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Research article

SCREENING OF MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK] GENOTYPES FOR SALT TOLERANCE

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ABSTRACT: Thirty nine mungbean genotypes exhibiting distinct and significant response during screening for salt tolerance at early seedling growth stage were screened at vegetative, flowering and pod-filling growth stages up to the harvest under two salinity stress levels i.e. 50 mM and 75 mM NaCl along with their respective control treatment. The experiment was conducted in earthen pots lined with polythene bags in complete randomized block design with reliable growth and physiological characteristics along with yield attributes. The results illustrated significant variations and adaptability among all the genotypes under salt stress. The tolerant genotypes were observed for less reduction in RWC, MSI, total chlorophyll and carotenoid contents, plant length, survival, K^+/Na^+ ratio, and grain yield even under high salinity level (75mM NaCl) with respect to their non-stressed plants. However, the susceptible genotypes showed greater reduction in the measured parameters under salinity stress. On the basis of low and best performance of each genotypes under high salinity levels, total eleven genotypes TCR86, PLM380, PLM562, WGG37, IC615, PLM891, IC2056, IC10492, PLM32, K851, and BB92R were selected from this study which will be screened further for salt tolerance for the identification of most salt tolerant and susceptible genotypes to be used in breeding for the genetic improvement of mungbean for saline soils. The study indicated that selection of genotypes according to their performance under saline condition is very important for the selection of salt tolerant genotypes.
Keywords: Mungbean, Salinity stress, Screening, Performance

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is an important, self-pollinated and environment friendly food grain legume of dry land agriculture with rich source of proteins, vitamins, and minerals for the poor's vegetarian diet in developing and underdeveloped countries [1]. Capacity to restores soil fertility and short life span makes it valuable in various cropping systems particularly rice and wheat. It is generally grown for its edible seeds, sprouts, noodles and consumed as dhal in Asian subcontinents. India is the largest producer and consumer of mungbean and accounts for about 65% of the world acreage and 54% of the world production of this crop [2]. It is the third most important pulse crop in India, occupying nearly 3.72 million ha area with 1.56 million tons production [3]. However, cultivated, weedy and wild germplasm of mungbean are available, very little is known regarding population structure, diversity, and gene flow and/or introgression. Additionally, the taxonomy of mungbean at varietal or subspecies level is still doubtful [4]. Its stagnant production in last few decades is due to susceptibility towards various biotic (Mungbean yellow mosaic virus, powdery mildew and *Cercospora* leaf spot) and abiotic (salinity, drought, temperature, and water-logging) stresses at different growth stages. Among the abiotic stresses, salinity stress is more atrocious limiting growth and grain yield world-wide where 50 mM NaCl can cause more than 60% yield losses [5]. The increased salinity of arable land is expected to have overwhelming global effects, resulting in up to 50% land loss by the middle of the twenty-first century [6]. It is continuously raising the concern for the researchers in this field to enhance the agricultural productivity of nutritious staple food crop, mungbean as per the demand of increasing population world-wide especially in the underdeveloped and developing countries. Authors reported that the greater accumulation of salt decreased the osmotic potential of soil solution eliciting water stress in plants and further interactions of the salts with mineral nutrition caused nutrient imbalance and deficiencies, oxidative stress or even pathology ultimately lead to plant death as a consequence of growth arrest and metabolic damage [7, 8].

To date, over 110 mungbean cultivars have been released by AVRDC in South and Southeast Asia and around the world. These cultivars are early and uniformly maturing (55-65 days), high yielding, and disease resistant. Salt tolerance is a polygenic, genotype dependent and developmental stage-specific phenomenon, therefore, tolerance at initial developmental stage may not be correlated with tolerance at later developmental stages. Because of the complex nature of salinity stress and lack of appropriate techniques for introgression little progress has been made to identify and develop salt tolerant mungbean varieties [9]. Therefore, it necessitate to enhance the productivity of the agronomically valuable food grain legumes to fulfill the demand of the geometrically increasing population by exploiting scarce natural resources more efficiently. Keeping the importance of all these aspects in mind, the present study was designed to observe the performance of earlier selected genotypes under saline conditions for later growth stages.

MATERIAL AND METHODS

Plant material

Thirty Nine mungbean genotypes selected from our earlier study of screening for salt tolerance at germination and early seedling growth stage were used as plant material for this study (data not shown). The seeds of all the genotypes were procured from core collection at National Bureau of Plant Genetic Resources (NBPGR), New Delhi and Division of Genetics, Indian Agricultural Research Institute, New Delhi (Tables 1).

Table 1 Details of the mungbean genotypes used for screening for salt tolerance

S.No.	Name of the accessions	Plant source	Genetic resource
1	PLM-184	*Vigna radiata* (C)	NBPGR, New Delhi-110012
2	PLM-734	,,	,,
3	IC-615	,,	,,
4	IC-2056	,,	,,
5	IC-10492	,,	,,
6	MH-96	,,	Division of Genetics, IARI, New Delhi-110012
7	PLM-32	,,	NBPGR, New Delhi-110012
8	PLM-256	,,	,,
9	PLM-303	,,	,,
10	T-44	,,	Division of Genetics, IARI, New Delhi-110012
11	PLM-884	,,	NBPGR, New Delhi-110012
12	ET-52196	,,	,,
13	PLM-231	,,	,,
14	PLM-562	,,	,,
15	PLM-891	,,	,,
16	PLM-380	,,	,,
17	PLM-953	,,	,,
18	PLM-707	,,	,,
19	PLM-777	,,	,,
20	PLM-334	,,	,,
21	PLM-111	,,	,,
22	PLM-748	,,	,,
23	PLM-975	,,	,,
24	WGG-37	,,	,,
25	IC-618	,,	,,
26	ET-52200	,,	,,
27	IC-10497	,,	,,
28	EC-5478	,,	,,
29	ET-52191	,,	,,
30	STV-2635	,,	,,
31	PLM-416	,,	,,
32	K851	,,	Division of Genetics, IARI, New Delhi-110012
33	ET-52194	,,	NBPGR, New Delhi-110012
34	LGG-450	,,	,,
35	BB-9-2R	*Vigna sublobata* (W)	,,
36	TCR-86	*Vigna trilobata* (W)	,,
37	ET-52201	*Vigna radiata* (C)	,,
38	PDM-11	,,	,,
39	PLM-666	,,	,,

W= wild relative of mungbean; C= cultigens

Salinity levels

Three salinity levels of 0mM NaCl (Control) , 50mM NaCl (T_1), and 75mM NaCl (T_2) were prepared by dissolving sodium chloride in the water used for irrigation to impose stress in the cultivated and wild relatives of mungbean. The control treatment was without sodium chloride.

Sowing of the seeds and salt treatment

Rhizobium treated seeds of all the selected mungbean genotypes were sown in 30 cm earthen pots (30 x 30 cm) containing 10 kg of soil, sand, and manure in 1:2:1 ratio. The pots were lined with 400 gauge polythene bags to avoid leaching of the salt during irrigation. The whole experiment was conducted in completely randomized block design (RBD) with 10 replications per treatment under an artificial rain shelter or hut made up of bamboos and polythene (PVC) with approximate 99% transparency or visibility so that the plants could absorb the sufficient light for photosynthesis and growth and the other contaminating or stress causing factors like natural rain, strong wind etc. interfering with the salinity treatment could be avoided. The removal of the weeds was done by hand regularly and the irrigation practice was maintained manually at regular intervals of time for the crop season. The plants were thinned to 5 plants per pot after one week of seed germination. The NaCl solutions of two concentrations i.e. 50mM (T_1) and 75mM (T_2) was applied to the plants i.e. 2.5 litre/kg of soil, after the emergence of fully expanded primary leaves in all the genotypes for imposing salinity stress. The plants applied with equal volume of water without NaCl were used as control (C). Scheduled routine of irrigation was practiced for both the control and the salt treated pots throughout the crop growth period.

Methodology used for the screening

The effect of salt stress on growth (root, shoot, and total plant length) and physiological characteristics and yield attributes was measured at different stages of the crop i.e. 1) vegetative, 2) flowering, and 3) pod filling growth stage. The biomass and yield related characteristics as (root and shoot dry weight, number of pods/plant, hundred seeds weight and yield /plant were recorded under both salinity treatments over control. The samples i.e. root and stem were dried at 80°C completely in hot air oven (NSW, New Delhi) for 2 days till constant weights were obtained and then incubated in desiccators before measuring the dry weight. Sodium and potassium contents were measured in dried root, stem, and leaf samples. Survival % was also measured at regular intervals of time after every 15 days after salinity treatment. The leaves samples for RWC, MSI, and total chlorophyll contents were collected early in the morning (6:00 – 7:00 A.M.) from the second fully expanded trifoliate from the top freshly during each growth stage. The leaf samples were brought to the laboratory in ice bouquet so that the loss of moisture can be minimized. All the observations were mean of three replications. The soil samples were also collected with 4 replications at different stages for the measurement of EC (units in dS/m) by Conductivity Bridge as per the method of Jackson [10].

Details of the methodology:

Relative water content (RWC)

Leaf relative water content (RWC) was estimated by recording the turgid weight of 0.5 g fresh leaf samples by keeping in water for 4 h, followed by drying in hot air oven till constant weight is achieved as per the method of Weatherley [11].

$$RWC = [(Fresh\ wt. - Dry\ wt.) / (Turgid\ wt. - Dry\ wt.)] \times 100$$

Membrane stability index (MSI)

Membrane stability index (MSI) was estimated as per Sairam *et al.,* [12]. For the estimation of membrane stability index 100 mg leaf material, in two sets, is taken in test tubes containing 10 ml of double distilled water. One set is heated at 40ºC for 30 min in a metabolic water bath and the electrical conductivity of the solution is recorded on a conductivity bridge (C_1). Second set is boiled at 100ºC on a boiling water bath for 10 min and its conductivity is measured on a conductivity bridge (C_2). Membrane stability index (MSI) is calculated as:

$$MSI = [1 - (C_1 / C_2)] \times 100$$

Chlorophyll contents and Carotenoids

Chlorophyll content was estimated by extracting 0.05 g of the leaf material in10 ml dimethylsulfoxide (DMSO) as per the method of Hiscox and Israelstam, [13]. Samples were heated in an incubator at 65ºC for 4 h and than after cooling to room temperature, the absorbance of extracts were recorded at 663nm and 645nm. Chlorophyll content was calculated as per the formula given by Arnon, 1949.

$$\text{Chl a: } [12.7 \times A_{663} - 2.69 \times A_{545}]$$

$$\text{Chl b: } [22.9 \times A_{645} - 4.68 \times A_{663}]$$

$$\text{Total chlorophyll} = 20.2 \times A_{645} + 8.02\ A_{663} \times V/W \times 1000$$

The values thus obtained were in ug/ml of extract (Solvent). Values in mg/g fresh wt. were obtained by multiplying the above values with "v/w x 1000," where V is volume of extract; W is fresh wt. of sample. The value of total carotenoids (mg g^{-1}) was determined as per the formula of (hichtenthaler and Wellburn, 1983).

$$\text{Carotenoids} = [1000\ A_{470} - (3.27\ \text{chl a} + 104\ \text{chl b})] / 229$$

Estimation of potassium and sodium

Digestion of plant samples

The plant samples were dried in oven at 65 ± 5°C and ground thoroughly by a wiley mill. A representative ground plant sample (0.5g) was taken for digestion. The samples were soaked overnight with 10ml of concentrated HNO_3 in conical flasks (100ml capacity) for pre-digestion and finally digested in a di-acid mixture (20ml) containing HNO_3 and $HClO_4$ acid (9:4) on digestion unit (Gerhardt Turbothernm). The digested material was cooled, diluted with distilled water and filtered through Whatman No. 42 filter paper. The volume was made up to 25 ml/40ml and stored in a polypropylene container (100ml capacity) for further analysis.

Estimation of potassium, sodium and their respective ratio (K^+/Na^+)

The K and Na content in the standard solutions and plant samples (leaf, stem, and root) were estimated by using K and Na - specific filters in a flame photometer (ELICO CL361). By plotting a standard curve with known concentration of K and Na, the content of K and Na were calculated in different plant parts. The K/Na ratio was calculated in all the plant samples by dividing their respective individual values.

Statistical analysis

The data obtained in this study was subjected to analysis of variance (ANNOVA) appropriate to the experimental design. F-test was carried out to test the significance of the treatment differences and the least significant difference (LSD) was computed to test the significance of different treatment at 5% level of probability by using OPSTAT program, HAU, Hisar.

RESULTS

The relative water content, membrane stability index, total chlorophyll, carotenoid contents, growth and survival of the plants, dry weight of roots and shoots gradually decreased with increase in salinity treatments from control to 50mM NaCl and 75mM NaCl in all the genotypes during all three growth stages as compared with their respective control. The effect of salinity was less during early vegetative stage but the effect increased significantly from flowering to pod-filling stage. The results showed that although salt stress increased the sodium level in all the plant parts in all the genotypes, however, the increments in leaves were significantly higher in susceptible genotypes. Interestingly, the tolerant genotypes TCR86, PLM380, PLM562, and WGG37 accumulated more Na^+ in the root and stem of the plant and thus allowing lesser amount of sodium in leaf. The reverse response was observed for the potassium content. Salinity drastically decreased the K^+/Na^+ ratio in all the plant parts in all the genotypes. However, the K^+/Na^+ ratio was significantly higher in the leaves of tolerant genotypes under salt stress than the other genotypes. The ultimate effect of reduction in all the physiological characteristics was the loss of economic yield and quality of produce in all the genotypes. The EC measured at all the growth stages was 1.66, 4.86, and 7.42 dS/m on an average for the control, 50mM, and 75mM NaCl stress levels, respectively. On the basis of low and best performance of each genotypes under high salinity levels in different parameters 39 genotypes were categorized. All the genotypes were grouped in low, medium and high performance and results were presented in Table 2. The results illustrated that all the susceptible genotypes showed low performance in each parameter while tolerant genotypes showed high value of all the studies parameters (Fig.1). It indicated that selection of genotypes according to their performance under saline condition is very important for the selection of salt tolerant genotypes. A significant variations and adaptability was noted among all the genotypes under salt stress. The tolerant genotypes i.e. TCR86, PLM380, PLM562, WGG37, IC615, and PLM891 were observed for less reduction in RWC, MSI, total chlorophyll and carotenoid contents, plant length, survival, K^+/Na^+ ratio, and grain yield even under high salinity level (75mM NaCl) with respect to their non-stressed plants. However, the susceptible genotypes IC2056, IC10492, PLM32, K851, and BB92R showed greater reduction in the measured parameters under salinity stress. The correlation studies showed that grain yield positively and significantly correlated with all the parameters except Na content in leaf, stem and root which was negatively non significant correlated. However, remaining parameters positively correlated with each other (Table 3). On the basis of screening results, total eleven genotypes TCR86, PLM380, PLM562, WGG37, IC615, PLM891, IC2056, IC10492, PLM32, K851, and BB92R were selected from this study which will be screened further for salt tolerance for the identification of most salt tolerant and susceptible genotypes.

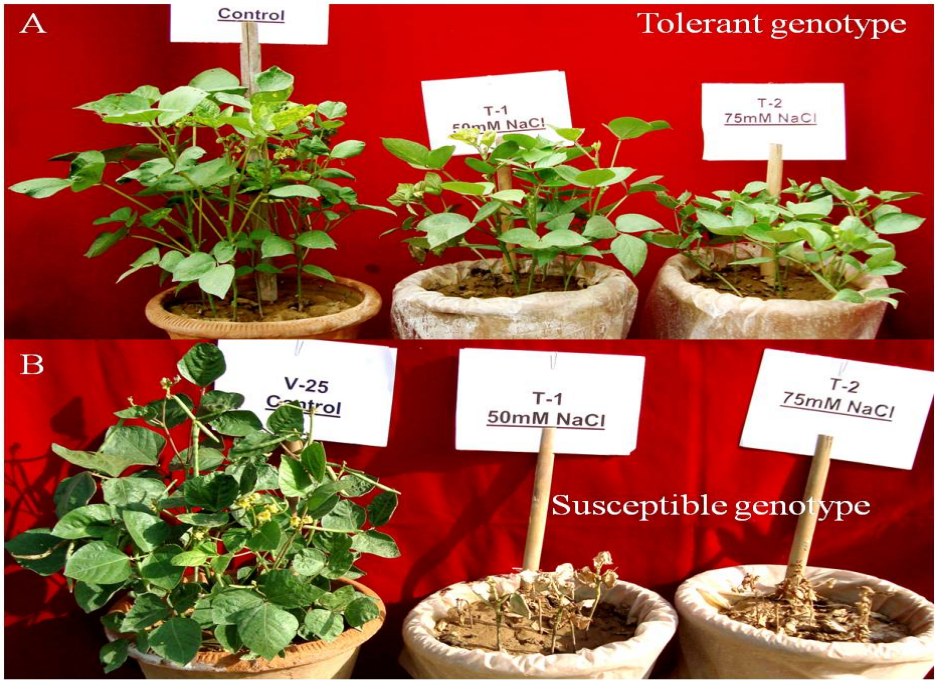

Fig.1 Performance of tolerant (A) and susceptible (B) genotypes of mungbean under salinity stress

Table 2 Low and high performance of selected 39 genotypes under salinity condition for different growth, physiological, biochemical and yield parameters (highlighted genotypes selected for further study)

S.No	Traits	Min.	Max.	Mean	Low performance/susceptible genotypes					High performance/tolerance genotypes				
1	Survival (%) -I	12.00	97.80	59.29	IC-10492	PLM-32	PLM-707	LGG-450	MH-96	WGG-37	PLM-184	PLM-562	PLM-380	TCR-86
	II	0.00	91.90	38.37	IC-10492	PLM-32	ET-52196	PLM-231	EC-5478	PLM-184	PLM-891	PLM-562	PLM-380	TCR-86
	III	0.00	84.00	23.94	IC-10492	PLM-32	ET-52196	PLM-231	EC-5478	IC-615	PLM-891	PLM-562	PLM-380	TCR-86
2	RWC (%) -I	57.88	85.52	72.32	IC-10492	PLM-32	BB-9-2R	K851	ET-52196	PLM-891	ET-52194	ET-52200	PDM-11	PLM-562
	II	0.00	82.79	66.20	IC-10492	PLM-32	PLM-303	IC-2056	T-44	PLM-884	TCR-86	WGG-37	ET-52194	PLM-707
	III	0.00	77.94	62.60	IC-10492	PLM-32	ET-52196	PLM-884	T-44	ET-52194	WGG-37	PLM-380	TCR-86	PDM-11
3	MSI (%) -I	31.72	85.03	64.52	PLM-303	PLM-256	T-44	STV-2635	PLM-231	PLM-562	WGG-37	ET-52194	ET-52200	TCR-86
	II	0.00	89.54	63.24	IC-10492	PLM-32	PLM-231	PLM-777	PLM-256	IC-615	PLM-380	PLM-562	TCR-86	WGG-37
	III	0.00	86.72	63.16	IC-10492	PLM-32	ET-52196	PLM-231	PLM-884	IC-615	PLM-380	PLM-891	WGG-37	TCR-86
4	Total chl. –I ($mg\ g^{-1}$ dwt.)	3.95	15.87	10.94	IC-10492	PLM-707	PLM-416	PLM-32	LGG-450	PLM-184	T-44	IC-615	PLM-562	PLM-380
	II	0.00	13.22	8.28	IC-10492	PLM-32	LGG-450	PDM-11	ET-52194	TCR-86	BB-9-2R	PLM-734	PLM-380	IC-615
	III	0.00	12.86	7.74	IC-10492	PLM-32	PLM-707	PLM-884	LGG-450	PLM-891	PLM-562	PLM-380	TCR-86	IC-615
5	Carotenoids -I ($mg\ g^{-1}$ dwt.)	0.89	3.31	2.25	IC-10492	PLM-707	PLM-32	PLM-416	LGG-450	PLM-666	ET-52201	PLM-380	PLM-562	IC-615
	II	0.00	2.95	1.92	IC-10492	PLM-32	LGG-450	PDM-11	PLM-884	TCR-86	IC-615	PLM-380	ET-52201	BB-9-2R
	III	0.00	3.04	1.85	IC-10492	PLM-32	PLM-884	PLM-707	LGG-450	MH-96	PLM-562	PLM-734	IC-615	TCR-86
6	Root L (cm)	0.00	35.00	19.99	IC-10492	PLM-32	ET-52196	PDM-11	PLM-707	PLM-380	PLM-734	PLM-562	IC-615	ET-52191
7	Shoot L (cm)	0.00	27.00	16.20	IC-10492	PLM-32	ET-52196	LGG-450	BB-9-2R	PLM-380	ET-52194	IC-615	WGG-37	TCR-86
8	Plant height ()	0.00	59.90	36.20	IC-10492	PLM-32	ET-52196	LGG-450	PLM-707	PLM-734	TCR-86	PLM-380	PLM-562	IC-615
9	Shoot dwt. (g)	0.00	5.84	1.40	IC-10492	PLM-32	ET-52196	ET-52200	LGG-450	TCR-86	PLM-891	PLM-562	IC-615	PLM-380
10	Root dwt. (g)	0.00	1.46	0.57	IC-10492	PLM-32	ET-52196	LGG-450	PDM-11	PLM-891	PLM-184	IC-2056	PLM-562	PLM-380
11	Root-Shoot ratio	0.00	1.29	0.45	IC-10492	PLM-32	ET-52196	BB-9-2R	PLM-777	MH-96	ET-52201	T-44	PLM-256	ET-52200
12	Na stem ($mg\ g^{-1}$ dwt.)	0.00	51.27	12.83	IC-10492	PLM-32	ET-52196	ET-52191	PLM-380	PDM-11	ET-52200	ET-52194	LGG-450	PLM-416
13	Na root ($mg\ g^{-1}$ dwt.)	0.00	38.75	12.33	IC-10492	PLM-32	ET-52196	PLM-184	ET-52191	PDM-11	WGG-37	ET-52194	PLM-884	LGG-450
14	Na leaf ($mg\ g^{-1}$ dwt.)	0.00	33.29	8.13	IC-10492	PLM-32	ET-52196	PLM-380	IC-10497	PLM-707	PLM-416	ET-52200	PDM-11	LGG-450
15	K stem ($mg\ g^{-1}$ dwt.)	0.00	40.87	25.73	IC-10492	PLM-32	ET-52196	PLM-666	ET-52200	PLM-334	PLM-562	PLM-891	PLM-380	TCR-86
16	K root ($mg\ g^{-1}$ dwt.)	0.00	15.24	7.67	IC-10492	PLM-32	ET-52196	ET-52200	PLM-666	PLM-334	IC-615	BB-9-2R	PLM-184	TCR-86
17	K leaf ($mg\ g^{-1}$ dwt.)	0.00	34.84	21.53	IC-10492	PLM-32	ET-52196	PLM-666	PLM-707	PLM-891	PLM-562	PLM-380	TCR-86	PLM-184
18	K/Na stem	0.00	10.12	3.85	IC-10492	PLM-32	ET-52196	ET-52200	PLM-416	PLM-891	TCR-86	PLM-562	PLM-380	ET-52191
19	K/Na root	0.00	2.57	0.94	IC-10492	PLM-32	ET-52196	ET-52200	LGG-450	PLM-380	PLM-334	IC-615	TCR-86	PLM-184
20	K/Na leaf	0.00	17.49	5.89	IC-10492	PLM-32	ET-52196	ET-52200	LGG-450	IC-615	IC-10497	TCR-86	PLM-562	PLM-380
21	Pods / plant	0.00	39.00	6.86	IC-10492	PLM-32	ET-52196	PLM-231	EC-5478	WGG-37	PLM-562	IC-615	PLM-380	TCR-86
22	100 seed wt.(g)	0.00	5.44	2.16	IC-10492	PLM-32	ET-52196	PLM-231	EC-5478	WGG-37	ET-52191	ET-52194	PLM-380	PLM-562
23	Seed wt. (g)	0.00	7.62	1.17	IC-10492	PLM-32	ET-52196	PLM-231	EC-5478	WGG-37	PLM-184	IC-615	PLM-562	PLM-380

(I, II, and III: vegetative, 50% flowering, and 50% pod-filling growth stage respectively)

Table 3 Correlation studies of 19 traits of 39 genotypes

S.No	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	0.422**	0.655**	0.510**	0.331	0.605**	0.665**	-0.069	-0.036	-0.131	0.664**	0.677**	0.596**	0.596**	0.669**	0.648**	0.805**	0.612**	0.780**
2	1.000	0.847**	0.559**	0.547**	0.373*	0.666**	0.381*	0.440*	0.358*	0.574**	0.503**	0.469**	0.255	0.260	0.241	0.301	0.448**	0.278
3		1.000	0.636**	0.569**	0.516**	0.734**	0.212	0.258	0.166	0.691**	0.551**	0.571**	0.426**	0.416**	0.475**	0.523**	0.496**	0.479**
4			1.000	0.948**	0.739**	0.574**	-0.414*	-0.353*	-0.429**	0.624**	0.653**	0.725**	0.662**	0.680**	0.711**	0.481**	0.180	0.446**
5				1.000	0.628**	0.482**	-0.403*	-0.340*	-0.407**	0.572**	0.601**	0.692**	0.604**	0.598**	0.642**	0.334*	0.031	0.283
6					1.000	0.640**	-0.473**	-0.403**	-0.504**	0.702**	0.625**	0.695**	0.814**	0.762**	0.735**	0.546**	0.413**	0.557**
7						1.000	0.166	0.225	0.088	0.623**	0.671**	0.633**	0.422**	0.480**	0.468**	0.624**	0.596**	0.540**
8							1.000	0.949**	0.978**	-0.168	-0.183	-0.333**	-0.578**	-0.534**	-0.541**	-0.155	0.299	-0.121
9								1.000	0.920**	-0.092	-0.129	-0.289	-0.543**	-0.531**	-0.504**	-0.107	0.289	-0.078
10									1.000	-0.186	-0.224	-0.358**	-0.578**	-0.532**	-0.571**	-0.197	0.281	-0.167
11										1.000	0.795**	0.864**	0.810**	0.716**	0.727**	0.491**	0.371*	0.468**
12											1.000	0.854**	0.681**	0.838**	0.700**	0.528**	0.323*	0.429**
13												1.000	0.774**	0.833**	0.818**	0.449**	0.254	0.435**
14													1.000	0.847**	0.893**	0.522**	0.303	0.550**
15														1.000	0.836**	0.553**	0.266	0.496**
16															1.000	0.634**	0.238	0.640**
17																1.000	0.426**	0.809**
18																	1.000	0.649**
19																		1.000

*showed significance level

1	**Survival %**	**11**	**K stem**
2	**RWC**	**12**	**K root**
3	**MSI**	**13**	**K leaf**
4	**Total chl.**	**14**	**K/Na stem**
5	**Carotenoids**	**15**	**K/Na root**
6	**Root L**	**16**	**K/Na leaf**
7	**Shoot L**	**17**	**Pods per plant**
8	**Na stem**	**18**	**100 seed wt.**
9	**Na root**	**19**	**Seed wt.**
10	**Na leaf**		

DISCUSSION

High concentration of salts in the root zone reduces soil water potential resulted in reduction of the relative water content, dehydration at cellular level and osmotic stress. The stability of the membrane decreased under salinity because of membrane disorganization responsible for higher leakage of salts/ ions from the leaves. The results obtained corroborates with the earlier reports [14, 15]. Salinity stress caused swelling of membranes in chloroplasts of sensitive plants which affects their chlorophyll content [16]. Therefore, the greater magnitude of these contents obtained in tolerant genotypes is responsible for their more resistance than the sensitive genotypes. This corroborates with the earlier reports [17, 18]. Substantial differences for salinity induced stunted plant growth were observed among the genotypes where shoot growth was far more affected than the root. Distraction of energy from growth to maintenance under salt stress caused growth retardation [19]. The result showed more decline in root and shoot dry weights in susceptible genotypes under salt stress over control. The results corroborates with the findings furnished by Saha *et al.,* [5] and Yupsains *et al*., [20].

Salinity caused decrease in xylem exudation rate and leaf water potential, relative water content and water retention capacity concurrently with increased water saturation deficit and water uptake capacity ultimately resulted in altered ionic homeostasis. Higher concentration of essential potassium ion in leaf tissue also contributes to the salt tolerance ability of plants [21]. Reduction in K^+ level was due to specific ion effect of Na^+ ion [22]. The K^+/Na^+ ratio was significantly higher in the leaves of tolerant genotypes under salt stress indicating their capacity to maintain favorable cellular environment for growth and other metabolic activities, which can be the basis of their tolerance towards soil salinity. The results are in accordance with the earlier reports [23, 24, 25]. Salinity stress affect pollination and impaired pod-setting resulting in more decrease in number of pods and grain yield [17, 26]. Salinity induced desiccation stress produced shriveled seeds resulted in low quality of produce [27]. The results corroborates with the earlier studies [28, 29, 30].

CONCLUSION

The present study concludes that the genotypes exhibited significant variations for adaptation towards salt stress. The control treatment showed clear differences among the genotypes for all the measured features. The selected genotypes from this study can be screened further for salt tolerance with more reliable parameters for the identification of most salt tolerant and susceptible genotypes that can be used in breeding as diverse resource of valuable traits assisting salt resistance for the genetic improvement of mungbean for saline soils.

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