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RESEARCH ARTICLE

Characterization of New Salt-Tolerant Rice Genotypes with Superior Agronomical and Cooking Traits

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ABSTRACT

Soil salinity is one of the major constraints affecting rice production worldwide. Goal of this research was evaluation of salt tolerance of new mutant rice germplasm and characterization of new salttolerant mutant rice promising lines with superior qualitative and quantitative traits. Salt tolerance of 56 promising mutant rice lines and 8 commercial and standard cultivars was investigated on standard evaluation scale of IRRI in an Augmented Design in salt affected soils of a rice farm with EC 6.5 dSm⁻¹ in Pirbazar region of Rasht, Guilan province of Iran. Then, yield and yield components of 13 selective salt-tolerant promising lines were evaluated in a three replicated randomized complete block design in the same farm in the second year. Yield and yield components and some cooking parameters of these genotypes were analyzed. Mean analysis, principal component factor and biplot analysis of traits related to yield of studied genotypes under salt stress represented that promising line HM5-250-42-1-E (M12) was the most salt-tolerant genotype. The promising line produced 80% higher paddy yield than its famous parental landrace Hashemi in salt affected soils. Also, this promising line had some superior cooking parameters than other genotypes even the most famous Iranian high-quality landraces Hashemi and Tarom Mahalli. It seems that promising line M12 (HM5-250-42-1-E) is an ideal option for development of rice cultivation and production particularly in regions that are faced with salinity problem.

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Introduction

Rice (*Oryza sativa* L.), the staple food for more than half of the world's population, is the most salt-sensitive cereal. One-fifth of irrigated agriculture is negatively affected by high soil salinity (Negrao et al., 2011). World population is growing and thousands of hectares of prone land for rice cultivation in the Iran and some regions in the world are faced with the problem of intense salinity annually. In Iran, parts of paddy fields in several northern and southern provinces (Mazandaran, Guilan, Golestan, Khuzestan and Fars) are confronted with soil and water salinity. In addition, the most important and marketable high-quality Iranian rice landraces, Hashemi and Tarom Mahalli, are sensitive to salinity conditions and plant yield decreases extremely in such conditions. Thus, developing salt-tolerant crops particularly in Iran is necessary. Existence

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of genetic variability for salt tolerance within species is paramount importance in the crop improvement program (Taliyil and Mammootty, 2010). Reliable and repeatable screening techniques are the mainstay of any successful breeding program specifically for biotic or abiotic stress breeding. Field screening is the best way to identify the most suitable genotypes because salt tolerance is very complex phenomena, but spatial variability in the field sometimes give the false positive results due to escape. The layout for such a test is generally augmented design or incomplete block design in which a set of check varieties is replicated many times. The involvement of a greater number of checks have been found better in data processing and finalizing the tolerant lines (International Rice Research Institute, 2006). Almost all the conventional breeding methods have been followed for the development of the salt-tolerant materials i.e. introduction, selection, hybridization, mutation and shuttle breeding approach (International Rice Research Institute, 2006).

Yichie et al. (2018) investigated variation in salinity tolerance among accessions of two wild rice species endemic to Australia, *O. meridionalis* and *O. australiensis*, with *O. sativa* cultivars Pokkali and IR29 providing salt-tolerant and sensitive controls, respectively and after 30 days of NaCl treatment, found that Pokkali and *Oa*-VR plants displayed the same absolute growth rate under 80 and 100 mM. Furthermore, Baloch et al. (2003) evaluated one mutant variety Shua-92 and two mutants of rice, derived through mutation breeding from the two standard varieties IR8 and Pokkali, for two years for their yield performance in salt affected soils with pH 7.63 to 7.68 and EC 7.11 to 8.0 dSm⁻¹. They indicated that the mutant variety Shua-92 produced 40 and 49% higher paddy yield on salt affected soils than the famous salt-tolerant varieties Nona Bokra and Pokkali.

To evaluate and compare different rice genotypes under salinity conditions, Saeidzadeh et al. (2016) conducted two separate experiments under two salinity and non-salinity fields in three replicated randomized complete block design in west of Guilan province (Astara) during 2009-2010. Distribution of the studied cultivars based on biplot of the grain yield and the indices presented that Hashemi, Tarom-Amiri, Tarom-Pakotah and Garib-Siahreihani were as tolerant varieties and IR29 was as sensitive variety to salinity stress. In order to study the effects of salt stress on yield and yield components of 21 rice genotypes, Mirdarmansouri et al. (2014) carried out a factorial experiment based on randomized complete block design on pots in greenhouse at Sari Agricultural Science and Natural Resources, during 2009. Salt stress was applied on reproductive stage in rice at 3 levels 0, 6 and 10 dSm⁻¹ NaCl. Their statistical analysis results indicated that in total, cultivars of Shastak mohammadi, Hassani and Tarom-Danesh were the most tolerant in response to salinity unlike other studied genotypes such as Tarom Mahalli and IR29.

To investigate salinity tolerance at seedling stage, Izaddoost et al. (2013) assessed 17 landraces and improved genotypes of rice (*Oryza sativa* L.) in a factorial experiment based on randomized complete block design and in four salinity levels (1.19, 4, 8 and 12 dSm⁻¹) in the early stage of vegetative growth. Results of principle component analysis and cluster analysis for clustering the studied genotypes using the indices exhibited that Shahpasand and Line 416 were most tolerant to salinity stress at seedling stage among the studied genotypes including landrace Hashemi. To evaluate genetic diversity of rice genotypes (45 Iranian landraces, 25 Iranian cultivars and 5 foreign cultivars) in relation to salt stress in seedling stage and determination of sensitivity and tolerance indexes based on dry matter, genotype code and Na/K ratio, Sabouri et al. (2008) performed an factorial experiment based on randomized complete block design in normal and salt stress (1.2, 4 and 8 dSm⁻¹) conditions in Rice Research Institute of Iran located in Rasht. Analysis of genotype code on IRRI standard method in stress condition indicated that Tarom Mahalli, Gharib, Shahpasand of Mazandaran and Ahlami Tarom with higher biomass, root and stem length and lower Na/K ratio are salt-tolerant cultivars. Kamyab-Talesh et al. (2014) evaluated salt tolerance of Iranian eight rice cultivars under four levels of irrigation water salinity (1, 2, 4 and 6 dSm⁻¹) with three replications, in Amol, Mazandaran province, north of Iran. Their results showed that Khazar cultivar was the most salt-sensitive cultivar in all salinity levels. In the irrigation salinity levels of 2 and 4 dSm⁻¹, Neda cultivar and in the level of 6 dSm⁻¹, Dasht cultivar were the most salt-tolerant cultivars. As some agricultural areas of Iran in the north and south of Iran are facing the serious problem of soil salinity and the yield of rice in these areas is greatly reduced, this research was conducted with goal of identification of new salt-tolerant mutant rice promising lines with superior agronomical and nutritional traits.

Materials and Methods

Plant Materials

146 mutant promising lines (i.e. 24 mutant promising lines with origin of landrace Tarom Mahalli, 4 mutant promising lines with origin of cultivar Fajr, 83 mutant promising lines with origin of landrace Hashemi and 35 mutant promising lines with origin of cultivar Khazar), 7 commercial cultivars (i.e. Hashemi, Ali Kazemi, Sepidrood, Sangjo, Tarom Mahalli, Khazar and Fajr) and an international salt-tolerant cultivar entitled FL476 were used as plant materials in this research. These promising lines were produced via gamma irradiation of seeds of high-quality landraces Hashemi and Tarom Mahalli and high-yield cultivars Fajr and Khazar in gamma cell of agriculture research school of Nuclear Science and Technology Research Institute of Iran six years ago.

Screening of Mutant Rice Populations Under Salinity Condition and Characterization of Salt-Tolerant Promising Lines

Screening criteria of salt tolerance

Though there is no single definite morphological marker available for salt tolerance or sensitivity in any crop, but a combination of criteria can be a good indication toward the salt response of crop plants. Therefore, several parameters such as survival of the plant, injury score, phenotypic expression and grain yield are used in combination for the effective and reproducible screening. These parameters in IRRI standard evaluation system for salinity, sodicity (2013) and Singh et al. (2002) technique for sodicity on 1-9 scale (Table 1) have been considered as critical limit for selection of the genotypes.

 Table 1. Modified standard evaluation score (MSES) of visual salt injury at seedling stage

Score	Observation	Description
1	Normal growth, no leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips or few leaves whitish and rolled	Tolerant
5	Growth severely retarded; most leaves rolled; only a few are elongating	Moderately tolerant
7	Complete cessation of growth; most leaves dry; some plants dying	Susceptible
9	Almost all plants dead or dying	Highly susceptible

Also, evaluation of yield of promising lines and commercial and standard cultivars under salinity condition was done on 1-9 scale of spikelet fertility (Table 2).

 Table 2. Standard evaluation score (SES) of spikelet fertility at reproductive stage

Score	Spikelet fertility	Description
1	> 80%	Highly tolerant
3	61%-80%	Tolerant
5	41%-60%	Moderately tolerant
7	11%-40%	Susceptible
9	< 11%	Highly susceptible

Field evaluation



Figure 1. Salinity in experimental rice farm

In the first year, screening of salt tolerance of promising lines and commercial and standard cultivars was performed in an augmented design in a salt affected soil with EC 6.5 dSm⁻¹ in Pirbazar region of Rasht, Guilan province of Iran. However, EC of farm soil reached to 8.5 dSm^{-1} at the end of growing season specially harvest time. In the second year, yield and yield components of selective salt-tolerant promising lines were evaluated in a three replicated Randomized Complete Block Design in the same salt land with the similar EC (Figure 1).

Evaluation of Some Cooking and Nutritional Parameters of the Promising Rice Lines

Percentages of total conversion, head rice and broken kernels were calculated for any genotype. Grain length and width before and after cooking of studied genotypes were estimated by photo enlarger. Also, elongation amount of the grain after cooking was measured for all genotypes. To classify studied promising lines and cultivars on Amylose Content (AC), rice seeds were milled with a commercial grinder to particles with size range of less than 800µm. The AC was determined by the simplified assay for milled rice described by Juliano (1985) in triplicate. Four classes of AC are recognized in rice breeding programs: high (>25%), intermediate (21-25%), low (10-20%) and very low (3-9%). Gel temperature was measured using method described by Little et al. (1958) with minor modifications. In this method, rice varieties are categorized into high (>74°C), intermediate (70-74°C) and low (<70°C) gel temperature classes or classified into high (1-2), intermediate (3-4) and low (5-6) gel temperature. Iranian rice genotypes were derived from Oryza sativa L. indica. Good quality indica cultivars have alkali spreading value >4. They are classified as grade 1 when grain length is 6.6-7.0 mm, L/W ratio >3.0 and AC 17-22% and as grade 2 when grain length is 5.6-6.5 mm, L/W ratio 2.5-3.0 and AC 23-25% or <17% (Juliano and Villareal, 1993).

Experimental Data Analysis

Mean analysis was done using SAS software version 9.1. In this software, t tests (LSD) were performed for all studied traits. Principle component analysis, the rice genotype-bytrait biplot and cluster analysis were performed for clustering the studied genotypes and traits under salt stress condition using Minitab software version 16.

Results and Discussion

In the first year of evaluation, 13 promising lines and two commercial cultivars Sepidrood and Ali Kazemi were characterized as salt-tolerant genotypes on vegetative characters. Among these genotypes, 12 promising lines were derived from landrace Hashemi. However, origin of one of salttolerant promising lines, TM6-B-7-1 was landrace Tarom Mahalli. Whereas other promising lines and commercial and standard cultivars did not express tolerance to salinity in this stage. Also, any salt-tolerant promising line with origin of cultivars Khazar and Fajr was not identified on vegetative characters. In maturity stage, 12 promising lines and one international standard cultivar known as FL478 (Adamu et al., 2018) were identified as salt-tolerant genotypes on yield of rice plants. Among them, 5 and 7 salt-tolerant promising lines were derived from landraces Tarom Mahalli and Hashemi, respectively. However, such as vegetative stage, any salttolerant promising line with origin of cultivars Khazar and Fajr was not found on yield and yield components. Totally, 12 salttolerant promising lines with origins of Tarom Mahalli and Hashemi were identified on two scales. But only promising line HM5-250-42-1-E with origin of Hashemi was highly salt-tolerant on two scales. Two parental cultivars Hashemi and Fajr had moderately tolerance to salt stress. But other two parental cultivars Khazar and Tarom Mahalli were salt sensitive. Finally, 5 salt-tolerant promising lines with origin Tarom Mahalli and 7 salt-tolerant promising lines with origin Hashemi and a highly salt-sensitive promising line M1 (TM6-220-10-4-1) with their parental landraces Hashemi and Tarom Mahalli were selected as plant materials for second year of evaluation. In the second year of evaluation, 8 genotypes including 4 promising lines with origin Hashemi and 3 promising lines with origin Tarom Mahalli and parental landrace Hashemi were characterized as salt-tolerant genotypes on vegetative scale. But among them, only 2 promising lines with origin Hashemi were salt-tolerant on yield and yield components. Such as the first year, the highest yield devoted to promising line M12 (HM5-250-42-1-E) with 2200 Kgha⁻¹. The height of 3 salt-tolerant promising lines was considerable higher than other promising lines, specially the most salt-tolerant genotype M12 with height of 144 cm. This issue indicated that salinity did not have any negative impact on height of these salt-tolerant genotypes and their height did not change compared to their parental landrace

under normal condition. Also, the highest of full seeds, spike length and thousand seed weight among all promising lines devoted to salt-tolerant promising line M12 This issue indicated that genotype HM5-250-42-1-E was well adapted with salt condition and reduction of its yield was not considerable compared to its parental cultivar, Hashemi and standard landrace, Tarom Mahalli under normal condition. Also, the lowest yield, plant height, full seeds and thousand seed weight was due to highly sensitive promising line M1. However, some plants in plot of this genotype could not survive in salt stress condition (Figure 2 and Table 3).



Figure 2. Plot of mutant promising line M12 (HM5-250-42-1-E) with origin of Hashemi in salt affected rice farm

Table 3. Comparison of yield and yield components of selective rice genotypes under salt stress condition in the second year of evaluation

Symbol	Genotype	TLVCh*	TLSF	PH (cm)	SPN	SPL (cm)	NFS	NES	PF (%)	ThSW (g)	Y (Kgha ⁻¹)
M1	TM6-220-10-4-1**	5	9	106	13	23.5	42	79	35	1.88	329
M2	ТМ6-В-7-1	5	7	116.5	14	22.5	59	34	63	2.17	1148
M3	ТМ6-В-19-1-Е	3	7	113	14	23.25	70	26	73	2.1	1056
M4	ТМ6-В-19-2	5	7	108	16	21.5	50	10	83	2.53	737.5
M5	ТМ6-230-1-1	3	7	117.5	17	25	72	40	64	2.53	1044
M6	TM6-250-11-5	3	7	114.5	15	22.75	53	35	61	2.11	778
M7	HM5-250-7-4-2	3	7	116.5	16	31	59	32	64	2.15	995
M8	HM5-250-7-4-3	5	7	127.5	16	29.75	60	20	75	2.25	1111
M9	HM5-250-7-5-2	5	5	129.5	17	28.5	53	16	77	2.51	1647.5
M10	HM5-250-25-1-3	3	3	142	16	31.5	70	29	71	2.23	1925
M11	HM5-250-26-1-E-1	3	3	130.5	15	28.25	83	38	68	2.09	1962.5
M12	HM5-250-42-1-E	3	3	144	13	32.75	92	24	80	2.55	2200
M13	HM5-300-16-1	5	3	142	16	32.25	85	20	81	2.12	1845.5
Н	Hashemi	3	7	144.5	16	30	58	24	70	2.15	1224.5
тм	Tarom Mahalli	5	7	138.5	18	24.5	52	27	66	2.12	858
HN	Hashemi (Normal condition)	-	-	145.2	13	27.95	101	8	93	2.6	3100
TMN	Tarom Mahalli (Normal condition)	-	-	147.5	14	25.75	107	8	93	2.91	3000

^{*}TLVCh, TLSF, PH, SPN, SPL, NFS, NES, PF, ThSW and Y are abbreviation of Tolerance Level on Vegetative Characteristics, Tolerance Level on Spikelet Fertility, Plant Height, Spike Number, Spike Length, Number of Full seeds, Number of Empty Seeds, Percentage of Fertility, Thousand Seed Weight and Yield. [•] In statistical analysis, 13 promising lines were symbolized with M1 to M13.

In addition, yield of two parental and commercial landraces Hashemi and Tarom Mahalli under salt stress was 1174.5 and 858 Kgha⁻¹, respectively (Figure 3). Whereas these landraces in natural condition had yield of 3100 and 3000 Kgha⁻¹, respectively. Mean analysis of data from experimental genotypes using SAS software indicated that there are considerable and significant differences (p<0.01) between genotypes in agronomic traits particularly yield and the most important component of yield, full seeds in salt stress condition (Table 4).

Table 4. Mean analysis of yield and yield components of studied rice genotypes under salt stress condition

			Mean Square									
Source	DF	Y [*] (Kg ha ⁻¹)	PH (cm)	SPN	SPL (cm)	NFS	NES	PF (%)	ThSW (g)			
Model	16	1800828.81**	645.84505**	6.2450980**	42.1256250**	1004.08088**	817.13480**	540.877451**	0.20849902**			
Error	34	327748.67	5.24725	1.4117647	0.3258824	38.92157	10.00000	16.019608	0.00076667			
Coeff Var		6.673337	1.785198	7.900525	2.106498	9.145573	11.40567	5.595531	1.206842			

Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight. "indicates that difference between treatments is significant in level of 1% (p<0.01).

Using t test (LSD), studied genotypes were categorized in different groups on yield. Landraces Hashemi and Tarom Mahalli under normal condition that had the highest yield among studied rice genotypes, were classified in a distinct group. However, these landraces did not have a suitable yield under salt stress condition and were included in separate groups compared to normal condition. Furthermore, promising line M12 (HM5-250-42-1-E) that had the highest yield among the genotypes under salt stress condition, was included in an independent group. Promising lines M10, M11 and M13 that had a good yield under salt stress condition were in another distinct class too. Highly salt sensitive promising line M1 with the lowest yield under salt stress condition was included in a separate group. Overall, salt stress had a negative effect on yield of studied rice genotypes. Nevertheless, four promising lines especially M12 had statistically a satisfactory yield under salt stress condition (Table 5).

Table 5. T test	s (LSD)) for traits related to	vield and vield	d components of studied	genotypes under salt	stress condition
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Symbol	Genotype	Mean										
Symbol	Genotype	Y [*] (Kgha ⁻¹)	PH (cm)	SPN	SPL (cm)	NFS	NES	PF (%)	ThSW (g)			
M1	ТМ6-220-10-4-1	379 ^{**}	106 ^н	13 ^e	23.5 ^H	42.3 ^F	79 ^A	35 ^J	1.88 ^H			
M2	ТМ6-В-7-1	1148 EF	116.5 ^E	13.7 DE	22.5 ^H	59 ^E	33.7 ^{CD}	63.3 ^{HI}	2.17 ^E			
M3	ТМ6-В-19-1-Е	1056 EF	111 ^{FG}	13.7 DE	23.25 ^H	70.3 ^{CD}	26.3 ^F	73 DEFG	2.1 FG			
M4	ТМ6-В-19-2	737.5 ^H	108 ^{GH}	15.7 ABCD	21.5	50 ^{ef}	10.3 '	82.7 ^B	2.53 ^c			
M5	TM6-230-1-1	1044 ^{EF}	117.5 ^E	16.7 ^{AB}	25 ^{FG}	71.3 ^c	40 ^B	64 ^{HI}	2.53 ^c			
M6	TM6-250-11-5	778 ^H	114.5 ^{EF}	14.7 BCDE	22.75 ^H	53.3 ^{EF}	35 ^{BC}	61	2.11 FG			
M7	HM5-250-7-4-2	995 FG	116.5 ^E	15.7 ABCD	31 ^c	58.7 ^E	32.3 CDE	65 ^{ні}	2.15 EF			
M8	HM5-250-7-4-3	1111 ^{EF}	127.5 ^D	16 ABC	29.75 ^D	59.7 DE	20.3 ^{GH}	74.7 CDEF	2.25 ^D			
M9	HM5-250-7-5-2	1647.5 ^D	129.5 ^D	16.7 ^{AB}	28.5 ^E	52.7 EF	16 ^н	76.7 BCDE	2.51 ^c			
M10	HM5-250-25-1-3	1925 ^c	142 ^{BC}	16 ABC	31.5 ^{BC}	70 ^{CD}	28.7 DEF	70.3 EFGH	2.23 ^D			
M11	HM5-250-26-1-E-1	1962.5 ^c	130.7 ^D	15 ^{BCDE}	28.25 ^E	82.7 ^B	38 ^{BC}	68 FGHI	2.09 ^G			
M12	HM5-250-42-1-E	2200 ^в	144 ^{AB}	13 ^E	32.75 ^	91.7 ^{AB}	24 ^{FG}	79.7 BCD	2.55 ^c			
M13	HM5-300-16-1	1845.5 ^c	142 ^{BC}	15.3 ^{BCD}	32.25 AB	85 ^B	20 ^{GH}	81 ^{BC}	2.12 EFG			
н	Hashemi	1224.5 ^E	144.5 AB	16 ABC	30 ^d	58 ^E	24 ^{FG}	70 EFGH	2.15 EF			
тм	Tarom Mahalli	858 ^{GH}	138.5 ^c	17.7 ^	24.5 ^G	52 ^{EF}	27.7 EF	66 GHI	2.12 EFG			
HN	Hashemi (Normal condition)	3100 ^A	145.2 AB	13 ^E	27.95 ^E	101.3 ^	8.3 ^J	92.7 ^	2.6 ^B			
TMN	Tarom Mahalli (Normal condition)	3000 ^A	147.5 ^	14 CDE	25.75 ^F	101.7 ^	7.7 ^J	93 ^A	2.91 ^A			

Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight. "In any column, *dissimilar letters* indicate *statistically significant* differences in *mean* values.

Height of studied genotypes was very variable. This trait was extremely influenced by salinity stress. All salt sensitive promising lines had a less height than their parental cultivars Hashemi and Tarom Mahalli and were classified in distinct groups. Nevertheless, height of the most salt-tolerant promising line, M12 did not change significantly under salinity condition in comparison with its parental cultivar. This promising line was categorized surprisingly in a common class with two parental cultivars Hashemi and Tarom Mahalli under normal condition and had a similar height. Mean of spike number in studied genotypes was variable as genotypes M1 and M12 in salt stress condition and Hashemi in normal condition had at least spikes with 13 and so, were included in a distinct group. Also, the highest mean of spike number was due to genotype Tarom Mahalli in salt stress condition with 17.7.

Salt stress had a considerable negative impact on spike length of parental landraces Tarom Mahalli and Hashemi as spike length of these landraces in normal condition with 25.75 and 27.95 cm decreased to 24.5 and 21 cm in salt stress condition. They were included statistically in separate groups from other genotypes. But the highest spike length was due to promising lines M12 and M13 with 32.75 and 32.25 cm, respectively and statistically were included in a similar group. Furthermore, landrace Hashemi in salt stress condition and promising line M4 produced the lowest spike length with 21 and 21.5 cm, respectively. These genotypes were categorized in a group too.

Mean of full seeds of studied rice genotypes indicated that salt stress has a considerable negative effect on yield components. Under salt stress condition, parental landraces Hashemi and Tarom Mahalli produced 58 and 52 full seeds, respectively. Whereas these landraces produced averagely 101.3 and 101.7 full seeds under normal condition and were included in a distinct group. In the salt stress condition, the highest full seeds was produced in promising line M12 with about 92. This genotype was included in a separate class statistically. Furthermore, two promising lines M13 and M11 produced averagely 85 and 82.7 full seeds under salt stress condition and jointly put in a group. The lowest full seeds and the highest empty seeds belonged to promising line M1. This genotype with 79 empty seeds was the most sensitive genotype to salt stress. Two parental landraces Hashemi and Tarom Mahalli under normal condition had the highest percentage of fertility compared to studied rice genotypes in salt stress condition and so, were in a distinct group. Also, the highest percentage of fertility among studied genotypes under salinity was due to promising lines M4, M13 and M12. Thousand seeds weight of parental landraces Hashemi and Tarom Mahalli under normal condition was higher than studied genotypes in salt stress condition. However, the highest thousand seeds weight among the genotypes under salt stress condition devoted to M12 with 2.553 g. The results of statistical analysis indicated that three important yield components, spike number, full seeds and thousand seeds weight in studied rice genotypes were strongly affected by soil salinity (Table 5).

Principal Component Factor Analysis of yield and yield components of the rice genotypes using Minitab 16 software represented that the first and second factors had the most influence on the amount of variation in the rice genotypes with variances of 2.2212 and 1.3091, respectively (Table 6).

Table 6. Principal C	component Factor	Analysis of the	Correlation Ma	atrix of yield and y	yield components of	the rice genotypes
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Variable	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7	Factor8	Communality
Υ*	0.401	0.589	-0.273	0.282	0.314	-0.415	-0.259	-0.000	1.000
PH	0.309	0.320	-0.435	-0.034	0.118	-0.773	-0.002	-0.001	1.000
SPN	0.082	-0.179	-0.058	-0.978	-0.034	-0.004	0.010	0.001	1.000
SPL	0.094	0.150	-0.959	-0.054	-0.017	-0.213	-0.013	-0.001	1.000
NFS	0.319	0.785	-0.219	0.314	0.256	-0.258	0.049	-0.002	1.000
NES	-0.939	-0.123	0.087	0.130	-0.219	0.167	0.018	-0.053	1.000
PF	0.861	0.331	-0.136	0.033	0.298	-0.187	-0.015	-0.076	1.000
ThSW	0.474	0.252	0.032	0.050	0.835	-0.109	-0.014	-0.000	1.000
Variance	2.2212	1.3091	1.2629	1.1594	1.0127	0.9554	0.0707	0.0087	8.0000
% Var	0.278	0.164	0.158	0.145	0.127	0.119	0.009	0.001	1.000

Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight.

Numerical amount of variances of five factors was more than 1. The first factor had a negative correlation (r = -0.939) with number of empty seeds. This factor had a positive correlation (r = 0.861) with percentage of fertility. Importantly, the second factor was positively correlated with yield and number of full seeds (r = 0.589 and r = 0.785), respectively. Furthermore, third, fourth and sixth factors had negative correlation with spike length, spike number and plant height (r = -0.959, r = -0.978, r = -0.773), respectively. However, the fifth factor was positively correlated with hundred seed weight (r = 0.835). Numerical amount of variances of the seventh and eighth factors was less than 1 and was not important and influencing factors.

Six factors specially the first and second factors had the

most influence on variation induced in the rice genotypes. So, considering the first and second factors, promising lines M12 and M11 under salt stress condition and parental cultivars Hashemi and Tarom Mahalli in normal condition that expressed similar characteristics, were included in domain 1. In this domain, x and y amounts are positive (Figure 3).

On yield and yield components, promising lines M12 and M11 that were the most salt-tolerant rice genotypes among all genotypes under salinity condition, were identified as selective genotypes of our research.

Also, after data analysis in Minitab 16 software, two traits of yield and number of full seeds that were included in domain 1, selected as the most influencing traits on variation between the rice genotypes (Figure 4).



Figure 3. Score plot of the rice genotypes on yield and yield components. H and TM are abbreviation of Landraces Hashemi and Tarom Mahalli. M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13 are indicator of promising rice lines



Figure 4. Loading plot of yield and yield components of the rice genotypes. Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight

Four rice genotypes (landraces Tarom Mahalli and Hashemi in normal condition and genotypes M12 and M11 under salt stress condition) with the highest yield and number of full seeds were included in domain 1. Landrace Hashemi and three promising lines derived from this landrace (M9, M10 and M13) under salinity stress were included in an independent category after Biplot analysis. Also, Minitab 16 software classified landrace Tarom Mahalli and two promising lines derived from this landrace (M4 and M5) and two promising lines derived from landrace Hashemi (M7 and M8) in a distinct domain. Other promising lines derived from landrace Tarom Mahalli (M1, M2, M3 and M6) were categorized in another domain (Figures 3 and 5).



Figure 5. View of the rice genotype-by-trait biplot- Yield and yield components. Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight



Figure 6. Cluster analysis of the rice genotypes on yield and yield components. Numbers of 1-15 indicate genotypes of M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13, Landraces Hashemi and Tarom Mahalli

Cluster analysis of the rice genotypes on yield and yield components indicated two landraces Tarom Mahalli and Hashemi in normal condition that had the highest similarity and were closely related, included in an independent category (Figure 6). Promising lines M13, M12, M11, M10 and M9 derived from landrace Hashemi under salt stress condition had similar properties and were categorized in a completely distinct category. Two landraces Tarom Mahalli and Hashemi and promising lines M2, M3, M4, M5, M6, M7 and M8 in salinity condition were classified in another category. Promising line M1 that was a salt sensitive genotype and had some unfavorable traits, was included in a completely distinct category.

Results of this research represented that the highest percentage of total conversion and percentage of head rice belonged to salt-tolerant promising line M12 (HM5-250-42-1-E) (Table 7).

Symbol	Genotype	PTC* (%)	PHR (%)	PBR (%)	AC (%)	GT	GL (mm)	GW (mm)	GL/GW Ratio	GLC (mm)	El Ratio
M1	TM6-220-10-4-1	62.92	44.94	17.98	20.3	4.33	5.86	1.8	3.26	11.13	1.9
M2	ТМ6-В-7-1	64.93	57.53	7.4	21.2	4.33	6.63	1.9	3.49	11.1	1.67
M3	ТМ6-В-19-1-Е	68.94	59.13	9.81	22.1	4.66	6.4	1.91	3.35	12.26	1.92
M4	ТМ6-В-19-2	66.35	55.41	10.94	20.7	4.66	6.03	1.96	3.08	11.33	1.88
M5	TM6-230-1-1	72.08	65.93	6.15	21.1	5	6.43	1.86	3.46	10.66	1.66
M6	TM6-250-11-5	62.45	52.71	9.74	21.6	4.33	6.2	2	3.1	12.2	1.97
M7	HM5-250-7-4-2	69.15	62.53	6.62	22	4.66	6.7	1.86	3.6	10.9	1.63
M8	HM5-250-7-4-3	66.97	57.65	9.33	21.6	4.66	6.53	1.86	3.51	11.13	1.71
M9	HM5-250-7-5-2	65.61	58.51	7.1	21.6	3.83	6.65	1.83	3.63	10.26	1.54
M10	HM5-250-25-1-3	67.06	56.97	10.09	22.7	5	6.43	1.86	3.46	10.6	1.65
M11	HM5-250-26-1-E-1	71.88	66.48	5.4	22.2	4.5	6.9	1.93	3.58	11.03	1.6
M12	НМ5-250-42-1-Е	73.19	68.83	4.36	20.1	4.5	6.83	2	3.42	11.66	1.71
M13	HM5-300-16-1	67.89	60.61	7.28	21.7	4.5	6.46	1.86	3.47	10.66	1.65
н	Hashemi	67.45	52.93	14.52	20.7	5	6.93	1.9	3.65	11.13	1.61
тм	Tarom Mahalli	70.75	63.27	7.48	22.6	4.5	6.5	2	3.25	11	1.7

Table 7.	Comparison of	f traits related	to cooking	and nutritional	qualities of	studied ge	enotypes
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^{*}PTC, PHR, PBR, AC, GT, GL, GW, GL/GW Ratio, GLC and El Ratio are abbreviation of Percentage of Total Conversion, Percentage of Head Rice, Percentage of Broken Rice, Amylose Content, Gelatinization Temperature, Grain Length, Grain Width, ratio of Grain Length/ Grain Width, Grain Length after Cooking and Elongation Ratio, respectively.

The lowest percentage of broken kernels was due to this promising line, too. Furthermore, percentage of total conversion and percentage of head rice of promising lines M5 and M11 were high compared to other genotypes. Amylose content of all promising lines was intermediate. However, amylose content of the highly salt-tolerant promising line M12 was near to intermediate (20.1). In addition, all promising lines except for M5 and M10 were intermediate gel temperature. These two promising lines and cultivar Hashemi were low gel temperature (5-6). The highest value of grain length devoted to landrace Hashemi and two promising lines derived from this landrace, M11 and M12 with 6.93, 6.9 and 6.83 mm, respectively. However, the highest value of grain width was due to landrace Tarom Mahalli and two promising lines M6 and

M12 with 2 mm. Grain length after cooking of three promising lines M3, M6 and M12 was higher than other genotypes. After cooking, grain length of these three promising lines increased to 12.26, 12.2 and 11.66 mm, respectively. But the highest grain elongation after cooking belonged to promising lines M6 and M3 with 6 and 5.83 mm, respectively. Whereas the lowest grain elongation after cooking was due to promising line M9 with 3.61 mm (Table 7).

Mean analysis of data from the studied rice genotypes using SAS software indicated that there are considerable and significant differences between genotypes in cooking and nutritional qualities specially percentage of head rice in level of 1% (Table 8).

Table 8. Mean analysis of traits related	to cooking and nutritional	qualities of studied genotypes
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Mean Square											
Source	DF	PTC* (%)	PHR (%)	PBR (%)	AC (%)	GT	GL (mm)	GW (mm)	GL/GW Ratio	GLC (mm)	El Ratio
Model	14	30.9660 403**	113.365 418 ^{**}	37.9388 000**	1.88279 365 ^{**}	0.28360 317 ^{**}	0.27314 984 ^{**}	0.01230 857 ^{**}	0.09719 270 ^{**}	0.92218 984 ^{**}	0.05214 667**
Error	30	0.0149 156	0.016 242	0.0265 133	0.04422 222	0.00560 222	0.00094 222	0.00052 667	0.00143 333	0.00097 333	0.00009 556
Coeff Var		0.180 016	0.216 393	1.819 998	0.978 906	1.639 805	0.472 305	1.206 584	1.106 928	0.280 101	0.568 990

^TPTC, PHR, PBR, AC, GT, GL, GW, GL/GW Ratio, GLC and El Ratio are abbreviation of Percentage of Total Conversion, Percentage of Head Rice, Percentage of Broken Rice, Amylose Content, Gelatinization Temperature, Grain Length, Grain Width, ratio of Grain Length/ Grain Width, Grain Length after Cooking and Elongation Ratio, respectively. ^{**}indicates that difference between treatments is significant in level of 1% (p<0.01).

Using t test (LSD), the rice genotypes on cooking and nutritional qualities were classified in different groups. The salt-tolerant promising line M12 (HM5-250-42-1-E) with 73.19

% that had highest percentage of total conversion, statistically was categorized in an independent category. Whereas parental landraces Hashemi and Tarom Mahalli had a lower percentage of total conversion with 67.45 and 70.75 %, respectively. This issue indicated that not only mutation breeding has induced salt tolerance in some mutant genotypes but also had a positive impact on some cooking and nutritional gualities of some genotypes. Also, promising line M12 (HM5-250-42-1-E) with the highest percentage of head rice and lowest percentage of broken rice was classified statistically alone in a distinct group. There were significant statistical differences in 1% level in amylose content of studied genotypes. However, all genotypes were intermediate amylose content. On amylose content, each of four salt-tolerant promising lines M10, M11, M12 and M13 were classified in completely separate categories compared to other genotypes. Whereas parental landraces were included in completely distinct groups too. Furthermore, three salt-tolerant promising lines M11, M12 and M13 that were low to intermediate gel temperature, categorized in an independent class. Another salt-tolerant promising line M10 that was low gel temperature, classified in a separate group. Parental landrace Hashemi and promising line M11 with highest grain length before cooking were categorized in a separate group. In addition, the most salt-tolerant genotype, M12 (HM5-250-42-1-E) was one of long and thin grain genotypes with length before cooking of 6.83 mm that was classified in an independent group too. The lowest grain width devoted to promising line M1 with 1.8 mm that was categorized in a separate group. Landrace Hashemi with the highest grain length/width ratio, categorized in a completely distinct group compared to other genotypes. On classification of Juliano and Villareal, 1993 for indica rice genotypes, promising lines M2, M7, M9, M11, M12 and cultivar Hashemi were classified as grade 1 indica genotypes. Each of promising lines M3 and M6 and the most salt-tolerant promising line, M12 with the highest grain length after cooking were classified in an independent category compared to other genotypes (Table 9).

Table 9. T tests (LSD) for traits related to cooking and nutritional qualities of studied genotypes

Symbol	Genotype	Mean										
Symbol		PTC* (%)	PHR (%)	PBR (%)	AC (%)	GT	GL (mm)	GW (mm)	GL/GW Ratio	GLC (mm)	El Ratio	
M1	TM6-220-10-4-1	62.93 ^{L**}	44.94 ^N	17.98 ^	20.3 ^G	4.33 ^D	5.86 ^J	1.8 ^F	3.26 ^F	11.13 ^E	1.9 ^c	
M2	TM6-B-7-1	64.95 ^к	57.53	7.4 ^G	21.2 ^E	4.34 ^D	6.63 ^D	1.9 ^{CD}	3.49 ^c	11.07 FG	1.67 ^F	
M3	ТМ6-В-19-1-Е	68.94 ^E	59. 13 ^G	9.81 ^E	22.13 ^в	4.66 ^B	6.41 ^G	1.91 ^c	3.36 ^E	12.26 ^A	1.92 ^B	
M4	TM6-B-19-2	66.35 ¹	55.41 ^ĸ	10.94 ^c	20.7 ^F	4.66 ^B	6.03 ¹	1.96 AB	3.08 ^G	11.33 ^D	1.88 ^D	
M5	TM6-230-1-1	72.08 ^B	65.93 ^c	6.15 ^J	21.1 ^E	5 ^	6.43 ^G	1.86 ^D	3.46 ^{CD}	10.66 ¹	1.66 FG	
M6	TM6-250-11-5	62.45 ^M	52.71 ^M	9.74 ^E	21.6 ^D	4.33 ^D	6.2 ^H	2 🔺	3.1 ^G	12.2 ^в	1.97 ^	
M7	HM5-250-7-4-2	69.15 ^D	62.53 ^E	6.62	22 ^{BC}	4.66 ^B	6.7 ^c	1.86 ^D	3.6 ^{AB}	10.9 ^н	1.63 ^н	
M8	HM5-250-7-4-3	66.97 ^н	57.65	9.33 F	21.6 ^D	4.66 ^B	6.53 ^E	1.86 DE	3.51 ^c	11.13 ^E	1.71 ^E	
M9	HM5-250-7-5-2	65.61 ^J	58.51 ^H	7.1 ^H	21.6 ^D	3.83 ^E	6.65 ^{CD}	1.83 EF	3.63 AB	10.25 ^к	1.54 ^J	
M10	HM5-250-25-1-3	67.06 ^н	56.97 ^J	10.09 ^D	22.7 ^	5 ^	6.43 ^G	1.86 DE	3.46 ^{CD}	10.6 ^J	1.65 ^G	
M11	HM5-250-26-1-E-1	71.88 ^B	66.48 ^B	5.4 ^ĸ	22.2 ^B	4.5 ^c	6.90 ^A	1.93 ^{BC}	3.58 ^B	11.03 ^G	1.6 ¹	
M12	HM5-250-42-1-E	73.19 ^A	68.83 ^A	4.36 ^L	20.1 ^G	4.5 ^c	6.83 ^B	2 *	3.42 DE	11.66 ^c	1.71 ^E	
M13	HM5-300-16-1	67.89 ^F	60.61 ^F	7.28 ^{GH}	21.7 ^{CD}	4.5 ^c	6.46 FG	1.86 DE	3.47 ^{CD}	10.66 ¹	1.65 ^G	
н	Hashemi	67.45 ^G	52.93 ^L	14.52 ^в	20.7 F	5 ^	6.93 ^A	1.9 ^{CD}	3.65 ^	11.12 EF	1.6 ¹	
тм	Tarom Mahalli	70.75 ^c	63.27 ^D	7.48 ^G	22.6 ^A	4.5 ^c	6.5 ^{EF}	2 *	3.25 F	11.07 FG	1.7 ^E	

^{*}PTC, PHR, PBR, AC, GT, GL, GW, GL/GW Ratio, GLC and El Ratio are abbreviation of Percentage of Total Conversion, Percentage of Head Rice, Percentage of Broken Rice, Amylose Content, Gelatinization Temperature, Grain Length, Grain Width, ratio of Grain Length/ Grain Width, Grain Length after Cooking and Elongation Ratio, respectively. ^{**} In any column, *dissimilar letters* indicate *statistically significant* differences in *mean* values.

Tuble To, This par component ractor Analysis of the correlation matrix of cooking properties of the field genot	The correlation matrix of cooking properties of the rice genotypes
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Variable	Factor1	Factor2	Factor3	Factor4	Factor5	Factor6	Factor7	Factor8	Factor9	Factor10	Communality
PTC*	0.759	-0.444	0.296	0.045	-0.241	-0.104	-0.261	0.000	0.000	0.000	1.000
PHR	0.835	-0.486	-0.052	-0.008	-0.223	-0.117	0.009	-0.000	-0.000	-0.000	1.000
PBR	-0.757	0.438	0.357	0.055	0.168	0.108	-0.252	0.001	0.000	-0.000	1.000
AC	0.331	-0.043	-0.183	-0.879	0.278	-0.028	-0.072	0.000	0.000	-0.000	1.000
GT	0.148	-0.113	0.937	-0.237	-0.007	0.069	0.161	-0.000	-0.000	0.000	1.000
GL	0.852	-0.043	0.034	0.269	0.440	0.069	-0.008	-0.001	-0.004	0.000	1.000
GW	-0.021	-0.900	-0.095	0.083	0.162	0.385	-0.017	-0.005	0.002	-0.000	1.000
GLWR	0.760	0.521	0.086	0.181	0.285	-0.169	0.012	-0.009	0.004	-0.000	1.000
GLC	-0.504	-0.698	0.089	0.152	0.383	-0.284	0.014	0.010	0.001	-0.000	1.000
El Ratio	-0.872	-0.430	0.046	-0.059	-0.013	-0.221	-0.006	-0.016	-0.002	0.000	1.000
Variance	4.2981	2.3953	1.1576	0.9718	0.6607	0.3524	0.1635	0.0005	0.0000	0.0000	10.0000
% Var	0.430	0.240	0.116	0.097	0.066	0.035	0.016	0.000	0.000	0.000	1.000

PTC, PHR, PBR, AC, GT, GL, GW, GL/GW Ratio, GLC and El Ratio are abbreviation of Percentage of Total Conversion, Percentage of Head Rice, Percentage of Broken Rice, Amylose Content, Gelatinization Temperature, Grain Length, Grain Width, ratio of Grain Length/ Grain Width, Grain Length after Cooking and Elongation Ratio, respectively.

Principal Component Factor Analysis of cooking properties of the rice genotypes using Minitab 16 software represented that the first and second factors had a 70% influence on diversity of the rice genotypes with variances of 4.2981 and 2.3953, respectively (Table 10).



Figure 7. Score plot of the rice genotypes on cooking properties. H and TM are abbreviation of Landraces Hashemi and Tarom Mahalli. M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13 are indicator of promising rice lines



Figure 8. Loading plot of cooking properties of the rice genotypes. PTC, PHR, PBR, AC, GT, GL, GW, GL/GW Ratio, GLC and El Ratio are abbreviation of Percentage of Total Conversion, Percentage of Head Rice, Percentage of Broken Rice, Amylose Content, Gelatinization Temperature, Grain Length, Grain Width, ratio of Grain Length/ Grain Width, Grain Length after Cooking and Elongation Ratio, respectively

Numerical amount of variances of three factors was more than 1. The first factor had positive correlation with percentage of total conversion, percentage of head rice, grain length and grain length/width ratio (r = 0.759, r = 0.835, r =0.852, r = 0.760), respectively. Although this factor had negative correlation with percentage of broken rice, grain length after cooking and elongation ratio (r = -0.757, r = -0.504, r = -0.872), respectively. The second factor was positively correlated (r = 0.521) with grain length/width ratio. But it had negative correlation with grain width and grain length after cooking (r = -0.900 and r = -0.698), respectively. Furthermore, third factor had a positive correlation (r = 0.937) with gelatinization temperature. Although numerical amount of variances of fourth factor was approximately 1, it was negatively correlated (r = -0.879) with amylose content. However, numerical amount of variances of other six factors was less than 1 and were not important and influencing factors. Four factors specially the first and second factors had the most influence factors on variation induced in the rice genotypes. So, considering the first and second factors, parental cultivar Hashemi, promising lines M2, M7, M8, M9, M10 and M13 derived from this landrace that represented similar cooking properties, were included in domain 1. In this domain, x and y amounts are positive (Figure 7).

After data analysis in Minitab 16 software, trait of grain length/width ratio that was included in domain 1, was selected

as the most influencing trait on variation between the rice genotypes (Figure 8).

Seven rice genotypes (parental cultivar Hashemi, promising lines M2, M7, M8, M9, M10 and M13 derived from this landrace with the highest grain length/width ratio were included in domain 1. Landrace Tarom Mahalli, promising line derived from this landrace (M5) and two salt-tolerant promising lines (M12 and M11) that had the highest percentage of total conversion and percentage of head rice were included in an independent group by Biplot analysis. Also, Minitab 16 software classified three promising lines derived from landrace Tarom Mahalli (M3, M4 and M6) in a distinct domain. The most salt sensitive promising line derived from landrace Tarom Mahalli (M1) was categorized in the last domain (Figures 7 and 9).

Cluster analysis of the rice genotypes on cooking properties indicated that the most salt-sensitive promising line M1 that had the least similarity with other genotypes, was included in an independent category (Figure 10).

Promising line M6 and landrace Hashemi had less similarity with other genotypes in their category. However, the most salt-tolerant promising line M12 had more similar properties with promising lines M11 and M5 in comparison with other genotypes in the category.



Figure 9. View of the rice genotype-by-trait biplot- Cooking properties. Y, PH, SPN, SPL, NFS, NES, PF and ThSW are abbreviation of Yield, Plant Height, Spike Number, Spike Length, Number of Full Seeds, Number of Empty Seeds, Percentage of Fertility and Thousand Seed Weight.



Figure 10. Cluster analysis of the rice genotypes on cooking properties. Numbers of 1-15 indicate genotypes of M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13, Landraces Hashemi and Tarom Mahalli. Numbers of 14 and 15 are indicator of landraces Hashemi and Tarom Mahalli

On mean comparisons of the grain yield and distribution of the studied cultivars based on biplot of the grain yield and indices, Saeidzadeh et al. (2016) indicated that the variety Hashemi had the highest grain yield among the studied genotypes and was characterized as a tolerant variety to salinity stress. Whereas in our research, this variety produced a moderately low yield and was almost sensitive to salt stress. Therefore, results of research Saeidzadeh et al. (2016) was in contradiction with our research results. In research of Mirdarmansouri et al. (2014), it was found that in total, cultivars of Shastak Mohammadi, Hassani and Tarom-Danesh were the highest tolerant cultivar in response to salinity (6 and 10 dSm⁻¹ NaCl) among other studied genotypes, whereas genotypes such as Tarom Mahalli and IR29 were salt stress sensitive. Results of this research confirm our research results that indicated landrace Tarom Mahalli was one of the most salt sensitive rice genotypes. Furthermore, Izaddoost et al. (2013), after principle component analysis and cluster analysis for clustering the studied genotypes under salt stress condition (4, 8 and 12 dSm⁻¹) exhibited that genotypes Shahpasand and Line 416 were the most salt-tolerant at seedling stage among the studied genotypes. However, landrace Hashemi in research of Izaddoost et al. (2013) such as our research was one of moderately tolerant genotypes in seedling stage.

In research of Sabouri et al. (2008), analysis of genotype code on IRRI standard method in salt stress (4 and 8 dSm⁻¹) conditions indicated that Tarom Mahalli with higher biomass, root and stem length and lower Na/K ratio is one of the salt-tolerant cultivars. These results were contrary with our results that represented landrace Tarom Mahalli is a salt sensitive cultivar. Also, research of Kamyab-Talesh et al. (2014)

indicated that Khazar cultivar was the most salt-sensitive cultivar in all salinity levels. This is accordance with our research results that represented this cultivar is one of the most salt sensitive cultivars. Baloch et al. (2003) indicated that the mutant variety Shua-92 derived from the standard varieties IR8 through mutation breeding, produced 40 and 49% higher paddy yield on salt affected soils than the famous salt-tolerant Indian varieties Nona Bokra and Pokkali. Similar results were achieved in our research. Thus, 2 mutant salt-tolerant promising lines M12 (HM5-250-42-1-E) and M11 (HM5-250-26-1-E-1) derived from the famous Iranian landrace Hashemi through mutation breeding, produced 80 and 60% higher paddy yield on salt affected soils than their salt moderately tolerant parental landrace Hashemi. Variety Shua-92 was evolved by irradiating the seeds of IR8 with 15 Gy fast neutrons in 1993. But 2 mutant salt-tolerant promising lines in our research was produced by gamma irradiation of the seeds of the famous landrace Hashemi. There were some contradictions between our research results and the results of other researchers. This greatly depended on salinity level of soil and water of the studied regions and plant growth stages and to some extent, climate conditions and kind of evaluation methods. For example, level of soil salinity in research of Saeidzadeh et al. (2016) was 4.77 dSm⁻¹ whereas soil salinity of our experimental rice farm was 6.5 dSm⁻¹ and this was impressive on different results obtained from two researches. This issue indicated landrace Hashemi had a lower salt tolerance in higher salinity condition. In research of Sabouri et al. (2008), landrace Hashemi was known as a salt tolerant cultivar on vegetative traits. In our research, evaluation of salt tolerance level of the genotypes was on yield and yield components and in result, landrace Tarom Mahalli was screened as one of the salt

sensitive genotypes. Results of Baloch et al. (2003) and our research represented that mutation breeding is an efficient tool for developing new abiotic stress tolerant rice genotypes with a favorable yield.

Conclusion

Overall, considering results of field evaluation, mean analysis and principal component factor analysis, the rice genotype-by-trait biplot and cluster analysis of yield and yield components of studied rice genotypes, promising line M12 (HM5-250-42-1-E) was selected as the most salt-tolerant genotype under salt stress condition. The most salt tolerant genotypes were derived from landrace Hashemi whereas any salt tolerant genotype with origin of cultivars Khazar and Fajr was not identified in this research. Promising line M12 can tolerate soil salinity up to EC of 8.5 dSm⁻¹ without any considerable reduction in yield. In addition, this promising line had unique and elite nutritional and cooking parameters such as the highest percentage of total conversion and percentage of head rice than other genotypes even the most famous Iranian high-quality landraces Hashemi and Tarom Mahalli. Also, promising line M12 is a marketable rice genotype and can bring a lot of economic income for rice farmers of the regions. It seems that promising line M12 (HM5-250-42-1-E) is an ideal option for development of rice cultivation and production especially in paddy fields and regions that are confronted with soil and water salinity in Iran and other regions of the world.

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