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Evaluation of Mungbean (Vigna radiata L. Wilczek) Genotypes Grown under Saline conditions

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ABSTRACT: Mungbean is a major pulse crop which provides dietary protein and many essential nutrients. It fixes biological nitrogen in soil and improves soil health but, sensitive to saline condition. The increased salinity of arable land is expected to have devastating global effects, resulting in up to 50 % land loss by the middle of the twenty-first century. The highest GCV and PCV were obtained for root dry weight, root fresh weight and root length and highest genetic advance as percentage of mean (GA) was obtained for seedling vigour index, shoot dry weight and shoot fresh weight. According to D-value the character shoot dry weight was the most sensitive under salinity and genotypes MVM-2 is more tolerant to salinity followed by RMG-1099 and RMG-1101 on the basis of reduction in mean value of shoot dry weight as compared to control.

Keywords: GCV, Mungbean, PCV, Salinity, Variability.

INTRODUCTION

Mungbean is an important short duration (65-90 days) legume crop of high nutritive values. It maintains soil fertility through biological nitrogen fixation in soil and thus plays a vital role in sustainable agriculture (Kannaiyan, 1999). Protein malnutrition remains a major nutrition problem in Asia and affects children most severely (WHO, 2000). Mungbean is a cheap source of protein and important nutritious dietary component of vegetarians in Asian countries especially in South-East Asia (Keatinge et al., 2011). Salinity is a main constraint in the production of mungbean where, 50 M NaCl can cause yield losses up to 70 % (Saha et al., 2010). Higher accumulation of salt decrease the osmotic potential of soil solution causing water stress in plants and further interactions of the salts with mineral nutrition cause nutrient imbalance and deficiencies, oxidative stress ultimately leading to plant death as a consequence of growth arrest and metabolic damage (Zhu, 2001; Tavakkoli et al., 2010; Hasanuzzaman et al., 2012). Salt stress alters plant growth and morphology, photosynthetic capacity, cell membrane integrity, cellular enzyme protection system and many physiological and biochemical activities (Chen et al., 2007). Levels of proteins, secondary metabolites, osmolytes, photosynthetic pigments, membrane damage and antioxidants were reduced at higher salt concentrations increased under salinity (Mankar et al., 2021).

A study on variability among available genotypes is the pre-requisite for initiating a varietal development

programme. Hence, it is necessary to analyses the nature and magnitude of the heritable genetic variation present among the genotypes. D-value represent the salinity stress index was used to find out the most tolerant genotype of mungbean. Mankar *et al.*, (2021) reported that germination and early seedling stage was more authentic to identify salt-tolerant mungbean varieties. The crosses between parents with maximum genetic diversity were generally the most responsive for genetic improvement (Arunachalam, 1981). An attempt was made to evaluate mungbean genotypes for their reaction to salt stress and to assess the genetic variability for salinity tolerance.

Due to complex nature of salinity stress and lack of appropriate techniques for introgression less progress has been made in developing salt stress varieties (Singh and Singh, 2011). Therefore, the general objective of this study was to assess the genetic variability and identify the salinity tolerant genotypes among some mungbean genotypes.

MATERIALS AND METHODS

A laboratory experiment during *Kharif* (2018-19) was carried out at Department of Plant Breeding and Genetics, S.K.N. College of Agriculture, Jobner at 32.3°C temperature and 53 % relative humidity. The seeds of 10 genotypes of mungbean *viz.*, RMG-1095, RMG-1078, RMG-975, MSJ-118, RMG-976, RMG-1101, MVM-2, RMG-1079, RMG-1099 and RMG-492 were surface sterilized by using 0.1 % mercuric chloride followed by three time rinsing with tap water. The three salinity levels were 0.0 % (control), 0.2 %

Kumawat & Gothwal Biological Forum – An International Journal 14(2): 287-292(2022)

and 0.4 % NaCl created by supplementing 0, 2 and 4 g NaCl to 1000 ml of double distilled water, respectively. The experiment was carried out in completely randomized design (CRD) with three replications. The observations were taken on 17^{th} day after sowing. The methods used for recording observations are described below:

A seed was considered as germinated at the emergence of both radicle and plumule up to 2 mm length (Chartzoulakis and Klapaki, 2000). The germination was recorded on 7^{th} day of planting and germination percentage (GP) was determined by using the following formula (Aniat *et al.*, 2012).

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

On 17^{th} day observations taken on various seedling characters *viz*; shoot length, root length, seedling length, shoot fresh weight, root fresh weight, seedling fresh weight, shoot dry weight, root dry weight, seedling dry weight. The root length/ shoot length ratio of seedling was calculated by the following formula.

Root length/Shoot length ratio =
$$\frac{RL}{SL}$$

The seedling vigour index was determined by the following formula (Iqbal and Rahmati, 1992):

Seedling vigour index $(SVI) = (RL+SL) \times (GP)$

D – **Value.** This represents salinity stress intensity and was derived by following formula:

$$D=1- \frac{Y_j}{Y_c}$$

Where,

 Y_j = Mean performance of a concerned character of all the genotypes in the salt stress environment

 Y_c = Mean performance of a concerned character of all the genotypes in the normal environment

The data obtained were subjected to analysis of variance following standard statistical methods (Panse and Sukhatme 1985) and the significant difference among the mean value were compared by least significant difference (LSD) test (P<0.05). Variability parameters were calculated by using various formulae given by Burton (1952); Johnson *et al.* (1955).

RESULTS AND DISCUSSION

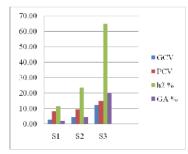
The pooled ANOVA of mungbean genotypes showed significant difference among the genotypes and all salinity levels for all the characters, indicated that genotypes showed differential response to different salinity levels (Table 1). Similar findings were also reported by Gogile *et al.*, (2013), in lentil by Tesfaye *et al.* (2015), in munbean by Hapsari and Trustinah (2018) for most of the characters.

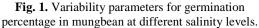
In mungbean all the characters under study showed variation at different levels of salinity (Table 2). Variability parameters for germination percentage were higher at highest salinity level (Fig. 1). Similar variation for germination percentage was reported by Kandil *et al.* (2012); Sehrawat *et al.*, (2014); Kamrul *et al.*, (2018) in mungbean. Variability parameters were increased with advancement of salinity levels in mungbean for germination percentage and seedling characteristics *viz.*, root length (Fig. 2), shoot length (Fig. 3), seedling length (Fig. 4), shoot fresh weight (Fig. 5), root fresh weight (Fig. 6), seedling fresh weight (Fig. 7), root dry weight (Fig. 8), shoot dry

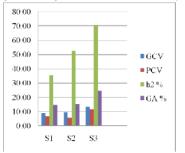
weight (Fig. 9), seedling dry weight (Fig. 10) root length/shoot length ratio (Fig. 11) and seedling vigour index (Fig. 12) and similar results were widely reported in mungbean (Subashree *et al.*, 2021); (Swarnakar, 2016), in lentil, chickpea and faba bean (Arslan *et al.*, 2016), in cowpea (Haleem, 2015), in *Pisum sativum* var. *abyssinicum* and *Lathyrus sativus* (Tsegay and Gebreslassie 2014), in moth bean and mung bean (Saroj and Soumana 2014).

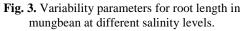
In general PCV were higher than GCV for all the characters indicating a positive effect of environment on the expression of characters. The highest GCV was obtained in root dry weight followed by root fresh weight and root length and highest PCV was obtained in root dry weight followed by root fresh weight and root length. Lowest GCV was obtained for shoot length followed by germination percentage and seedling length and lowest PCV was obtained for seedling length followed by shoot length and root length/shoot length ratio across the salinity gradients. Huda et al., (2017) in rice under saline condition reported higher percentage of GCV and PCV for root dry weight. Kumawat and Gothwal (2018) reported lowest GCV for germination percentage which was similar with investigated results. Heritability in broad sense was generally increased with increasing salinity level for germination percentage, seedling length, seedling fresh weight, shoot dry weight, root length/shoot length ratio and seedling vigour index. Characters having high heritability were not more affected by the environment (Chen et al., 2007). Increase in heritability with increased salinity level indicated that variability was increased as advancement in salinity level due to expression of gene for salinity tolerance (Saranga et al., 1992; Foolad 1996; Khan et al., 2003).

Increasing trend in genetic advance with increasing salinity level for most of the traits indicated that higher variability was obtained at higher salinity level therefore; selection at higher salinity level is more responsive for obtaining salinity tolerant genotypes (Kumawat and Gothwal 2018; Gupta 1994). On the basis of D-value (Table 3) the characters shoot dry weight was the most sensitive under salinity. It is suggested that major emphasis should be given on shoot dry weight while screening for salinity tolerance. According to reduction in mean value of shoot dry weight as compared to control genotypes (Table 4) mungbean genotypes MVM-2 is more tolerant to salinity followed by RMG-1099 and RMG-1101.









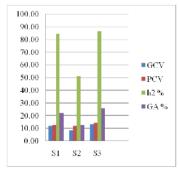
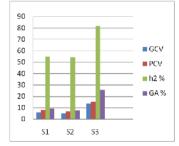
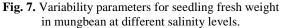


Fig. 5. Variability parameters for root fresh weight in mungbean at different salinity levels.





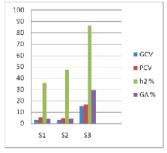


Fig. 9. Variability parameters for shoot dry weight in mungbean at different salinity levels.

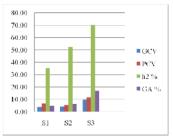


Fig. 2. Variability parameters for shoot length in mungbean at different salinity levels.

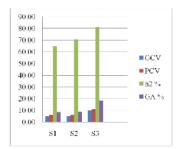


Fig. 4. Variability parameters for seedling length in mungbean at different salinity levels.

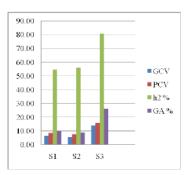


Fig. 6. Variability parameters for shoot fresh weight in mungbean at different salinity levels.

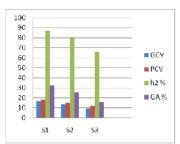


Fig. 8. Variability parameters for root fresh weight in mungbean at different salinity levels.

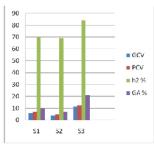
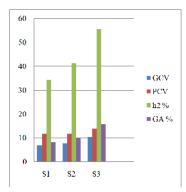


Fig. 10. Variability parameters for seedling dry weight in mungbean at different salinity levels.



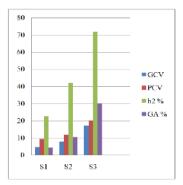


Fig. 11. Variability parameters for root legth/shoot length ratio in mungbean at different salinity levels.

Fig. 12. Variability parameters for seedling vigour index in mungbean at different salinity levels.

Characters	Source of variation with degree of freedom							
	Genotypes df=9	Salinity levels df=2	Genotype × Salinity df=18	Pooled Error df= 60				
Germination Percentage	160.85**	6584.92**	108.95**	43.21				
Root length	5.88**	235.41**	3.19**	1.29				
Shoot length	10.27**	1266.19**	2.09**	0.48				
Seedling length	23.69**	2590.11**	7.81**	1.50				
Root fresh weight	3375.05**	539233.25**	912.32**	214.95				
Shoot fresh weight	109708.62**	7810807.85**	45330.83**	10235.28				
Seedling fresh weight	132712.53**	12454031.49**	41854.77**	11243.43				
Root dry weight	100.83**	1006.35**	32.03**	3.51				
Shoot dry weight	184.52**	101640.69**	64.57**	24.47				
Seedling dry weight	485.50**	122863.93**	86.69**	24.24				
Root length/shoot length	0.01**	0.01**	0.01**	0.01**				
Seedling vigour index	279579.44**	38731214.71**	148872.80**	59899.00				

 Table 2: Variability parameters for germination percentage and seedling characteristic in mungbean at different salinity levels.

Salinity	Germination percentage					Seedling Fresh Weight					
Level	Mean	GCV	PCV	h2 %	GA %	Mean	GCV	PCV	h2 %	GA %	
S_1	95.21	2.82	8.27	11.61	1.98	2356.87	5.98	8.07	55.02	9.14	
S_2	78.09	4.55	9.36	23.58	4.55	2249.53	5.14	6.98	54.29	7.80	
S_3	65.71	12.10	15.01	65.04	20.11	1191.10	13.96	15.44	81.65	25.98	
			Shoot Lengtl	h		Root Dry weight					
S_1	26.67	3.93	6.61	35.26	4.80	33.20	16.88	18.07	87.17	32.46	
S_2	25.44	4.06	5.60	52.26	6.06	29.12	13.65	15.16	80.99	25.30	
S_3	14.85	9.75	11.62	70.40	16.85	21.27	9.49	11.69	66.01	15.89	
			Root length			Shoot Dry weight					
S_1	11.69	8.99	6.61	35.26	14.81	153.29	3.47	5.80	35.86	4.28	
S_2	10.72	9.48	5.60	52.56	15.30	115.74	3.38	4.90	47.55	4.80	
S_3	6.42	13.31	11.62	70.40	24.62	39.08	15.46	16.67	86.01	29.53	
		S	eedling leng	th		Seedling Dry Weight					
S_1	38.36	5.14	6.38	64.90	8.52	186.49	5.77	6.90	70.12	9.96	
S_2	36.16	5.03	5.98	70.65	8.70	144.85	3.95	4.75	69.17	6.77	
S ₃	21.28	9.88	10.97	81.07	18.33	60.86	11.23	12.23	84.28	21.24	
		Ro	ot Fresh We	ight		Root Length /Shoot length					
S_1	276.80	11.84	12.60	84.57	21.94	0.44	6.82	11.62	34.42	8.24	
S_2	257.26	8.46	11.84	51.00	12.44	0.42	7.60	11.82	41.34	10.06	
S_3	35.03	13.44	14.44	86.61	25.76	0.43	10.23	13.73	55.51	15.70	
	Shoot Fresh Weight					Seedling Vigour Index					
S_1	2080.79	6.33	8.58	54.55	9.64	3648.08	4.49	9.43	22.66	4.40	
S_2	1992.27	5.62	7.52	55.89	8.65	2826.37	7.77	11.94	42.21	10.43	
S_3	1156.08	14.12	15.71	80.77	26.15	1402.36	17.09	20.16	71.84	29.83	

Where, \mathbf{GV} = genotypic variance, \mathbf{PV} = phenotypic variance, \mathbf{GCV} = genotypic coefficient of variation, \mathbf{PCV} = phenotypic coefficient of variation, \mathbf{h}^2 = heritability in broad sense, \mathbf{GA} = genetic advance as percentage of mean

Character	Control	Salt stress	D- value	Rank
Germination Percentage	95.21	71.9	0.245	8
Root length	26.67	20.15	0.245	9
Shoot length	11.69	8.57	0.267	6
Seedling length	38.36	28.72	0.251	7
Root fresh weight	276.08	146.14	0.471	2
Shoot fresh weight	2080.8	1574.2	0.243	10
Seedling fresh weight	2356.9	1720.3	0.27	5
Root dry weight	33.2	25.45	0.234	11
Shoot dry weight	153.29	77.41	0.495	1
Seedling dry weight	186.49	102.86	0.448	3
Root length/shoot length	0.44	0.43	0.025	12
Seedling vigour index	3648.1	2114.4	0.42	4

Table 3: D- value of different characters of green gram grown under saline conditions.

Table 4: Mean performance of different genotypes and % reduction under salinity in comparison to control
for shoot dry weight.

Sr. No.	Genotypes	Mean performance				% reduction in				
SI. No. Genotypes		S_1	S_2	S_3	Mean	S_2	S ₃	Sm	Rank	
1.	RMG- 1095	2049.33	1755.43	1031.67	1612.14	14.34	49.66	32.00	10	
2.	RMG- 1078	1915.13	1914.43	1033.33	1620.97	0.04	46.04	23.04	4	
3.	RMG- 975	2094.00	2037.77	1130.33	1754.03	2.69	46.02	24.35	5	
4.	MSJ-118	2161.33	2003.53	1258.77	1807.88	7.30	41.76	24.53	6	
5.	RMG- 976	2437.33	2240.00	1210.00	1962.44	8.10	50.36	29.23	9	
6.	RMG-1101	1909.80	1907.07	1064.33	1627.07	0.14	44.27	22.21	3	
7.	MVM-2	2031.67	1996.00	1485.00	1837.56	1.76	26.91	14.33	1	
8.	RMG- 1079	2100.33	2026.80	1077.67	1734.93	3.50	48.69	26.10	7	
9.	RMG- 1099	2009.00	1963.37	1347.67	1773.34	2.27	32.92	17.59	2	
10.	RMG- 492	2100.00	2078.33	922.00	1700.11	1.03	56.10	28.56	8	

CONCLUSION

The present investigation indicated that pooled analysis of variance showed significant differences among genotypes, salinity levels as well as the interactions between genotype \times salinity levels. Different variability parameters viz., GCV, PCV, h² and GA as percentage of mean showed differential response to salinity levels. The development of salt-tolerant variety of mungbean is a cheaper and easier technology to overcome the reduce productivity in saline soil. Selection based on variability parameters and D-value will be use for selection of salt tolerant genotypes, although use of molecular marker linked with salinity tolerant OTLs or genes are more appropriate techniques to obtain saline tolerance genotypes when it combined to conventional morphological approach, where trials should also be evaluated under different field conditions by creating sick plots of salinity.

Future scope: Salt tolerant genotypes MVM-2, RMG-1099 and RMG-1101will be involved in different breeding program of mungbean to develop elite salt tolerant variety of mugbean after extensive field trial under saline condition.

Conflict of Interest. None.

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Kumawat & GothwalBiological Forum - An International Journal14(2): 287-292(2022)

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