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COMBINING ABILITY FOR YIELD, OIL CONTENT, AND PHYSIO-BIOCHEMICAL CHARACTERS OF CANOLA (*BRASSICA NAPUS* L.) UNDER SALT STRESS CONDITIONS

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SUMMARY

Creating a half-diallel cross succeeded among seven diverse canola genotypes. The obtained 21 F_1 hybrids with their seven parents underwent three salinity stress levels exposure—3.91 dsm^{-1} (Normal), 6.24 dsm^{-1} (S1), and 7.81 dsm^{-1} (S2) —during the 2020/2021 growing seasons. Salinity treatments significantly reduced days to 50% flowering, plant height, number of primary branches, pods/plant, 1000-seed weight, seed yield/plant, seed oil content, relative water content, calcium, potassium, and the ratio between K^+ and Na+ compared with a normal condition. Proline content, osmotic pressure, and Na+ were considerably higher under salinity stress conditions. Highly significant differences showed among the parents and hybrids for all traits across the tested environments. General (GCA) and specific (SCA) combining ability effects were highly significant for all attributes. The parental genotypes Serw4 and Pactol resulted as good general combiners for increased seed oil content (SOC), seed yield/plant (SYPP), and some of its components in research environments. The hybrid combinations H2/S × Serw4 and Serw4 × Serw6 were good specific combiners for days to first flower (DTF), number of primary branches (NPB), number of pods per plant (NP), a thousand seed weight (TSW), seed yield per plant (SYPP), seed oil content (SOC), proline content (ProC), Ca++, and K+/Na+. The SDS-PAGE analysis of seed proteins indicated high levels of genetic variability and revealed some vital biochemical markers for salt tolerance.

Keywords: canola (*Brassica napus* L.), combining ability, gene action, saline environments, seed yield, oil content, physio-biochemical traits

Key findings: Parents and F_1 hybrids showed high genetic variation for all attributes in nonsaline and saline environments. The parental genotypes Serw4 and Pactol were effective general combiners for enhancing seed yield and other features under stressed and non-stressed situations. H2/S × Serw4 and Serw4 × Serw6 were good specific combiners for most traits and can benefit future hybrid development to improve canola salt tolerance.

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INTRODUCTION

Canola (*Brassica napus* L.) has become the third most valuable edible oilseed crop worldwide after soybean and cotton, accounting for 12% of the annual global oil production (FAOSTAT, 2020). The importance of canola could be due to the suitable fatty acids, high oil content of grains, and utilization as a promising bio-diesel crop (Tian *et al*., 2020). Moreover, it has several advantages in crop rotation because of the earlier harvest than winter cereals (Menendez *et al*., 2019). Many abiotic stresses affect the successful cultivation of canola (Ahmed *et al*., 2021). In arid and semi-arid locations, soil salinity from soluble salts (mainly NaCl) severely threatens crop production. Salt accumulation results from less rainfall, greater evapotranspiration, salts in irrigation water, rocks, and poor water handling (Ding *et al*., 2020).

Salt-affected soils are generally distributed worldwide (Tahmasebpour *et al*., 2018). Almost 6% of the earth's total cultivated area has salinity stress affecting it, accounting for more than 800 million ha of the global land. Moreover, 20% of the global arable land currently experiences salt stress, which will continue to increase to 50% by 2050 (Shrivastava and Kumar, 2015; Liu et al., 2015). Generally, reduced germination percentage and seedling growth in different plant species are common responses to salt stress, including *B. napus* (Choudhary *et al*., 2015; Verma *et al*., 2016; Kanwal *et al*., 2019). Low levels of salts lead to shoots' dehydration, and high levels alter physio-chemical properties of the soils, such as, decreased soil porosity, water movement, nutritional imbalances, and soil aeration, which negatively affect plant uptake of essential nutrients and the oil quality and quantity (Hafez *et al*., 2020).

The harmful impact of salinity on yield attributes comes from accumulated sodium ions that restrict the availability of potassium ions, leading to decrease crop yield (Hussain *et al*., 2013; Saha *et al*., 2015). Sensitive cultivars collect sodium ions faster than tolerant ones, killing *Brassica napus* cells. Plants mitigate the deleterious effects of salinity through osmotic adjustment of the Na^+/K^+ ion ratio by regulating potassium absorption and restricting sodium ions from entering the cell (Ashraf and McNeilly, 2004). Salinity also decreases the chemical activity of water, resulting in hyperosmotic shock (Oghan *et al*., 2018). The analysis of protein patterns using SDS-PAGE could help understand the expression of salinity-responsive genes.

Canola breeding programs must understand physiological, ionic, and agronomic characteristics under salt stress conditions to increase seed production (Ashraf and McNeilly, 2004). Diallel mating is efficient for testing the GCA effects of selected genotypes. Diallel analysis can identify superior parents and hybrids, analyze gene function, and estimate the GCA and SCA of parents and crosses. SCA has non-additive gene effects, while GCA has additive gene outcomes (Sprague and Tatum, 1942). Many researchers have examined combining canola features in nonsaline situations (Ishaq *et al*., 2017). Few researchers have explored the inheritance of these features in saline environments (Kanwal *et al*., 2019).

Therefore, this study materialized to a) evaluate the performance of seven canola genotypes and their 21 F_1 crosses under saline conditions, b) estimate the GCA of the parents and SCA of the hybrids, c) determine the mode of gene action controlling seed yield, oil content and other physio-biochemical characters, and d) identify promising parents and hybrids for future breeding programs of salt tolerance to ensure possible highest yields.

MATERIALS AND METHODS

Plant material and growing conditions

Seven canola genotypes served as parents in this investigation (Table 1). Said parents' crossing in the half diallel mating scheme (7 × 7) excluding reciprocals ran in the 2019/2020 season to obtain 21 F_1 hybrids. In the 2020/2021 season, the seven parents with 21 F_1 hybrids gained evaluation in three environments at two locations with differing soil salinity degrees. The first was at the experimental farm, Faculty of Agriculture, Suez Canal University, Ismailia, as a normal condition (EC 3.91 dsm^{-1}) and the other at the experimental farm of Desert Research Center, Ras-Sudr Research Station, South Sinai, Egypt (29° 35′ N, 32° 41′ E) under two salinity levels: 6.24dsm^{-1} (S_1) and 7.81dsm^{-1} (S_2). Soil and irrigation water chemical analysis for each environment displays in Table 2. Each surrounding had a randomized complete block design with three replications. Each plot consisted of three rows 3 m long, adopting a 0.5 m × 0.15 m space between and within rows, respectively. The over-planted parcels received thinning 21 days after sowing. Recommended agronomic practices for canola production continued at the proper time.

Data recorded

Days to 50% flowering (DTF), plant height (PH), number of primary branches (NBP), the number of pods per plant (NP), a thousand-seed weight (TSW), seed yield per plant (SYPP), and seed oil content (SOC) determination employed the Soxhlet extraction apparatus according to A.O.A.C. (1975).

Ions content and physiological traits

Ion concentrations came from extractions of 0.5 g plant material. The milled plant samples from each genotype in each saline treatment underwent drying at 70 °C for 48 h. Afterward, digesting plant samples followed with 10 ml H_2So_4, extracted to 100 ml. Flame photometers measured K+ and Na+, and atomic absorption assessed Ca^{++}.

Table 1. Name and origin of canola genotypes used in the study.

Name	Origin
H2/S	Egypt
Serw4	Egypt
Topaz	Germany
AD/201	Germany
Pactol	French
Serw46	Egypt
Serw6	Egypt

Table 2. Soil and irrigation water chemical analysis for each of the experimental conditions.

Soil analysis										
Regions	$CaCO_3$%	Ec dsm^{-1}	pH	Cations meq/L				Anions meq/L		
				Ca^+	Mg^+	Na^+	K^+	Cl^-	So_4^{2-}	HCO_{3-}
Normal	0.52	3.91	7.45	5.2	3.9	19.6	0.72	15	8.1	2.1
S1(S1)	1.23	6.25	7.82	28	38.5	74.6	0.91	102	34.82	3.35
S2(S2)	1.47	7.81	7.95	30.0	39.2	76.9	0.95	105.0	37.80	3.65
Water analysis										
Regions	$CaCO_3$%	Ec dsm^{-1}	pH	Cations meq/L				Anions meq/L		
				Ca^+	Mg^+	Na^+	K^+	Cl^-	So_4^{2-}	HCO_{3-}
Normal	0.42	1.9	7.9	2.1	2.1	6.7	0.4	3.4	3.4	3.0
S1(S1)	1.62	3.6	8.2	22.2	4.14.5	23.3	1.2	7.4	11.2	5.2
S2(S2)	1.79	3.8	8.5	27.8	5.0	26.2	1.3	8.12	11.8	6.3

Leaf relative water content (RWC)

The leaf relative water content detection resulted in the fully expanded topmost leaf of the main shoot. Upon noting the sample leaves' weight, specimens got placed in distilled water in a Petri dish. Removing the leaves from the plate after 2 h with surface water wiped, the turgid weight measurement ensued. Samples attained oven-drying at 70 °C to constant weight (Weatherley, 1950) computed leaf relative water content using the following equation:

$$\text{RWC}\,\% = \frac{\text{Fresh weight - dry weight}}{\text{Turgid weight - dry weight}} \times 100$$

Leaf proline content (ProC)

The 0.5 g of complete leaves, ground in 5 ml ethanol (95%), had its upper zone washed with ethanol 70% twice, centrifuged at 3500 rpm for 10 min and measured by spectrophotometer at 515 nm wavelength for proline and 625 nm for total soluble carbohydrate (Bates *et al*., 1973).

SDS-PAGE analysis

Sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) performed engaged the method of Laemmli (1970) and modified by Studier (1973). After electrophoresis, gel fixing and staining followed with 0.25% (w/v) Coomassie Brilliant Blue R-250. The gel photography, scanning, and analysis used Gel Doc 2000 Bio-Rad system.

Statistical analysis

The recorded data went through the analysis of variance (ANOVA) technique according to Steel and Torrie (1986). Combining ability analysis followed Griffing's (1956) method II model I, using the DIALLEL-SAS program (Zhang *et al*., 2005). Cluster dendrogram and matrix plot of the genotypes based on morphological traits and the principal component analysis (PCA) interaction between genotypes and morpho-physiological analysis used Past software (Hammer *et al*., 2001). A hierarchical clustering heatmap to conduct physiological parameters with studied genotypes used TBtools Software (Chen *et al*., 2020).

RESULTS

Analysis of variance

The ANOVA results for each environment (Table 3) showed highly significant differences among the genotypes (parents and their F_1 hybrids) for all traits. Moreover, general combining ability (GCA) and specific combining ability (SCA) mean squares were vastly substantial for all qualities. The magnitude of SCA mean squares was higher than that of GCA mean squares (less than the unity) for all the studied traits under nonsaline and salinity stress environments.

Mean performance

Morphological traits

The mean values of DTF, PH, and NBP significantly decreased by 12.4% and 38.2%, 23.5% and 47.7%, and 36.34% and 55.4% under both levels of salinity (S1 and S2), respectively, compared with the normal condition (Table 1). The parents Topaz and Serw4 and the crosses Serw4 × Serw6 and Serw4 × Serw46 exhibited the earliest flowering, while Pactol and Serw46 and Topaz × Pactol and Pactol × Serw46 displayed the latest flowering under the three environments (Figure 1). Moreover, the parent Topaz and the cross AD/201 × Pactol were the shortest genotypes, whereas the parent Serw46 and the cross Serw4 × Pactol were the tallest ones (Figure 2). Likewise, the parent AD/201 and the cross Serw4 × Serw6 recorded the highest number of primary branches, with the lowest values assigned for the parent Topaz and the cross H2/s × Serw6 under all environments (Figure 3).

Table 3. Analysis of variance for all the studied traits under normal and salinity stress conditions.

Environment	SOV	df	DTF	PH	NPB	NP	TSW	SYPP	SOC
Normal	Rep	2	0.257	4.16	128.41**	1.12	630.37*	0.014**	11.61**
	Genotypes	27	3.25**	158.68**	206.03**	5.54*	1835.38*	1.15*	28.67**
	GCA	6	0.231**	51.03**	58.19**	1.89**	627.18**	1.02**	13.38**
	SCA	21	1.33**	53.43**	71.67**	1.83**	607.39**	0.20	8.46**
	Error	54	0.451	0.424	6.810	0.169	60.79	0.103	0.82
	GCA /SCA		0.17	0.96	0.81	1.03	1.03	5.10	1.58
S1	Rep	2	18.3**	11.04	0.64	7.50	0.23*	1.71**	12.0**
	Genotypes	27	449.78**	41.74**	2.10**	1699.69**	0.71**	14.67**	42.85**
	GCA	6	171.76**	20.90	0.51	281.01**	0.340**	2.11**	18.60**
	SCA	21	143.69**	11.91**	0.75**	648.14**	0.21**	5.68**	13.08**
	Error	54	0.481	1.45	0.12	5.64	0.02	0.04	0.03
	GCA /SCA		1.20	1.75	0.68	0.43	1.62	0.37	1.42
S2	Rep	2	18.37**	0.25	0.60	0.57	0.27	0.26*	1.09**
	Genotypes	27	51.93**	54.60**	2.39**	504.87**	1.37**	6.15**	22.02**
	GCA	6	20.54**	11.63**	0.33**	96.61**	0.36**	1.19*	7.42**
	SCA	21	16.38**	20.07**	0.96**	188.76**	0.48**	2.29**	7.31**
	Error	54	1.20	1.66	0.09	0.66	0.07	0.02	0.05
	GCA /SCA		1.25	0.58	0.34	0.51	0.75	0.52	1.02
Environment	SOV	df	RWC	ProC	Na+	K+	Ca++	K+/ Na+	
Normal	Rep	2	0.57	0.210	0.15	0.02**	3.09	0.003	
	Genotypes	27	23.52**	12.26**	107.19**	15.53**	16.10**	3.63**	
	GCA	6	19.43**	6.64**	3.54**	5.33**	11.11**	0.38	
	SCA	21	24.69**	3.35**	44.92**	5.13**	3.72*	1.45**	
	Error	54	0.57	0.09	0.001	0.008	0.17	0.004	
	GCA /SCA		0.79	1.98	0.08	1.04	2.99	0.26	
S1	Rep	2	22.95	0.003**	27.53	0.00	0.02	0.0012*	
	Genotypes	27	7.25**	0.16**	121.22	7.26**	17.91**	0.0035**	
	GCA	6	2.68**	0.06*	22.89	3.85**	5.49**	0.000**	
	SCA	21	2.34**	0.05**	45.41**	0.91**	6.10**	0.01**	
	Error	54	0.09	0.0001	9.27	2.85	0.008	0.0001	
	GCA /SCA		1.15	1.20	0.50	4.23	0.90	0.00	
S2	Rep	2	31.61	0.004**	6.04**	0.01	2.34	0.001	
	Genotypes	27	131.37	0.14**	58.56**	7.07**	24.60**	0.005**	
	GCA	6	27.61**	0.05**	13.53**	2.59**	3.76	0.001**	
	SCA	21	48.41**	0.04**	21.22**	2.28**	9.46**	0.017**	
	Error	54	0.06	0.0002	2.78	0.01	1.54	0.0001	
	GCA /SCA		0.57	1.25	0.64	1.14	0.40	0.06	

* and **: significant at $P < 0.05$ and 0.01, respectively. DTF: days to 50% flowering, PH: plant height (cm), NPB: No. of primary branches, NP: No. of pods/plant, TSW: 1000-seed weight (g), SYPP: seed yield/plant (g), SOC: seed oil content; RWC: relative water content (%); ProC: proline content.

The hierarchical cluster dendrogram for morphological characters of 28 canola genotypes treated with two salinity stresses has computations in Figure 4. The cluster showed two major groups; first group contains five parents (H2/S, Topaz, Pactol, AD/201, and Serw6) and nine hybrids (P1 × P6, P1 × P2, P2 × P4, P2 × P5, P2 × P7, P3 × P4, P3 × P5, P4 × P5, and P6 × P7). The plot matrix in Figure 5 provided the correlation between studied canola genotypes and morphological traits measured in control and salinity stress. Red indicates the highest correlation, and blue indicates the lowest correlation.

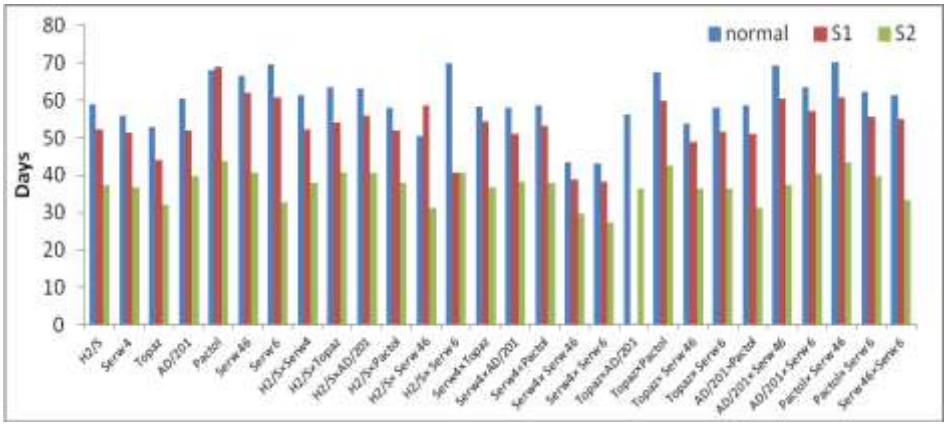

Figure 1. Days to 50% flowering of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

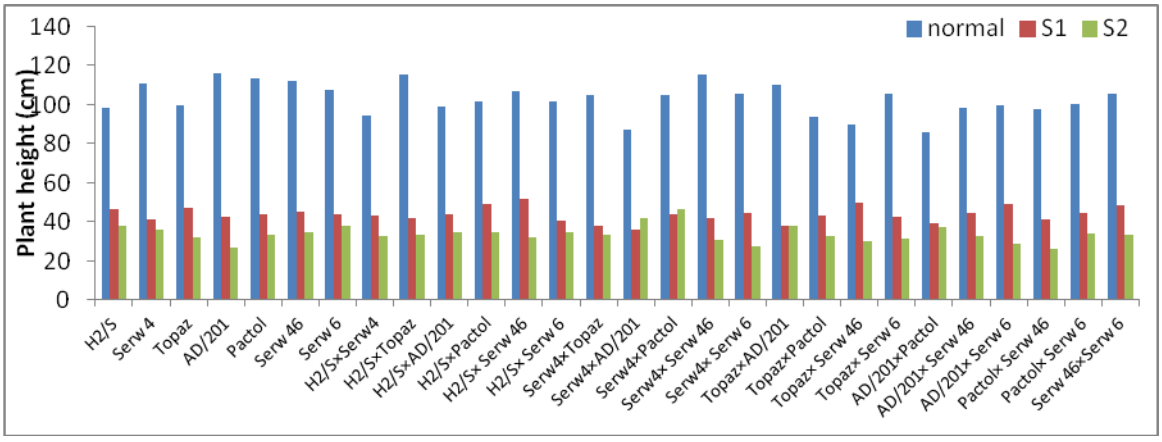

Figure 2. Plant height of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

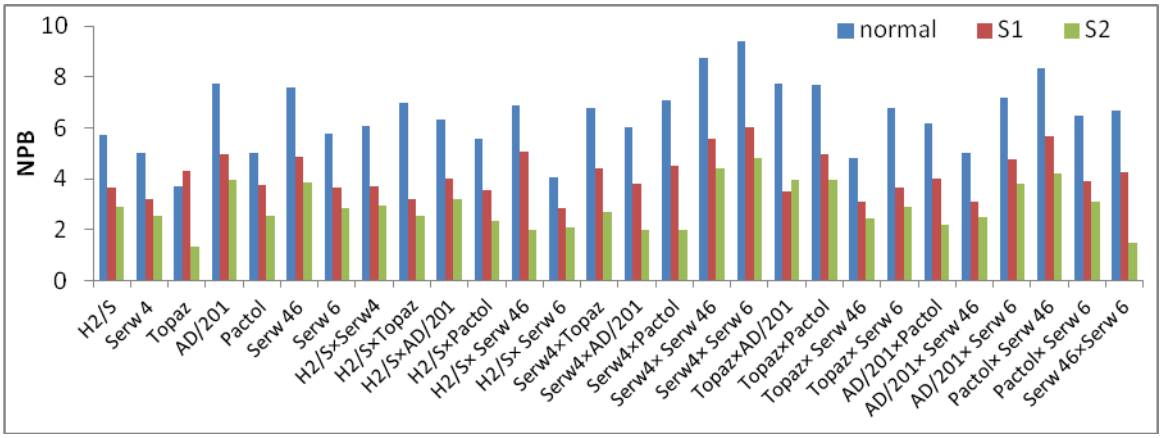

Figure 3. No. of primary branches (NPB) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

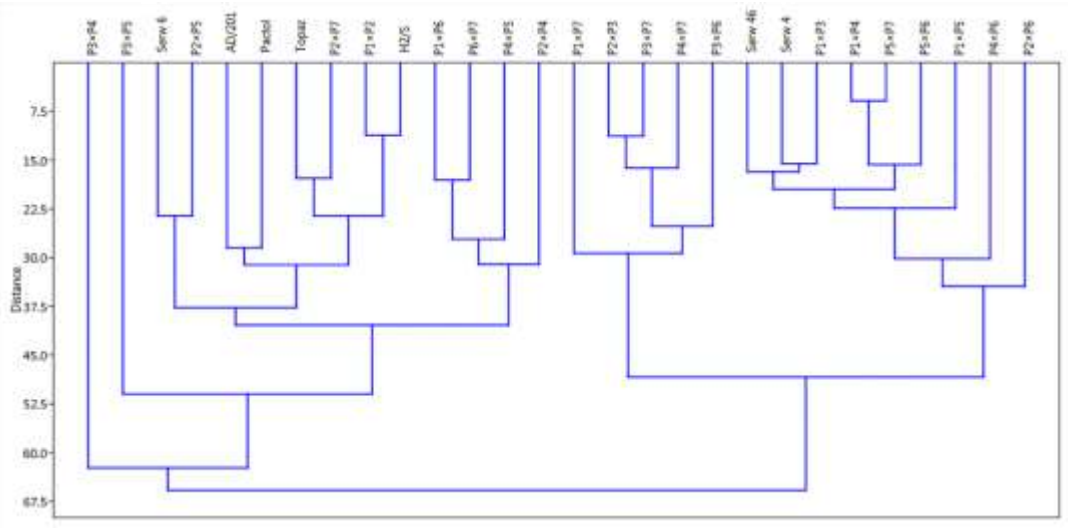

Figure 4. Hierarchical cluster dendrogram of 28 canola genotypes treated with two salinity stresses based on morphological characters.

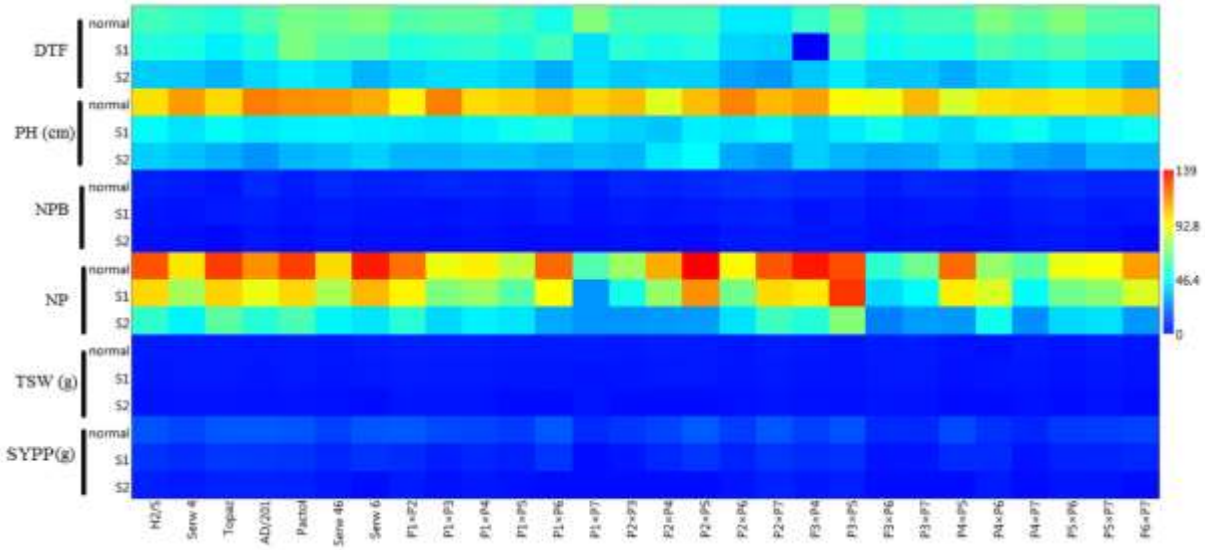

Figure 5. Plot matrix for morphological traits at control and salinity stress for studied canola genotypes.

Seed yield, its attributes, and seed oil content

The means of NP, TSW, SYPP, and SOC of all genotypes declined considerably under the two salinity treatments (S1 and S2) versus normal conditions, by 22.7% and 59.6%, 12.5% and 37.4%, 45.1% and 66.21%, and 9.5% and 21.5%, respectively. The highest NP resulted in the parents Serw.6 at normal and S1 conditions and Topaz under S2. Meanwhile, the cross Serw4 × Pactol under normal conditions and Topaz × Pactol under S1 and S2 levels recorded the highest means for this trait (Figure 6). The parents Pactol and Topaz and the cross H2/s × Serw.4 had the heaviest

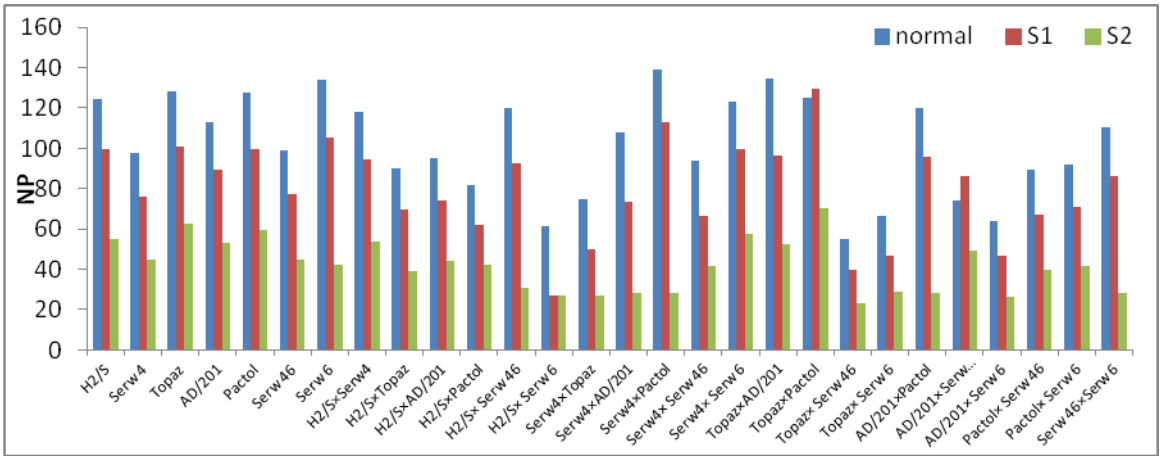

Figure 6. Number of pods/plant (NP) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

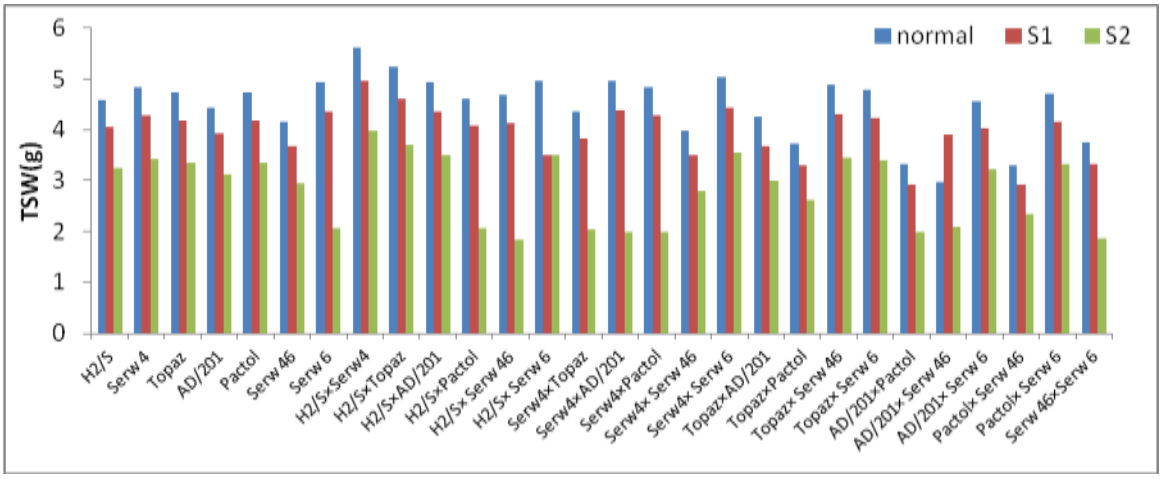

Figure 7. A Thousand seed weight (TSW) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

TSW, while the parent Serw.46 and the cross Pactol × Serw.46 expressed the lightest weight (Figure 7). Additionally, the parents, AD/201, Topaz, and Pactol, as well as, the cross combination Serw4 × Serw6, Topaz × Pactol, H2/S × Serw4, and Serw4 × Pactol, gave the highest SYPP over all environments (Figure 8). Moreover, the parents H2/S and Serw46 and the cross Serw4 × Pactol, Pactol × Serw6, Topaz × Serw6, and H2/s × Pactol presented the highest SOC (Figure 9).

Ions content and physiological traits

The two salinity treatments (S1 and S2) increased ProC and OP while decreasing RWC (Figures 8–13). The parents Topaz and H2/S and the cross combinations H2/s × Serw46 and Serw4 × AD/201 had the highest RWC under the three treatments (Figure 10). The parents Serw6 and Serw46 and the hybrids H2/s × Topaz, H2/s × AD/201, and Serw4 × Serw6 had the maximum ProC under all conditions

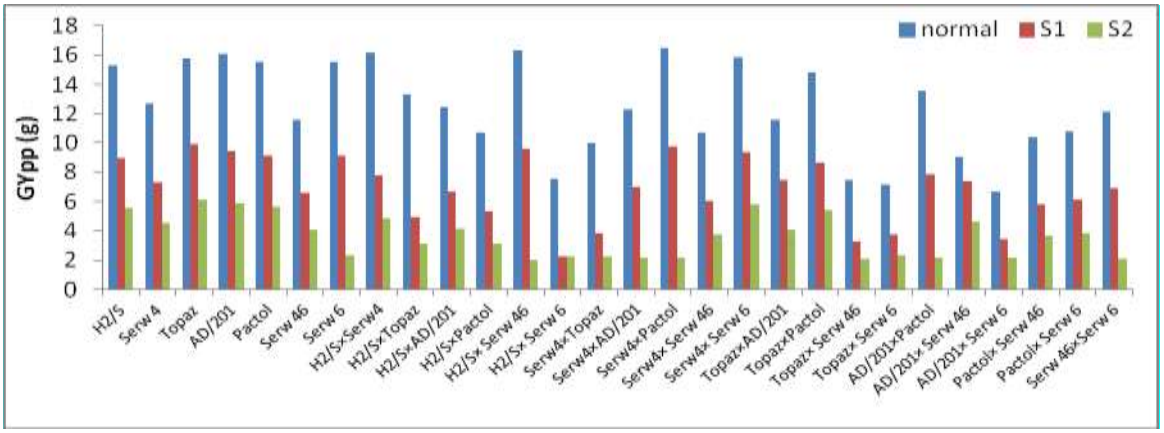

Figure 8. Seed yield per plant (SYPP) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

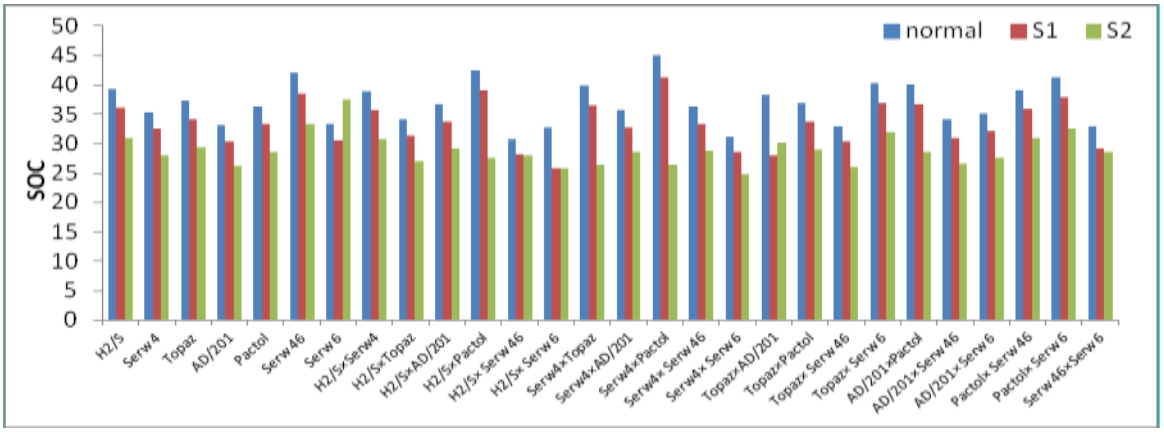

Figure 9. Seed oil content (SOC) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

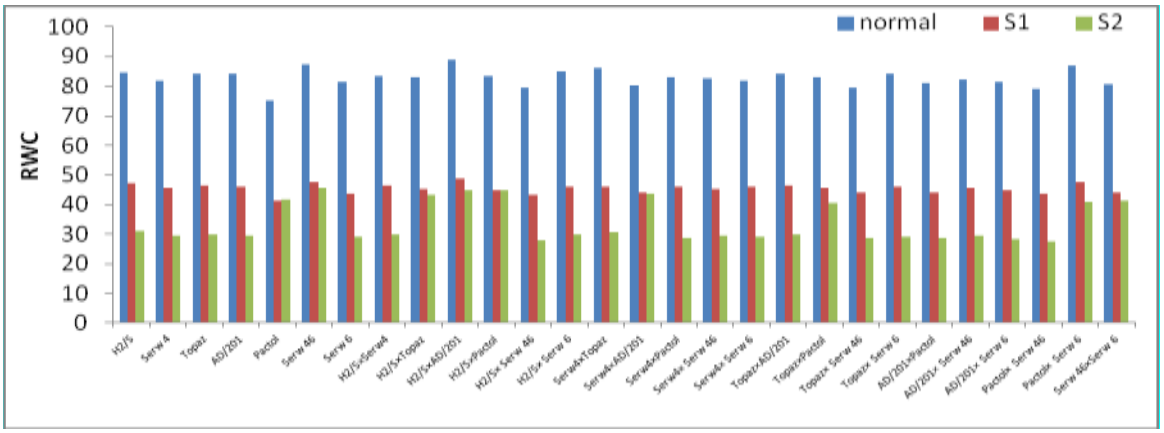

Figure 10. Relative water content (RWC) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

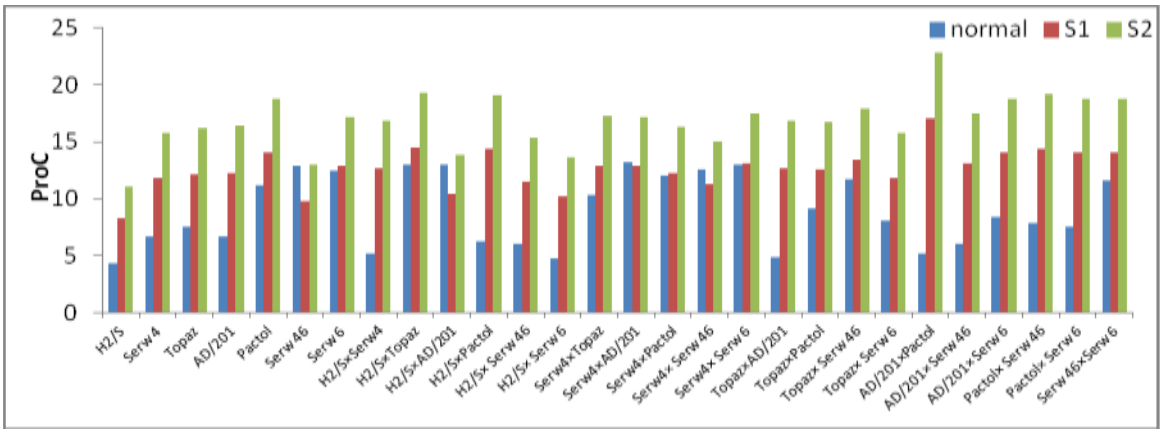

Figure 11. Proline content (ProC) of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

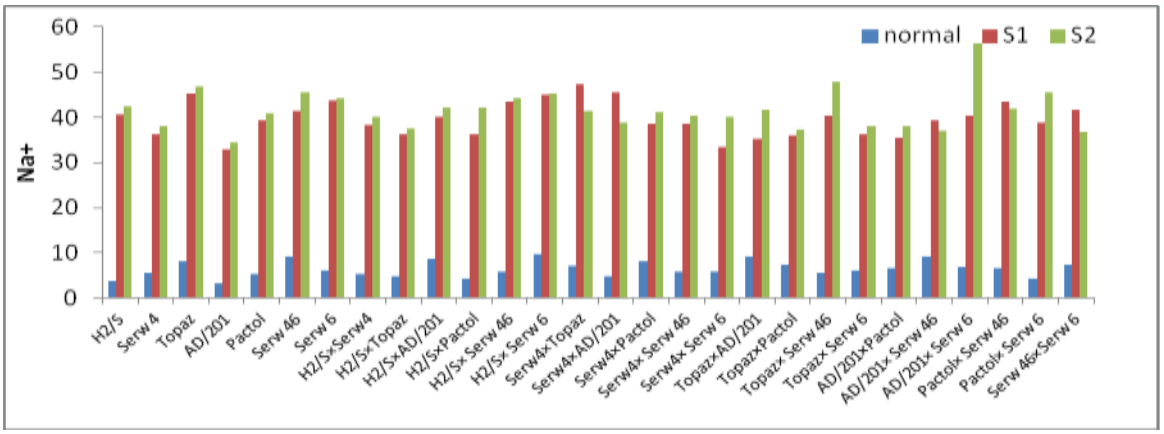

Figure 12. Na^+ of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

(Figure 11). An increased salinity increases canola leaf Na^+ concentration, but K^+, Ca^{++}, and K^+/Na^+ ratio declines (Figures 12, 13, 14, and 15). The parents, AD/201 and Serw4, and the cross combinations Topaz × Pactol, AD/201 × Pactol, Serw4 × Serw6, and H2/s × Topaz exhibited the lowest Na^+ value and highest K^+/Na^+ ratio. The parent Serw4 and crosses Topaz × Serw46, Serw4 × Serw6, and Topaz × AD/201 indicated greatest K^+ values. Under both salinities, the parents, AD/201 and Pactol, and the cross combinations H2/S × Serw4, Pactol × Serw46, and Serw4 × AD/201 maintained an increased Ca^{++}. Canola's K^+/Na^+ ratio may indicate salinity tolerance. These genotypes may be salinity-tolerant.

Hierarchical clustering of the heatmap appeared in Figure 16 to visualize the physiological parameters of canola genotypes over salinity stress. The heatmap generation comprised the genotype of the parents and hybrids. The first cluster of heatmap represented by physiological metabolites that responded to salinity stress divided into two cluster groups; one group includes proline and K^+ under two salinity stresses (S1, S2) and Na^+ content at control treatments, and the second group includes leaf RWC, Ca^{++} content, leaf OP, SOC at the control and salinity stresses, in addition to ProC and K^+ content at the control, and Na^+ at salinity stress. The second cluster of the heatmap for studied genotypes has a

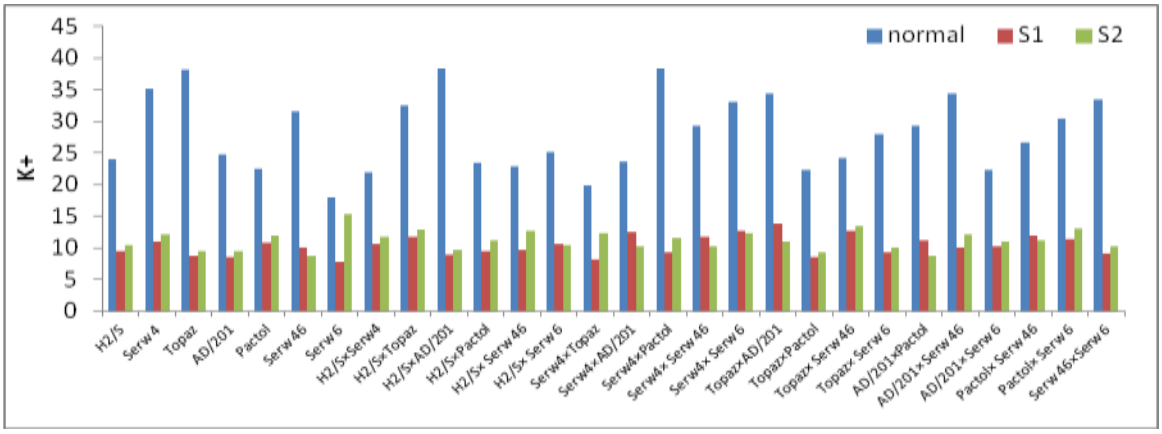

Figure 13. Ka^{+} of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

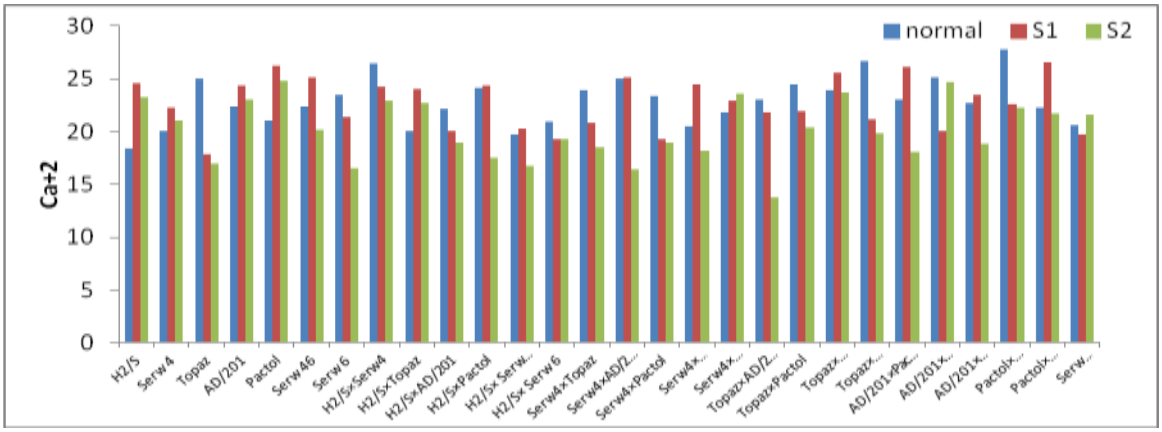

Figure 14. Ca^{+2} of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

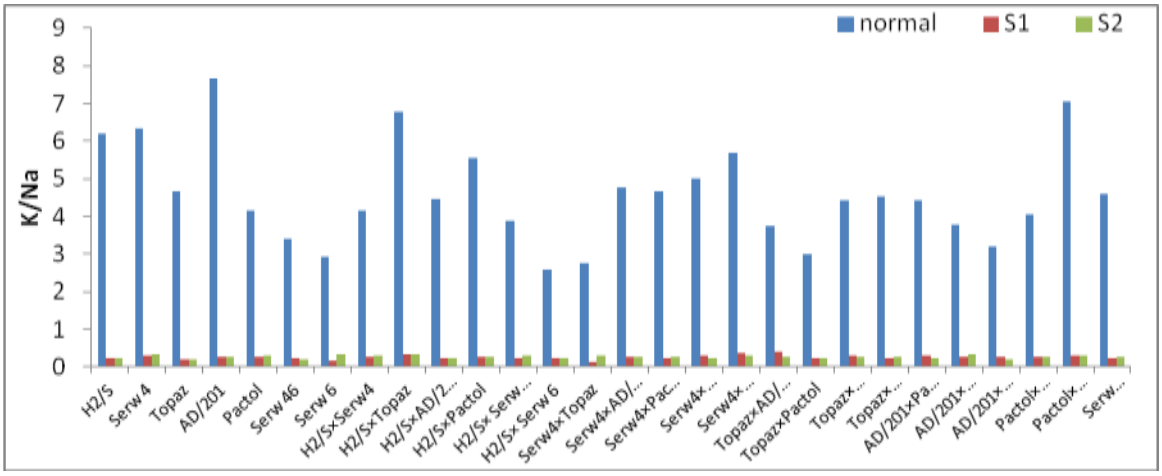

Figure 15. K/Na of all genotypes grown under normal and salt stress (S1) and (S2) conditions.

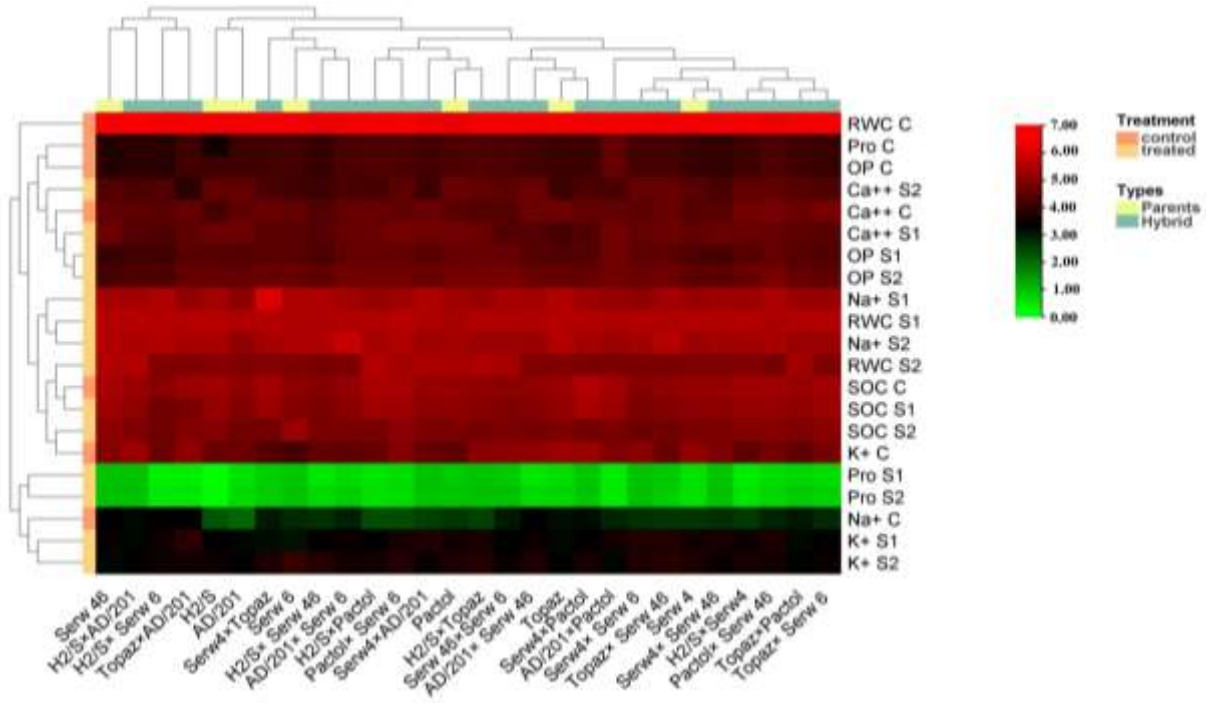

Figure 16. Hierarchical clustering heatmap for physiological parameters in 28 genotypes under salinity stresses.

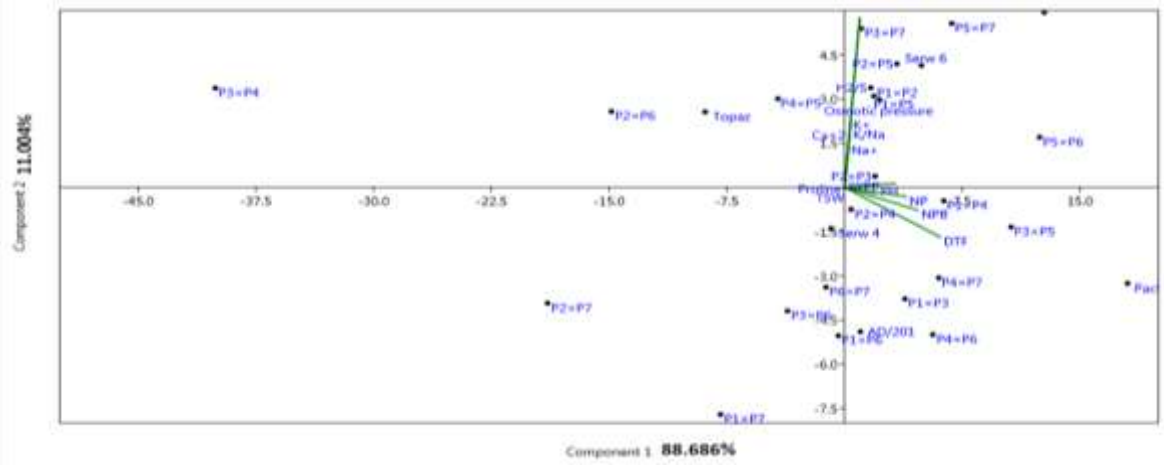

Figure 17. Principal component analysis (PCA) of morpho-physiological parameters for canola genotypes at salinity stress.

two-cluster classification; the first cluster includes Serw.46, H2/S × AD/201, H2/S × Serw.6, and H2/S, and the second group contains other genotypes. Thus, physiological parameters appeared closely correlated with salinity stresses. Principal component analysis (PCA) for six morphological traits and seven physiological parameters' explanation showed superimposed, suggesting an interaction between genotypes and morpho-physiological parameters under salinity stress (Figure 17). PCA signified physiological parameters (RWC)

and morphological traits DTF and NPB are the most effective parameters in the interaction. The first principal component (PC1) explained approximately 88.686% of the variance in the data, and the second (PC2) explained 11.004%.

General combining ability effects

Estimates of GCA effects for each parent are in Table 4. High positive values of GCA effects were interesting for all studied characteristics except DTF, PH, and Na^+ content, where high negative values would be desirable from the breeder's point of view. The parents H2/S at S1, Serw6 under S2, and Serw4 under the three environments had significant and adverse GCA effects for DTF. Moreover, the parents Pactol under normal conditions, Serw.4 and AD/201 under S1, as well as, Topaz and Serw46, showed dismissive and sizable effects toward dwarfness, and the parents H2/S and Serw6 expressed positive and meaningful outcomes toward tallness. The parent's AD/201 at S2 and Serw46 at typical and S1 situations had notable and positive GCA effects for NBP. Furthermore, the parents Serw4 and AD/201 under nonsaline conditions, H2/S and Topaz at S2, and Pactol under the three environments expressed significant and favorable GCA effects for NP. Similarly, the parents Serw.6 under the normal condition, Topaz under S2, Serw4 under normal and S2, and H2/S under the three environments exhibited affirmative and weighty GCA effects for TSW. The highest GCA effects for SYPP came from H2/S and Serw4 under normal and S2, and H2/S under the three environments, Pactol under a nonsaline condition, Serw4, AD/201, and Pactol at S1, and H2/S, Serw4, Topaz, AD/201, and Pactol under S2 environment. The parent Pactol, followed by Serw4 and Topaz, recorded the highest GCA estimates for SOC under nonsaline and S1 conditions.

Regarding RWC, four parents under nonsaline conditions had significant and positive effects, with H2/S being the best, while in saline conditions, Serw4 and Pactol recorded the highest results for this trait. Under all conditions, Serw4, Topaz, Serw46, and Serw6 exhibited the greatest positive and significant effects for ProC. Similarly, Serw4 recorded the utmost adverse and suggestive impacts for Na^+. Under all environments, Serw4 and Pactol gave the maximum positive and noteworthy outcomes for K^+ and Ca^{++}, respectively. Finally, Serw4 and AD/201 under a nonsaline condition and S1 level, and Serw4, Pactol, and Serw46 under S2 level had substantial and desirable GCA effects for K^+/Na^+. Based on the results, the parents Serw4, Topaz, and Pactol had the supreme GCA effects for most measured traits.

Specific combining ability effects

Estimates of SCA effects of the 21 F_1 crosses under normal and saline conditions appear in Tables 5a–c. The highest significant and negative (desirable) SCA effects under the three environments were notable in the crosses: H2/S × Serw46, Serw4 × Serw46, and AD/201 × Pactol for DTF, Pactol × Serw46 for PH, and H2/S × Serw4, H2/S × Topaz, and Serw4 × Serw46 for Na^+. On the contrary, the hybrids: Serw4 × Serw46, Serw4 × Serw6, Topaz × Pactol, and Pactol × Serw46 for NBP; H2/S × Serw4, Serw4 × Serw6, Topaz × AD/201, and Topaz × Pactol for NP; H2/S × Serw4 and Topaz × Serw46 for TSW; H2/S × Serw4, Serw4 × Serw6, and Topaz × Pactol for SYPP; H2/S × Serw4, H2/S × AD/201, Topaz × Serw6, AD/201 × Pactol, and Pactol × Serw6 for SOC; H2/S × Serw46, Serw4 × AD/201, and Serw46 × Serw6 for RWC; H2/S × Topaz, H2/S × AD/201, Serw4 × AD/201, and Serw4 × Serw46 for ProC; H2/S × Topaz, Topaz × AD/201, and AD/201 × Serw46 for K^+; H2/S × Serw4 and Topaz × Serw6 for Ca^{++}, and H2/S × Topaz, Serw4 × Serw6, and Topaz × Serw46 for K^+/Na^+ had the highest significant and positive SCA effects (desirable) under all conditions. Interestingly, the crosses that showed high SCA effects for SYPP also showed desirable SCA effects for some other traits.

Table 4. General combining ability effects of the parental lines under normal and salinity stress conditions.

Parents character		H2/S	Serw.4	Topaz	AD/201	Pactol	Serw.46	Serw.6	LSD $_{0.05}$	LSD $_{0.01}$
	Normal	0.43*	−5.13**	−1.90**	1.06**	3.59**	0.10	1.86**	0.40	0.54
DTF	S1	−1.24**	−3.36**	−2.45**	0.03	5.29**	1.90**	-0.17	0.44	0.40
	S2	0.78*	−1.74**	−0.37	0.75*	2.60**	-0.48	-1.55**	0.68	0.91
	Normal	−0.85	1.25*	−0.47	−1.15	−1.43*	1.54*	1.11	1.18	1.57
PH	S1	1.49**	−2.21**	−0.26	−1.60**	−0.08	1.89**	0.78*	0.75	1.18
	S2	0.89*	1.56**	-0.81*	−0.33	0.86*	-1.66**	-0.51	0.80	1.06
	Normal	−0.53**	0.24	−0.28*	0.22	−0.08	0.40**	0.01	0.25	0.33
NPB	S1	−0.38**	0.14	−0.27*	0.06	0.11	0.37**	−0.03	0.22	0.25
	S2	−0.25*	0.09	−0.27**	0.21*	−0.04	0.18	0.08	0.19	0.26
	Normal	−1.34	2.79**	−2.61**	3.08**	8.54**	−5.89**	−4.56**	1.55	2.06
NP	S1	−2.19**	1.07	−0.64	1.36	11.05**	−5.02**	−5.64**	1.47	1.55
	S2	1.39**	−0.95*	3.64**	0.04	3.93**	−3.46**	−4.57**	0.74	0.99
	Normal	0.31**	0.23**	0.03	−0.12**	−0.27**	−0.34**	0.14**	0.09	0.11
TSW	S1	0.21**	0.23**	0.05	−0.08*	−0.20**	−0.27**	0.06	0.08	0.09
	S2	0.25**	0.05	0.23**	−0.08	−0.19*	−0.28**	0.02	0.17	0.23
	Normal	0.70**	0.68**	−0.54**	0.16	0.80**	−0.77**	−1.04**	0.25	0.33
SYPP	S1	−0.09	0.33**	−0.40**	0.38**	0.72**	−0.34**	−0.60**	0.13	0.25
	S2	0.15**	0.11*	0.26**	0.22**	0.28**	−0.32**	−0.70**	0.09	0.13
	Normal	−0.04	0.33**	0.24**	−0.95**	2.52**	−0.48**	−1.62**	0.07	0.09
SOC	S1	−0.10	0.71**	−0.16**	−1.30**	2.71**	−0.20**	−1.67**	0.11	0.07
	S2	−0.12	−1.04**	−0.21**	−0.90**	0.12	0.47**	1.67**	0.15	0.20
	Normal	0.71**	0.66**	0.50**	0.66**	−1.38**	−0.81**	−0.34*	0.27	0.36
RWC	S1	0.43*	0.41*	0.23	0.31	−0.74**	−0.44*	−0.21	0.41	0.27
	S2	−0.33	1.23**	−0.45*	0.68**	0.10	−1.25**	0.02	0.34	0.45
	Normal	−0.09**	0.04**	0.02**	−0.05**	−0.06**	0.09**	0.05**	0.01	0.02
Pro	S1	−0.15**	0.07**	0.01*	−0.06**	−0.01*	0.08**	0.06**	0.01	0.01
	S2	−0.15**	0.04**	0.01*	−0.04**	0.00	0.08**	0.06**	0.01	0.01
OP	Normal	−0.56**	−0.57**	−0.05	0.34**	1.53**	−0.77**	0.09	0.19	0.26
	S1	−0.57**	−0.59**	0.05	0.07	1.69**	−0.92**	0.25*	0.21	0.19
	S2	−0.67**	−0.62**	0.13	-0.08	1.67**	−0.83**	0.41**	0.26	0.35
	Normal	-0.62**	-0.38**	0.54**	0.00	-0.39**	0.77**	0.08*	0.07	0.09
Na+	S1	1.10**	-1.26**	0.36**	-1.78**	-0.57**	1.34**	0.82**	0.03	0.07
	S2	-0.10	-1.32**	0.09	-0.85**	-0.84**	0.96**	2.07**	0.18	0.24
	Normal	−1.44**	1.24**	1.39**	0.74**	−1.04**	0.97**	−1.85**	0.02	0.03
K+	S1	−0.36**	0.45**	−0.19**	−0.37**	−0.07*	−0.05	0.59**	0.06	0.02
	S2	0.03*	0.37**	−0.12**	−0.34**	0.09**	0.08**	−0.10**	0.03	0.04
Ca++	Normal	−1.43**	−0.21**	1.03**	0.33**	0.45**	−0.06*	−0.11**	0.06	0.07
	S1	−0.01	−0.01	−1.17**	0.41**	1.29**	0.15**	−0.66**	0.06	0.06
	S2	0.38**	−0.08*	−0.94**	−0.49**	0.79**	0.70**	−0.36**	0.06	0.09
	Normal	0.40**	0.33**	−0.25**	0.33**	0.03	−0.47**	−0.36**	0.11	0.15
K+/ Na+	S1	−0.02**	0.02**	−0.01**	0.00**	0.00	−0.01**	0.01**	0.00	0.11
	S2	0.00	0.02**	0.00	0.00	0.00*	0.00*	−0.01**	0.00	0.00

* and **: significant at $P < 0.05$ and 0.01, respectively.

Table 5a. Estimates of SCA effects of the 21 F_1 crosses for all the studied traits under normal and salinity stress conditions.

Crosses	DTF			PH			NPB			NP			TSW		
	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2
H2/S× Serw.4	5.82**	4.28**	1.83*	−8.87**	−0.17	−3.24**	−0.15	−0.22	0.21	13.42**	15.75**	11.35**	0.53**	0.54**	0.83**
H2/S×Topaz	5.32**	5.04**	3.13**	14.09**	−2.89**	−0.54	1.28**	−0.29	0.18	−9.32**	−7.49**	−7.45**	0.33**	0.38**	0.37
H2/S×AD/201	2.16**	4.56**	2.02*	−1.90	0.37	0.65	0.11	0.22	0.35	−9.74**	−4.87**	1.10	0.19	0.25*	0.47*
H2/S×Pactol	−6.23**	−4.69**	−2.50**	1.31	3.81**	−0.87	−0.32	−0.32	−0.28	−28.88**	−26.68**	−5.07**	0.01	0.08	−0.84**
H2/S×Serw.46	−10.28**	−2.98**	−6.09**	3.14*	4.55**	−0.69	0.51	0.93**	−0.83**	23.87**	19.98**	−8.68**	0.16	0.21*	−0.99**
H2/S×Serw6	7.76**	−10.57**	4.31**	−1.85	−5.60**	0.50	−1.94**	−0.87**	−0.64**	−36.27**	−44.80**	−11.63**	−0.04	−0.75**	0.39
Serw.4×Topaz	5.22**	7.49**	1.65	1.47	−3.43**	−1.20	0.33	0.38	−0.05	−28.53**	−30.41**	−17.45**	−0.47**	−0.43**	−1.10**
Serw.4×AD/201	1.86**	1.67**	2.20*	−15.62**	−3.98**	6.98**	−0.92**	−0.54	−1.20**	−1.36	−8.95**	−12.85**	0.30**	0.25*	−0.82**
Serw.4×Pactol	0.40	−1.25*	0.02	1.94	2.50**	10.13**	0.40	0.11	−0.95**	24.51**	20.97**	−16.40**	0.34**	0.27**	−0.70**
Serw.4×Serw.46	−12.12**	−12.20**	−5.24**	9.57**	−1.33	−3.02**	1.59**	0.91**	1.26**	−6.70**	−9.25**	4.27**	−0.48**	−0.45**	0.19
Serw.4×Serw.6	−14.08**	−10.79**	−6.50**	0.14	2.27*	−7.17**	2.67**	1.80**	1.76**	21.78**	24.13**	21.55**	0.11	0.17	0.64**
Topaz×AD/201	−2.91**	−8.08**	−1.17	8.87**	−3.86**	5.02**	1.31**	0.04	0.66**	31.05**	15.72**	7.28**	−0.21*	−0.28**	0.01
Topaz×Pactol	5.70**	4.51**	3.31**	−7.14**	−0.17	−0.83	1.56**	0.99**	1.38**	16.06**	39.28**	21.12**	−0.59**	−0.54**	−0.26
Topaz×Serw.46	−4.62**	−3.10**	0.06	−14.21**	4.33**	−0.98	−1.78**	−1.15**	−0.35	−39.99**	−34.47**	−18.66**	0.64**	0.55**	0.65**
Topaz×Serw.6	−2.17**	1.64**	1.13	2.13	−1.59	−1.13	0.54	−0.17	0.22	−29.48**	−26.97**	−12.21**	0.06	0.14	0.28
AD/201×Pactol	−6.33**	−6.97**	−9.13**	−14.56**	−2.65**	2.69**	−0.45	−0.28	−0.91**	4.72*	3.56	−17.73**	−0.84**	−0.76**	−0.58**
AD/201×Serw.46	8.09**	5.75**	−0.06	−5.24**	0.19	1.20	−2.12**	−1.48**	−0.82**	6.63**	10.06**	10.91**	0.34**	0.26**	−0.39
AD/201×Serw.6	1.00	4.49**	4.02**	−3.06*	6.06**	−4.28**	0.47	0.58*	0.60*	−37.96**	−28.75**	−11.07**	−0.02	0.07	0.43*
Pactol×Serw.46	6.36**	0.82	4.09**	−5.28**	−4.24**	−6.65**	1.50**	1.03**	1.18**	−16.34**	−18.69**	−2.35*	−0.64**	−0.59**	−0.04
Pactol×Serw.6	−3.39**	−2.10**	1.50	−2.57	−0.07	−0.13	0.02	−0.31	0.15	−15.09**	−14.13**	0.30	0.28*	0.32**	0.64**
Serw.46×Serw.6	−0.71	0.62	−1.76*	0.01	1.99*	1.72	−0.23	−0.21	−1.66**	17.32**	16.87**	−5.72**	−0.60**	−0.45**	−0.73**
$LSD_{0.05}$	1.00	1.08	1.68	2.92	1.84	1.98	0.62	0.55	0.48	3.83	3.64	1.83	0.21	0.19	0.42
$LSD_{0.01}$	1.33	1.44	2.24	3.89	2.46	2.63	0.82	0.74	0.63	5.10	4.85	2.44	0.28	0.26	0.56

Table 5b. Estimates of SCA effects of the 21 F_1 crosses for all the studied traits under normal and salinity stress conditions.

Crosses	SYPP			SOC			RWC			ProC		
	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2
H2/S×Serw.4	2.19**	0.65**	0.96**	1.74**	1.72**	3.08**	−1.75**	−1.01*	−5.23**	−0.17**	−0.19**	−0.15**
H2/S×Topaz	0.58	−1.47**	−0.97**	−2.89**	−1.76**	−1.64**	1.14**	0.65	−2.72**	0.37**	0.43**	0.38**
H2/S×AD/201	−1.03**	−0.52**	0.16	0.85**	1.73**	1.21**	0.54	0.47	−3.88**	0.54**	0.50**	0.44**
H2/S×Pactol	−3.41**	−2.19**	−0.93**	3.20**	3.05**	−1.41**	−6.05**	−3.40**	7.77**	−0.04*	−0.04**	−0.04**
H2/S×Serw.46	3.80**	3.13**	−1.47**	−5.53**	−4.79**	−1.26**	5.56**	3.02**	14.04**	−0.22**	−0.14**	−0.03**
H2/S×Serw6	−4.71**	−4.02**	−1.02**	−2.46**	−5.78**	−4.65**	−1.76**	−1.04*	−4.59**	−0.14**	−0.21**	−0.20**
Serw.4×Topaz	−2.74**	−3.00**	−1.75**	2.40**	2.64**	−1.16**	−0.78*	−0.47	8.66**	0.03*	0.02**	0.01
Serw.4×AD/201	−1.16**	−0.61**	−1.80**	−0.58**	−0.05	1.53**	3.72**	1.98**	9.23**	0.26**	0.29**	0.26**
Serw.4×Pactol	2.44**	1.79**	−1.83**	5.31**	4.52**	−1.49**	1.16**	0.56	10.11**	−0.02	0.17**	0.16**
Serw.4×Serw46	−1.78**	−0.88**	0.31**	−0.32**	−0.50**	0.35	−2.89**	−1.62**	−5.26**	0.18**	0.12**	0.12**
Serw.4×Serw6	3.64**	2.68**	2.76**	−4.34**	−3.75**	−4.78**	1.86**	1.00	−4.73**	0.11**	0.17**	0.14**

Table 5b. (Cont'd).

Crosses	SYPP			SOC			RWC			ProC		
	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2
Topaz×AD/201	−0.64*	0.57**	−0.04	2.12**	−3.81**	2.37**	−4.07**	−2.19**	9.61**	−0.25**	−0.24**	−0.25**
Topaz×Pactol	2.00**	1.44**	1.22**	−2.79**	−2.13**	0.18	1.72**	0.90	−3.67**	0.07**	0.01	0.12**
Topaz×Serw46	−3.80**	−2.88**	−1.54**	−3.57**	−2.69**	−3.12**	−0.13	−0.11	−2.73**	0.07**	0.11**	−0.03**
Topaz×Serw6	−3.87**	−2.20**	−0.90**	4.86**	5.47**	1.61**	−1.47**	−0.76	−4.33**	−0.10**	−0.12**	−0.07**
AD/201×Pactol	0.00	−0.18	−2.00**	1.64**	1.98**	0.37*	1.54**	0.79	4.76**	−0.11**	−0.20**	−0.28**
AD/201×Serw46	1.48**	0.43*	1.05**	−1.25**	−0.97**	−1.80**	−2.65**	−1.48**	−4.70**	−0.18**	−0.23**	−0.14**
AD/201×Serw6	−5.00**	−3.27**	−1.02**	0.78**	1.77**	−2.03**	0.67*	0.22	−4.76**	−0.05**	−0.04**	0.04**
Pactol×Serw.46	−2.18**	−1.45**	0.03	0.25**	0.05	1.52**	1.01**	0.52	−3.53**	−0.17**	−0.15**	−0.16**
Pactol×Serw.6	−1.53**	−0.95**	0.56**	3.55**	3.48**	1.87**	0.14	0.04	−4.96**	−0.02	−0.14**	−0.19**
Serw.46×Serw.6	1.36**	0.95**	−0.56**	−1.77**	−2.22**	−2.54**	4.57**	2.50**	8.37**	−0.04*	0.05**	0.09**
LSD $_{0.05}$	0.61	0.33	0.23	0.18	0.26	0.36	0.67	1.00	0.84	0.03	0.02	0.02
LSD $_{0.01}$	0.81	0.44	0.31	0.23	0.35	0.49	0.89	1.34	1.11	0.04	0.02	0.03

Table 5c. Estimates of SCA effects of the 21 F_1 crosses for all the studied traits under normal and salinity stress conditions.

Crosses	Na+			K+			Ca++			K+/ Na+		
	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2	Normal	S1	S2
H2/S×Serw.4	−0.20*	−0.31**	−0.51*	−6.07**	−0.01	0.29**	5.27**	1.61**	2.46**	−1.18**	0.00	0.01*
H2/S×Topaz	−1.59**	−3.98**	−4.53**	4.38**	1.80**	1.78**	−2.44**	2.49**	3.14**	2.03**	0.08**	0.07**
H2/S×AD/201	2.73**	1.96**	0.93**	10.94**	−1.14**	−0.82**	0.42**	−3.08**	−1.14**	−0.85**	−0.04**	−0.03**
H2/S×Pactol	−1.25**	−3.15**	0.98**	−2.28**	0.05	−0.66**	2.19**	0.43**	−3.84**	0.53**	0.03**	−0.02**
H2/S×Serw.46	−0.75**	2.03**	1.18**	−4.84**	1.58**	−0.35**	−1.71**	−2.58**	−4.49**	−0.63**	0.02**	−0.01**
H2/S×Serw.6	3.76**	4.30**	1.11**	0.24**	−1.42**	0.76**	−0.41**	−2.78**	−0.88**	−2.04**	−0.06**	0.01
Serw.4×Topaz	0.57**	1.53**	0.62**	−10.94**	0.50**	−2.01**	0.21**	−0.66**	−0.65**	−1.93**	0.00	−0.05**
Serw.4×AD/201	−1.16**	2.92**	5.56**	−6.52**	0.86**	0.32**	2.05**	2.06**	−3.15**	−0.47**	0.00	−0.03**
Serw.4×Pactol	2.50**	1.41**	1.15**	10.04**	−0.41**	−1.13**	0.20**	−4.71**	−1.93**	−0.28*	−0.02**	−0.03**
Serw.4×Serw.46	−1.02**	−0.50**	−1.38**	−1.08**	−0.33**	−0.20**	−2.08**	1.66**	−2.64**	0.56**	−0.01**	0.00
Serw.4×Serw.6	−0.35**	−5.04**	−2.73**	5.52**	0.13	2.12**	−0.76**	0.90**	3.85**	1.12**	0.05**	0.07**
Topaz×AD/201	2.18**	−2.30**	0.20	4.20**	2.87**	1.51**	−1.14**	−0.10	−4.95**	−0.93**	0.10**	0.03**
Topaz×Pactol	0.81**	−2.56**	−3.99**	−6.17**	−1.98**	−1.39**	0.14*	−0.90**	0.35**	−1.38**	−0.04**	−0.01*
Topaz×Serw.46	−2.28**	−0.12**	4.57**	−6.25**	2.03**	2.73**	0.10	3.89**	3.81**	0.53**	0.05**	0.03**
Topaz×Serw.6	−0.92**	−3.70**	−6.09**	0.25**	−1.87**	−0.48**	2.92**	0.25**	0.98**	0.54**	−0.02**	0.02**
AD/201×Pactol	0.53**	−1.02**	−2.42**	1.44**	0.01	−0.90**	−0.64**	1.66**	−2.37**	−0.53**	0.01**	−0.01*
AD/201×Serw.46	1.83**	1.02**	−5.28**	4.53**	0.99**	0.41**	1.98**	−3.18**	4.27**	−0.67**	0.02**	0.04**
AD/201×Serw.6	0.38**	2.44**	13.08**	−4.76**	−0.80**	0.79**	−0.36**	1.03**	−0.43**	−1.36**	−0.04**	−0.03**
Pactol×Serw.46	−0.26**	2.27**	1.22**	−1.36**	0.44**	1.13**	4.46**	−1.50**	0.64**	−0.10	0.00*	0.02**
Pactol×Serw.6	−1.83**	−0.28**	2.26**	5.27**	0.95**	1.51**	−0.91**	3.21**	1.12**	2.78**	0.03**	0.02**
Serw.46×Serw.6	−0.05	−4.29**	−3.44**	6.22**	−1.97**	−0.91**	−2.05**	−2.50**	1.15**	0.84**	−0.02**	−0.01
LSD 0.05	0.16	0.08	0.44	0.06	0.15	0.07	0.14	0.14	0.16	0.27	0.00	0.01

* and ** significant at P < 0.05 and 0.01, respectively.

SDS-PAGE

Extracting proteins ran from the seeds of all canola genotypes. The results of the electrophoretic separation of protein are in Figure 5. The computer imaging analysis enabled in identifying 10 major protein bands R1–R10 in 14 genotypes. The number and intensity of protein bands resolved by SDS-PAGE ranged widely depending on salinity level and genotypes. Therefore, significant differences emerged between non-stress and stressed protein extraction when the size and migration properties of proteins in canola genotypes underwent scrutiny in this study. As arrows indicate, the 10 regions of major protein bands R1–R10, which ranged from 19 to 86 KDa, resulted in most genotypes. Moreover, the major differences between the banding proteins occurred in the R4, R5, and R6 regions with molecular weights of 34 to 47 KDa. The crosses H2/S × Serw.4, H2/S × Topaz, Serw.4 × Pactol, and AD/201 × Serw6 showed the most remarkable differences in R4, R5, and R6 bands compared with other genotypes (Figure 18). The average linkage procedure, UPGMA clustered the investigated 28 canola genotypes based on differences in the number of bands and their intensity, as evident in Figure 19.

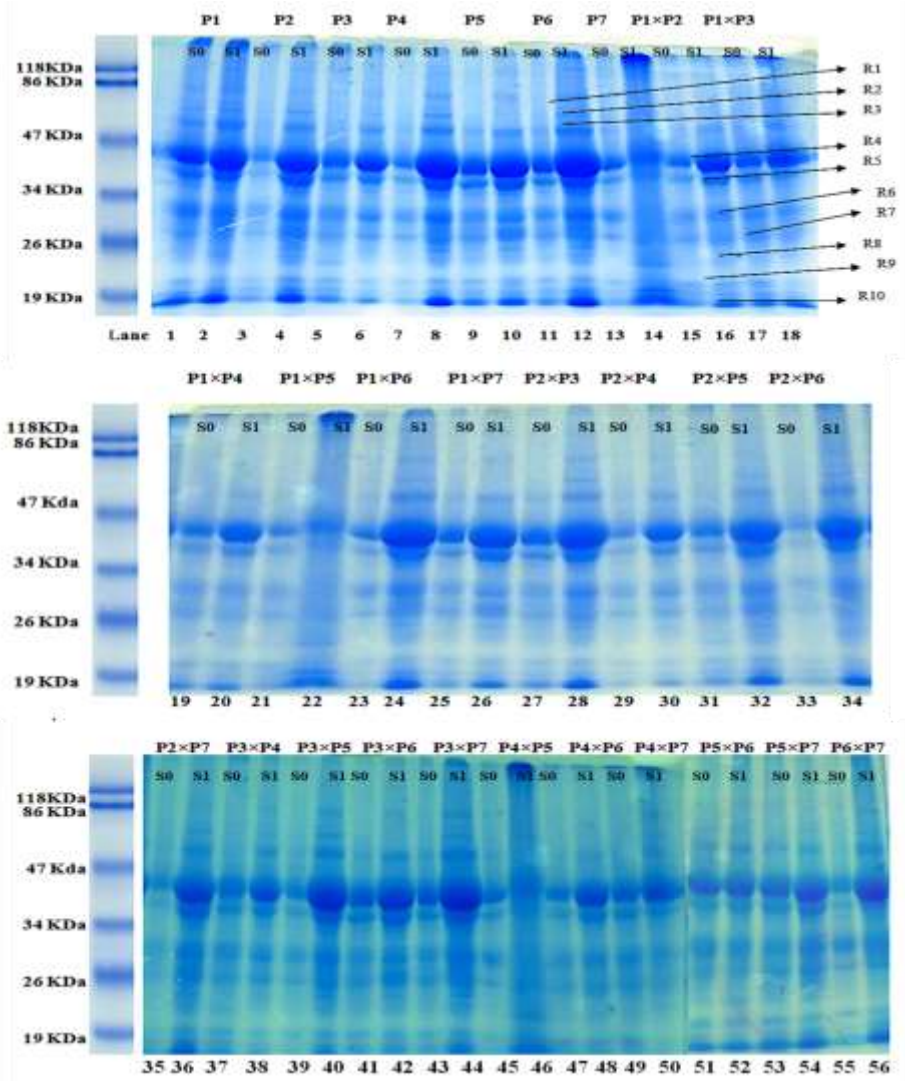

Figure 18. SDS-PAGE patterns of canola protein under normal (S0) and salinity (S1) conditions.

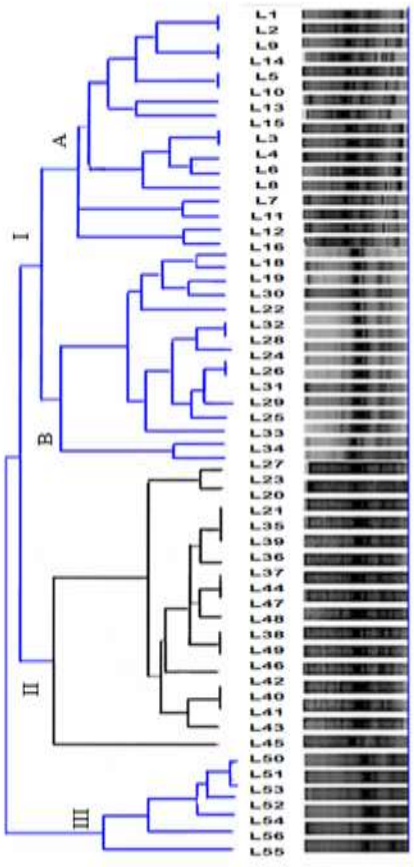

Figure 19. A dendrogram showing the relationship among genotypes of canola based on total seed protein under normal and salinity stress conditions.

At the 20% similarity level, genotypes subdivide into three major clusters. Cluster 1, distinctly separated from other bundles, included the most genotypes. Among Cluster 1, genotypes split into two subgroups (A1 and A2). The subgroup (A1) comprised the parents and some crosses, mainly under nonsaline conditions. Meanwhile, A2 contained most crosses under saline conditions. Cluster II showed the maximum similarity among crosses and included the most crosses at a similarity level of 100% compared with the total number of genotypes. The genotypes in Cluster II may be a stable and heritable variation that may have arisen due to a gene or chromosome variation. Cluster III showed more genetic variability than others and included six genotypes at 69.2% similarity.

DISCUSSION

Salinity tolerance is a genetically complex trait with regulations from several genes (Oghan *et al*., 2018). This study materialized to estimate combining ability and identify the type of gene action controlling the inheritance of salt tolerance in canola through the evaluation of 21 F_1 with their seven parents under normal and two salinity stress levels, i.e., 6.24 dS m^{-1} (S1) and 7.81 dS m^{-1} (S2).

The highly significant variations observed among the parental genotypes and their F_1 hybrids for all the measured traits under nonsaline and saline conditions suggested adequate genetic differences, which allows the selection of preferred genotypes under each environment. Previous

investigations revealed significant differences among canola genotypes grown under saline and nonsaline soils (Dezfouli *et al*., 2019). The analysis of combining ability estimates showed extremely notable variances in GCA and SCA effects for all measured traits. It indicates that both additive and non-additive gene actions were essential in controlling the inheritance of these traits under all tested environments. Similarly, significant GCA and SCA effects occurred for multiple attributes in canola (Channa *et al*., 2018). The magnitude of the GCA/SCA variance ratio revealed that all measured traits were under control by the non-additive gene action across environments. This finding is in agreement with Channa *et al*. (2018) and Dezfouli *et al*. (2019), who found a multitude of non-additive genetic effects in the inheritance of plant height, days to 50% flowering, 1000-seed weight, oil content, and seed yield per plant in canola under a normal condition. However, these results contradict the findings of other studies (Shehzad *et al*., 2015), reporting that additive gene effects showed to be more important in controlling canola seed yield and oil content. The discrepancy in results could be due to variations in germplasm and environmental conditions under which the experiment proceeded (Ishaq *et al*., 2017). It is imperative to note that information concerning genetic effects governing canola seed yield and other traits under salt stress is limited to the study's best knowledge.

Salinity stress treatments (S1 and S2) decreased all genotype traits except ProC and hazardous ion absorption Na^+, with Sharaan *et al*. (2012) and Ishaq (2017) finding similar results. DTF reduced significantly during salinity stress. Partial salinity stress escape may favor earlier-flowering genotypes (Kazan and Lyons, 2016). Salinity may reduce PH due to water absorption, cell elongation, and division inhibition (Raza, 2020; Zheli *et al.,* 2021). SOC decreased gradually with increasing salinity from S1 to S2. It matches the results from Ashraf and McNeilly (2004).

In this investigation, salinity stress treatments (S1 and S2) increased Na+ and lowered K^+, Ca^{++}, and K^+/Na^+ ratios. Raza (2020) found similar results. Na^+ and Cl^+ compete with other essential ions like K^+ and Ca^{++} at the root ion absorption site, causing ion toxicity. With their molecular similarities, high Na^+ concentrations reduced K^+ uptake (Oghan *et al*., 2018). S1 and S2 treatments increased proline content in all genotypes, matching the findings of Raza (2020). Proline scavenges reactive oxygen species, regulates cell redox equilibrium, and supplies energy in addition to osmoprotection. Many physiological processes during development result in yield. SYPP is the most vital agronomic parameter for abiotic stress resistance, particularly salinity. Under salt stress, yield qualities like NP and TSW may decrease, lowering SYPP. Salinity steadily diminished these components. Salinity stress reduced NP and TSW (Valiollah, 2013). This study's 66.21% SYPP reduction under high salinity level (S2) compared with nonsaline treatment was similar to Farouk and Arafa (2018). The study found that evaluating genotypes under different environmental conditions helps discover the optimal genotypes for a given environment. Since they had the sizable mean values for SYPP and most characteristics, the parent's AD/201, Topaz, and Pactol and the crosses Serw4 × Serw6, Topaz × Pactol, H2/S × Serw4, and Serw4 × Pactol were promising salinity-tolerant genotypes. These genotypes need thorough evaluation in multilocation experiments and are potential for salinity resistance.

The success of any plant breeding program relies on the precision selection of parents (Kamara *et al*., 2020). In the presented study, GCA effects for the evaluated parents differed significantly for each trait. Moreover, none of the parents showed significant GCA effects for all the determined traits under any assessed environment. The significant and negative GCA effects observed with H2/S at S1, Serw.6 under S2, and Serw4 for DTF under the three conditions suggested that these parents could be essential sources of favorable alleles for earliness under the tested conditions. Likewise, the parents Serw4, AD/201, Topaz, and Serw46 were the best general combiners for shortness, while H2/S and Serw6 emerged as excellent combiners for tallness under saline conditions. High seed and oil yields under all possible ecosystems are the

most critical objective in canola breeding programs (Ishaq *et al*., 2017). The parents Serw4 and Pactol signified as good general combiners for increasing SYPP and some of its components, as well as, SOC in both nonsaline and saline conditions, since they exhibited high GCA values for these traits. Interestingly, the parent Serw.4, which had desirable GCA effects for SYPP, was also a good general combiner for DTF, RWC, ProC, K^+, and K^+/ Na^+ under stressed and non-stressed environments. Thus, this parent could transfer these desirable alleles to its offspring to develop salinity-tolerant hybrids.

SCA effects help choose the best hybrids by showing better or worse results than envisaged versus their parents' average performance. In this study, the most specific combiners for SYPP and some of its components were H2/S × Serw4, Serw4 × Serw6, and Topaz × Pactol under all environments. These findings suggest that those hybrids provide a better source to develop canola genotypes for salt tolerance. These crosses consisted of at least one parent with a high GCA effect and increased concentration of favorable alleles for canola seed yield. Kanwal *et al*. (2019) found similar results. In this study, the crosses H2/S × Serw4, H2/S × AD/201, and Topaz × Serw.6 across all environments proved promising specific combiners for improving SOC. Similar findings also came from Channa *et al*. (2018) and Farouk and Arafa (2018). However, the hybrids H2/S × Serw4 and Serw4 × Serw6 were the best specific combiners for more than one trait, such as, DTF, NPB, NP, TSW, SYPP, SOC, ProC, Ca^{++}, and K^+/Na^+. Accordingly, these hybrids might improve these traits under both conditions.

In this study, changes in protein profiles occurred under salinity stress treatment compared with normal conditions, as distinguished by an absence or induction of new protein bands. In addition, the increase or decrease of protein band intensity in response to salinity stress has also manifested. This result agrees with the findings of Dolatabadi and Toorchi (2017), who reported the presence or the absence of new protein bands in canola genotypes under salinity stress. The changes in protein profiles may be due to an inhibiting or stimulating translation of mRNAs under salinity stress or a result of the regulation of mRNA transcription (Hurkman and Tanaka, 1987). Moreover, the latest research results proved that cluster analysis based on protein pattern data benefits categorizing the evaluated canola genotypes into similar groups under stressed and non-stressed conditions, including validity in exposing variation.

The Hierarchical cluster heatmap is one visual method that can help clarify the associations and relations between different parameters of samples under diverse treatments. The benefit of heatmap is better in combination with hierarchical clusters based on similarity or distance between them. The principal component analysis is a multivariate data assessment in visualizing relationships, similarities, and dissimilarities among various plant parameters against salinity tolerance. PCA explains the maximum variations in interaction by morphological and physiological traits (Khan *et al*., 2019).

CONCLUSIONS

Parents and F_1 hybrids showed high genetic variation for all attributes in nonsaline and saline environments. Salinity stress reduces canola output. Non-additive action controls salt resistance in canola genotypes. Seed protein SDS-PAGE verified the materials' considerable variety. The parental genotypes Serw4 and Pactol were effective general combiners for enhancing seed yield and other attributes under stressed and non-stressed conditions. Similarly, H2/S × Serw4 and Serw4 × Serw6 were good specific combiners for most traits and can benefit future hybrid development to improve canola salt tolerance.

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