

CHARACTERIZATION AND YIELD VARIATION IN MUNGBEAN GENOTYPES UNDER WATER STRESS

M. Belayet Hossain¹, M. A. Karim², J. U. Ahmed², M. M. Haque² and M. Waliur
Rahman³

ABSTRACT

An investigation was carried out at the experimental field of Bangabandhu Shiekh Mujibur Rahman Agricultural University, Gazipur to characterize different plant parameters related to yield performance of twenty seven mungbean (*Vigna radiata* L.) genotypes under water stress condition. Four clusters were found from a scattered diagram formed by function 1 and function 2 values obtained from PCA. Among the 4 clusters, the cluster IV showed the highest distance unit of 94.224 with cluster I, 17.676 and 24.810 with cluster II and III. Intermediate distanced cluster was found between cluster IV and cluster I. This intermediate distanced cluster pairs may act as good source of distant parents in hybridization program.

Keywords: Mungbean, water stress, yield variation

INTRODUCTION

Mungbean (*Vigna radiata* L. *wilezek*) is one of the important grain legumes extensively grown in the tropics and subtropics. Mungbean is the fifth important pulse crop of Bangladesh and it occupies about 43680 ha of land producing 25655 tons of dry grain annually (BBS, 2005). Climatic conditions of Bangladesh favor growth of mungbean on well drained soil almost throughout the year, even though its cultivation still remains concentrated mainly in the post monsoon dry season. The crop being normally grown under non-irrigated condition, encounters water stresses of varying degrees at different growth stages depending on soil moisture condition. Hence, the yield of mungbean in Bangladesh is quite low compared to that in other mungbean growing countries. Plant performance under conditions of water shortage has been extensively studied. Water stress affects various physiological processes associated with growth, developed and economic yield of a crop (Hsiao and Acevedo, 1974; Begg and Turner, 1976). Water deficit disturbs normal turgor pressure, and the loss of cell turgidity may stop cell enlargement that causes reduced plant growth. Water deficit may change the pattern of growth. Often root shoot ratio increases, leaf area index decreases and the thickness of cell walls and amount of cutinization and lignifications increase by water stress.

Mungbean is reported to be more susceptible to water deficits than many grain legumes (Pandey *et al.*, 1984). Water stress reduces photosynthesis, which are the most important physiological processes that regulate development and productivity of crop plants. A number of researchers reported that reduction in crop photosynthesis and development of water stressed plant is due to reduction in leaf area and dry matter accumulation (Pandey *et al.*, 1984; Kriedemann 1986; Hamid *et al.*, 1990). Although water stress imposed at any growth stage

¹Jabor Hat College, Pirgonj, Thakurgaon, ²Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur-1706, ³Hajee Mohammad Danesh Science and Technology University (HSTU), Dinajpur 5200, Bangladesh

causes reduction in dry matter but their effects on seed yield differ depending on growth stage when exposed to stress (Agrawal *et al.*, 1976). Sadasivan *et al.* (1988) reported that stress during vegetative phase reduce grain yield through reducing plant size, limiting root growth, and leaf area, restricting dry matter accumulation, number of pods and harvest index. Water deficits at the flowering and the post-flowering stages have been found to have a greater adverse impact than at the vegetative stage (Cortes and Suidaria, 1986). The reproductive stage is well known for its sensitivity to drought stress (Brown *et al.*, 1985); the seed yield and harvest index being most sensitive to water stress treatment imposed at post flowering and pod development stages (Upreti and Bhatia, 1989). Hesketh (1963) reported tenfold differences/in net photosynthesis among species. However, genotypic differences under varying degrees of water stress have not been elucidated. An understanding of genotypic difference to water stress can aid in identifying cultivars that can tolerate drought and produce reasonably high seed yield. Thus the present experiment was conducted to asses the performance of mungbean cultivars (genotypes) to water stress.

MATERIALS AND METHODS

The experiment was carried out at the experimental field of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur during the kharif season (April 2004 to June 2004). The experiment was conducted under rain free shed condition. The field was possible to cover by a moving house made by stainless steel frame and transparent polythene sheet was used as shed. The soil type of the experimental field belongs to the Shallow Red Brown Terrace type under Salna Series of Madhupur Tract (Brammer, 1971; Saheed, 1984) of Agro Ecological Zone (AEZ) 28, which is characterized by silty clay with pH value of 6.5. Twenty seven mungbean genotypes collected from Asian Vegetables Research and Development Centre (AVRDC), Taiwan were included in the present investigation. The accession numbers of the genotypes were GK 11, GK 13 GK 15, GK 16, GK 17, GK 18, GK 19, GK 22, GK 23, GK 24, GK 25, GK 26, GK 27, GK 28, GK 29, GK 30, GK 32, GK 33, GK 35, GK 37, GK 38, GK 39, GK 40, GK 42, GK 43, GK 45 and GK 47. The doses of manures and fertilizers were applied as per recommendation of Fertilizer Recommendation Guide 1997. The experimental field was kept weed free by hand weeding. Weeding was done at 15 days interval and it was continued up to pod harvesting stage. The crop was protected from the attack of insect pests by spraying of Malathion 57 EC @ 1 ml/L of water. At physiological maturity, dry pods were harvested at different days after sowing (DAS) for different genotypes. The harvesting was started from 57 DAS and continued up to 68 DAS for different genotypes. The data of different physio-morphological, reproductive, seed yield and related attributes were recorded from the investigation to obtain the precise information pertaining to genotypic differences.

Principal components were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jeger *et al.*, 1983).

Clustering was done using non-hierarchical classification. Starting from some initial classification of the genotypes into required group, the algorithm repeatedly transfers genotypes from one group to another so long as such transfers improve the value of criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swapping two genotypes of different classes, and so on. Using Canonical Vector Analysis a linear combination of original variability's that maximize the ratio in between group to with in group variation to be find out and there by giving functions of the

original variability's that can be used to discriminate between groups. The canonical varieties are based on the roots and vectors of $W^{-1}B$, where W is the pooled within groups covariance matrix and B is the among the groups covariance matrix.

When the clusters are formed, the average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n , where D^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

Cluster diagram was drawn using the intra and inter cluster distance. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

RESULTS AND DISCUSSION

Genetic diversity and Cluster Analysis

The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. Thus, the results obtained through PCA were confirmed by non-hierarchical clustering. Table 1 represents the cluster occupied by 27 genotypes of mungbean. The cluster I contained higher number of genotypes (17) followed by cluster II and cluster IV containing five and four genotypes respectively. The cluster III consisted two genotypes. Nataranjan and Palanisammy (1990) reported five clustering with eight genotypes and their 15 hybrids in mungbean. Cluster I was composed of GK 11, GK 13, GK 15, GK 16, GK 17, GK 18, GK 19, GK 23, GK 24, GK 26, GK 28, GK 29, GK 39, GK 40, GK 42, GK 45 and GK 47. Cluster II had five genotypes named GK 22, GK 32, GK 33, GK 35 and GK 43. Cluster III was formed by genotypes viz. GK 25 and GK 27 and cluster IV by GK 30, GK 37 and GK 38 (Fig. 1).

Mahalanobis (D^2) distance among the clusters were also calculated (Table 2) by Discriminant Function Analysis. Among the 4 clusters, the cluster IV showed the highest distance unit of 94.224 with cluster I, 17.676 and 24.810 with cluster II and III.

Now the question would arise what were the effects of the whole 7 variables considered in the analysis under each cluster. To find out the answer of the question, the test of equality of groups means were done by Discriminant Function Analysis (Table 3).

Table 1. List of selected 27 mungbean genotypes under 4 clusters

Cluster No.	Number of genotypes in cluster	Name of genotypes
I	17	GK 11,GK 13,GK 15,GK 16,GK 17, GK 18,GK 19,GK 23,GK 24,GK 26, GK 28, GK 29,GK 39,GK 40,GK 42, GK 45, GK 47
II	5	GK 22,GK 32,GK 33,GK 35GK 43
III	2	GK 25,GK 27
IV	3	GK 30,GK 37,GK 38

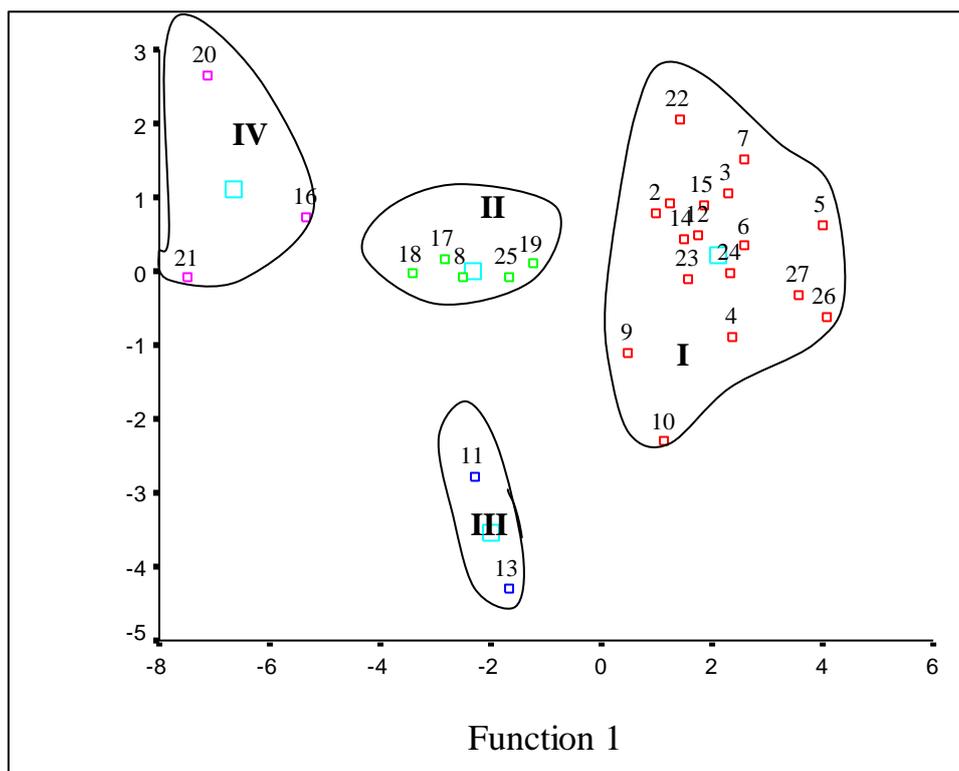


Fig. 1. Graphic illustration of Discriminatory Function Analysis of 4 groups of 27 mungbean genotypes based on 8 variables

Table 2. Pairwise Mahalanobis (D^2) distance between 4 clusters of 27 mungbean genotypes

Clusters Number	1	2	3
1	36.528		
2	26.484	8.735	
3	94.224	17.676	24.810

Table 3. Tests of Equality of 4 Group Means of variables evaluated for 27 mungbean genotypes by hierarchical cluster analysis and Discriminant Function Analysis

Name of variables	Wilks' Lambda	F	df1	df2	Sig.
Branches per plant	0.740	2.701	3	23	0.069
Pods per Plant	0.431	10.105	3	23	0.000
Pod length (cm)	0.768	2.316	3	23	0.102
Seeds Per Pod	0.816	1.730	3	23	0.189
1000 seeds weight (g)	0.299	17.946	3	23	0.000
Seeds yield (g / p)	0.540	6.539	3	23	0.002
Total dry weight (g)	0.606	4.994	3	23	0.008

CONCLUSION

From this study, it was concluded that genotypes GK 37, GK 19 and GK 11 performed better than the other 24 genotypes under water stress condition.

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