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Explore salt tolerant fenugreek genotypes seedlings using salt tolerance index

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Abstract

Saline condition is increasing at a global level and study of tolerance to salinity during germination is an important for the establishment of plants and growing in saline soil. This laboratory experiment was carried out to assess the germination and early seedling growth response to salinity stress. Evaluation of 10 genotypes of Fenugreek at five different salinity levels (0.0, 40, 80, 120 and 160 mM NaCl) was carried out during the 2016-2017 in the laboratory of SKN College of Agriculture, Jobner. To determine the salt tolerant Fenugreek genotypes using salt tolerance index, experiment consist of following genotypes namely RMT - 305, RMT - 351, RMT - 361, RMT - 354, RMT - 365, UM - 383, RMT - 1, RMT - 143, RMT - 303 and UM - 385. Fifteen seeds of each genotype were sown per sterilized petridish layered with autoclaved germination papers. Each petridish was irrigated with 3 ml of test solutions after draining out the previous days solutions. The temperature was 23 ± 2 °C in the culture room and the set was maintained in dark for the first two days followed by exposure to light of tube lights and incandescent bulbs. The experimental design was RBD with three replications. The experiment was terminated after 8th day of sowing in petri dishes and average germination percentage, shoot length, root length, shoot fresh weight, root fresh weight, shoot dry weight, root dry weight, total dry weight and salt tolerance index were recorded. The salt tolerance index (STI) of the genotypes, expressed as the ratio of dry matter yield produced under the NaCl treatments compared to the control treatment, was found to be a reliable criterion for ranking genotypes for their tolerance to NaCl. Genotypes UM-385, RMT-365, RMT-143 and RMT-351 were found most tolerant among above ten genotypes. These lines can be utilized to develop new varieties and hybrids with high germination and better seedling establishment in salinity with higher yielding ability. Cultivation of these salt tolerant genotypes on saline land would be a viable option to ensure food security under this climate change scenario.

Keywords: Fenugreek, salinity, salt tolerance index (STI), seedling, NaCl

Introduction

Salinity is one of the important factors affecting germination and seedling growth of plant. Salinity is the major abiotic constrain of crop production in arid and semi-arid regions where soil salt content that is naturally high and precipitation can be insufficient for leaching (Zhao *et al.*, 2007) [26]. Over 6% of the world's land is affected by salinity/sodicity, this accounts for more than 800 million ha of land (Food and Agriculture Organization of the United Nations (FAO), 2010 [11]). Therefore, genetically stress-tolerant varieties are basic need for the plant breeder. The identification of salt-tolerant genotypes is the starting point for such breeding studies. This study was conducted to determine and assess the tolerance of fenugreek genotypes under saline conditions and identify the salt tolerant genotype. Soil salinity is a condition in which the soluble salt content of the soil reaches a level harmful to crops through the reduced osmotic potential of the soil solution and the toxicity of specific ions. Fenugreek (*Trigonella foenum-graecum* L.) is a self-pollinated, small seeded, annual legume which belongs to family fabaceae. It has chromosome number $2n = 2x = 16$. It is an important multipurpose winter season seed spice crop. It is moderately tolerant to salinity. Generally, most of the plants cannot survive under high soil salinity conditions. Salinity leads to weak growth and development resulting in drastic loss in yield and quality. Due to increasing the salinity problems in all over the world, we need to focus to overcome this abiotic stress by given more attention to crop breeding for salinity. The development of salt tolerant crop has a significant importance on agricultural and economical aspects (Dulai, *et al.*, 2011) [9]. Besides germplasm resources, the use of efficient selection criteria would help breeders. However, it is difficult to say that the breeders have efficient selection criteria and tools for improvement of salt tolerant varieties.

Rather than a long-term breeding program, the determination of more tolerant varieties to grow in saline soils may be a short-term solution (Khalid *et al.*, 2001)^[17].

Salinity affects the morphological, physiological and biochemical activities in plant such as reduction in seed germination decrease in shoot and root length, alterations in the integrity of cell membranes, changes in different enzymatic activities and photosynthesis. It also affects metabolic activities by reducing the ability of plants to take up water that reduces plant growth. Seed germination is a complicated process and is sensitive to salt stress. Salinity influence seed germination by reducing the osmotic potential and toxicity of specific ions such as sodium and chlorine, as well as reducing essential nutrients such as calcium and potassium. Both, phase of germination and seedling establishment is most critical stage for determine the crop yield. Salinity affects all stages of growth and development, resulting in stunted growth, restricted lateral shooting and reduction in the size of leaves, fruits and seeds and ultimately reduced yield. The deleterious consequences of high saline conditions in the plant cells are hyper-osmotic shock and ionic imbalance. Although, salt stress affects all growth stages of a plant but seed germination and seedling growth stages are known to be more sensitive for most of the plant species.

Material and Method

The laboratory experiment was carried out at Department of Plant Breeding and Genetics, Sri Karan Narendra Agriculture University, Jobner-303329, Rajasthan, India in December, 2016 where the temperature was 23±2 °C. The seeds of ten genotypes of fenugreek namely RMt - 305, RMt – 351, RMt – 361, RMt – 354, RMt – 365, UM – 383, RMt – 1, RMt – 143, RMt – 303 and UM – 385 were used for evaluation. Prior to germination, the seeds were surface sterilized with 0.1% mercuric chloride for 1 minute and washed 3 times under running tap water followed by washing with double distilled water.

Treatments and experimental design: The experiment consists of 10 genotypes and 5 salinity levels were laid out in randomized block design with three replications. The number of petri dishes needed for this experiment was 150 (10×5×3). Five different salinity levels designated as S0, S1, S2, S3, and S4 viz., 0.0, 40, 80, 120 and 160 mM NaCl were prepared by dissolving 0.0, 584.4, 1168.8, 1753.2 and 2337.6 mg NaCl in 250 ml double distilled water, respectively.

Preparations and sterilization of Petri dishes and germination papers: petri dishes of 9 cm diameter are sterilized at 165 °C for 4 hours in hot air oven and germination papers were autoclaved at 15 psi and 121 °C for 20 minutes.

Procedure for germination: The 15 seeds of each genotype were germinated in petri dishes layered with germination papers and then moistened with 3 ml of test solutions daily after removing previous day solution. The set was maintained in dark for first two days. The germination was recorded on 7th day after seed planting.

Observations recorded: All observations were recorded on 8th day of planting on different characters. Five seedlings were randomly selected from each petridish to observe the data on shoot length, root length, shoot fresh weight, root fresh

weight, shoot dry weight, root dry weight and total dry weight. The data on shoot dry weight and root dry weight was recorded after drying in hot air oven for 48 hours at 65 °C. The methods used for recording observations are described below:

Germination Percentage: A seed was considered as germinated at the emergence of both root and shoot up to 2 mm length (Chartzoulakis *et al.*, 2000)^[6]. The germination was recorded on 7th day after planting and germination percentage was determined by using the following formula (Aniat *et al.*, 2012)^[3].

$$\text{Germination Percentage} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds sown}} \times 100$$

Shoot and Root Length: On 8th day the shoot and root length of germinated seeds was recorded. For this, randomly selected five seedlings were divided into two parts viz., shoot and root and length was measured using measuring scale in centimeter and averaged. The hypocotyl length was included in shoot length.

Shoot and Root Fresh Weight: The fresh weight of shoots and roots from the five seedlings which were selected already from each replication and in each treatment was measured in milligram by using a sensitive electronic balance and averaged.

Shoot, Root and Total Dry Weight: The fresh shoots and roots which were taken for weight were kept into paper bags. The name of genotypes and levels of salinity were written on paper bags by marker for further identification. After taking fresh weight these were kept in oven at 65 °C for 48 hours for drying. After drying, the dried shoots and roots were weighed by sensitive electronic balance in milligram and average was calculated. The total dry weight was calculated by adding dry weight of shoot and root.

Salt Tolerance Index: Salt tolerance index of already selected five seedlings was calculated by the following formula Kokten *et al.*, 2000^[19]:

$$STI = \frac{\text{TDW at one of the salinity level}}{\text{TDW at control}} \times 100$$

Where, STI = Salt tolerance index and TDW = Total (root + shoot) dry weight

Statistical Analysis

The data obtained from this study were subjected to analysis of variance following standard statistical methods (Panse and Sukhatme)^[21] and significant differences among the mean values were compared by least significant difference (LSD) test ($P < 0.05$).

Experimental Results

Analysis of Variance

The pooled analysis of variance indicated that the genotypes, salinity levels and genotype x salinity interaction exhibited significant mean sum of squares for all the characters except germination percentage due to genotypes. This indicated differential response of genotypes to salinity levels for all the characters.

Effect of Salinity on Mean Performance

The mean values at different salinity levels for various genotypes and characters are presented in Table 3.2. Perusal of table revealed that the mean values of all the characters varied along the salinity gradient. The values were maximum in the control (S₀) and were minimum at the highest salinity level (S₄) for majority of characters.

Germination percentage: The magnitude of germination percentage decreased with increase in salt concentration. It was highest in S₀ (96.89%) then decreased progressively in S₁ (93.33%), S₂ (89.11 %), S₃ (88.44%) and S₄ (82.67%). It ranged from 91.11 % (RMT-354) to 100 % (RMT-1, RMT-303 and UM-385) in S₀, 88.89% (RMT-1) to 97.78% (RMT-303) in S₁, 82.22% (RMT-351) to 95.55% (RMT-303& RMT-305) in S₂, 80.00 % (RMT-351) to 95.55 % (RMT-303& RMT-305) in S₃ and 75.55 % (RMT-365& UM-385) to 91.11 % (RMT-303) in S₄ salinity level. The range was wider in S₃ and S₄ as compared to S₀ and S₁ salinity level indicated that higher salinity adversely affected germination.

Shoot length (cm): The shoot length was also decreased with increasing level of salinity. It was highest in S₀ (7.16 cm) then decreased progressively in S₁ (6.98 cm), S₂ (5.78 cm), S₃ (4.24 cm) and S₄ (2.71 cm). It ranged from 5.71 cm (RMT-361) to 7.79 cm (UM-383) in S₀, 6.51 cm (RMT-351) to 7.87 cm (UM-385) in S₁, 5.07 cm (RMT-361) to 6.61 cm (UM-385) in S₂, 3.40cm (RMT-305) to 5.19 cm (RMT-143) in S₃ and 2.05cm (RMT-305) to 5.19 cm (UM-383) in S₄ salinity level.

Root length (cm): The root length was highest in S₀ (4.50 cm) and it was decreased with increasing salinity levels as following in S₁ (4.21 cm), S₂ (4.05 cm), S₃ (3.99 cm) and S₄ (3.99 cm). It ranged from 3.67 cm (RMT-305) to 5.39 cm (UM-385) in S₀, 3.47 cm (RMT-365) to 5.38 cm (RMT-143) in S₁, 3.11 cm (UM-383) to 4.79 cm (RMT-143) in S₂, 3.17 cm (RMT-365) to 4.51 cm (RMT-303) in S₃ and 2.29 cm (RMT-143) to 3.16 cm (RMT-303) in S₄ salinity level.

Shoot fresh weight (mg): In case of shoot fresh weight also decreased with increasing level of salinity except in S₁. The magnitude of this parameter was highest in S₁ (110.68 mg) as compared to S₀ (107.78 mg), then decreased in S₂ (95.12 mg), S₃ (70.58 mg) and in S₄ (54.45 mg). It ranged from 95.53 mg (UM-383) to 138.83 mg (RMT-303) in S₀, 78.91 mg (RMT-1) to 138.76 mg (RMT-303) in S₁, 70.93 mg (RMT-365) to 119.41 mg (RMT-303) in S₂, 60.22 mg (RMT-1) to 81.13 mg (RMT-143) in S₃ and 45.40 mg (RMT-305) to 68.56 mg (RMT-303) in S₄ salinity level.

Root fresh weight (mg): There was also a decreasing trend with increasing salinity level but it did not affect with slightly increase salinity upto 40 mM. It was found maximum in S₀ and S₁ (31.44 mg) and later decreased in S₂ (31.16 mg), S₃ (28.63 mg) and S₄ (16.36 mg). It ranged from 20.91 mg (RMT-303) to 39.56 mg (RMT-305) in S₀, 23.17 mg (RMT-351) to 37.15 mg (UM-383) in S₁, 22.60 mg (RMT-365) to 39.38 mg (RMT-303) in S₂, 24.15 mg (RMT-1) to 34.69 mg (RMT-303) in S₃ and 13.94 mg (RMT-365) to 17.86 mg (RMT-354) in S₄.

Shoot dry weight (mg): In case of Shoot dry weight also decreased with increasing level of salinity except in S₁. The

magnitude of this parameter was highest with quite similar in S₁ (78.6 mg) as compared to S₀ (78.5 mg), then decreased in S₂ (7.76 mg), S₃ (7.03 mg) and in S₄ (6.98 mg). It ranged from 5.92 mg (RMT-365) to 10.25 mg (RMT-303) in S₀, 5.87 mg (RMT-1) to 10.33 mg (RMT-303) in S₁, 6.10 mg (RMT-1) to 10.45 mg (RMT-303) in S₂, 5.48 mg (RMT-351) to 8.58 mg (UM-385) in S₃ and 5.34 mg (RMT-365) to 9.33 mg (RMT-303) in S₄ salinity level.

Root dry weight (mg): The Root dry weight also decreased with increasing level of salinity. It was highest in control S₀ (1.20). The magnitude of this parameter was quite similar in S₁ (1.15 mg) and S₂ (1.16 mg), then decreased in S₃ (1.09 mg) and in S₄ (0.88 mg). It ranged from 0.90 mg (RMT-354) to 1.29 mg (UM-383) in S₀, 0.91 mg (RMT-1) to 1.35 mg (RMT-361) in S₁, 0.99 mg (RMT-1) to 1.36 mg (UM-385) in S₂, 0.84mg (RMT-365) to 1.22 mg (RMT-361) in S₃ and 0.74 mg (RMT-365) to 1.17 mg (UM-385) in S₄ salinity level.

Total dry weight (mg): The Total dry weight also decreased with increasing level of salinity. It was highest in control S₀ (9.05) then decreased in S₁ (9.00 mg) and S₂ (8.92 mg), in S₃ (8.12 mg) and in S₄ (7.85 mg). It ranged from 6.89 mg (RMT-365) to 11.51 mg (RMT-303) in S₀, 6.78 mg (RMT-1) to 11.54 mg (RMT-303) in S₁, 7.09 mg (RMT-1) to 11.63 mg (RMT-303) in S₂, 6.61 mg (RMT-351) to 9.79 mg (UM-385) in S₃ and 6.08 mg (RMT-365) to 10.23 mg (RMT-303) in S₄ salinity level.

Salt tolerant index (%): The mean effect of Salt tolerance index was found maximum (100%) under control condition and decreased with increasing salinity levels but at moderate level of salinity (S₁) was found slightly larger (100.80%) than the control (S₀). It was decreased in S₂ (99.49%) followed by S₃ (91.20%) and S₄ (87.53%). The magnitude of salt tolerance index was higher for some genotype RMT-351 (124.42%), UM-385 (122.27%), RMT-365 (111.19%), UM-383 (102.73%) and RMT-303 (100.50%) at lower salinity level (S₁) than the control. The magnitude of salt tolerance index was found maximum for mostly genotype at S₂ salinity level RMT-365 (119.07%), UM-385 (108.10%), RMT-143 (106.04%), RMT-305 (104.26%), RMT-361 (103.56%), RMT-351 (102.62%) and RMT-303 (101.30%) than the control. At the higher level of salinity (S₃), salt tolerance index was found higher for some genotype RMT-365 (110.99%), UM-385 (106.79%) and RMT-143 (104.73%) than the control. Most tolerant genotype at highest salinity level S₄ was RMT-143 (98.49%). The wide range of salt tolerance index with the increasing level of salinity was found. It varied from 67.83% to 124.42% in S₁, 70.61% to 119.07% in S₂, 66.74% to 110.99% in S₃ and 71.20% to 98.49% in S₄.

Based upon the rank totals of a genotype, the genotype UM-385, RMT-365, RMT-143 and RMT-351 were found to be most tolerant genotype over different salinity levels. RMT-36, RMT-354 and RMT-303 genotype were found moderately tolerant to saline conditions. RMT-1, UM-383 and RMT-305 genotypes were found least tolerant to saline land.

Discussion

Fenugreek is an important spice crop and also used as a medicinal plant, which is cultivated in various agro climatic region of the country. Fenugreek is regarded as moderately tolerant to salinity (Niknam and McComb, 2000) ^[20].

Development of salinity tolerant lines is an ideal way to mitigate the negative effects of salinity on fenugreek cultivation. The findings emanating from the present investigation are discussed here in the light of available literature.

Analysis of Variance

Analysis of variance revealed significant difference among the genotypes for all the traits except for germination percentage at low levels of salinity (S_0 and S_1). Similar results have also been reported by Asaadi, 2009^[4] and Ratnakar and Rai, 2013^[23] in fenugreek and by Ashagre *et al.*, 2013^[5] in chickpea. Significant difference indicated presence of sufficient genetic variability in the material used for this investigation.

Effect of salinity on mean performance of genotypes:

Comparison of mean values of different characters indicated that for most of the characters, these values decreased under saline condition particularly for germination percent and various seedling traits like shoot length, root length, shoot and root fresh weight and dry weight. Decrease in mean performance with increasing salinity levels was less in root length, shoot dry weight and root dry weight. This reduction in mean performance was very well expected, owing to the reduction in overall plant growth in stress (saline) environment (Jain and Agarwal, 1991; Abdelmoumen and EL-Idrissi, 2009)^[14, 1]. It might be concluded that effect of salinity on different characters was not uniform; some characters were influenced more while other less. This reduction in mean performance was due to salts of different nature and concentration because increased water potential, restricted the movement of water towards the seed surface (Houimli *et al.*, 2008)^[13]. Variation for germination and

seedling characteristics at different salinity levels was widely reported in wheat (Khayatnezhad *et al.*, 2010)^[18], in fenugreek (Ghorbanpour *et al.*, 2011; Soughir *et al.*, 2013; Kapoor and Pande, 2015; and Ratnakar and Rai, 2013)^[12, 25, 15, 23], in spinach (Keshavarzi *et al.*, 2011)^[16], in chickpea (Ashagre *et al.*, 2013)^[5], in mungbean (Dutta and Bera, 2014)^[10], in sorghum (Dadar *et al.*, 2014)^[8] and in oat (Chauhan *et al.*, 2016)^[7]. The salinity gradient adversely affected the mean values of all the characters with increase in the salinity gradient except in S_1 shoot fresh weight. There is no difference for root fresh weight in S_1 and S_2 . Like root length that was less affected by salinity because shoot length was found to be more sensitive than root length. Root fresh weight and Total dry weight reduced highly at high salinity levels, it has been reported previously by Ramoliya *et al.*, (2004)^[22] and Asaadi (2009)^[4]. Generally, the mean values were maximum in the control and then decreased in S_1 , S_2 and S_3 and minimum at the highest level of salinity (S_4). Such observations were reported earlier in fenugreek (Kapoor and Pande, 2015^[15] and Ratnakar and Rai, 2013)^[23], in spinach (Keshavarzi *et al.*, 2011)^[16] and in oat (Chauhan *et al.*, 2016)^[7]. Interestingly reduction in the mean values of shoot dry weight was not much significantly different in 40 mM as compared to the control (0.0 mM). Such stimulatory effect of low salinity has been reported earlier by Jain and Agarwal (1991)^[14]. Since the genotype x salinity interaction was significant for all the traits except germination percentage. This indicated the differential response of genotypes to the salinity levels. It reported earlier by Asaadi, 2009^[4]; and Ratnakar and Rai, 2013^[23] in fenugreek. It would be worthwhile to compare the genotypes over different salinity levels for different characters, rather than the pooled mean alone. None of the genotypes showed uniform response under different salinity levels for any given character.

Table 1: The Pooled ANOVA for various traits under different salinity levels

Characters	Source of variation with degree of freedom				
	Genotypes (9)	Salinity levels (4)	Replication/ Salinity (10)	Genotype x Salinity (36)	Error (90)
Germination (%)	167.217**	866.278**	30.207	29.169	20.343
Shoot length (cm)	1.417**	107.260**	0.203	0.572**	0.125
Root length (cm)	1.399**	14.140**4**	0.053	0.608**	0.062
Shoot fresh weight (mg)	1056.196**	17887.158**	3.747	269.856**	2.757
Root fresh weight (mg)	84.874**	1270.848**	3.271	54.101**	1.891
Shoot dry weight (mg)	15.756**	6.065**	0.065	2.177**	0.117
Root dry weight (mg)	0.193**	0.505**	0.008	0.041**	0.004
Total dry weight (mg)	18.246**	9.435**	0.08	2.274**	0.131

* and ** represent significant at 5% and 1% level of significance, respectively.

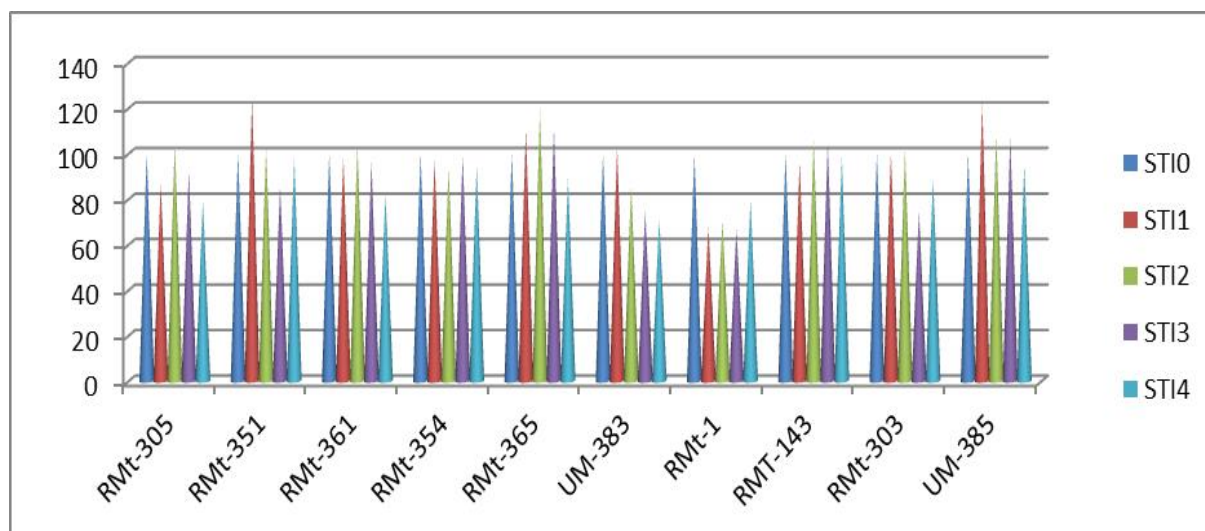
Table 2: The mean values of genotypes for different characters over different salinity levels

Genotype	Germination Percentage					Shoot Length (cm)					Root Length (cm)				
	S_0	S_1	S_2	S_3	S_4	S_0	S_1	S_2	S_3	S_4	S_0	S_1	S_2	S_3	S_4
RMt-305	95.55	95.55	95.55	95.55	88.89	7.33	7.30	5.67	3.40	2.05	3.67	3.97	3.85	3.45	2.30
RMt-351	95.55	91.11	82.22	80.00	84.45	6.95	6.51	5.75	4.01	2.83	3.85	3.74	3.88	4.29	2.94
RMt-361	97.78	95.55	93.33	91.11	84.45	5.71	6.53	5.07	3.42	2.61	3.69	3.53	4.06	3.69	2.66
RMt-354	91.11	91.11	84.45	82.22	80.00	7.31	7.27	5.68	4.92	2.68	4.67	4.71	4.45	3.87	3.07
RMt-365	95.55	91.11	88.89	88.89	75.55	7.41	6.87	5.79	4.19	2.93	4.60	3.47	3.81	3.17	3.00
UM-383	95.56	95.55	84.45	84.44	77.78	7.79	6.89	5.39	4.36	3.20	5.29	4.36	3.11	4.16	2.43
RMt-1	100.00	88.89	88.89	86.67	82.22	6.91	6.75	6.03	3.98	2.75	4.69	4.51	3.67	3.89	2.88
RMT-143	97.78	93.33	86.67	91.11	86.67	6.93	6.83	6.08	5.19	2.75	4.47	5.38	4.79	4.49	2.29
RMt-303	100.00	97.78	95.55	95.55	91.11	7.49	6.95	5.74	5.17	2.85	4.65	4.53	4.51	4.51	3.16
UM-385	100.00	93.33	91.11	88.89	75.55	7.73	7.87	6.61	3.71	2.46	5.39	3.94	4.32	4.39	2.43
Overall mean	96.89	93.33	89.11	88.44	82.67	7.16	6.98	5.78	4.24	2.71	4.50	4.21	4.05	3.99	2.72
CD	6.26	6.99	8.03	8.64	8.50	0.71	0.69	0.75	0.45	0.31	0.40	0.44	0.53	0.43	0.32
CV (%)	3.77	4.37	5.25	5.69	5.99	5.75	5.79	7.60	6.16	6.68	5.20	6.05	7.65	6.22	6.84

Genotype	Shoot fresh weight(mg)					Root fresh weight(mg)					Shoot dry weight(mg)				
RMt-305	122.04	121.31	100.67	70.88	45.40	39.56	31.81	29.91	28.23	14.47	9.14	7.81	9.53	8.40	7.20
RMt-351	103.77	121.36	99.99	69.59	50.69	29.00	23.17	25.72	24.71	17.39	6.69	8.45	6.85	5.48	6.69
RMt-361	98.41	108.67	90.59	71.43	53.67	27.81	33.41	33.76	30.59	17.27	7.66	7.82	8.40	7.75	6.85
RMt-354	105.14	101.41	90.39	68.18	51.94	30.50	29.80	29.58	27.07	17.86	7.30	6.80	6.67	6.93	6.87
RMt-365	105.95	108.87	70.93	70.59	60.95	30.99	33.35	22.60	27.29	13.94	5.92	6.60	7.11	6.77	5.34
UM-383	95.53	106.31	86.83	78.00	59.57	35.76	37.15	38.86	28.31	17.31	7.89	8.26	6.63	5.67	5.63
RMt-1	103.69	78.91	82.20	60.22	46.39	32.94	27.19	33.45	24.15	15.81	8.76	5.87	6.10	5.67	7.20
RMT-143	95.55	110.24	97.21	81.13	46.33	30.46	24.67	30.54	29.41	14.63	6.87	6.75	7.28	7.59	7.11
RMt-303	138.83	138.76	119.41	67.16	68.56	20.91	42.14	39.38	34.69	17.48	10.25	10.33	10.45	7.42	9.33
UM-385	108.90	110.92	112.93	68.65	60.95	36.51	31.72	27.78	31.89	17.41	7.97	9.88	8.55	8.58	7.54
Overall mean	107.78	110.68	95.12	70.58	54.45	31.44	31.44	31.16	28.63	16.36	7.85	7.86	7.76	7.03	6.98
CD	2.36	3.09	3.43	2.68	2.54	3.22	2.52	2.25	2.17	1.15	0.93	0.55	0.63	0.28	0.28
CV (%)	1.28	1.63	2.10	2.22	2.72	5.97	4.67	4.21	4.43	4.08	12.94	11.39	12.67	8.72	13.83
Genotype	Root dry weight (mg)					Total dry weight (mg)					Salt tolerant index (%)				
RMt-305	1.23	1.17	1.25	1.15	0.98	10.37	8.97	10.78	9.55	8.18	100.00	86.83	104.26	92.19	79.13
RMt-351	1.01	1.13	1.05	1.13	0.83	7.70	9.58	7.90	6.61	7.52	100.00	124.42	102.62	85.91	97.64
RMt-361	1.69	1.35	1.27	1.22	0.81	9.35	9.17	9.67	8.97	7.67	100.00	98.42	103.56	96.25	82.22
RMt-354	0.90	1.16	1.03	1.19	0.86	8.20	7.96	7.70	8.13	7.73	100.00	97.10	93.91	99.16	94.41
RMt-365	0.97	1.03	1.05	0.84	0.74	6.89	7.63	8.16	7.61	6.08	100.00	111.19	119.07	110.99	88.73
UM-383	1.29	1.15	1.21	1.18	0.91	9.18	9.41	7.84	6.85	6.53	100.00	102.73	85.45	74.63	71.20
RMt-1	1.27	0.91	0.99	1.00	0.75	10.03	6.78	7.09	6.67	7.95	100.00	67.83	70.61	66.74	79.53
RMT-143	1.22	1.04	1.25	0.85	0.83	8.09	7.79	8.53	8.43	7.93	100.00	96.67	106.04	104.73	98.49
RMt-303	1.27	1.21	1.17	1.15	0.90	11.51	11.54	11.63	8.57	10.23	100.00	100.50	101.30	74.59	88.94
UM-385	1.19	1.33	1.36	1.21	1.17	9.17	11.21	9.91	9.79	8.71	100.00	122.27	108.10	106.79	95.01
Overall mean	1.20	1.15	1.16	1.09	0.88	9.05	9.00	8.92	8.12	7.85	100.00	100.80	99.49	91.20	87.53
CD	0.13	0.13	0.12	0.11	0.09	0.94	0.63	0.69	0.30	0.30	0.00	12.27	12.96	10.31	9.38
CV (%)	6.28	6.39	5.88	5.65	5.66	6.07	4.06	4.48	2.18	2.22	0.00	7.10	7.59	6.59	6.25

Table 3: Ranking of genotypes based upon salt tolerance index (STI)

Genotype	Salinity levels and rank of genotypes										
	S0	S1		S2		S3		S4		Rank	Overall
	STI	STI	Rank	STI	Rank	STI	Rank	STI	Rank	Total	Rank
RMt-305	100.00	86.83	9	104.26	4	92.19	6	79.13	9	28	8
RMt-351	100.00	124.42	1	102.62	6	85.91	7	97.64	2	16	4
RMt-361	100.00	98.42	6	103.56	5	96.25	5	82.22	7	23	5
RMt-354	100.00	97.10	7	93.91	8	99.16	4	94.41	4	23	5
RMt-365	100.00	111.19	3	119.07	1	110.99	1	88.73	6	11	2
UM-383	100.00	102.73	4	85.45	9	74.63	8	71.20	10	31	9
RMt-1	100.00	67.83	10	70.61	10	66.74	10	79.53	8	38	10
RMT-143	100.00	96.67	8	106.04	3	104.73	3	98.49	1	15	3
RMt-303	100.00	100.50	5	101.30	7	74.59	9	88.94	5	26	7
UM-385	100.00	122.27	2	108.10	2	106.79	2	95.01	3	9	1

**Fig 1:** Ranking of genotypes based upon salt tolerance index (STI)

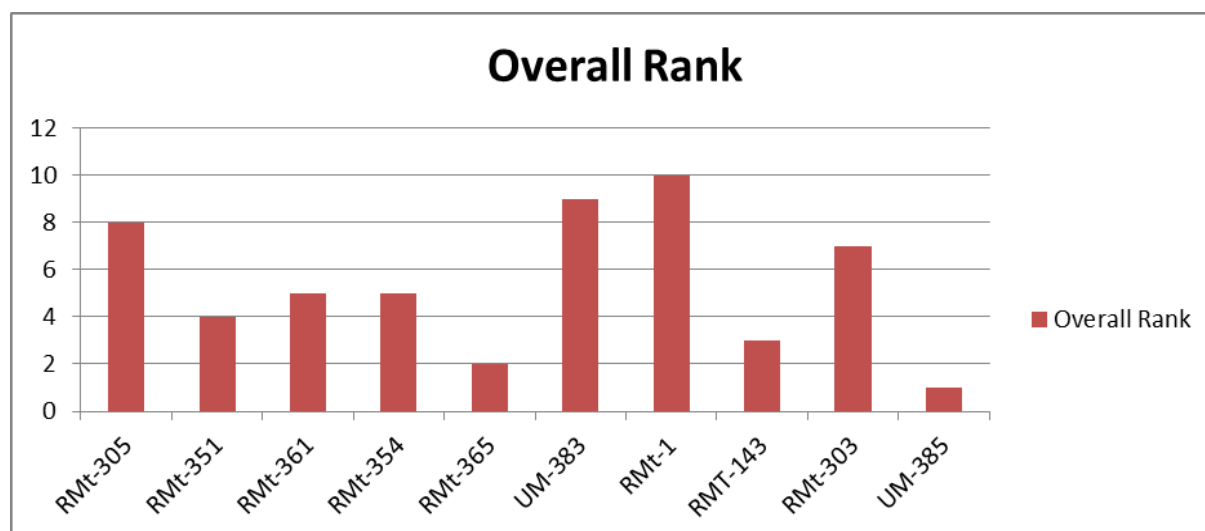


Fig 2: Overall Ranking of genotypes based upon salt tolerance index (STI)

Conclusion

The early seedling parameters of genotype showed significantly variation at higher salinity in comparison to 0 to 40 mM NaCl salinity level for most of the characters. Various salt tolerance indices were shown to be useful for estimation of stress level and identification of salt tolerant elite genotypes. Several studies proposed the use of STI in screening program for salt tolerance rather than other indices (Ali *et al.* 2007; Shahzad *et al.* 2012) [2, 24]. The genotype UM-385, RMT-365, RMT-143 and RMT-351 were found to be most tolerant genotype over different salinity levels using STI. Such potential lines could serve for effective exploitation for further breeding purposes as a source for salt-responsive candidate genes suitable for crop improvement in saline land as viable option to ensure food security under this climate change era.

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