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Uncovering the tolerance of mungbean (*Vigna radiata* L. Wilczek) genotypes under saline conditions using *k-mean* cluster analysis

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Abstract

Mungbean is very important legume crop. Short growth duration, adjustment in different cropping rotations, higher protein profile and nitrogen fixing properties further highlights the importance of this crop. Salinity is very damaging abiotic stress which effects the crop plants. To increase the productivity of mungbean it is very important that saline areas should be explored for mungbean cultivation. Seventeen mungbean genotypes were evaluated under three salinity treatments and grouped into tolerant and susceptible genotypes. Three different saline treatments were imposed under hydroponic growth medium. Salinity treatments were $7dsm^{-1}$ and $14dsm^{-1}$ alongwith normal water treatment. Different morphological and biochemical parameters like root length, shoot length, root weight, shoot weight, chlorophyll-a, chlorophyll-b and phenolic contents were targeted for evaluation of mungbean response. Analysis of variance for factorial treatment structure under completely randomized block design, Dunnett's multiple comparisons with a control treatment and K-mean cluster analysis were used for uncovering the responses of mungbean genotypes under diverse saline conditions. Genotypic and treatment effects were found significant for various traits and mean comparison showed that increased level of salt stress showed severely adverse effects on morphological, physiological and biochemical parameters of mungbean. AUM-18 and AUM-24 were tolerant while AUM562-1 was most susceptible genotype under all subjected salinity treatments according to the grouping of K-mean cluster analysis.

Keywords: Mungbean, salinity stress, tolerance, plant growth, chlorophyll contents, phenolic contents, photosynthesis, growth inhibition and germplasm screening.
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Introduction

Mungbean (*Vigna radiata* L. Wilczek) is a short season annual summer legume and grown as opportunity crop in rotation between cereals. Protein profile of mungbean is high relative to others which is upto 25% of seed dry weight and amino acid profile of mungbean is complementary to cereals (Karuppanapandian *et al.,* 2006). It is advantageous crop because it is fitted into rotations due to short duration (75-90 days), little water requirement, increasing soil fertility and lack of nitrogen fertilizer requirement (Ghallab *et al.,* 2007). Exploration of mungbean potential on saline areas is of due importance for promotion of mungbean cultivation on marginal lands. Main lands are occupied by main crops with tight cropping pattern so, exploitation of saline areas for mungbean cultivation is the main theme of current research experiment.

Problem of salinity stress can be assessed on global level by reviewing reported data which depicted that about half of total irrigated land and almost 20% of cultivated area affected from salinity stress (Zhu, 2001). Salinity is serious issue of arid and semi-arid tropics. It is a major problem for agricultural productivity not only from main agricultural crops but also from legumes (Abd-Alla, 1998). Early growth stages like seed germination and seedling development were reported to be adversely affected by salinity stress in all the crops (Mishra and Dwivedi, 2004). Both salinity and sodicity are the most severe stresses because these produced multiple problems including direct ionic toxicity, osmotic stress, oxidative stress and ionic imbalance (Zhu, 2001; Munns, 2002; Eker *et al.,* 2006; Munns *et al.,* 2006) and affected more than 800 million hectares globally (Munns, 2005). Saline condition induces multiple stresses therefore perceived as most severe abiotic stress. Like water uptake is reduced under saline conditions and metabolic processes are affected as in case of drought stress (Munns, 2002). Sodium chloride (NaCl) is most prominent and most damaging salt among different types of salt ions. Pulses are amongst most sensitive plants to salinity stress (Rogers *et al.,* 2005) and significant reduction in mungbean yield is reported due to saline conditions. Threshold level of mungbean is 1.8 dSm^{-1} (Maas, 1990). Significant yield losses had been reported in mungbean due to salinity stress. Breeding of mungbean for abiotic stresses is ignored field of research (Kumar *et al.,* 2012). Pioneer attempt to launch foundation of solid breeding program is screening of already available mungbean germplasm for salinity tolerance. Inter and intra crop genetic diversity for salinity tolerance is reported in scientific findings (Shannon, 1997). Based on these findings it was mandatory to assess the genetic variation

between mungbean genotypes for salinity tolerance. Basic approach to sort out the source of genetic variability is screening of mungbean genotypes for salinity tolerance. These attempt have been made previously in different crops (Aslam *et al.,* 2015; Maqbool *et al.,* 2015a, b).

Partitioning of data set into disjoint groups or classes is described as clustering of data. Pattern within a cluster is more likely to be similar than between clusters. Clustering pattern has resemblance with blocking pattern in experimental designs of field experiments as variation between the blocks is greatly higher than within the blocks. Neural network and k-mean clustering were extensively used for grouping, classification and clustering of disease attack on aerial parts of plants (Al-Hiary *et al.,* 2011). Different clustering techniques along with Kohonen self-organising map (non-linear neural network; Kohonen, 1982) were used for prioritizing the pest species in targeted locality by development of pest assemblage profile (Worner *et al.,* 2013). K-mean clustering is used to partition the data into k-groups or classes. This is an unsupervised algorithm used for grouping. K-mean clustering is effective method and have practical applications in grouping of results from different fields of research (Fahim *et al.,* 2006; Margaret, 2006; Koheri and Ali, 2007). K-mean cluster analysis is broadly used in remote sensing (Chehata and Bretar, 2008; Zheng *et al.,* 2008). This analysis is sensitive for selection of cluster number (Pham *et al.,* 2004) and initialization (Yang *et al.,* 2010). In present research work k-mean cluster analysis on the basis of its practical workability and applicability was uniquely used for grouping of mungbean genotypes based on their performance and selection of tolerant genotypes under different saline conditions.

Materials and Methods

Research experiment was conducted following aquaculture in screenhouse of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during 2013. Total 17 mungbean genotypes i.e. M-2004, AUM6375, AUM38, M-2006, AUM-31, AUM-18, AUM 24, NM54, AUM 19, AUM 28, M 2002, AUM 9, AUM 27, NM 92, AUM 56-2, AUM 562-1 and NM98 were collected from the same department and Nuclear Institute for Agriculture and Biology (NIAB). Seeds were grown in sand filled trays following completely randomized design, allowed to germinate and grow using tap water (EC≈1.5-2.0ds/m) for irrigation. At three leaves stage, seedlings were carefully uprooted and transferred in aquaculture tubs containing Hoagland nutrient solution (Hoagland and Arnon, 1950) with floating polystyrene sheets bearing 100 holes in each sheet. One seedling per hole was carefully and softly fixed providing cushion using sponge and allowed to stabilize for two days. Proper aeration was applied by installing aeration pumps and pH was maintained up to 6.5 in each tub. After stability of seedlings three different salinity treatments following one for each tub were applied. Genotypes were sown using factorial treatment structure under completely randomized block design. Three different stress levels were maintained as following;

Treatment-1: ≈1.5-2.0dsm^{-1} (no salt applied)
Treatment-2: 7dsm^{-1}
Treatment-3: 14dsm^{-1}

pH and electric conductivity (EC) were properly maintained and monitored on daily basis. Water in the tubs was changed after 15 days of transplantation and refilled maintaining same strengths.

Temperature (°C) of leaves with uniform maturity and exposure to sun was measured by using infrared thermometer (model) before harvest. Seedlings of all the entries were harvested 30 days after transplantation in aquaculture to record data for measurement of different parameters like root length (cm), shoot length (cm), root weight (g), shoot weight (g), chlorophyll-a (mg/100 mg), chlorophyll-b (mg/100mg), phenolic contents (100 µg/ml) and leaf temperature (°C). Chlorophyll contents were determined by using spectrophotometer readings in following equations;

Chlorophyll-a = [0.999A663-0.0989A645 (mg/100ml)],
Chlorophyll-b = [0.328A663+1.77A645 (mg/100ml)],

Phenol contents were determined by following Julkenen-Titto (1985).

Statistical Analysis

Data were statistically analyzed by using two factor factorial analysis of variance to assess the treatment, genotypic and their interaction effects (Steel *et al.,* 1997). Dunnett's multiple comparisons with a control was done for treatment mean comparison. Statictix 9.1 free version of software was used for analysis of variance and treatment mean comparison. To evaluate the genotypic performance and to sort out best performing genotypes under saline conditions *K-mean* cluster analysis (Mac Queen, 1967) was used for grouping of mungbean genotypes based on their performance. XLStat software (free version) was used for K-mean cluster analysis of subjected data.

Results

Table-1: Mean squares with level of significance for different morpho-physiological traits of mungbean

SOV	DF	Root length	Root Weight	Shoot length	Shoot weight	Chlorophyll a	Chlorophyll b	Leaf Temp	Phenolics
Replication	2	10.75	1.004	21.22	2.049	0.00016	0.00042	0.704	0.0038
Genotype	16	47.05*	0.551ns	14.93**	2.744**	2.022**	2.999**	1.045ns	0.0012ns
Treatment	2	1685.3**	17.66**	1505.5**	123.76**	4.233**	73.13**	11.82**	0.13*
Genotype× Treatment	32	33.24ns	0.849**	15.69**	2.65**	0.818**	1.921**	0.959ns	0.0018ns
Error	100	27.08	0.445	6.48	1.268	0.0000116	0.0000279	0.644	0.0039
Total	152								

Table-2: Dunnett's Multiple Comparisons with a Control for morphometric and physiological traits

Treatment	Leaf temperature (°C)		Shoot length (cm)		Root length (cm)		Root weight (g)	
	Mean value	Difference	Mean	Difference	Mean	Difference	Mean	Difference
Normal	29.88		28.15		26.53		1.903	
7dsm^{-1}	30.50	0.616*	19.29	-8.86*	18.01	-8.514*	0.989	-0.913*
14dsm^{-1}	30.83	0.950*	18.27	-9.88*	15.58	-10.95*	0.803	-1.099*
Treatment	Shoot weight (g)		Chlorophyll a contents (mg/100mg)		Chlorophyll b contents (mg/100mg)		Phenolic contents (100 µg/ml)	
	Mean value	Difference	Mean	Difference	Mean	Difference	Mean	Difference
Normal	4.22		2.63		4.94		0.6358	
7dsm^{-1}	1.88	-2.34*	2.05	0.570*	2.93	2.014*	0.6357	-0.0001ns
14dsm^{-1}	1.27	-2.95*	2.08	0.552*	2.69	2.249*	0.6358	-0.0000ns

Analysis of variance showed that genotypic effects were highly significant for shoot length, shoot weight, chlorophyll a and chlorophyll b contents while genotypic effects were significant for root length. Genotypic effects were non-significant for root weight, leaf temperature and phenolic contents (Table-1). Treatment effects were highly significant for root length, root weight, shoot length, shoot weight, chlorophyll a, chlorophyll b and leaf temperature while significant for phenolic contents (Table-1). Genotype × Treatment interaction effects were highly significant for root weight, shoot length, shoot weight, chlorophyll a and chlorophyll b contents while non-significant for root length, leaf temperature and phenolic contents (Table-1).

Dunnett's multiple comparisons with a control treatment was done to analyze the generalized trends in responses of genotypes across the treatments for subjected traits (Table-2). Mean leaf temperature was increased across the treatments for studied mungbean genotypes. Shoot length, root length, root weight, shoot weight, chlorophyll a and b contents were reduced in mungbean genotypes with increased level of salt stress. Total phenolic contents were rendered unaltered in mungbean genotypes across the salinity environments (Table-2).

All the genotypes were classified on the basis of K-mean cluster analysis against three salinity treatments. Three groups per treatment were made and under treatment-1, genotypes AUM562-1, NM54 and AUM-24 were in center of group-1, group-2 and group-3 respectively. In second treatment genotypes, M-2006, AUM-18 and AUM19 were central in group-1, 2 and 3 respectively. In third treatment genotypes, AUM-24, AUM56-2 and AUM562-1 were central in group-1, 2 and 3 respectively (Table-3). First group in each treatment constitutes genotypes with superior performance, second group having genotypes of average performance and third group comprised of poor performer genotypes. Distance between central genotypes of three k-mean groups were shown in Table-4. Under treatment-1, central genotype of first group was 17.136 units apart from central genotype of second group. Centre of first and third groups were 15.437 units apart and centers of second and third groups were 4.482 units apart. Closeness of second and third groups showed that genetic variation between these groups is lesser. Central points of first and third groups were more apart than other group combinations (first and second group; second and third group) under treatment-2. Second and third groups were more diverse than other group combinations (first and second group; first and third group) under treatment-3 (Table-4).

Table-3: Central genotypes for all of three k-mean classes under three salinity treatments

Class	Treatment	Genotype	Root length (cm)	Shoot length (cm)	Leaf temperature (°C)	Root weight (g)	Shoot weight (g)	Chlorophyll, a (mg/100mg)	Chlorophyll, b (mg/100mg),	Phenolic contents (100 µg/ml)
	1	AUM562-1	20.500	26.267	30.000	0.960	2.667	2.665	4.601	0.636
1										
	2	NM54	16.200	16.267	29.833	0.857	1.743	2.254	4.912	0.600
	3	AUM-24	13.633	18.867	31.433	1.387	1.387	1.702	2.610	0.589
	1	M-2006	29.600	26.700	30.967	1.967	5.130	2.649	4.878	0.649
2	2	AUM-18	19.067	19.733	30.500	0.837	1.553	1.677	3.280	0.603
	3	AUM19	14.000	17.667	30.800	1.013	1.333	0.683	2.058	0.579
	1	AUM-24	25.933	29.033	30.467	2.300	5.823	2.631	5.211	0.636
3	2	AUM56-2	21.333	21.500	30.267	1.107	1.700	1.864	3.723	0.611
	3	AUM562-1	19.400	22.400	29.267	1.220	2.070	0.695	3.251	0.577

First group comprised of 5 genotypes while second and third groups consist of 6 genotypes each. Second group had highest within group variance which showed that variability within this group is higher than others under treatment-1. First group had five, second had nine and third had three genotypes under treatment-2 when subjected to k-mean clustering analysis. Within group variance of second group is highest which showed highest variation within group relative to other two groups under treatment-2. Under treatment-3, within group variance is lower in first group which showed higher homogeneity within this group relative to other groups. First, second and third groups have 5, 8 and 4 genotypes respectively under treatment-3 (Table-5). Minimum, average and maximum distances from centroids were shown in Table-5 which showed the relative closeness and differences among genotypes from central accessions within groups under salinity treatments.

Analysis of variance for k-mean groups was presented in Table-6. Model degree of freedom is based on number of groups. Root length and root weight were showing significant differences for three k-mean groups under three salinity treatments. Shoot weight was significant for three k-mean group model under treatment-1 and 2 while non-significant for treatment-3. Significance of traits for three k-mean cluster showed that these traits were decisive in grouping of mungbean genotypes. Chlorophyll a contents showed significant differences under treatment-1 and 3 while non-significant under treatment-2. Chlorophyll b contents, leaf temperature and phenolic contents exhibited non-significant difference for three k-mean model analysis of variance under all the three salinity treatments (Table-6).

At normal condition, following k-mean cluster analysis, 17 mungbean genotypes were distributed into genetically distant three groups. M-2004, NM54, AUM19, AUM9 and AUM562-1 were superior performers and placed in group-1, genotypes AUM6375, M-2006, AUM-31, AUM28, AUM27 and NM92 were average performers which fall in group-2 while rest of six genotypes were poor performer and got position in group-3 in hydroponic under normally treated conditions. At 7dsm^{-1}, k-mean cluster analysis distributed mungbean genotypes in three user defined groups. Group-1 comprised of superior genotypes like M-2004, AUM6375, AUM-24, NM54 and AUM28. Genotypes with average performance like AUM38, M-2006, AUM-18, AUM19, M2002, AUM9, AUM27, NM92 and NM98 were placed in group-2. AUM-31, AUM56-2 and AUM562-1 were poor performers at 7dsm^{-1} and fall in group-3. Similarly, at 14dsm^{-1}, relative performance of mungbean genotypes was assessed by grouping them in three users defined groups. The superior genotypes M-2004, AUM-18, AUM-24, AUM27 and AUM56-2 were allotted group-1, Genotypes AUM6375, M-2006, AUM-31, AUM19, AUM28, AUM9, NM92 and NM98 with average performance were present in group-2 and poor performing genotypes like NUM38, NM54, M-2002 and AUM562-1 were placed in group-3 (Table-7). Overall performance of M-2004 was the best as it was present in group-1 at all the salinity levels. Genotypes AUM-18 and AUM-24 were present in group-1 at both 7dsm^{-1} and 14dsm^{-1} levels which showed that these genotypes were more stable under salinity stress. Genotypes M-2006, AUM19, AUM9, NM92 and NM98 were present in group-2 at both 7dsm^{-1} and 14dsm^{-1} levels which proved that these genotypes had average level of performance whereas the genotype AUM562-1 got position in group-3 at both 7dsm^{-1} and 14dsm^{-1} salinity levels which reflected the consistent poor performance under salinity stress. Rest of the genotypes did not perform consistently at all the salinity levels therefore categorized as poor performers at different saline environments (Table-7).

Table-4: Distance between k-mean class central genotypes

	Treatment-1				Treatment-2				Treatment-3			
	Distances between the class centroids:				Distances between the class centroids:				Distances between the class centroids			
Class		1	2	3		1	2	3		1	2	3
	Genotype	AUM562-1	M-2006	AUM-24		NM54	AUM-18	AUM56-2		AUM-24	AUM19	AUM562-1
1	AUM562-1	0	17.136	15.44	NM54	0	9.31	13.73	AUM-24	0	3.94	10.95
2	M-2006	17.14	0	4.48	AUM-18	9.31	0	4.91	AUM19	3.94	0	13.96
3	AUM-24	15.44	4.48	0	AUM56-2	13.73	4.91	0	AUM562-1	10.95	13.96	0

Table-5: General Summary Results for three k-mean classes under three salinity treatments

	Treatment-1			Treatment-2			Treatment-3		
Class	1	2	3	1	2	3	1	2	3
Genotypes	5	6	6	5	9	3	5	8	4
Sum of Weights	5	6	6	5	9	3	5	8	4
Within-Class variance	14.82	52.20	16.31	41.23	6.69	5.43	10.34	23.47	24.15
Minimum distance to centroid	1.75	2.95	2.24	2.87	0.79	1.34	1.74	2.22	2.27
Average distance to centroid	3.207	6.169	3.529	5.104	2.356	1.792	2.82	4.265	3.934
Maximum distance to centroid	5.402	9.041	5.511	10.146	3.146	2.687	3.335	6.432	6.425

Table-6: Analysis of variance for morpho-physiological traits under three salinity treatments for three k-mean classes

Parameters	DF (Model)	Mean squares (Model; T-1	Mean squares (Model;T-2)	Mean squares (Model;T-3)	DF (Error)	Mean squares Error (T-1)	Mean squares Error (T-2)	Mean squares Error (T-3)	Pr > F (T-1)	Pr > F (T-2)	Pr > F (T-3)
Root length	2	103.488	25.522	60.657	14	6.284	3.566	6.832	0.000	0.007	0.003
Root Weight	2	18.822	18.590	35.285	14	2.819	1.851	2.765	0.009	0.002	0.001
Shoot length	2	0.075	0.118	0.394	14	0.418	0.332	0.289	0.837	0.708	0.288
Shoot weight	2	2.129	0.478	0.123	14	0.227	0.106	0.125	0.003	0.031	0.399
Chlorophyll a	2	6.444	0.794	0.514	14	1.494	0.297	0.135	0.035	0.104	0.048
Chlorophyll b	2	0.001	1.416	0.344	14	0.011	0.586	0.541	0.913	0.126	0.545
Leaf Temperature	2	1.518	1.233	0.028	14	0.552	1.168	0.515	0.098	0.374	0.948
Phenolic contents	2	0.000	0.000	0.000	14	0.000	0.000	0.000	0.681	0.887	0.507

Note: if Pr value is ≤0.05 then significant, if Pr value is ≤0.01 then highly significant, if Pr value >0.05 then non-significant

Discussion

Growth of mungbean plants was declined with the increase in intensity of salinity stress. This reduction might be due to lesser availability of micronutrients to plant from full strength Hoagland solution under saline environment as micronutrient deficiency indicators were evident on plants. Yellowing and chlorosis were prominent symptoms of micronutrients deficiency which reflected reduced chlorophyll contents. Yellowing and chlorosis resulted in inhibition of photosynthetic activity, carbohydrate synthesis, supply to growing regions and plant growth. Intensity of these symptoms was parallel with severity of stress. Growth parameters (root length, shoot length, root weight and shoot weight) of group-1 were higher relative to genotypes in other groups under different salinity treatments. Whereas, mean values also showed that growth parameters were reduced or lower in 3rd k-mean group under each salinity treatment. It was reported that root length, shoot length, dry mass accumulation, branching and number of leaves were

TABLE-7: GENOTYPES IN EACH K-MEAN CLASS UNDER THREE SALINITY TREATMENTS

TREATMENT	Class	Genotypes
1	1	M-2004, NM54, AUM19, AUM9, AUM562-1
	2	AUM6375, M-2006, AUM-31, AUM28, AUM27, NM92
	3	AUM38, AUM-18, AUM-24, M2002, AUM56-2, AUM-24
2	1	M-2004, AUM6375, AUM-24, NM54, AUM28
	2	AUM38, M-2006, AUM-18, AUM19, M2002, AUM9, AUM27, NM92, NM98
	3	AUM-31, AUM56-2, AUM562-1
3	1	M-2004, AUM-18, AUM-24, AUM27, AUM56-2
	2	AUM6375, M-2006, AUM-31, AUM19, AUM28, AUM9, NM92, NM98
	3	AUM38, NM54, M2002, AUM562-1

reduced under saline conditions and this suppression was reduced by foliar application of micronutrients (Boron and Zinc; Arora *et al.,* 2012). Reduction in growth of mungbean plants under salinity stress might be due to reduction in cell elongation, cell wall plasticity and cellular metabolism as reported in previous research that these mechanisms were affected by salinity stress (Alpaslan and Gunes, 2001). Reduction in cell elongation, plasticity of cell wall and cellular metabolism might be responsible for reduction in root length, shoot length, root weight and shoot weight.

Chlorophyll contents of tolerant (1st group) mungbean genotypes were higher relative to susceptible (3rd group) genotypes. Chlorophyll contents are important for plant life as these assist the plants to remain functionally active and to provide photosynthates for longer period of time to plants. Photosynthesis is not carried out without chlorophyll contents, which is important physiological process for maintaining growth and crop productivity (Bharud and Sagare, 2003). Plant growth is critical index that determine the plant salinity tolerance level. Root shoot length and weight of mungbean plants were reduced by salinity stress and such results were also mentioned by numerous researchers in different crops (Kasukabe *et al.,* 2006; Ibrahim *et al.,* 2007; Keutgen and Pawelzik, 2008).

Phenolic contents increased under prevalence of saline conditions. Tolerant genotypes (1st group) has greater phenolic contents than susceptible genotypes (3rd group). This increase might be due to cellular adaptive mechanism for scavenging the reactive oxygen species (Mohamed and Aly, 2008). Phenols act as antioxidants because these are hydrogen donators, quencher of singlet O_2, and reducing agents (Rice-Evans *et al.*, 1997). Results of current studies showed that phenol contents were not affected significantly due to different salinity treatments. Differences among genotypes were non-significant while differences were significant under different treatments. It is reported that at reproductive stage, phenolic contents are higher (Bravo, 1998). Phenolic contents are also different under different growth stages (Hichem *et al.,* 2009). Suppressed water absorption, inhibited metabolic activity were due to Na^+ and Cl^- ion toxicity and nutrient uptake deficiency (Ghoulam *et al.,* 2002; De Lacerda *et al.,* 2003). It was reported that exogenous application of arginine and polyamines promotes cell division, cell elongation, cell wall stability, cell differentiation and plant growth under saline conditions (Velikov *et al.,* 2000; Mo and Pua, 2002). These findings supported the perception that all these processes/mechanism (cell division, cell differentiation, cell elongation and cell wall stability) were adversely effected by saline conditions which resulted in plant growth reduction. More energy expenditure for repair mechanism and osmotic adjustment were responsible for growth reduction in plants under saline conditions (Pasternak, 1987). Salinity tolerance is credited to the exclusion of Na^+ ions from shoots (Greenway and Munns, 1980), compartmentalization and selective uptake of ions (Hossain et al., 2008). Water use efficiency and water potential of plants is decreased under salinity stress which leads to further losses and damages in plants (Mansour *et al.,* 2005).

Higher salt concentration in root zone, decreases the water potential and water availability. Osmotic stresses prevail due to reduction of water contents at cellular level and subsequent processes are also badly affected (Lloyd *et al.,* 1989). Under saline conditions photosynthesis is adversely affected either due to stomatal factors viz, stomatal closure, reduction in CO_2 diffusion and intracellular CO_2 concentration or due to non-stomatal factors viz, photosynthetic apparatus, photosynthetic pigments (Stepien and Klobus, 2006). Growth was inhibited in beans with increase in salinity level. Concentration of plastid pigments was decreased under salinity stress. Salinity reduced growth in Basil plants (Heidari, 2012). Due to accumulation of higher salt contents the cells of transpirating leaves injured resultantly plant growth and photosynthesis were adversely affected (Munns *et al.,* 2006). Decrease in chlorophyll contents under saline conditions is attributed to the photoinhibition and ROS accumulation. Decrease in chlorophyll contents is a reason for reduction of photosynthetic activity in plants under salt stress.

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