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Screening of Mungbean (*Vigna radiata*) Genotypes for Nutrient Stress Tolerance

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ABSTRACT

Generally nutrient deficiency of a soil is corrected through application of chemical fertilizers. Fertilizers on one hand are costly and on the other hand it may lead to water pollution by nitrogen and phosphorus from agricultural land. Screening of genotypes for nutrient stress tolerance could be the best alternative to overcome the situation. The present study evaluates the plant growth characters with emphasis on root growth and nutrient uptake of selected mungbean genotypes and examines the efficiency of certain growth parameters for predicting their adaptation in sub-optimal nutrient environment. Some genotypes (VC 6153B, GK3 & VC 6144A) were found to be high nutrient acquiring genotypes and some (PDM 54, IPSA 25 & VO 1443 A-G) were low nutrient acquiring genotypes.

Key words: Mungbean, genotypes, nutrient stress.

INTRODUCTION

Due to rapid growth and early maturity, mungbean is adopted into multiple cropping systems in the drier and warmer climates of the lowland tropics and sub-tropics. Although mungbean has a number of advantages in terms of food value, production and crop management, the area and production is not increasing proportionately in comparison with other cereals. With the advent of high yielding varieties of rice and wheat the production of cereal crops increased manifold during the past four decades with the concomitant decrease in area and production of pulses. In view of growing demand of the cereal crops it is unlikely that the HYV cereals would give way to pulses like mungbean. In Bangladesh, extensive cultivation of mungbean is constrained by strong competition with rice, particularly during wet season.

There are two approaches to overcome nutritional deficiency of soils and crops, one is to fit the soil through supplement nutrients to the crops and the other is to fit the crops or crop varieties to the soils.

MATERIALS AND METHODS

The treatment variables comprised 200 mungbean genotypes (both native and exotic). Seeds were collected from the Genetic Resources Unit of the Department of Agronomy, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur. The experiment was conducted during the period of June 1999 to August 2000 in four batches taking 50 genotypes each time.

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The experiment was laid out in a Completely Randomized Design (CRD) with five replications each for genotype and age. Healthy and uniform seeds of each genotype were sorted out from their stock, treated with vitavex 200 @ 1g kg^{-1} seed. After soaking in water for 4 hours 3 imbibed seeds were sown in each polyvinyl pot filled with low fertility field soil.

The soil used in the study was clay loam having low N (0.09%), low P (6.58µg/g soil) and medium K (0.26 meq/100 g soil). No fertilizer and organic amendments were used for growing the crops up to 21 days after emergence (DAE). Seedlings were raised at optimal soil moisture condition (i.e. about 50% available water content). On the 21st day seedlings of each genotype were carefully uprooted from the soil followed by washing the soil with tap water. After harvest, plants were separated into stem, leaf, petiole and root. Leaf area, root volume and root length were recorded just after harvest. Dry mass of the seedling was recorded. Root length density (RLD), root weight density (RWD), root surface area (RSA), specific leaf weight (SLW), plant growth rate (PGR) and net assimilation rate (NAR) were calculated. Tissue N, P and K concentration were determined in the laboratory following standard methods (Micro-Kjeldahl method, molybdate blue method of Murphy and Riley (1962) and wet oxidation methods).

As large number (200) of genotypes were involved in the study, analysis of variance (ANOVA) was not employed to evaluate the genotypic variation in seedling growth, instead, cluster and discriminant function analysis (DFA) were performed for classifying the genotypes (accessions) into a number of homogenous groups using MS Excel and SPSS software's following four steps.

i. Estimation of degree of association among the different characters analyzed, according to Pearson's coefficient (Clifford and Stephenson, 1975).
ii. Derivation of orthogonal variables, using principal component analysis (PCA) based on the correlation matrix (Hair *et al*., 1992).
iii. Classifications of accessions in similar groups by the hierarchical technique of cluster analysis (Hair *et al*., 1992).
iv. Verification of the significance of groups by multiple groups DFA to determine the power of each variable to separate groups (Hair *et al*., 1992).

RESULTS AND DISCUSSION

There was variation in morphological parameters among the genotypes (Table 1). Variation in root length was the highest among the parameters that ranged between 598 cm to 5464 cm per plant while RWD, RSA and root volume showed little variation. Correlation between pairs of parameters satisfied some aspects of relationship (Table 2).

Table 1. Variation in morphological characters among 200 mungbean genotypes

Character	Range	Mean	SD*	CV* (%)
a. Morphological				
Plant height (cm)	5.9 - 15.0	10.4	1.80	29.54
Leaf weight (mg)	141 - 427	291	55.3	11.90
Specific leaf weight (mg cm^{-2})	2.11 - 4.23	4.18	1.80	22.08
Leaf area (cm^2)	21.70 - 167.30	80.50	31.90	30.95
Stem weight (mg)	16 - 325	40	52.31	38.04
Root weight (mg)	85 - 241	155	34.74	21.99
Root weight density (mg cm^{-3})	0.12 - 1.05	0.31	0.14	3.22
Root length (cm)	598 -5464	1891	1076.03	47.74
Root length density (cm cm^{-3})	0.69 - 6.31	2.18	1.24	26.51
Root surface area (cm^2)	6.16 - 42.10	20.76	6.49	5.02
Root volume (cm^3)	1.0 - 6.6	3.4	1.00	5.06
NAR (mg cm^{-2} day^{-1})	0.36 - 1.19	0.61	0.17	15.74
PGR (mg day^{-1})	14.6 - 43.0	28.6	6.08	20.57
b. Physiological				
Nitrogen uptake (mg $plant^{-1}$)	2.11 - 15.07	6.50	2.30	10.53
Phosphorus uptake (mg $plant^{-1}$)	0.031- 1.454	0.326	0.207	24.54
Potassium uptake (mg $plant^{-1}$)	0.039- 0.302	0.152	0.064	26.31

Note: * Significant at 5% level.

Table 2. Correlation coefficients among 16 quantitative characters weighted to measure the diversity among 200 mungbean genotypes

	PHT	LFWT	SMWT	RWT	RV	LA	SLW	PGR	NAR	RL	RLD	RWD	RSA	N-up	P-up
PHT															
LFWT	0.388**														
SMWT	0.651**	0.679**													
RWT	0.590**	0.788**	0.776**												
RV	-0.044	0.402**	0.219	0.329**											
LA	0.471**	0.631**	0.716**	0.661**	0.210										
SLW	-0.326**	-0.165*	-0.368**	-0.309**	-0.025	-0.778**									
PGR	0.584**	0.913**	0.899**	0.920**	0.349**	0.735**	-0.302								
NAR	-0.317**	-0.157	-0.342**	-0.275**	0.093	-0.714**	0.857**	-0.302							
RL	-0.035	0.426**	0.239	0.349**	0.960**	0.246**	-0.066	0.857**	0.062						
RLD	-0.232**	0.172*	-0.101	0.003	0.758**	-0.120	0.231**	-0.066	0.370**	0.715**					
RWD	-0.022	0.223**	0.051	0.182*	0.477**	-0.013	0.143*	0.166*	0.249**	0.408**	0.634**				
RSA	-0.035	0.426**	0.239**	0.349**	0.960**	0.246**	-0.066	0.373**	0.062	1.000**	0.715**	0.408**			
N-up	0.187*	0.597**	0.606**	0.549**	0.193*	0.463**	-0.162*	0.647**	-0.186*	0.260**	-0.133**	-0.268**			
P-up	0.265**	0.471**	0.364**	0.453**	0.274**	0.232**	0.020	0.469**	0.036	0.269**	0.274**	0.546**	0.104		
K-up	0.409**	0.595**	0.763**	0.614**	0.256**	0.594**	-0.245**	0.726**	-0.323**	0.265**	0.040	0.277**	0.377**	0.467**	-

Note: PHT=Plant height, LFWT= leaf weight, SMWT= stem weight, RWT= root weight, RV= root volume, LA= leaf area, SLW= specific leaf weight, PGR= plant growth rate, NAR= net assimilation rate, RL= root length, RLD= root length density, RWD= root weight density, RSA= root surface area, N-up= nitrogen uptake, P-up= phosphorus uptake and K-up= potassium uptake

*, ** significant at 5% and 1% level, respectively

Among the morphological variables, the highest correlation correspond to root length (r = 1.00) and root volume (r = 0.96). Traits presenting highly significant correlations with these two characters were RSA and root volume (r = 0.96) and leaf weight (r = 0.913) indicate that higher the root and leaf weight higher the PGR. NAR was positively correlated with SLW (r = 0.857) but negatively correlated with leaf area (r = -0.714) which indicate that NAR increases with increasing SLW whereas decreases with increasing leaf area (Table 2). Leaf area higher than optimum reduces the light interception due to mutual shading and thereby reduces the photosynthetic efficiency. Root weight was positively correlated with nitrogen uptake (r = 0.549), phosphorus uptake (r = 0.435) and potassium uptake (r = 0.614), which indicate that accessions having higher root weight were efficient in N, P and K uptake.

A dendrogram was constructed on the basis of cluster analysis (Fig. 1), which gave a preliminary idea about the number of clusters to be done using 16 variables in 200 mungbean genotypes. The discriminant functions that differentiated among these clusters were obtained by the stepwise procedure. The 200 mungbean genotypes were grouped into four (Figure 2) by hierarchical cluster analysis followed by DFA to verify the precision of the groups originally made by cluster analysis. The graphic illustration of the discriminant analysis would provide an idea about the discrimination of the genotypes among clusters. From the figure it was observed that the 4 clusters were oriented in different positions of the origin of X and Y ordinates. As hierarchical clustering was done in the analysis, the genotypes were clustered mainly on the basis of the higher values of discriminating variables contributing to functions 1 and 2.

Dendrogram using Average Linkage (Within Group)

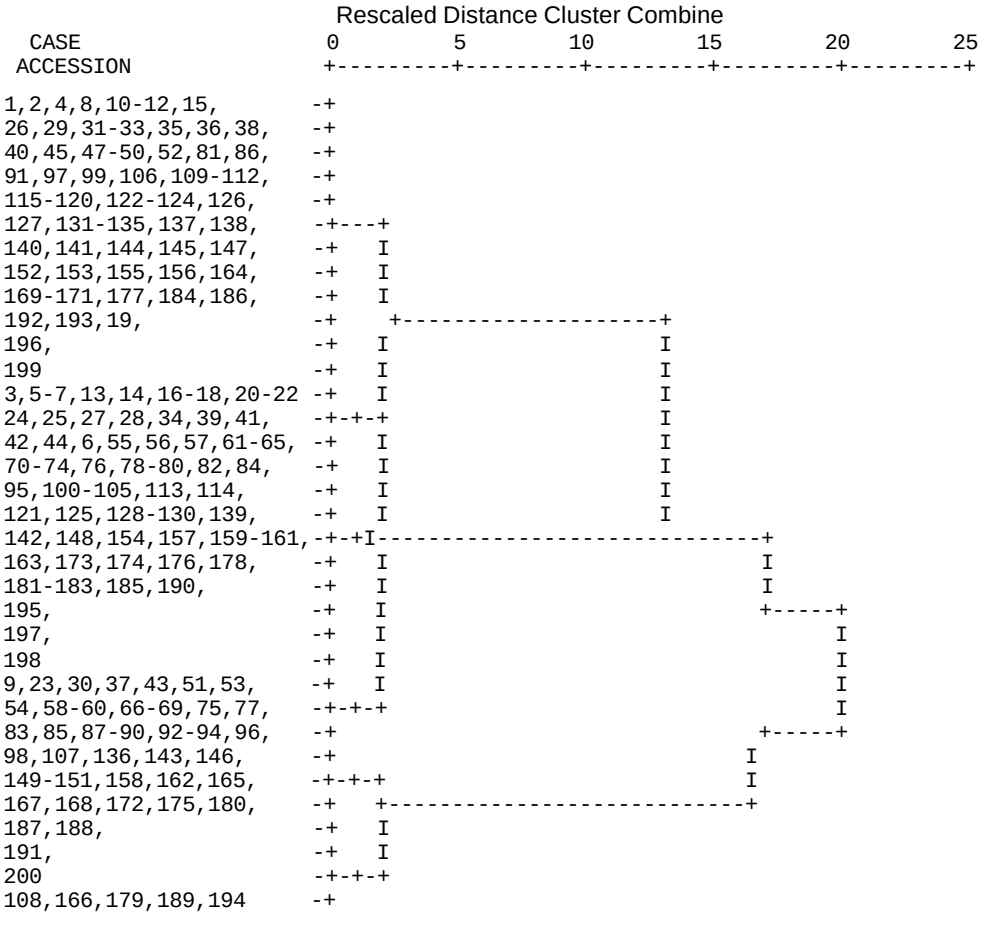

Fig. 1. Dendrogram showing the relationship among the mungbean accessions (genotypes) in relation to their contribution to diversity

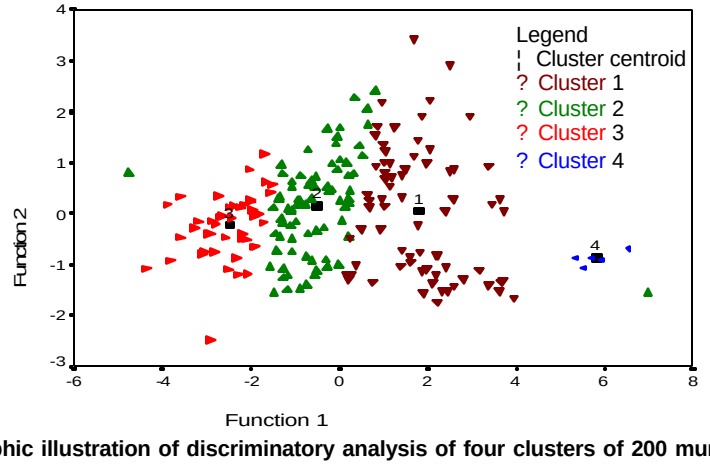

Fig. 2. Graphic illustration of discriminatory analysis of four clusters of 200 mungbean genotypes based on their principle component scores

According to D2 analysis, cluster 1 and 3 were the most distant with 480.852 units among the clusters (Table 3). The four clusters were also statistically different from each other. Each of the clusters included accessions from all the regions except cluster 4. Cluster 2 included the maximum (96) accessions followed by cluster 3 (81) and cluster 1 (28), whereas cluster 4 included the lowest number (5) of accessions. However, this graphical illustration did not provide any indication about the best cluster; rather it indicated the effects of variables contributing to functions 1 and 2 on the genotypes under each cluster.

Table 3. Pair wise Mahalanobis distances (D^2) between four clusters of mungbean genotypes

Cluster	1	2	3	4
1	0.00	-	-	-
2	192.031**	0.00	-	-
3	480.852**	97.585	0.00	-
4	79.791**	192.768**	307.087**	0.00

Note: ** distances differing from zero at a 99% confidence interval

Accordingly, based on 16 variables under functions 1 and 2, the genetic diversity among clusters 1 and 4 was lesser compared to the other clusters. It may provide the basic information to the breeders for selecting parents in the breeding program. D^2 analysis was done by other workers to identify the distinct clusters in different studies (Mannan, 2000; Islam, 2003; Momin, 2003). The genotype or genotypes oriented at or very near to the group centroid mean that the deviation of the genotype or genotypes in response to discriminating variables was very close to the cluster centroid and might be considered as the most representative (might not be the best) of that cluster. Accordingly, the accession nos.49, 36 and 153 (genotypes VC 6153B, GK 3 and VC 6144A) in cluster 2 and the accession nos. 43, 167 and 191 (genotypes PDM 54, IPSA 25 and VO 1443 A-G) in cluster 3 might be considered as more representative of their respective clusters. The discriminant functions that differentiated among these clusters were obtained by the stepwise procedure (Table 4). All discriminatory functions were statistically significant at a probability of 0.001 according to the Chi-square test. However, latent roots indicate that the first four functions accounted for more than 84.75% of the total variance (Table 4).

Table 4. Discriminant functions that distinguish between clusters of mungbean genotypes

Function	Latent root	Variance (%)		R^2 coefficient	Wilks ?	$?^2$	df	P
		Function	Cumulative					
1	6.655	41.594	41.594	0.566	0.987	104.85	66	0.002
2	3.889	24.307	65.901	0.808	0.769	59.84	127	0.000
3	1.690	10.561	76.462	0.858	0.873	0.00	199	0.000
4	1.311	8.194	84.656	0.829	0.805	0.99	198	0.000
5	0.647	4.044	88.700	0.947	0.292	64.45	122	0.000
6	0.475	2.968	91.668	0.906	0.923	63.52	107	0.001
7	0.383	2.392	94.060	0.932	0.987	143.49	48	0.001
8	0.236	1.476	95.536	0.976	0.785	23.20	179	0.000
9	0.228	1.422	96.958	0.898	0.990	59.00	139	0.001
10	0.162	1.013	97.971	0.963	0.225	23.20	179	0.000

The contribution of each of 10 canonical discriminant functions for explaining the variance along with their corresponding *eigen* values and canonical correlation coefficient have been described in Table 4. It appeared that the function 1 (the first principal component) alone explained 41.6% of the total variance while the function 2 (the second principal component) explained 24.3% and together they explained 65.9% of the total variance.

Table 4 described the variables mostly contributed to the discriminant functions along with their coefficients under each function. It was found that the coefficients of leaf area (0.855), leaf weight (0.795), root weight (0.875), stem weight (0.854), PGR (0.945), N (0.945), P (0.521) and K (0.761) uptake were more in function 1 and than those in function 2. It meant that contribution of these variables to function 1 was higher for explaining 41.6% of total variance in 200 mungbean genotypes. On the other hand, the coefficients of root weight (0.885), root length (0.702), root volume (0.738), NAR (0.603) were higher in function 2 than those in function 1. It meant that contribution of these variables to function 2 was higher in explaining 24.3% of the total variance in 200 mungbean genotypes. Gonzales (1996), Chen *et al*. (1997) and Pandey *et al*. (1999) showed that a set of variables corresponded the different principal components (functions) under different studies in grouping rice genotypes.

Canonical vector analysis (CVA) revealed that in canonical vector, the major axes of differentiation- root weight, leaf weight, root length and root surface area were the most important characters responsible for the genetic divergence; which accounted for 84.7% of total diversity. The given values of these four principal component axes were more than unity. The given values of the 1st, 2nd, 3rd and 4th principal component axis- root weight, leaf weight, root length and root surface area are 6.665, 3.889, 1.690 and 1.311 contributing 41.6%, 24.3%, 10.6% and 8.2% of the total diversity in mungbean genotypes under study (Table 5). As the integrated sum of all single root parameters, the root surface area can indicate root efficiency in adsorbing water and mineral nutrients (De Willigen and Van Noordwijk, 1987).

Table 5. Latent roots and latent vectors associated with the first four principal components

	Principal components			
	1st	2nd	3rd	4th
Latent roots	6.655	3.889	1.690	1.311
Percentage variance	41.594	24.307	10.561	8.194
Latent vectors				
a. Morphological				
Plant height (cm)	0.536	- 0.424	0.246	- 0.196
Leaf weight (mg)	0.855	1.976E-02	0.212	0.177
Specific leaf weight	- 0.424	0.488	0.637	0.329
Leaf area (cm^2)	0.795	- 0.397	- 0.315	- 0.134
Stem weight (mg)	0.854	0.739	0.178	7.633E-02
Root weight (mg)	0.875	- 0.144	0.197	6.097E-02
Root weight density (mg cm^{-3})	0.279	0.626	- 0.101	- 0.563
Root length (cm)	0.579	0.702	0.558	0.136
Root length density (cm cm^{-3})	0.204	0.885	- 0.342	- 0.121
Root surface area (cm^2)	0.579	0.702	0.248	0.136
Root volume (cm^3)	0.551	0.738	- 0.305	7.689E-02
NAR (mg cm^{-2} day^{-1})	- 0.372	0.603	0.558	0.291
PGR (mg day^{-1})	0.945	- 0.151	0.215	0.123
b. Physiological				
Nitrogen uptake (mg $plant^{-1}$)	0.596	- 0.208	1.443E-02	0.662
Phosphorus uptake (mg $plant^{-1}$)	0.521	0.235	0.459	- 0.406
Potassium uptake (mg $plant^{-1}$)	0.761	- 0.117	0.204	- 0.170

Considering overall results seedling leaf weight, root weight, root length and root surface area may be treated as important traits for screening large number of mungbean genotypes for sub-optimal nutrient environment.

CONCLUSION

Multivariate analysis revealed that roots contributed significantly to nutrient uptake in mungbean genotypes. Among the four clusters genotypes viz. VC6153B, GK 3 and VC 6144A of cluster 2 were identified as high growth and high N, P, K acquiring genotypes and genotypes viz. PDM 54, IPSA 25 and VO 1443 A-G were identified as low growth and low N, P, K acquiring genotypes. The nitrogen efficient genotypes can be used in the breeding program for development of new high yield potential varieties of mungbean that would fit in the low fertility marginal lands.

LITERATURE CITED

Chen, Z. Q., Li, J. and Li, H. 1997. Studies on plant type design and selection target of high quality varieties in indica rice. I. Correlativity and principal components analysis of major characters. *J South China Agril Univ* **18**(3), 7-12.

Clifford, H. T. and Stephenson, W. 1975. An introduction to numerical classification. Academic Press, New York, USA.

Gonzales, L. M. 1996. Principal component analysis and variety classification in relation to rice seedling salinity tolerance. *Int Rice Res Notes* **21**, 2-3, 55-56.

Gunawardena, S. F. B. N., Danso, S. K. A. and Zapata, F. 1992. Phosphorus requirements and nitrogen accumulation by three mungbean (*Vigan radiata* (L.) Wliczek) cultivars. *Plant and Soil* **147**, 267-274.

Hair, J.F., Anderson, R. E., Tatham, R. L. and Black, W. C. 1992. Multivariate data analysis. Macmillan Publishing Company, New York, USA.

Islam, M. R. 2003. Eco-physiology of soil flooding tolerance in mungbean. Unpublished [PhD Thesis], Dept. of Agronomy, BSMRAU, Gazipur.

Islam, M. T. 1994. Eco-physiological studies on photosynthesis and dry matter production in mungbean (*Vigna radiata* (L.) Wilczek). Unpublished [PhD Thesis], Kyushu University, Fukuoka, Japan.

Mamin, M. S. I. 2003. Photosynthesis, shoot reserve translocation, lodging and nitrogen use efficiency of modern and traditional varieties of rice. Unpublished [PhD Thesis], BSMRAU, Gazipur.

Mannan, M. A. 2000. Plant Biodiversity in the homesteads of Bangladesh and its utilization in crops environment. Unpublished [PhD Thesis], Dept. of Genetics and Plant Breeding, BSMRAU, Gazipur.

Pandey, D. K., Gupta, H. S. and Pandey, P. S. 1999. Assessment of divergence in rice grown in iron toxic soil of Meghalaya. *Indian J Agril Sci* **69**(1), 69-70.

Van Noordwijk, N. and De Willigen, P. 1979. Calculation of the root density required for growth in soils of different P-status. *In* "The Soil-Root Interface" (J. L. Harley and R. S. Russell, Eds.), Academic Press, New York, London. pp. 381-390.