

Estimation of Genetic Variability and Correlation Coefficients of Different Salinity Levels in Mungbean Genotypes

Saravanan T., Thangavel P., Johnny Subakar Ivin J.

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ABSTRACT

For this study eight mungbean genotypes viz., ADT 2, BM-2002-1, ML 5, AKM 4, Vishal, Vamban, TARM 1 and Utkarsh were used. Observations were taken on seven seedling characters and 7 quantitative characters. Statistical analysis of the seedling and quantitative characters showed that the PCV was higher than that of GCV for all the characters studied. Highest GCV and PCV were expressed by seedling shoot dry weight at 6 dSm⁻¹ salinity level followed by seedling shoot fresh weight at 6 dSm⁻¹, indicating that variation among the genotypes was highest for these traits. The PCV and GCV values were lowest in germination percentage followed by the shoot length at control. Among the growth characters

heritability (broad sense) was found to range from 41.57 % to 100 % in control, while in salinity levels broad sense heritability ranged from 50 % to 100 %. Under control, heritability was high for all characters except for germination percentage, shoot length and plant height. While in salinity condition, it was high for all characters except for number of pods/plant at 6 dsm⁻¹ salinity level. The genetic advance was high in nature only for the germination percentage whereas, the remaining character revealed low GA estimates. The maximum genetic advance in percent of mean (GAMP) was obtained for seedling shoot dry weight followed by seedling root dry weight at 6 dsm⁻¹ and the lowest was for plant height followed by germination percentage at control. The study revealed that all the 14 characters were positively correlated with each other. For all the characters, the genotypic correlation was at higher level than the phenotypic correlation. Four elite genotypes were found to be superior based on the mean performance namely Utkarsh, TARM 1, Vamban and Vishal among the various levels of salinity.

Keywords Genetic correlation, morphological traits, Heritability, Salinity score, Genetic divergence.

INTRODUCTION

The widespread dietary use of mungbean on the Indian subcontinent renders it a crucial pulse crop. In the arid and semi-arid tropics, as well as in the plains in irrigated areas, salinity stress is a severe issue

Saravanan T.^{1*}, Thangavel P.², Johnny Subakar Ivin J.³

²Professor

^{1,2}Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar 608002, Tamil Nadu, India

³Assistant Professor

Mother Teresa College of Agriculture, Mettusalai, Illuppur, Pudukkottai 622102, Tamil Nadu, India

Email : saravthiyagu@gmail.com

*Corresponding author

(Kumar *et al.* 2022). Mungbean incurs the merged adverse effects of other environmental factors such as insects, pests, high temperatures, pod shattering, and salinity due to global climate change, eventually resulting in a high yield loss (Kandil 2012). Relatively, minor research attention has been given to mungbean breeding compared to the cereals and soybean (Kim *et al.* 2015). Yield is unstable over locations and seasons due to the susceptibility of mungbean cultivars to environmental stress and disease (Bhajan *et al.* 2019). One of the most important strategies adopted by plant scientists to overcome salinity is to exploit genetic variability of the available germplasm to identify tolerant genotypes that may sustain a reasonable yield on salt affected soils (Neikr *et al.* 2019). This study, therefore, aimed at investigating the different agronomic performance of some accessions of mungbean to select for salt tolerance with the objectives of studying the variability parameters among various salinity levels and correlation among various characters under different levels of salinity.

MATERIALS AND METHODS

The experiment was conducted in the Seed Science and Technology (SST) Laboratory and at Pot Culture Yard, Department of Genetics and Plant Breeding, Faculty of Agriculture Annamalai University, Annamalai Nagar, Tamil Nadu during January 2016 to December 2017. For this study, eight mungbean genotypes collected based on their geographical and ecological adaptations to semi-arid and semi-humid regions of India such as ADT 2, BM-2002-1, ML 5, AKM 4, Vishal, Vamban, TARM 1 and Utkarsh were used.

The laboratory experiment was made to screen best performing accessions to assess the salt tolerance of mungbean at germination and seedling growth such as Germination percent, seedling shoot and root length, seedling shoot and root fresh weight and seedling shoot and root dry weight. The pot culture experiment focused on evaluation of variation in morphological, yield and yield related traits such as days to flowering, plant height number of branches/plants, number of pods/plants, number of seeds/pods, 100 seed weight and seed yield/plant of mungbean accessions. The design of both experiments was Ran-

domized Block Design (RBD) with three replications for each treatment and control.

The experiment was conducted using plastic earthen pot of 19 cm width at the base, 20 cm at the top and 18 cm height in Pot Culture Yard, with four salt treatments (0, 2, 4 and 6 dSm⁻¹). The soil was analyzed in Soil Science Laboratory, Department of Soil Science and Agricultural Chemistry, Faculty of Agriculture, Annamalai University sandy loam soil was sieved through a four mm sieve to get rid of large particles. The seeds were surface sterilized. The pots were filled with 3 kg sandy loam soil and seven sterilized seeds were sown in each pot and irrigated with tap water for three weeks at three days interval after sowing (Sunil Kumar *et al.* 2012). Then, each pot was treated with 360 ml of selected salt solutions for one month in three days intervals (Esechie *et al.* 2002). Equal amount of tap water was used to irrigate the control pots for the same duration.

Data on morphological and agronomical characters such as Germination percentage (GP), Seedling shoot length (SSL), Seedling root length (SRL), Seedling shoot fresh weight (SSFW), Seedling root fresh weight (SRFW), Seedling shoot dry weight (SSDW), Seedling root dry weight (SRDW), Days to first flowering (days), Plant height (cm), Number of branches/plant, Number of pods/plant, Number of seeds/pod, 100 seed weight (g) and Seed yield/plant (g) were collected from three randomly selected plants per pot and their mean data were recorded for all observations.

Statistical analysis

Analysis of variance (ANOVA) was calculated by TNAU STAT (Manivannan 2014). Genotypic and phenotypic coefficient of variation (GCV and PCV) were enumerated by the system of Burton (1952) and graded in the range; low (< 10%), moderate (10 - 20%), high (> 20%) (Sivasubramanian and Madhavamenon 1973). Broad sense heritability was deliberated using the formula by Lush (1940) and distinguished as high (> 60%), moderate (30- 60%) and low (0-30%). The genetic advance in mean per cent was estimated by employing the technique provided by Johnson *et al.* (1955) wherein classification was done to the extent of

low (< 10%), moderate (10- 20%), high (> 20%). The correlation of yield with its constituent attributes and among characters were calculated applying formula given by Weber and Moorthy (1952) wherein analysis was enacted utilizing the software, TNAUSTAT (Manivannan 2014).

RESULTS AND DISCUSSION

Due to the mung bean's intricate, fragile floral structure and the extremely precise micro circumstances requisite to pollen dehiscence and fertilization, the inherent variability for yield and traits pertaining to yield is very restricted, resulting in further selection for improvement not feasible. Nevertheless, breeders could benefit enormously from proper assessment of the magnitude of genetic variation existing for yield components, their heritability values, and genetic advance in order to identify superior genotypes for improvement.

The analysis of variance (ANOVA) for fourteen characters is furnished in Tables 1 - 4 individually for the various salinity levels viz., control at (Table 1), 2 dSm⁻¹ at (Table 2), 4 dSm⁻¹ (Table 3), and 6 dSm⁻¹. The 't' values were highly significant for all the 14 characters studied.

For all the characters, the PCV values were generally marginally greater than the GCV values, indicating a favorable impact of environment on character expression. The seedling shoot dry weight at 6 dSm⁻¹ salinity level and seedling shoot fresh weight at 6 dSm⁻¹ revealed the largest GCV and PCV values, indicating that these traits disclosed the most genotype variation. In terms of germination percentage, the PCV and GCV values were lowest, followed by the shoot length at control, indicating that these were the least variable characters (Fig. 1). When GCV and PCV values for each character were contrasted across salinity levels, it became apparent that while mean values ascended with salinity, CV values also stood up, potentially suggesting a complex response mechanism that culminated in genotype variations and the likelihood of determining responsive genotypes. This is particularly applicable for each of the fourteen characters, as Jat (2009) has previously stated. Superior values of heritability observed, revealed the possibility of improvement in the traits. Estimates of heritability in broad sense ranged from 41.57 % to 100 % in control, while in salinity levels broad sense heritability ranged from 50 % to 100 %. Under control, heritability was high for all characters except for germination percentage, shoot length and plant height. While in salinity condition, it was high for all characters except for number of pods/plant at 6 dsm⁻¹ salinity level. Higher broad sense heritability

Table 1. Analysis of variance among mungbean genotypes for fourteen characters in control.

Source	df	Germination (%)	Shoot length (c)	MSS				
				Root length (c)	Seedling shoot fresh weight (g)	Seedling root fresh weight (g)	Seedling shoot dry weight (g)	Seedling root dry weight (c)
Replication	2	2.619	0.378	0.085	0.001	0.002	0.-001	0.001
Treatment	7	28.572	1.776	1.653	0.406	0.026	0.025	0.004
Error	14	9.115	0.417	0.116	0.001	0.002	0.001	0.001

Table 1. Continued.

Source	df	Days to first flowering	Plant height (cm)	MSS				
				Number of /plant branches (days)	Number of pods /plant	Number of seeds/pod	100 seed weight (g)	Seed yield/ plant (g)
Replication	2	3.125	0.459	0.001	0.500	0.375	0.041	0.097
Treatment	7	5.881	3.651	1.714	2.381	5.238	1.179	2.338
Error	14	0.792	1.161	0.001	0.310	0.327	0.063	0.0526

Table 2. Analysis of variance among mungbean genotypes for fourteen characters at 2 dSm⁻¹ salinity level.

Source	df	Germination (%)	Shoot length (cm)	MSS				
				Root length (cm)	Seedling shoot fresh weight (g)	Seedling root fresh weight (g)	Seedling shoot dry weight (g)	Seedling root dry weight (g)
Replication	2	1.046	0.133	0.069	0.005	0.001	0.002	0.001
Treatment	7	151.819	29.644	7.679	0.642	0.022	0.046	0.012
Error	14	2.698	0.099	0.049	0.007	0.001	0.001	0.001

Table 2. Continued.

Source	df	Days to first flowering (days)	Plant height (cm)	MSS				
				Number of branches /plant	Number of pods /plant	Number of seeds/pod	100 seed weight (g)	Seed yield/ plant (g)
Replication	2	1.167	0.976	0.001	0.792	0.167	0.001	0.002
Treatment	7	38.452	50.316	2.946	2.071	2.738	2.943	13.544
Error	14	0.881	0.696	0.001	0.268	0.309	0.009	00.021

magnitude revealed that greater proportion of the entire variance was due to the greater genotypic variance influenced less by environmental factors therefore having high heritable variations. Such findings were suitable for reliable selection of traits, which are the key components for any crop improvement program (Thiyagarajan 1990). The low broad sense heritability magnitude revealed traits under examination had lower genetic potentials. Kandic *et al.* (2009) suggested that the heritability of physiological traits is lower than the heritability of morphological traits.

Numerous studies have evaluated the relationship between heritability and the degree of variation between phenotypic and genotypic coefficients of variability (Khan *et al.* 2007). The evaluation of the results demonstrated that traits like fresh root weight and excised leaf water retention in stressful environments have minimal variation between phenotypic and genotypic coefficient of variability and therefore are highly heritable. The characters expressed a smaller PCV and GCV difference with high heritability as the salinity levels were normal and varied. It became

Table 3. Analysis of variance among mungbean genotypes for fourteen characters at 4 dSm⁻¹ salinity level.

Source	df	Germination (cm)	Shoot length (cm)	MSS				
				Root length (cm)	Seedling shoot fresh weight (g)	Seedling root fresh weight (g)	Seedling shoot dry weight (g)	Seedling root dry weight (g)
Replication	2	0.563	0.133	0.059	0.014	0.003	0.001	0.001
Treatment	7	38.105	9.435	3.807	0.523	0.0205	0.040	0.005
Error	14	5.784	0.230	0.055	0.017	0.001	0.001	0.001

Table 3. Continued.

Source	df	Days to first flowering (days)	Plant height (cm)	MSS				
				Number of branches /plant	Number of pods /plant	Number of seeds/pod	100 seed weight (g)	Seed yield/ plant (g)
Replication	2	1.042	0.002	0.001	0.042	0.500	0.009	0.016
Treatment	7	17.470	5.974	1.714	1.691	4.381	1.684	2.901
Error	14	1.042	1.008	0.001	0.280	0.309	0.029	0.020



Fig. 1. Genetic components of variance and heritability for germination percentage, seedling shoot length, seedling root length, seedling shoot fresh weight, seedling root fresh weight, seedling shoot dry weight, Seedling root dry weight, days to first flowering in mungbean.

evident that selection would be successful for traits with high heritability and minor variations between phenotypic and genotypic coefficients of variability.

The maximum genetic advance (GA) was observed in respect of germination percentage among the fourteen characters. The minimum genetic ad-

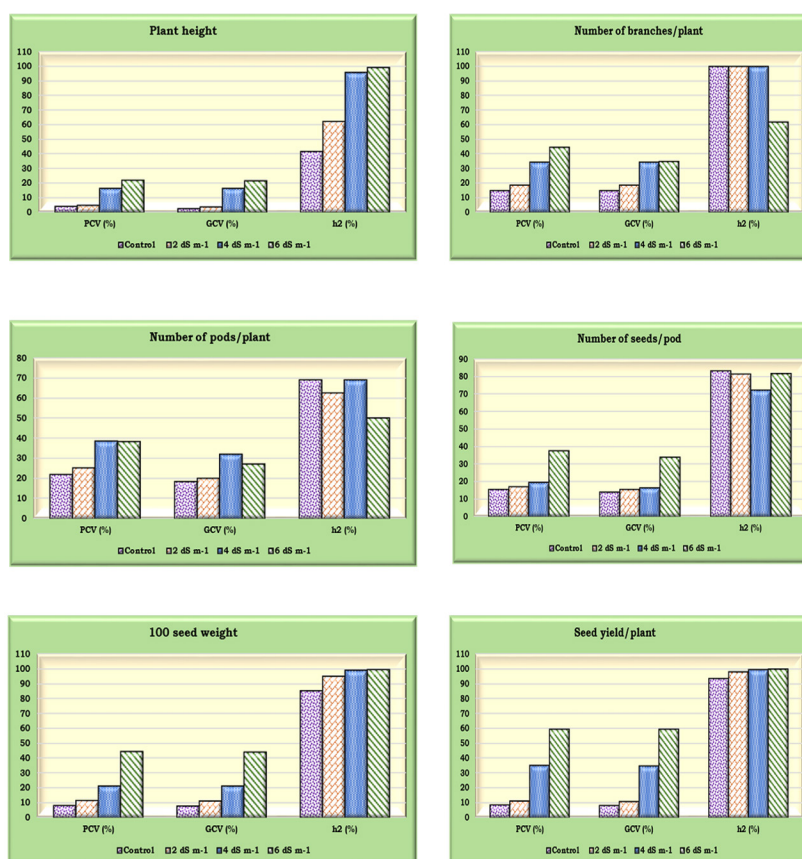
vance was found for the character seedling root fresh weight. The maximum genetic advance in percent of mean (GAMP) was obtained for seedling shoot dry weight followed by seedling root dry weight at 6 dS m⁻¹ and the lowest was for plant height followed by germination percentage at control.

Table 4. Analysis of variance among mungbean genotypes for fourteen characters at 6 dSm⁻¹ salinity level.

Source	df	Germination (%)	Shoot length (cm)	MSS				
				Root length (cm)	Seedling shoot fresh weight (g)	Seedling root fresh weight (g)	Seedling shoot dry weight (g)	Seedling root dry weight (cm)
Replication	2	0.108	0.018	0.002	0.011	0.001	0.001	0.001
Treatment	7	571.486	28.735	20.283	0.504	0.011	0.039	0.012
Error	14	1.716	0.102	0.009	0.014	0.001	0.001	0.001

Table 4. Continued.

Source	df	Days to first flowering (days)	Plant height (cm)	MSS				
				Number of pods /plant	Number of seeds/pod	100 seed weight (g)	Seed yield/ plant (g)	
Replication	2	1.125	0.722	0.292	0.042	0.542	0.001	0.005
Treatment	7	63.024	72.443	1.423	0.7381	4.357	5.815	17.866
Error	14	3.506	0.228	0.244	0.185	0.304	0.009	0.012

**Fig. 2.** Genetic components of variance and heritability for plant height, Number of branches/plants, Number of pods/ plants, Number of seeds / pods, 100 seed weight, Seed yield / plant.

Characters of crop plants, especially quantitative characters show different levels of interrelationship. Correlation analysis is a tool to study interrelationship of characters so as to identify variables that show maximum relationship with others. Fourteen characters of the eight genotypes of mungbean were subjected to correlation analysis. The study revealed that all the 14 characters were positively correlated with each other. The genotypic correlation was more significant than the phenotypic correlation for every single characteristic. Out of the various characters studied, seed yield/plant the genotypic correlation was recorded at higher level than the phenotypic correlation. Seed yield/plant was in positive and significant correlation with germination percentage ($G=0.78, 0.74$) ($P=0.76, 0.73$) at 4 and 6 dSm^{-1} , shoot length ($G=0.80, 0.85, 0.79$ under control, 4 and 6 dSm^{-1}), ($P=0.84, 0.79$ at 4 and 6 dSm^{-1}), seedling shoot fresh weight ($G=0.85, P=0.85$) at 6 dSm^{-1} , days to first flowering ($G=0.87, 0.90, 0.96$), ($P=0.72, 0.88, 0.88$) under control, 4 and 6 dSm^{-1} , plant height ($G=0.84, 0.89, 0.84$ control, 4 and 6 dSm^{-1}), ($P=0.86, 0.80$ at 4 and 6 dSm^{-1}), number of branches/plant ($G=0.87, 0.95$), ($p=0.86, 0.74$) at 4 and 6 dSm^{-1} , number of pods/plant ($G=1.01, 0.73$) under control and 4 dSm^{-1} , number of seeds/pod ($G=0.73, 0.77, 0.92, 0.88$ control, 2, 4 and 6 dSm^{-1}), ($P=0.79, 0.80$ at 4 and 6 dSm^{-1}); 100 seed weight ($G=0.94, 0.90, 0.95$), ($P=0.78, 0.90, 0.95$) under control, 4 and 6 dSm^{-1} salinity levels, respectively (Table 4, Fig. 2).

Significant association with days to first flowering were in accordance with Rathor *et al.* (2015) and Hemavathy *et al.* (2015); for plant height, similar results were obtained by Patel *et al.* (2014) and Rathor *et al.* (2015), Hemavathy *et al.* (2015) and Keerthinandan *et al.* (2016); for number of pods/plant, similar results were also observed by Gadakh *et al.* (2013), Titumeer *et al.* (2014), Rathor *et al.* (2015), Hemavathy *et al.* (2015) and Das and Barua (2015).

Positive and significant correlation between number of pods/plant and number of seeds/pod were reported by Raselmiah *et al.* (2016). The genotypic correlation of 100 seed weight was positive and significant with seed yield per plant which was in accordance with the results of Raselmiah *et al.* (2016).

The current experiment resulted in a significant amount of insight on the mean performance, variability among the 8 genotypes of mungbean, heritability,

genetic advance, genetic divergence, and character association within them. The chosen characters were all positively correlated with one another.

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