Using artificial neural network to evaluate salinity indices to identify rapeseed salinity tolerant cultivars

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Article Info	ABSTRACT
Article type: Research Article	**Objective**: This study aims to evaluate the salt tolerance of various canola genotypes in arid and semi-arid regions, particularly focusing on the identification of salt-tolerant varieties that can perform well under saline conditions.
	Methods: A total of 39 cultivars and lines of rapeseed were assessed for their tolerance to salinity using eight different indices. The evaluation was conducted through a randomized complete block experiment with four replications under two irrigation conditions: normal (0.831 dSm^{-1}) and saline (8.7 dSm^{-1}) in Kerman, Iran. Statistical analyses, including analysis of variance, regression, and artificial neural network (ANN) modeling, were employed to assess the performance of the canola varieties.
	Results: The results indicated significant differences between the cultivars and a notable interaction effect between environmental conditions and cultivar performance. Additionally, there was a non-significant correlation (0.021) between cultivar performance in the two irrigation conditions, suggesting genetic diversity among the genotypes for breeding purposes. The endurance indices—harmonic mean, stress tolerance index, mean product, and geometric mean product—demonstrated positive and significant correlations with seed performance in both irrigation scenarios, making them effective predictors of salinity tolerance. High-yielding varieties such as Talaye, Talaieh, T98007, Ahmadi, Modena, Option 500, and PP-4010 were identified as suitable for cultivation in saline soils.
	Conclusions:This research contributes to the understanding of salt tolerance in canola genotypes, providing valuable insights for breeding programs aimed at enhancing crop performance in saline environments. The identification of specific endurance indices as reliable predictors of tolerance offers a methodological advancement in the selection of salt-tolerant cultivars.

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1 Introduction

Salty soil and water are the main limiting climatic factors that make planting crops difficult and this difficult is caused by the high concentration of salt in the soil solution around the plant roots (Di-Caterina *et al.* 2007; Ravari et al. 2015). The reason for the decrease in the growth of plants in salty conditions is lack of water due to the creation of a negative potential in the soil solution around the roots, the creation of ionic toxicity conditions due to the absorption of Na^+ and Cl^- ions, which leads to a decrease in the absorption of K^+, $Ca2^+$ and $NO3^-$ (Isayenkov & Maathuis 2019).

The important role of rapeseed (Brassica napus L.) in the production of oilseeds in Iran is undeniable due to its wide adaptability to different conditions. Rapeseed also improves the soil structure due to its deep and extensive roots, and as

(SSI)[2], (GMP)[3], (MP)[4], (TOL)[5], (HM)[6], (STI)[7], (YSI)[8], and (YI)[9], had been proposed to select the superior genotypes

(Bouslama & Schapaugh 1984; Fernandez 1992; Gavuzzi *et al.* 1997; Sio-Se Mardeh *et al.* 2006; Shirani Rad & Abbasian 2011; Bchini *et al.* 2011).

The efficiency of these indicators appears to be dependent on the selection objective and target climate. Therefore, to increase rapeseed production in different conditions, it is necessary to introduce indicators that can be used to identify genotypes with good performance in the field. (Amit *et al.* 2018). Different techniques, including grouping, regression, biplot, and Artificial Neural Network (ANN), can be used to evaluate the efficacy of these indices for genotype screening (Dehghani *et al.* 2006; Ravari *et al.* 2015). The Multilayer Perceptron (MLP) is a common ANN model used among researchers. This model has three layers, which are the input, hidden, and output layers respectively (Ravari *et al.* 2015). The mean squared error (MSE) and the coefficient of determination (R^2) between the anticipated and actual values are two of the most popular metrics for evaluating the model's validity (Przyby *et al.* 2020; Niedbała *et al.* 2022). So far, the use of artificial intelligence has not been used in

a result, its rotation with cereals as a pre-sowing plant significantly increases the yield of cereals. Rapeseed planting is facing restrictions due to the spread of salinity in Iran (Rameeh 2011; Saberi et al 2021). The main strategy to increase production in saline conditions is to use improved cultivars using the hybridization method (Amiri-Oghan *et al.* 2012).

To check the salinity tolerance trait and use a proper breeding method, the influence of the relevant genes on this trait should be checked. (Muhammad *et al.* 2014). Also, in order to accurately estimate genetic indices and obtain sufficient information about the studied plant, reliable information about gene function in the studied population should be obtained (Rozema & Schat 2013).

A number of indicators including in terms of tolerance to salinity according to the relationship between (Yp)[10] and (Ys)[11] the determination of salinity-tolerant cultivars, especially in rapeseed. Ji *et al.* (2007) used this method to forecast the yield of Fujian rice under normal mountain weather conditions. They claimed that when comparing a regression model with rice to an ANN model, ANN model consistently predicts field performance more accurately. Niedbała *et al.* (2019) compared three artificial intelligence models to determine the performance of canola before harvest. The outcomes indicated that the lowest mean absolute percentage error, (MAPE), and R^2 (the coefficient of determination) were 6.88% and 0.69, respectively, related to the QQWR31_5 program. Ravari *et al.* (2015) also used this system to rate the salinity tolerance indices in determining the wheat salinity tolerant cultivars. The results of their investigation showed that ANN is a fast, cheap, and at the same time efficient solution for detecting genotypes that tolerate salinity to a great extent. So this experiment was conducted to identify the superior index(s) in order to identify the rapeseed genotype(s) tolerant to salinity through ANN.

2 Materials and Methods

This design involved the succeeding 39 canola genotypes: (1) Talaieh, (2) Sarigol, (3) Zarfam, (4) Zafar, (5) Delgan, (6) Ahmadi, (7) Hyola401, (8) Hyola 60, (9) pp-401015E, (10) T98007, (11) Talaye, (12) SLM046, (13) Geronimo, (14) Modena, (15) Opera, (16) Symbol, (17) KS-11, (18) Colvert, (19) Ks-7, (20) Okapi, (21) Licord, (22) Orient, (23) Option500, (24) H-19, (25) Shiralee, (26) San-14, (27) San-12, (28) SPN178, (29) SPN179, (30) SPN181, (31) SPN182, (32) SPN183, (33) SPN184, (34) SPN185, (35) SPN192, (36) SPN193, (37) RGS003, (38) Dalgon, and (39) SAN56 was carried out in two randomized complete block designs (designs 1 and 2) with four replicates for each design under two irrigation conditions, design 1; 0.931 dSm^{-1} and design 2; 8.7 dSm^{-1}, at The Kerman Education and Agriculture and

Natural Resources Research Center, Kerman, Iran in 2020. The seeds were planted in six rows 4 meters long in each plot with a 0.4 meters distance between rows and 40 plants per square meter. The required amount of fertilizer before planting (130 kg of nitrogen and 40 kg of phosphorus per hectare) was used based on the soil sample analysis. From the four middle rows in each plot, 25 cm were removed from both sides of each row (top and bottom) and the seed yield of the middle four rows was calculated. The following

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[2] -Sensitivity stress index
[3] - Geometric Mean product
[4] - Mean Product
[5] - Tolerance
[6] - Harmonic Mean

[7] - Stress Tolerance Index
[8] - Yield Stability Index
[9] - yield index
[10] - Yield in non-saline Environment
[11] - Yield in saline Environment

expressions were used to calculate each of the eight stress tolerance indices:

$$MP = \frac{(Y_s + Y_p)}{2}, \text{ (Bouslama \& Schapaugh 1984);}$$

$$TOL = (Y_p - y_s) \text{ (Hossain } et \, al. \text{ 1990);}$$

$$GMP = \sqrt{Y_s \times Y_p} \text{ (Sio-Se Mardeh } et \, al. \text{ 2006);}$$

$$SSI = \frac{1 - \frac{Y_s}{Y_p}}{\frac{\overline{Y_s}}{\overline{Y_p}}} \text{ (Fischer \& Maure 1978);}$$

$$YI = \frac{Y_s}{\overline{Y_p}} \text{ (Gavuzzi } et \, al. \text{ 1997);}$$

$$YSI = \frac{Y_s}{\overline{Y_p}} \text{ (Bouslama \& Schapaugh 1984);}$$

$$STI = \frac{Y_s \times Y_p}{\overline{Y_p}^2} \text{ (Gavuzzi } et \, al. \text{ 1997);}$$

$$HM = \frac{2(Y_s \times Y_p)}{(Y_s + Y_p)} \text{ (Rosielle \& Hamblin 1981).}$$

All calculations were done based on seed yield and average seed yield under stress and non-stress conditions. MLP model was combined with ANN in this experiment. The data set was randomly divided into three sets: training, testing, and validating sets, containing 95, 36, and 25 of the total data, respectively. The network was trained, tested and evaluated with the proposed method by Bagheri *et al.* (2012).

In its most basic form, weighted connections allow data to flow within the network between the layers so that a node accepts data from the preceding layer, and a weighted sum of all its net input is computed using the succeeding formula (Shearer *et al.* 2000):

$$t_i = \sum_{j=1}^{n} (W_{ij}X_j + b_i)$$

In this formula, X, n, W, and b_i are the input from node j, the number of inputs, the weight of communication between nodes i and j paths, and a bias, respectively. The weighted values, t_i, are then subjected to a transfer function to determine the output values (o_i).

The most typical activation or transfer equation in hidden and output layers are sigmoidal functions (Gholipoor *et al.* 2012):

$$f(t_i) = \frac{1}{1 + e^{-ti}}$$

Information is frequently transferred from the input layer to hidden layers using a linear transfer function (Kaul *et al.* 2005). Several indicators have been introduced in research papers to check the validity of a model. MSE and coefficient of determination (R^2), two of the most popular

indices, are calculated using the formula shown below (Keskin & Taylan 2009):

$$R^2 = \frac{\left(\sum_{i=1}^{n}(a_i - \bar{a})(p_i - \bar{p})\right)^2}{\sum_{i=1}^{n}(a_i - \bar{a})^2(p_i - \bar{p})^2} \quad [3]$$

$$MSE = \frac{\sum_{i=1}^{n}(ai - pi)^2}{n} \quad [4]$$

In the above formulas, a_i, p_i, $\bar{a}$, $\bar{p}$, and n are the the ith real output variable, ith forecasted output variable produced by model, the average of real variables, average of forecasted output variables, and the number of output variables, respectively

The importance of each predictor is calculated using a sensitivity analysis, which also determines the significance of the absolute variables. Afterwards, each predictor's importance and normalized importance (relative importance) are displayed in a table and a chart, respectively. The total error in the lack of a variable is divided by the entire network error in the existence of all the input variables to determine the values of the sensitivity (importance) factors for the input variables. Consequently, if the sensitivity of the input variable is greater than one, the output variable will be significantly affected. The total error in the absence of a variable is divided by the entire network error in the presence of all the input variables to determine the values of the sensitivity (importance) factors for the input variables. Consequently, if the sensitivity of the input variable is greater than one, the output variable will be significantly affected. By dividing the importance of every variable by the highest value of its importance, the relative importance of each variable is calculated. The model that has the lowest MSE and the highest R^2 is placed in the group of the best models. All statistical analyzes were performed in SPSS version 20 (SPSS. 2010).

3 Results and Discussion

The outcomes indicated that there is a significant difference between cultivars and the interaction effect of environment × variety (Table 1). Also, the correlation coefficient between Yp and Ys (Table 2) was not significant. These results show that the responses of cultivars are different in two environments and there is genetic diversity among the varieties.

These results showed that the selection of superior genotype with high performance in non-stress environment (Yp) does not always lead to the selection of genotypes with high performance in stress environment (Ys). These results were consistent with the results of Ravari *et al.* (2015); Isayenkov & Maathuis (2019); and Hosseini *et al.* (2012).

The outcomes of the index test indicated the significance of the difference of each index between the genotypes (Tables 3 and 4). Considering that GMP, MP, HM and STI indices had a positive and significant correlation with Yp and Ys (P < 0.01), therefore the selection according to the high quantity of the mentioned indices led to the selection of high-yielding cultivars such as Talaieh, Talaieh, T98007 and Ahmadi in both environments.

Table 1- Mean squares of 39 rapeseed varieties for grain yield in combined analysis of variance for Yp, first environment (design 1) and Ys, second environment (design 2)

Source of variation	df	MS
Environment (E)	1	7008.822**
Error 1 (R/E)	4	8.359
Genotype (G)	38	193.539**
Environment × Genotype (E × G)	38	19.018**
Error 2 (R × G/E)	152	0.192

Accordingly, these four indicators are used to separate cultivars belonging to group A (genotypes with similar good performance in stress and stress-free environments), group B (genotypes with good performance only in stress-free environments), group C (genotypes with performance good only in stress environments) and group D (genotypes with poor performance in both environments) (Fernandez 1992). These consequences are in accordance with the results published by Bchini *et al.* (2011) and Shokri-Gharelo *et al.* (2018). Henfy *et al.* (2003) reported that these four indices were suitable in research on sorghum.

The selected cultivars based on the discussed indices were introduced as salinity-sensitive cultivars despite the low YS,

and this is related to the inability of the two mentioned indicators to separate the varieties belonging to the two groups (A and C) from each other (Table 3).

These results are agreeing with the findings of Sio-Se Mardeh *et al.* (2006) and Talebi *et al.* (2009). The non-weighted paired group method with arithmetic average (UPGMA) and similarity matrix based on Euclidean distance measurement were used to perform the cluster analysis (Figure 1).

Table 2 Correlation coefficient between Yp, Ys and eight salt tolerance indices of rapeseed varieties based on grain yield

	YP	YS	TOL	MP	GMP	SSI	YI	STI	HM	YSI
YP	1									
YS	0.021ns	1								
TOL	0.78**	-0.84**	1							
MP	0.99**	0.99**	-0.91**	1						
GMP	0.99**	0.98**	-0.85**	0.99**	1					
SSI	0.68**	-0.79**	0.55**	-0.75**	-0.70**	1				
YI	0.06ns	0.99**	-0.56**	0.75**	0.703**	0.70**	1			
STI	0.97**	0.99**	-0.98**	0.98**	0.968**	-0.73**	0.76**	1		
HM	0.69**	0.999**	-0.76**	0.99**	0.991**	-0.85**	0.76**	0.99**	1	
YSI	-0.78**	1**	-0.94**	0.99**	0.98**	-0.77**	0.79**	0.99**	0.99**	1

The outcome showed that the studied cultivars were grouped into four class: sensitive (S), semi-sensitive (MS), moderately tolerant (MT), and tolerant (T). The results of step-by-step regression analysis (Table 5) among salinity indices and genotype reactions to salinity including sensitive, semi-sensitive, semi-tolerant, and tolerant as independent variables and dependent variables, respectively, show that YSI in the first stage entered into the equation ($R^2 = 0.92$).

GMP entered to the equation in the second stage with ($R^2 = 0.91$).

The following steps involved entering the parameters SSI, MP, STI, TOL, and HM into the equation, with R^2 values of 0.91, 0.90, 0.91, 0.9, and 0.9, respectively. Additionally, the yield index (YI) was left out of the calculation.

Table 3 Mean grain yield and indices of 39 rapeseed varieties under stress and non-stress conditions (data sorted by Ys−Yp)

G.N.D	Name	YP	Ys	TOL	MP	GMP	SSI	YI	YSI	STI	HM	Ys-Yp
3	Zarfam	2285	3967	1682	3126	3010.7	-1.66	1.736	1.376	1.09	2899.74	1682
4	Zafar	2500	3402	-902	2951	2916.3	-0.81	1.361	1.18	1.02	2882.07	902
1	Talaieh	3001	3685	-684	3343	3325.5	-0.51	1.228	1.278	1.33	3308.01	684
2	Sarigol	2758	3375	-617	3066.5	3050.9	-0.5	1.224	1.171	1.12	3035.46	617
5	Delgan	1968	2408	-440	2188	2176.9	-0.5	1.224	0.835	0.57	2165.88	440
6	Ahmadi	2947	3386	-439	3166.5	3158.9	-0.34	1.149	1.174	1.2	3151.28	439
8	Hyola60	2873	3224	-351	3048.5	3043.4	-0.28	1.122	1.118	1.11	3038.4	351
9	PP4010	2850	3198	-348	3024	3019	-0.27	1.122	1.109	1.1	3013.99	348
7	Hyola401	3011	3307	-296	3159	3155.5	-0.22	1.098	1.147	1.2	3152.07	296
10	T98007	2990	3260	-270	3125	3122.1	-0.2	1.09	1.131	1.17	3119.17	270
11	Talaye	3866	4122	-256	3994	3991.9	-0.15	1.066	1.43	1.92	3989.9	256
14	Moderna	2879	2967	-88	2923	2922.7	-0.07	1.031	1.029	1.03	2922.34	88
15	Opera	950	955	-5	952.5	952.5	-0.01	1.005	0.331	0.11	952.493	5
12	Slm046	2271	2256	15	2263.5	2263.5	0.015	0.993	0.782	0.62	2263.48	-15
13	Geranimo	2590	2382	208	2486	2483.8	0.181	0.92	0.826	0.74	2481.65	-208
22	Orient	281	150	131	215.5	205.3	1.05	0.534	0.052	0.01	195.592	-131
23	Option50	2856	2454	402	2655	2647.4	0.317	0.859	0.851	0.84	2639.78	-402
24	H-19	2844	2322	522	2583	2569.8	0.413	0.816	0.805	0.79	2556.63	-522
17	Ks-11	886	342	544	614	550.47	1.382	0.386	0.119	0.04	493.505	-544
18	Colvert	2266	1202	1064	1734	1650.4	1.057	0.53	0.417	0.33	1570.78	-1064
16	Symbol	2743	1383	1360	2063	1947.7	1.116	0.504	0.48	0.46	1838.86	-1360
19	Ks-7	2972	1474	1498	2223	2093	1.135	0.496	0.511	0.53	1970.64	-1498
20	Okapi	2777	1156	1621	1966.5	1791.7	1.314	0.416	0.401	0.39	1632.45	-1621
21	Licord	2544	902	1642	1723	1514.8	1.453	0.355	0.313	0.28	1331.8	-1642
34	Spn185	2820	1153	1667	1986.5	1803.2	1.331	0.409	0.4	0.39	1636.78	-1667
35	Spn192	2843	1153	1690	1998	1810.5	1.338	0.406	0.4	0.39	1640.63	-1690
32	Spn183	2805	1003	1802	1904	1677.3	1.446	0.358	0.348	0.34	1477.63	-1802
33	Spn184	2973	1158	1815	2065.5	1855.5	1.374	0.39	0.402	0.41	1666.78	-1815
36	Spn193	2975	921	2054	1948	1655.3	1.554	0.31	0.319	0.33	1406.56	-2054
37	Spn194	2770	623	2147	1696.5	1313.7	1.745	0.225	0.216	0.21	1017.22	-2147
38	Rgs003	2975	779	2196	1877	1522.3	1.662	0.262	0.27	0.28	1234.7	-2196
39	Dalgon	3930	1543	2387	2736.5	2462.5	1.367	0.393	0.535	0.73	2215.97	-2387
27	San-12	2577	35	2542	1306	300.32	2.221	0.014	0.012	0.01	69.062	-2542
28	Spn178	4196	1621	2575	2908.5	2608	1.382	0.386	0.562	0.82	2338.56	-2575
25	Shiralee	2850	83	2767	1466.5	486.36	2.186	0.029	0.029	0.03	161.302	-2767
26	San-14	4151	1348	2803	2749.5	2365.5	1.52	0.325	0.468	0.67	2035.11	-2803
29	Spn179	3007	37	2970	1522	333.56	2.224	0.012	0.013	0.01	73.1005	-2970
30	Spn181	4196	1621	2575	2908.5	2608	1.382	0.386	0.562	0.82	2338.56	-2575
31	Spn182	2850	83	2767	1466.5	486.36	2.186	0.029	0.029	0.03	161.302	-2767

*Group Number in Dendogram

**Table 4** Mean squares of eight tolerance indices for grain yield

S.O.V	df	TOL	MP	GMP	SSI	YI	YSI	STI	HM
Replication	2	4.5**	7.34**	6.33**	0.0001ns	0.0001ns	0.0001ns	0.008*	5.48*
Variation	38	38.3**	96.7**	88. 7**	0.014**	0.004**	0.1218	0.48**	80.7**
Error	76	0.373	0.099	0.80	0.001	0.0003	0.001	0.001	0.081
CV%		12.25	8.3	7.32	17.82	12.46	15.8	13.11	8.9

Table 5 Stepwise linear regression equations

Steps	Indices Entered	Equations	R^2
1	X1(YSI)	$Y=-0.434 + 0.345X_1$	0.92
2	X2(GMP)	$Y=0.478 +0.35X1 + 0.45X2$	0.89
3	X3(SSI)	$Y=0.551 + 0.446X1 + 0.47X2 + 0.43X3$	0..88
4	X4(MP)	$Y=0.5862 + 0.38X1 + 0.53X2 + 0.41X3 + 0.54X4$	0.88
5	X5(STI)	$Y=0.64234 + 0.49X1 + 0.57X2 + 0.35X3 + 0.49X4 + 0.43X5$	0.89
6	X6(TOL)	$Y=0.69021 + 0.476X1 + 0.54X2 + 0.42X3 + 0.48X4 + 0.39X5 + 0.21X6$	0.85
7	X7(HM)	$Y=0.6742 + 0.31X1 + 0.57X2 + 0.41X3 + 0.52X4 + 0.37X5 + 0.18X6 + 0.19X7$	0.88

YI was not entered in the equation;(regression calculations were made using average data)

Figure 1 Dendrogram on the basis of the UPGMA method for tolerance indices of grain yield in 39 rapeseed varieties
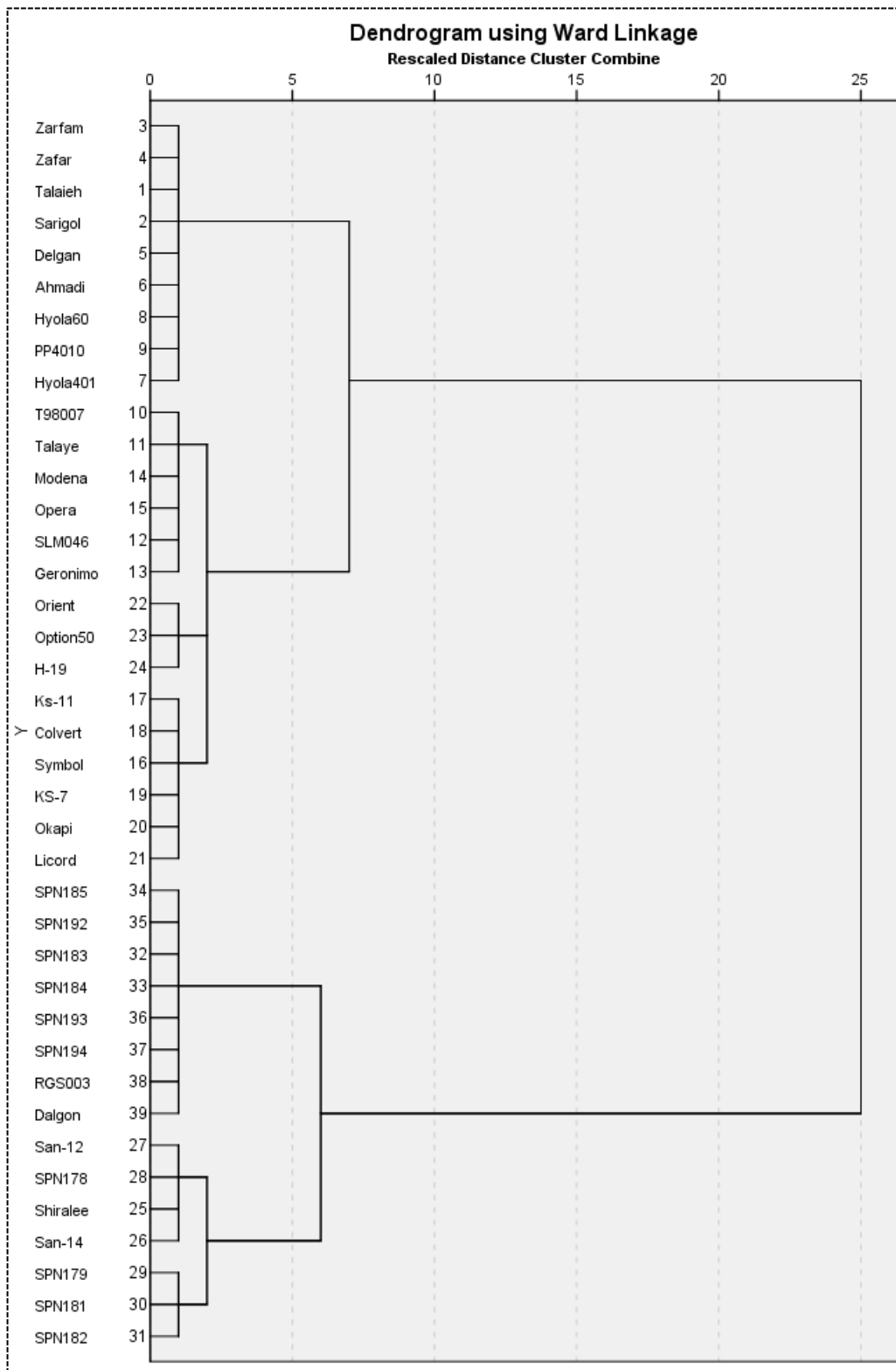

The input layer in the ANN analysis had eight neurons that represented eight indicators related to salinity, and the output layer had one neuron representing the response of genotypes to salinity (Figure 2).

The neurons's number in the hidden layer was determined through a process of trial-and-error, which started with one and then increased sequentially. At this stage, the learning rate, the number of learning round (or "epochs"), and the momentum were constant at 0.8, 10000, and 0.6, respectively.

Figure 2 The schematic structure of multilayer-perceptron neural networks model.
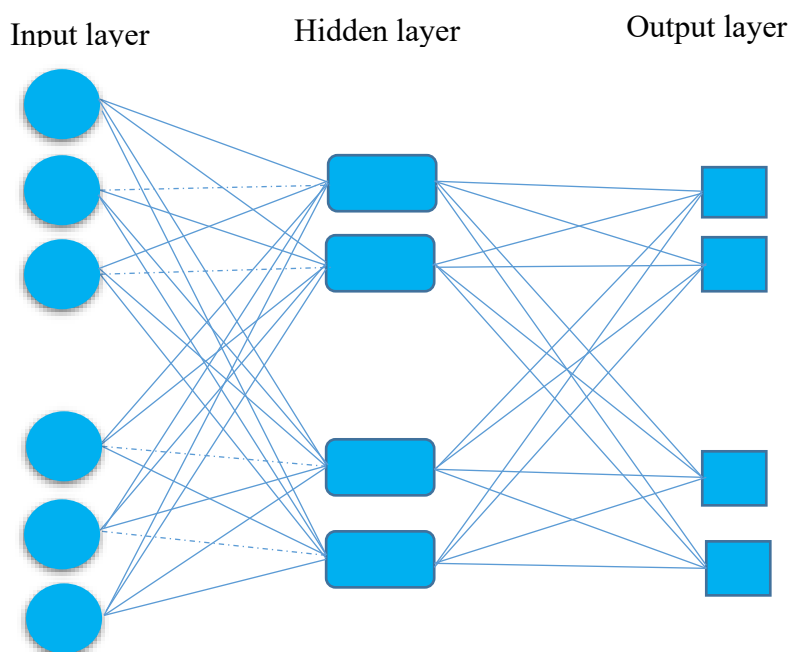
The momentum is a tuning parameter to avoid inconstancy arising from a high learning rate. The network's training process speed is governed by learning rate and for faster training network it will be between 0 and 1. The number must be greater than zero, represent the maximum number of epochs (p) or sources (data transferred from training sample) that can be used to bring the initial learning rate down to the lower boundary. Training stops if the number of epochs exceeds the maximum number allowed. These three network evaluation parameters were determined based on the research done by Bagheri et al (2012). This operation will be successively repeated several times on the training data set to ensure the correct performance of the network. According to a review of the network's performance, its execution tended to get better as the hidden layer's number of neurons was raised to the ideal level (Table 6).

In this experiment, the learning phase's MSE curve was lower than the validating phase, indicating accurate training. The two curves' close proximity to one another revealed that 0.0054 was the best MSE value (Table 7; Figure 3).

Table 6 Error variations with different number of neurons in the training, testing and validating phases

No. of Neurons Hidden	Validating		Testing		Training	
Layer	R^2	MSE	R^2	MSE	R^2	MSE
2	0.742	3.1320478	0.421	2.320405	0.731	3.3951033
3	0.783	2.2306459	0.582	1.764093	0.782	2.879032
4	0.888	1.0056124	0.734	0.72145	0811	1.093418
5	0.945	0.4521126	0.789	0.478089	0.838	0.790541
6	0.959	0.00842160	0.812	0.05621	0.879	0.0034861
7	**0.980**	**0.0002183**	**0.849**	**0.00312**	**0.895**	**0.00085967**
8	0.963	0.00064034	0.831	0.00682	0.893	0.0005782
9	0.969	0.00437512	0.801	0.0090523	0.874	0.000305
10	0.972	0.00120548	0.798	0.083701	0.831	0.000222

The bold values show the optimum number of neurons in hidden layer and the best training steps that established minimum error, respectively.

Eight neurons were selected in the 18th training step of an experienced network with a hidden layer. The proximity of R^2 values, 0.969 and 0.977, respectively, in the training and testing phase indicated the correct training of the ANN and the good performance of the network in determining the reaction of varieties to salinity according to the relevant indicators (Figure 4).

Similar outcomes were reported by Bagheri *et al.* (2012) for the prediction of silage maize yield; they noted that their model's best validation performance occurred at step 10 with an MSE of 0.0032. The high R^2 of 0.98 between the

calculated and actual dry yields demonstrated the effectiveness and superiority of the planned network.

According to the ANN outcomes, the YSI index (140.6) was discovered to be crucial in identifying salt-tolerant varieties (Figure5).

**Table 7** MSE values at different training steps of the network

Training Steps	MSE		
	Validating	Testing	Training
2	4.321	4.515	3.793
4	2.869	3.021	2.439
6	1.309	1.068	0.931
8	0.672	0.421	0.556
10	0.0831	0.058	0.234
12	0.015	0.024	0.015
14	0.0069	0.007	0.008
16	0.0073	0.0041	0.0053
18	**0.0071**	**0.0043**	**0.0051**
20	0.0098	0.0056	0.0049
22	0.0091	0.0068	0.0069
24	0.0085	0.0059	0.06

The bold values show the optimum number of neurons in hidden layer and the best training steps that established minimum error, respectively

This index demonstrated a significant (P= 0.01) negative and positive correlation with Yp and Ys, respectively. The cultivars that were selected based on high values of this index had high performance under stressful conditions, but their performance may be low in a non-stress environment. Even though choosing tolerant varieties won't lower Ys, selection based on this index is appropriate. The following parameters, in order of importance, were indices listed in figure 5, respectively.

Figure 3 Change in the mean square error during the training steps
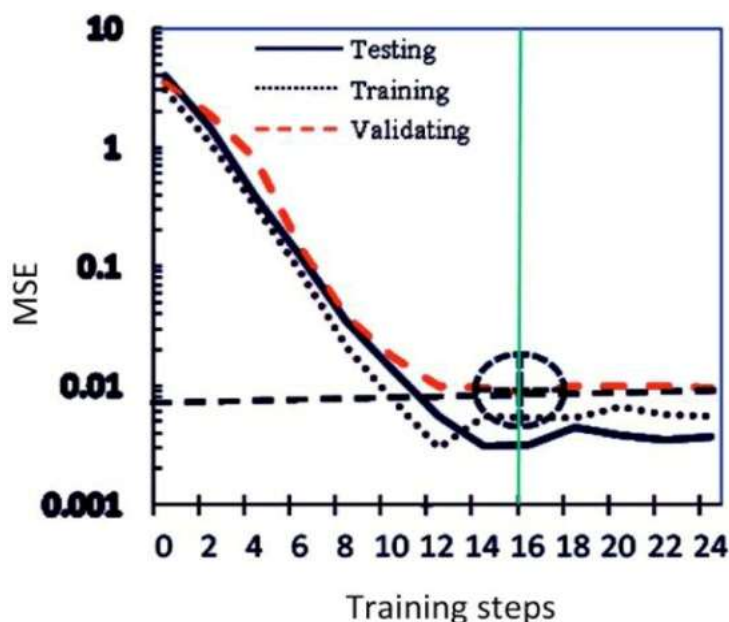
According to the findings of ANOVA, regression, and neural networks, the best indicators that can distinguish group A varieties from other groups are the first four indicators according to figure 5. The evaluation overall findings demonstrated that these four indices are appropriate for choosing genotypes tolerant to salinity.

Figure 4 Predicted values of tolerance by MLP neural network versus observed values in testing (left) and training (right) phases
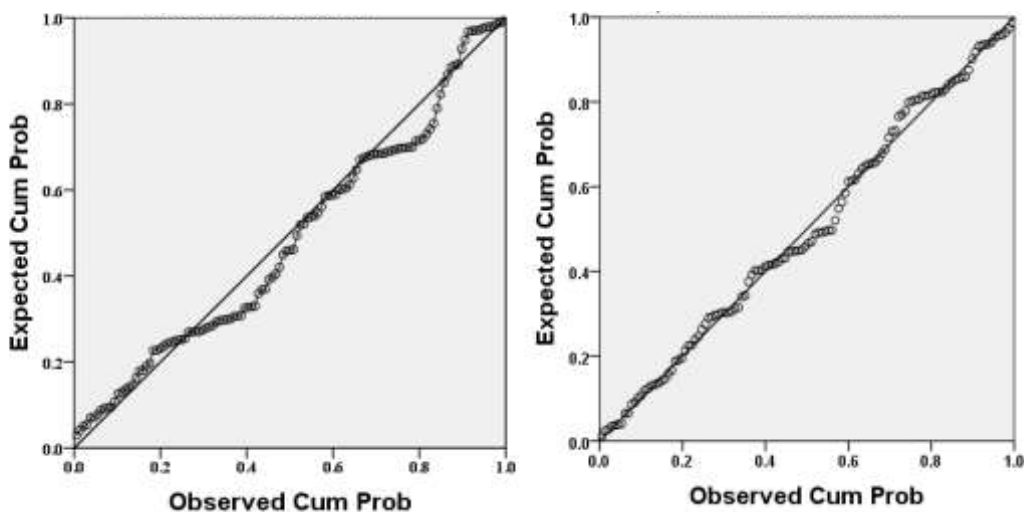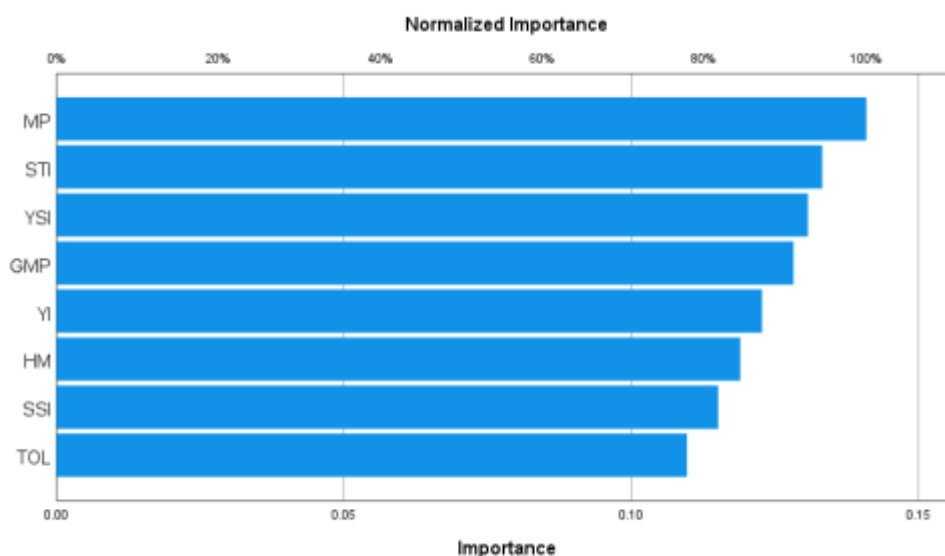

Figure 5 The relative importance of the effective parameters in determining salt-tolerant varieties

4: Conclusions

Finally, it should be noted that further experiments using other genotypes at different stress levels (more than two) would be useful to more accurately evaluate the salinity tolerance of different canola cultivars. What is important about the ANN is to know that this method is a useful manner for predicting the tolerance of agricultural and gardening plants to various stresses quickly, cheaply, accurately and objectively. However, the results of this article provide valid evidence that it is possible to carefully select plants that tolerate different biotic and abiotic stresses by using artificial neural networks, and it is also valuable to use this method in different fields of agriculture.

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