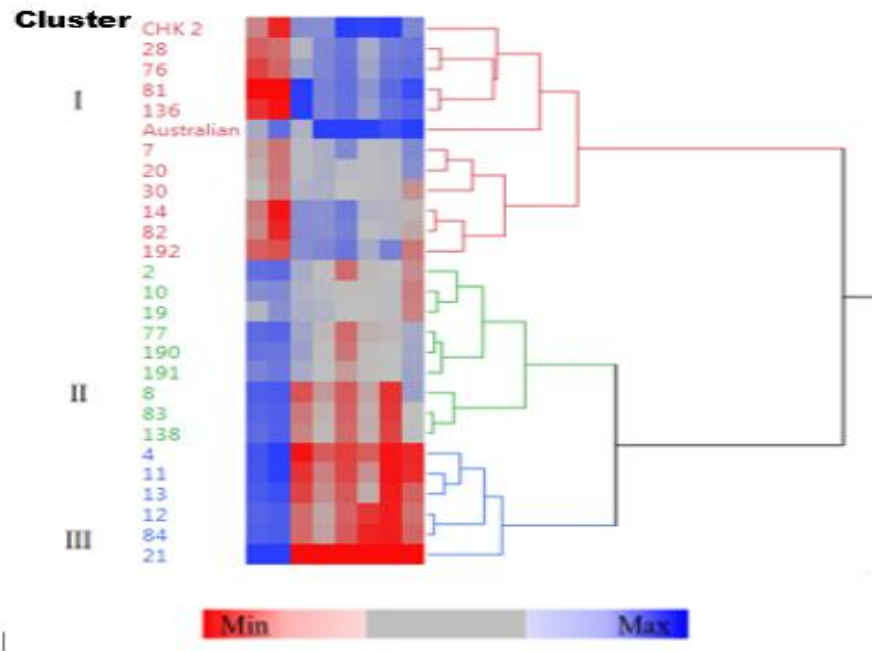


Fig. 1: Hierarchical cluster analysis dendrogram (Ward's method) and pattern map of the values of the qualitative traits of 27 barley genotypes.

4. Conclusion

Grain yield/plant had a high phenotypic variation coefficient, indicating that there is enough variety for genetic improvement by selection. Breeding genotypes and their parents were divided into three categories based on their performance in salt conditions using hierarchical clustering: highly, intermediately, and poorly. Furthermore, broad sense heritability ranged from 70.61 to 96.52 for all investigated characteristics. The genetic progress, expressed as a percentage of mean projections, varied from 4.82 for days to maturity to 45.14 for grain yield/plant. High heritability with high genetic advance was observed for No. of spikes/plant, seed index and grain yield/plant. However phenotypic correlation coefficients displayed positive and highly associations between grain yield/plant with plant height, No. of spikes/plant, spike length, No. of grains/spike and seed index. Furthermore, the number of spikes/plant, grains/spike, seed index, and days to maturity had the most positive direct influence on grain yield, whereas plant height, days to heading, and spike length had the greatest negative direct effect on yield, indicating the relevance of these variables in improving production.

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