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**Research Article**

# Evaluation of salt tolerance indices in contrast to rice (*Oryza sativa* L.) cultivars and mutants

**Farhad Bagheri[1], Hemmatollah Pirdashti*[2], Gorban Ali Nematzadeh[3], Yasser Yaghoubian[1]**

**[1] Department of Agronomy, Sari Agricultural Sciences and Natural Resources University, Sari, Iran**
**[2] Department of Agronomy, Genetics and Agricultural Biotechnology Institute of Tabarestan, Sari Agricultural Sciences and Natural Resources University, Sari, Iran**
**[3] Genetics and Agricultural Biotechnology Institute of Tabarestan, Sari Agricultural Sciences and Natural Resources University, Sari, Iran**
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## Abstract

**Salinity is one of the most important and widespread abiotic stresses that limit the growth of crops and productivity. To evaluate the yield and salt tolerance indices in contrast rice genotypes, a factorial experiment was conducted based on a randomized complete block design with three replications in 2022. The treatments included three levels of salinity stress (control, 4 and 8 dS.m$^{-1}$) and 17 genotypes, including two sensitive and two tolerant check cultivars and 13 advanced (M10) mutant lines. Also, the investigated traits in this study were stress tolerance index (STI), stress susceptibility index (SSI), tolerance index (TOL), geometric mean productivity (GMP), mean productivity index (MP), and harmonic mean (HM) along with rice paddy yield (PY) in both normal and salt stress conditions. The results showed that salinity stress at both levels of 4 and 8 dS.m$^{-1}$ markedly reduced PY in all the studied genotypes. The lowest values of STI (0.04) and TOL (-11.79) were recorded in IR29 and Deilamani cultivars, respectively. When the cultivars were grown at 4 dS.m$^{-1}$ of salt stress, the MP10 genotype was superior in terms of GMP (1.32), MP (16.83), and HM (16.05) indices. By comparison, at salinity stress of 8 dS.m$^{-1}$ the highest values for GMP, MP and HM indices were obtained in the MP10, MP6 and MP10 genotypes with 1.21, 8.32 and 5.42, respectively. Cluster analysis at salinity levels of 4 and 8 dS.m$^{-1}$ showed that the studied mutants have a significant variation in stress tolerance indices. The MP10 mutant line achieved the highest PY, which was close to the Deilamani tolerant check cultivar when grown at under 8 dS.m$^{-1}$ of salinity stress. Also, this promising line recorded the highest value of tolerance indices in both salinity levels of 4 and 8 dS.m$^{-1}$. Therefore, the advanced mutant line of MP10 could be recommended for further research on salinity stress tolerance mechanisms.**

**Keywords: Mutant, Rice, Salinity stress, Tolerance indices**

## Introduction

The stress caused by the salinity of soil and water is one of the most important abiotic stresses in agricultural systems that exist in wide areas of the world (Ahmad *et al*., 2018; Hosseini *et al*., 2019; Hosseini *et al*., 2020; Khalvandi *et al*., 2019). Around 340 to 900 million hectares of land are faced with salinity worldwide. Also, many parts of Iran have the problem of salinity and drainage. Almost 20% of the total area of Iran, totaling 25 million hectares, is adversely affected by different degrees of salinity (FAO, 2007; Munns, 2002). Salinity has significantly affected plants through ionic toxicity, osmotic stress, imbalance of nutrients, and extensive changes in the synthesis of biochemical compounds (Abdel Latef *et al*., 2021; Khan, 2018). Also, salinity leads to a consequence series of morphological, physiological, biochemical, and molecular changes that hurt the growth and plant productivity (Ghonaim *et al*., 2021; Munns, 2002; Munns *et al*., 2020).

95% of the rice (*Oryza sativa* L.) is now cultivated in the two provinces of Mazandaran and Gilan (Jafari Rad *et al*., 2014). The statistics show that between 200 and 300 thousand hectares of rice fields in Guilan, Mazandaran, and Golestan provinces are threatened by salinity (Mirdar Mansouri, 2012). Among different solutions, rice plant improvement can be more promising and significant compared to other soil improvement processes. By introducing salt-tolerant rice cultivars and identifying effective traits, millions of hectares of saline and non-cultivable land can be

*Corresponding Author, Email: h.pirdashti@sanru.ac.ir

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properly exploited (Kibria *et al*., 2017). Studies have shown that the rice plant is tolerant to salinity during the germination stage but shows the highest sensitivity to salinity during the seedling and flowering stages (Hussain *et al*., 2017). Therefore, it is necessary to identify and introduce salt-tolerant lines using different breeding approaches.

Mutation breeding is a shortcut method to improve many important agricultural traits, such as tolerance to abiotic stresses, resistance to diseases, improved quality, and marketability (Negrao *et al*., 2017). Therefore, mutation induction is an important method to increase the mutant frequency (Da Luz *et al*., 2016; Majidi and Amiri Fahliani, 2016). More than 3402 mutant varieties have been introduced worldwide, of which 64% have been improved by gamma rays (Musavizadeh *et al*., 2018). Oladi *et al*. (2014) used the International Rice Research Institute (IRRI) standard to evaluate 42 rice mutant lines with Sang-e-Tarom, Nemat, and Hashemi in soil with a salinity of 7 $dS.m^{-1}$. Cluster analysis classified 35% of the lines in the tolerant group, 57% in the moderate tolerance group, and 8% in the sensitive group. Meanwhile, stress resistance indices are also used to check the response of different cultivars to salinity stress (Hossain *et al*., 1990). Selection based on the stress susceptibility index (SSI) often resulted in selecting genotypes with relatively low performance under normal conditions and high performance under stress conditions (Farshadfar and Sutka, 2003). In general, cultivars with SSI greater than one are considered sensitive. Rosielle and Hamblin (1981) introduced the tolerance index (TOL) and mean productivity (MP). Then, stress tolerance indices (STI) and geometric mean productivity (GMP) were proposed by Fernandez (1992) to identify genotypes that produce optimal yield under both normal and stressful conditions. Fernandez (1992) introduced the STI as a suitable index to distinguish genotypes to achieve high performance under stress conditions. Accordingly, GMP and STI indicators were introduced as the best indicators and the most suitable rice genotypes (Erfani *et al*., 2012). Also, Asadi *et al*. (2012) introduced STI and GMP as the most appropriate criteria for determining wheat tolerance and achieving higher yields in both saline and non-saline conditions. Various studies applied salinity tolerance indices and the correlation between them to select the salt-tolerant cultivars (e.g., Jafari Rad *et al*., 2014; Mirdar Mansori *et al*., 2011). Since these mutant lines were improved in a breeding program for tolerance to salinity (Oladi *et al*., 2020), the purpose of the present research is to evaluate the performance of the advanced generation of rice mutant lines (M10) to salt stress conditions using various tolerance indices.

## Materials and methods

The current research was carried out as a factorial experiment based on a randomized complete block design with three replications at the Genetics and Agricultural Biotechnology Institute of Tabarestan (GABIT) located in the Sari Agricultural Sciences and Natural Resources University (SANRU) in 2022. In this experiment, 17 rice genotypes including 13 advanced mutant lines (M10 generation), were used which had been obtained by gamma-ray irradiation from Cobalt spring 60 from Sang-e-Tarom (P1), Hashemi (P3) and Khazar (P18) varieties (Oladi *et al*., 2019), (Table 1). Two international (IR29) and naive (Sepidrood) sensitive controls were also used along with two international (Nonabukra) and native (Deylamani) tolerant controls. Salinity stress using NaCl solutions was imposed at three levels including control (no salinity stress) and 4 and 8 $dS.m^{-1}$.

First, the genotype seeds were disinfected with fungicide and then transferred to the germinator. The seeds were kept in the dark for 48 hours at a temperature of 25 C until they germinated. Then the germinated seeds were exposed to the optimum light for initial growth and, after that, planted in a seed tray filled with paddy soil. Seedlings with three leaves (BBCH: 13) from each genotype were transferred to the pots with a capacity of seven kilograms of soil (with an opening diameter of 26 cm and a height of 24 cm) and planted at a distance of 20×20 cm. After the establishment of the plants (about a week after transplanting), saline treatments will be applied. The amount of NaCl needed to apply each of the salinity levels will be calculated using Equation 1 (Hasheminia *et al*., 1997).

$$TDS = 0.6\ EC$$

Where EC is electrical conductivity and TDS is total dissolved solids.

At the time of fully ripening (BBCH: 89), the PY was determined in terms of grams per plant based on the IRRI standard (SES, 2013) in the stress (Ys) and normal or potential (Yp) conditions. After harvesting, tolerance indices to salinity stress (Table 2) were calculated using the Yp and Ys and the average yield of all genotypes in non-stressed ($\bar{Y}p$) and stressed conditions ($\bar{Y}s$).

Finally, the data obtained from the experiment were analyzed with SAS statistical software version 9.2, and the correlation coefficient and cluster analysis (Ward method) between indicators were calculated with SPSS software version 16. Duncan's multiple range test ($\alpha$=0.05) was used to compare the mean yields of genotypes in different treatments.

## Results and discussion

The results of ANOVA related to all studied indices in different rice genotypes under salinity stress are shown in Table 3. Based on the obtained results, it was observed that the simple effect of salinity and genotype, as well as their interaction effect, was highly significant for all tolerance indices. Similarly, Afkhami *et al*. (2021) showed a considerable difference between rice genotypes when grown at both 4 and 8 $dS.m^{-1}$ of salinity. Also, Izaddoost *et al*. (2013) and Sabouri *et al*. (2008) reported a significant difference among

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**Table 1. The list of studied mutants along with native and international sensitive and tolerant controls**

| Row | Lines code | Abbreviated line code | Row | Lines code | Abbreviated line code |
|---|---|---|---|---|---|
| 1 | M10-P1-1-1-1-4-1 | MP1 | 10 | M10-P3-4-7-1-1-1 | MP10 |
| 2 | M10-P1-4-2-1-2-1 | MP2 | 11 | M10-P18-1-4-2-1-1-1 | MP11 |
| 3 | M10-P1-7-1-1-1-1 | MP3 | 12 | M10-P18-1-4-3-3-1-1-1 | MP12 |
| 4 | M10-P1-7-1-1-2-1 | MP4 | 13 | M10-P18-1-7-3-4-2-1-1 | MP13 |
| 5 | M10-P3-4-4-6-1-1 | MP5 | 14 | Nonabukra (International tolerant control) | Nonabukra |
| 6 | M10-P3-4-4-7-1-1 | MP6 | 15 | Sepidrood (Native sensitive control) | Sepidrood |
| 7 | M10-P3-4-4-7-1-2 | MP7 | 16 | Deilamani (Native tolerant control) | Deilamani |
| 8 | M10-P3-4-4-10-11 | MP8 | 17 | IR29 (International sensitive control) | IR29 |
| 9 | M10-P3-4-5-7-1-1 | MP9 | | | |

**M = Mutant, P1 = Sang-e Tarom, P3 = Hashemi, P18 = Khazar**

**Table 2. The calculated tolerance indices used in the experiment**

| Row | Index name | Abbreviations | Relation | References |
|---|---|---|---|---|
| 1 | Stress Tolerance Index | STI | $STI = \frac{YP \times YS}{(\overline{YP})^2}$ | Fernandez (1992) |
| 2 | Stress Susceptibility Index | SSI | $SSI = \frac{1 - \frac{YS}{YP}}{1 - \frac{\overline{YS}}{\overline{YP}}}$ | Fisher and Maurer (1978) |
| 3 | Tolerance Index | TOL | $TOL = YP - YS$ | Rosiel and Hamblin (1981) |
| 4 | Geometric mean productivity | GMP | $GMP = \sqrt{YS \times YP}$ | Fernandez (1992) |
| 5 | Mean productivity index | MP | $MP = \frac{YP + YS}{2}$ | Rosiel and Hamblin (1981) |
| 6 | Harmonic mean | HM | $HM = \frac{2(YP \times YS)}{YP + YS}$ | Fernandez (1992) |

**Table 3. Variance analysis of the salinity effect on salt tolerance indices at different rice genotypes**

| Source of Variation | df | STI | SSI | TOL | GMP | MP | HM |
|---|---|---|---|---|---|---|---|
| Replication | 2 | 0.00563 | 0.0338 | 0.08237 | 0.00010 | 0.4560 | 1.0680 |
| Salinity (S) | 1 | 40.478** | 896.797** | 2403.701** | 0.354** | 600.925** | 21633.31** |
| Genotypes (G) | 16 | 2.395** | 23.940** | 104.603** | 0.0269** | 68.107** | 666.66** |
| S×G | 16 | 1.5637** | 30.4965** | 49.207** | 0.00149** | 12.301** | 442.865** |
| Error | 66 | 0.00014 | 0.00971 | 0.00174 | 1.480 | 0.00043 | 0.015730 |
| CV (%) | - | 1.48 | 2.66 | 1.66 | 0.10 | 0.27 | 0.60 |

****: Significant at 1% levels**

**Stress tolerance index (STI), stress susceptibility index (SSI), tolerance index (TOL), geometric mean productivity (GMP), mean productivity index (MP), and harmonic mean**

genotypes regarding various indices.

The results of the average comparison between the studied different genotypes based on STI, SSI, TOL, GMP, MP, and HMP indices under the salinity stress of 4 dS.m$^{-1}$ have been shown in Table 4. The highest value for the STI (3.5) was obtained for the MP10 genotype, while the lowest value (0.04) was obtained for the IR29 cultivar. Also, two genotypes of MP11 and MP8, which had the lowest values of stress susceptibility index (SSI), respectively, are among the tolerant cultivars. According to this index, the sensitive and tolerant genotypes can be determined regardless of their performance potential (Fischer and Maurer, 1978). Also, the lowest stress tolerance index (TOL), whose low values indicate the relative tolerance of cultivars, was related to Deilamani cultivar with -11.79. The highest values for GMP and MP indices were obtained in the MP10 genotype, with 1.32 and 16.83, respectively. Selection based on the MP index allows the choice of genotypes with high potential yield (Fernandez, 1992). Based on the comparison results, the highest amount of HM (16.05) was related to the MP10 genotype, and the lowest amount (1.72) was recorded in the IR29 genotype. Since the high numerical values of MP, GMP, STI, and HM indices indicate relative tolerance to stress (Table 4), the MP10 line has the highest value in all these indices. This line can be introduced as a tolerant line in salinity of 4 dS.m$^{-1}$. Aminpanah *et al*. (2018) also selected the STI, MP, GMP, and HM as the best indices and used them to introduce stress-tolerant genotypes with high yield under both stress and non-stress conditions.

The results of the average comparison between the different studied genotypes based on STI, SSI, TOL, GMP, MP, and HMP indices under the salinity stress of 8 dS.m$^{-1}$ are shown in Table 5. The average comparison

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**Table 4. Mean comparison of salt tolerance indices for different rice genotypes at salt stress of 4 dS m$^{-1}$**

| Genotypes | Tolerance Indices | | | | | |
|---|---|---|---|---|---|---|
| | STI | SSI | TOL | GMP | MP | HM |
| MP1 | 1.03 h | 4.72 $^{g}$ | 0.06 $^{h}$ | 1.24 $^{g}$ | 8.93 $^{j}$ | 8.93 $^{h}$ |
| MP2 | 1.01 $^{i}$ | 4.42 $^{h}$ | 0.79 $^{e}$ | 1.24 $^{g}$ | 8.79 $^{k}$ | 8.77 $^{i}$ |
| MP3 | 2.26 f | 8.70 $^{c}$ | -9.72 $^{P}$ | 1.29 $^{e}$ | 14.08 $^{d}$ | 12.40 $^{e}$ |
| MP4 | 3.14 b | 6.79 $^{e}$ | -6.82 $^{l}$ | 1.31 $^{b}$ | 15.93 $^{b}$ | 15.20 $^{b}$ |
| MP5 | 0.26 $^{m}$ | 8.78 $^{c}$ | -3.35 $^{j}$ | 1.16 $^{k}$ | 4.79 $^{o}$ | 4.20 $^{m}$ |
| MP6 | 2.51 d | 4.26 $^{h}$ | 1.94 $^{d}$ | 1.30 $^{d}$ | 13.97 $^{e}$ | 13.90 $^{c}$ |
| MP7 | 1.79 $^{g}$ | 4.65 $^{g}$ | 0.31 $^{g}$ | 1.27 $^{f}$ | 11.75 $^{h}$ | 11.75 $^{f}$ |
| MP8 | 0.08 $^{n}$ | 1.98 $^{k}$ | 3.64 $^{b}$ | 1.09 $^{l}$ | 3.12 $^{p}$ | 2.05 $^{o}$ |
| MP9 | 2.64 c | 7.10 $^{d}$ | -7.02 $^{m}$ | 1.30 $^{c}$ | 14.70 $^{c}$ | 13.87 $^{c}$ |
| MP10 | 3.50 $^{a}$ | 6.80 $^{e}$ | -7.23 $^{n}$ | 1.32 $^{a}$ | 16.83 $^{a}$ | 16.05 $^{a}$ |
| MP11 | 0.48 $^{k}$ | 1.81 $^{k}$ | 10.25 $^{a}$ | 1.19 $^{i}$ | 7.97 $^{l}$ | 4.68 $^{l}$ |
| MP12 | 1.78 $^{g}$ | 3.91 $^{i}$ | 2.94 $^{c}$ | 1.27 $^{f}$ | 11.82 $^{g}$ | 11.63 $^{g}$ |
| MP13 | 0.27 $^{m}$ | 17.49 $^{a}$ | -7.41 $^{o}$ | 1.16 $^{k}$ | 5.89 $^{m}$ | 3.55 $^{n}$ |
| Nonabukra | 0.35 $^{l}$ | 5.87 $^{f}$ | -1.37 $^{i}$ | 1.17 $^{j}$ | 5.26 $^{n}$ | 5.17 $^{k}$ |
| Sepidrood | 2.30 $^{e}$ | 6.74 $^{e}$ | -5.73 $^{k}$ | 1.29 $^{e}$ | 13.63 $^{f}$ | 13.03 $^{d}$ |
| Deilamani | 0.83 $^{j}$ | 15.66 $^{b}$ | -11.79 $^{q}$ | 1.23 $^{h}$ | 9.95 $^{i}$ | 6.45 $^{j}$ |
| IR29 | 0.04 $^{o}$ | 3.53 $^{j}$ | 0.69 $^{f}$ | 1.05 $^{m}$ | 1.79 $^{q}$ | 1.72 $^{p}$ |

**In each column, means with similar letters were not significantly different (P≤ 0.05).**

**Table 5. Mean comparison of salt tolerance indices for rice genotypes at salt stress of 8 dS.m$^{-1}$**

| Genotypes | STI | SSI | TOL | GMP | MP | HM |
|---|---|---|---|---|---|---|
| MP1 | 0.13 j | 0.84 $^{ef}$ | 7.85 $^{j}$ | 1.12 $^{h}$ | 5.04 $^{i}$ | 2.00 $^{i}$ |
| MP2 | 0.13 $^{j}$ | 0.85 $^{de}$ | 8.04 $^{i}$ | 1.12 $^{h}$ | 5.13 $^{h}$ | 1.99 $^{i}$ |
| MP3 | 0.15 $^{h}$ | 0.83 $^{g}$ | 8.02 $^{i}$ | 1.13 $^{g}$ | 5.22 $^{g}$ | 2.23 $^{g}$ |
| MP4 | 0.18 $^{g}$ | 0.89 $^{b}$ | 11.50 $^{d}$ | 1.14 $^{f}$ | 6.78 $^{cd}$ | 2.04 $^{h}$ |
| MP5 | 0.04 $^{l}$ | 0.59 $^{k}$ | 2.21 $^{m}$ | 1.06 $^{k}$ | 2.05 $^{m}$ | 1.58 $^{l}$ |
| MP6 | 0.32 $^{c}$ | 0.86 $^{d}$ | 13.25 $^{a}$ | 1.17 $^{b}$ | 8.28 $^{a}$ | 3.04 $^{d}$ |
| MP7 | 0.14 $^{i}$ | 0.90 $^{b}$ | 10.95 $^{e}$ | 1.12 $^{g}$ | 6.45 $^{e}$ | 1.78 $^{k}$ |
| MP8 | 0.02 $^{n}$ | 0.90 $^{b}$ | 4.53 $^{k}$ | 1.03 $^{m}$ | 2.67 $^{k}$ | 0.76 $^{o}$ |
| MP9 | 0.33 $^{b}$ | 0.75 $^{i}$ | 8.89 $^{h}$ | 1.17 $^{b}$ | 6.74 $^{d}$ | 3.83 $^{c}$ |
| MP10 | 0.58 $^{a}$ | 0.69 $^{j}$ | 9.80 $^{f}$ | 1.21 $^{a}$ | 8.27 $^{a}$ | 5.42 $^{a}$ |
| MP11 | 0.09 $^{k}$ | 0.94 $^{a}$ | 12.5 b | 1.10 $^{i}$ | 6.83 c | 1.08 $^{m}$ |
| MP12 | 0.23 $^{d}$ | 0.87 $^{c}$ | 11.87 $^{c}$ | 1.15 $^{c}$ | 7.36 $^{b}$ | 2.47 $^{f}$ |
| MP13 | 0.04 $^{l}$ | 0.12 $^{l}$ | 0.55 $^{o}$ | 1.06 $^{j}$ | 1.86 $^{n}$ | 1.84 $^{j}$ |
| Nonabukra | 0.03 $^{m}$ | 0.84 $^{ef}$ | 3.99 $^{l}$ | 1.05 $^{l}$ | 2.55 $^{l}$ | 1.03 $^{n}$ |
| Sepidrood | 0.20 $^{e}$ | 0.83 $^{fg}$ | 9.25 $^{g}$ | 1.14 $^{d}$ | 6.16 $^{f}$ | 2.57 $^{e}$ |
| Deilamani | 0.19 $^{f}$ | -0.07 $^{m}$ | 0.35 $^{p}$ | 1.14 $^{e}$ | 3.85 j | 3.84 $^{b}$ |
| IR29 | 0.01 $^{o}$ | 0.76 $^{h}$ | 1.75 $^{n}$ | 0.99 $^{n}$ | 1.24 $^{o}$ | 0.69 $^{p}$ |

**In each column, means with similar letters were not significantly different test (P≤ 0.05).**

results showed that the highest value of STI was obtained for genotype MP10 and the lowest for IR29 with 0.58 and 0.011, respectively. The highest values for MP and GMP indices were obtained in genotypes MP6 and MP10 with 8.32 and 1.21, respectively. For the HMP index, the highest value was obtained in the MP10 genotype at 5.42, while the lowest value was recorded in the IR29 genotype at 0.69. Similarly, higher values of STI, GMP, MP, and HM indices in seven-day-old rice seedlings resistant to salt stress (Hosseini *et al.*, 2012) and also in salt-resistant genotypes of rice at the seedling stage (Mirdarmansouri *et al.*, 2012; Izaddoost *et al.*, 2013) was reported earlier. The genotype with high GMP and MP and less TOL is more tolerant of stress (Saberi *et al.*, 2015; Rezaei *et al.*, 2010; Jabbari *et al.*, 2008). The best value of SSI index related to the Deilamani genotype was obtained with -0.078. The SSI indicates that if a genotype performs better in both stress and non-stress conditions, but shows a large percentage of changes, it is not identified as a tolerant genotype. For this reason, selection based on this index reduces the performance potential in suitable and stress-free environments (Schnider *et al.*, 1997). Also, the highest value of the TOL index related to MP10 genotype while the lowest one was for the Deilamani cultivar with values of 13.25 and 0.39, respectively. Selection based on the TOL index often leads to the selection of genotypes that have relatively low performance under normal conditions. In the other words, the TOL cannot distinguish genotypes that are tolerant to stress conditions (Jafari Rad, 2014).

Based on the cluster results using Ward's minimum variance method and Euclidean distance square measure, the studied genotypes were placed in four

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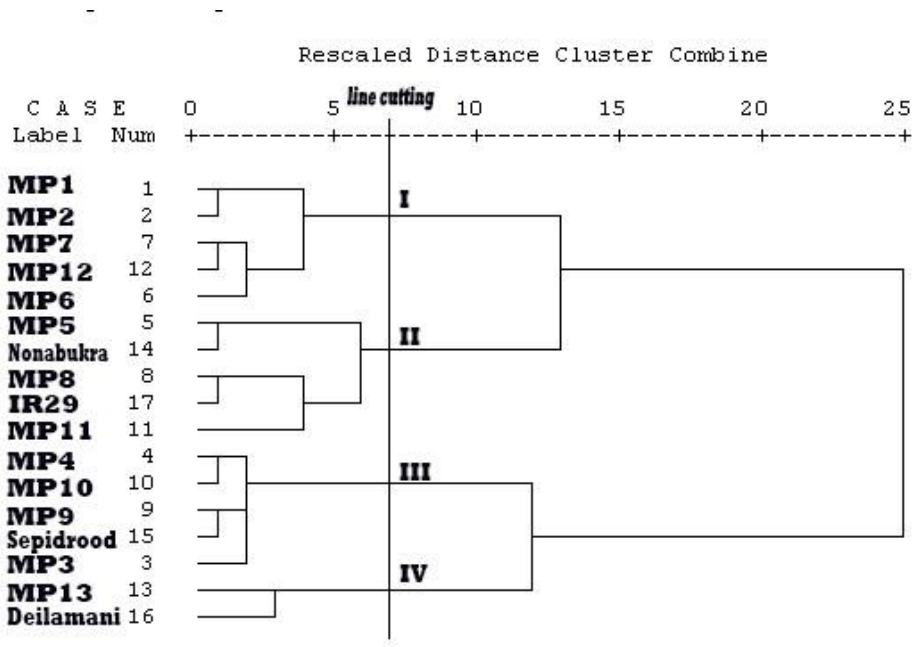



**Figure 1. Dendrogram obtained from cluster analysis using Ward's method based on all studied genotypes under salinity stress of 4 dS.m$^{-1}$**

**Table 6. The results of the discriminant function for the validity of the clustering of rice genotypes at a salinity of 4 dS.m$^{-1}$**

| Group | | Group Membership | | | | TOTAL |
|---|---|---|---|---|---|---|
| | | 1 | 2 | 3 | 4 | |
| Original | 1 | 5 | 0 | 0 | 0 | |
| | 2 | 0 | 5 | 0 | 0 | 5 |
| | 3 | 0 | 0 | 5 | 0 | 5 |
| | 4 | 0 | 0 | 0 | 2 | 5 |
| Percent | 1 | 100 | 0 | 0 | 0 | 2 |
| | 2 | 0 | 100 | 0 | 0 | 100 |
| | 3 | 0 | 0 | 100 | 0 | 100 |
| | 4 | 0 | 0 | 0 | 100 | 100 |
| | | | | | | 100 |

**100.0% of originally grouped cases were correctly classified**

groups at the salinity stress level of 4 dS.m$^{-1}$ (Figure 1). To ensure the accuracy of the groupings obtained from the analysis method, a cluster discriminant function was used (Table 6). Nonabukra and IR29 cultivars (internationally sensitive and tolerant, respectively) were included in one group. The Sepidrood (native sensitive) variety was placed in the second group, and the Deilamani (native tolerant) variety was placed in the third group. The dendrogram obtained from the evaluation of salinity tolerance at a salinity level of 4 dS.m$^{-1}$ by Sabouri *et al*. (2008) showed that all studied genotypes of rice were placed in three separate groups. The discriminant function showed that all the genotypes were correctly grouped, and the success rate of the whole discriminant function was 100%. The success rate indicates how successful the discriminant function was in grouping or classifying between groups (Safari *et al*., 2007).

Cluster analysis divided the studied genotypes into three separate groups at the salt stress level of 8 dS.m$^{-1}$ (Figure 2). A discriminant function was used to ensure the accuracy of the groupings obtained from the cluster analysis (Table 7). Deilamani, Nonabukra, and IR29 cultivars were placed in the third group, and the Sepidrood cultivar (native sensitive check) was placed in the first group. Similar results were reported in another study by Izaddoost *et al*. (2013) in 8 dS.m$^{-1}$ of salt stress in different rice genotypes. Cluster analysis is usually used as a multivariate statistical method to separate and group contrast genotypes (Hossain *et al.*, 1990; Li *et al.*, 2021; Mazlomi *et al.*, 2020).

The results of the correlation coefficient between the various studied indicators under the salinity stress of 4 dS.m$^{-1}$ in different rice genotypes are shown in Table 7. Based on the results, it was observed that PY had a positive and significant correlation with STI, HMP, MP, and GMP indices. STI index also positively and significantly correlated with GMP, MP, and HMP

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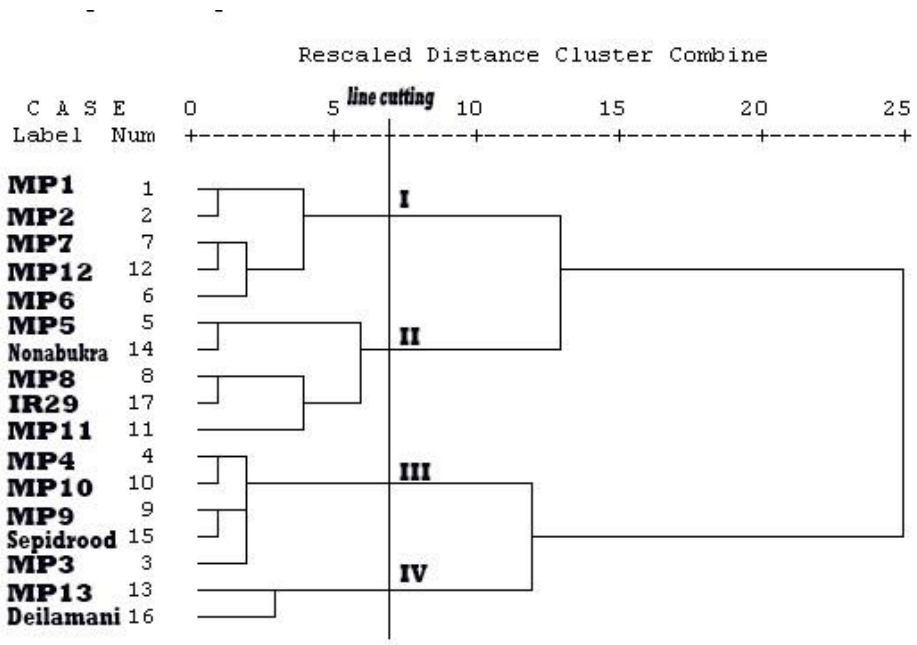



**Figure 2. Dendrogram obtained from cluster analysis using Ward's method based on all studied genotypes under salinity stress of 4 dS m$^{-1}$**

**Table 7. Correlation coefficient of salinity stress indices and PY in 4 and 8 dS.m$^{-1}$ conditions**

| | STI | SSI | TOL | GMP | MP | HM | Yield |
|---|---|---|---|---|---|---|---|
| | | | | 4 dS.m$^{-1}$ | | | |
| STI | 1 | | | | | | |
| SSI | -0.05 | 1 | | | | | |
| TOL | -0.38 | -0.77 $^{**}$ | 1 | | | | |
| GMP | 0.90 $^{**}$ | 0.04 | -0.34 | 1 | | | |
| MP | 0.96 $^{**}$ | 0.04 | -0.39 | 0.96 $^{**}$ | 1 | | |
| HMP | 0.97 $^{**}$ | -0.07 | -0.33 | 0.95 $^{**}$ | 0.97 $^{**}$ | 1 | |
| Yield | 0.87 $^{**}$ | 0.38 | -0.74 $^{**}$ | 0.86 $^{**}$ | 0.91 $^{**}$ | 0.86 $^{**}$ | 1 |
| | | | | 8 dS.m$^{-1}$ | | | |
| STI | 1 | | | | | | |
| SSI | 0.03 | 1 | | | | | |
| TOL | 0.51 $^{*}$ | 0.69 $^{**}$ | 1 | | | | |
| GMP | 0.87 $^{**}$ | 0.04 | 0.66 $^{**}$ | 1 | | | |
| MP | 0.78 $^{**}$ | 0.40 | 0.91 $^{**}$ | 0.89 $^{**}$ | 1 | | |
| HMP | 0.92 $^{**}$ | -0.31 | 0.23 | 0.84 $^{**}$ | 0.59 $^{*}$ | 1 | |
| Yield | 0.73 $^{**}$ | -0.61 $^{**}$ | -0.057 | 0.67 $^{**}$ | 0.35 | 0.93 $^{**}$ | 1 |

*** and **: Significant at 5 and 1% levels, respectively**

indices as well as GMP index with MP and HMP and PY. Also, the TOL index was negatively and significantly correlated with PY and SSI. The results of this research are similar to the results of Yarahmadi *et al*. (2020) in wheat and Jafari Rad *et al*. (2014) in rice genotypes, which showed that tolerance indices such as STI, GMP, HM, MP, and YI had a positive and significant correlation with PY in both normal and stress conditions.

Table 7 displays the correlation coefficients between the different studied indicators in various rice genotypes under salinity stress of 8 dS.m$^{-1}$. There was a positive and significant correlation between PY with STI, GMP. Also, HMP indices and STI index with TOL, GMP, MP showed a positive and significant correlation. Similar results was observed between HMP indices and SSI index with TOL, TOL index with GMP and MP indices and MP index with HMP. The SSI index had a negative and significant correlation with the PY. The correlation coefficient between the salinity tolerance indices at the level of 8 dS.m$^{-1}$ in the assessment of salinity tolerance in rice cultivars and lines by Izaddoost *et al*. (2013) showed that STI index with TOL, GMP, and MP indices and TOL index with STI, MP, and GMP as well as GMP index had a positive and significant correlation with STI, TOL, MP and HM indices and then MP with STI, TOL and GMP indices as well as STI and GMP indices. The correlation coefficient between the various studied indices under the salinity stress of 8 dS.m$^{-1}$ in different genotypes of rice which was investigated by

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**Table 8. Mean comparison of PY (g/plant) of different rice genotypes under control and salt stress conditions**

| Genotypes | Control | 4 dS.m$^{-1}$ | 8 dS.m$^{-1}$ |
|---|---|---|---|
| MP1 | 8.96 $^{k}$ | 8.91 $^{k}$ | 1.134 $^{i}$ |
| MP2 | 9.19 $^{j}$ | 8.41 $^{l}$ | 1.127 $^{i}$ |
| MP3 | 9.22 $^{i}$ | 18.95 $^{c}$ | 1.27 $^{h}$ |
| MP4 | 12.52 $^{e}$ | 19.36 $^{b}$ | 1.11 $^{i}$ |
| MP5 | 3.11 $^{o}$ | 6.47 $^{m}$ | 1.07 $^{j}$ |
| MP6 | 14.94 $^{a}$ | 13.01 $^{g}$ | 1.70 $^{d}$ |
| MP7 | 11.91 $^{f}$ | 11.61 $^{h}$ | 0.93 $^{k}$ |
| MP8 | 4.94 $^{l}$ | 1.31 $^{p}$ | 0.42 $^{n}$ |
| MP9 | 11.19 $^{g}$ | 18.22 $^{d}$ | 2.32 $^{c}$ |
| MP10 | 13.21 $^{c}$ | 20.46 $^{a}$ | 3.42 $^{b}$ |
| MP11 | 13.10 $^{d}$ | 2.86 $^{o}$ | 0.57 $^{m}$ |
| MP12 | 13.29 $^{b}$ | 10.35 $^{i}$ | 1.37 $^{g}$ |
| MP13 | 2.18 $^{p}$ | 9.27 $^{j}$ | 1.59 $^{e}$ |
| Nonabukra | 4.57 $^{m}$ | 5.96 $^{n}$ | 0.59 l |
| Sepidrood | 10.76 $^{h}$ | 16.17 $^{e}$ | 1.47 $^{f}$ |
| Deilamani | 4.05 $^{n}$ | 15.85 $^{f}$ | 3.66 $^{a}$ |
| IR29 | 2.14 $^{q}$ | 1.45 $^{p}$ | 0.42 $^{n}$ |

**In each column, means with similar letters were not significantly different based on Duncan's multiple range test (P≤ 0.05).**

Afkhami *et al*. (2021) showed that the HM index showed positive and significant correlation with MP, GMP, and STI indices and STI index with MP and GMP as well as SSI index with TOL and GMP index with MP.

According to the findings, the salinity stress of 4 dS.m$^{-1}$ had a negative effect only in four genotypes of MP6, MP8, MP11 and MP12. However, the salinity of 8 dS.m$^{-1}$ reduced the PY of all the studied genotypes except the Deilamani cultivar, which was considered a native tolerant control. When the salinity of plots reached 8 dS.m$^{-1}$, the Deilamani cultivar showed the lowest (9.6%), and the MP11 showed the highest reduction (95%) compared to the normal conditions. In the control conditions, the highest and the lowest PY was recorded in MP6 (14.94 g/plant) and IR29 (2.14 g/plant). In contrast, at 4 dS.m$^{-1}$ of salinity conditions, MP10 (20.46 g/plant) and IR29 (1.45 g/plant), and at 8 dS.m$^{-1}$ of salt tress, Tarem Deilamani (3.66 g/plant) and IR29 (0.42 g/plant) and MP8 (0.42 g/plant) showed the maximum and minimum PY, respectively (Table 8). Among the genotypes, at a salinity level of 8 dS.m$^{-1}$, PY of MP10 was found to be close to the Tarem Deilamani salt-tolerant cultivar. This result shows the high potential of seed production of this cultivar in saline conditions. Hasamuzzaman *et al*. (2009) observed that although different rice cultivars respond differently to salinity stress, the PY of rice cultivars decreased with increasing salinity levels. The decrease in PY of rice cultivars under salt conditions has been previously reported by Saeedzadeh *et al*. (2018), Jafari Rad *et al*. (2014), Biabani *et al*. (2012) and Gain *et al*. (2004).

## Conclusion

The results of this research clearly showed that salinity stress at both levels of 4 and 8 dS.m$^{-1}$ markedly reduced PY in all studied genotypes. According to the yield of advanced mutant lines at the salinity level of 8 dS.m$^{-1}$ the MP10 line yield was close to that of the Deilamani tolerant control. Based on the results of the tolerance indices, the MP10 line showed the highest value in both salinity levels of 4 and 8 dS.m$^{-1}$, therefore, could be introduced as a superior line for further and supplementary research.

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