

Assessment of genetic diversity in mungbean (*Vigna radiata* L. Wilczek) landraces under tropical environment of Andaman & Nicobar Islands

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Abstract

A study was conducted to determine the genotypic and phenotypic variance and genetic diversity for yield and its attributing traits in 56 germplasms of mungbean. Significant variation among the landraces and genotypes was recorded. Using cluster analysis by UPGMA method, all the genotypes were grouped into 3 major and one minor groups. Cluster I consisted 10 genotypes, cluster II 20, Cluster III 24 and cluster IV 2 genotypes. The pattern of distribution of genotypes from different locations into four clusters was random, demonstrating that geographical isolation may not be the only factor causing genetic diversity. More emphasis should be given on cluster III for selecting genotypes as parents for crossing with the genotypes of cluster I. Principal component analysis explained nearly 74% of total variation among genotypes. By plot of first two components score for genotypes confirmed the results of cluster analysis.

Key words: Landraces, mungbean, genetic diversity, principal component analysis

Mungbean (*Vigna radiata* L. Wilczek) is a widely cultivated pulse crop. This crop is popular due to its suitability in various crop rotation practices and well suited in both dry and irrigated conditions. The Andaman & Nicobar Islands are the custodian of genetic diversity of so many flora and fauna in general and *Vigna* spp. and their wild relatives in particular. The objectives of the study were to determine the genetic diversity and relationships within 56 genotypes/landraces of mungbean under Bay island conditions, and to determine which accessions should

be included in a mungbean breeding programme.

The 56 mungbean germplasm accessions included 42 indigenous landraces (from Andaman and Nicobar Islands), 9 advanced breeding lines and 5 established cultivars. The experiment was carried out in the field of Garacharma Farm, Division of Field Crops, Central Agricultural Research Institute, Port Blair, Andaman & Nicobar Islands, India during *rabi* 2011-12 and 2012-13. The climatic conditions were hot and humid. Plants were grown in 3.0 m x 1.2 m plots in a replicated trial. Row to row distance was 30 cm and plant to plant distance was 10 cm. In each accession, 10 plants were randomly chosen for biometric measurements. Observations were recorded on days to 50 % flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length, seeds per pod, 100 seed weight and seed yield per plant. All the agronomical management practices were done as per the recommendation for the crop. Plants were harvested when 90% of the pods showed physiological maturity and turned brown and black. Analysis of variance (ANOVA) was done to know the significant variation among the genotypes based on the 9 morphological traits applying SAS 4.2. An unweighted pair-group method of the arithmetic average clustering procedure (UPGMA) was employed to construct dendrograms. Principal component analysis was also performed to establish the importance of different traits in explaining the total variation.

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The landraces showed enough range of variation for all nine quantitative traits. Significant differences among the genotypes for all the traits at 0.01 % level of significance were found. In general, the germplasm with desirable characters were identified for each trait in different groups. However, some preferable characters such as high seed yield per plant, more number of seeds per pod, more number of pods per plant and more seed weight existed in rather low frequency in the present germplasm set. Highest variation was observed for seed yield in the genotypes ANM-11-12 followed by ANM-11-46, ANM-11-07-2, ANM-11-05, ANM-11-47, ANM-11-08, ANM-11-11, ANM-11-01 and ANM-11-44 which were significantly different from other genotypes.

The magnitude of differences between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were minimal for number of branches per plant, days to flowering, days to maturity and 100-seed weight suggesting minimum role of environment on the expression of genes controlling these traits. The minimum and maximum values of the coefficient of variation for each quantitative trait indicated that there is considerable morphological variation among the accessions. Therefore, the possibility to obtain superior genotypes for various morphological traits needs to be explored through field evaluation and characterization of diversity, present among genotypes. The variability present for morphological traits in mungbean has been previously studied [1, 2].

Estimates of mean, range, genotypic variance (σ_g^2), phenotypic variance (σ_p^2), coefficient of variation (CV) and heritability (H_{bs}) for nine morphological traits

are given in Table 1. The mean morphological and seed yield showed significant differences ($p < 0.01$) for all the nine quantitative traits. Highest phenotypic variance (>20%) was observed for plant height followed by number of pods per plant. The number of pods per plant, days to flowering and days to maturity exhibited moderate phenotypic variance, while lowest genetic variation (<10%) was observed for the traits such as length of pods, seeds per pod and 100-seed weight among the accessions. The genotypic variance was observed highest for plant height followed by seed yield per plant and lowest genetic variation (<10%) was observed for other characters, including length of pods, seeds per pod and 100-seed weight.

Estimates of PCV and GCV were highest for seed yield/plant followed by number of branches per plant over the seasons, respectively. The estimated PCV and GCV values for the other traits ranged between 6.19% to 14.22% and 4.97% to 16.44%, respectively. Broad senses of heritability (Table 1) estimates ranged from 31.89% for number of pods per plant to 92.79% for number of branches per plant. The traits such as, 100-seed weight, seed yield per plant, days to maturity and days to flowering exhibited higher heritability estimates (>50%) while, plant height, length of pods and number of seeds per pod showed lower magnitude (<50%) of heritability estimates.

In the present study several diverse accessions, were identified, with high yield potential and a few of which exceeded the varieties used as checks. The present results are however, not in conformation with previous reports [3] and indicate that for seed and pod traits, genotypic effect is much greater than environmental effect [2-4].

Table 1. Basic statistics for 9 quantitative traits in landraces of mungbean

Characters	Mean with SE	Range		σ_g^2	σ_p^2	GCV (%)	PCV (%)	h_b^2
		Minimum	Maximum					
Days to 50% flowering	36.72 \pm 2.51	28.0	46.0	10.09	16.42	8.65	11.03	61.46
Days to maturity	68.08 \pm 2.53	64.0	77.0	11.44	17.77	4.97	6.19	64.39
Plant height (cm)	46.74 \pm 5.80	28.0	75.0	16.01	44.15	8.56	14.22	36.26
Number of branches per plant	4.19 \pm 1.05	02.0	07.0	1.24	1.33	26.53	27.54	92.79
Number of pods per plant	22.33 \pm 4.55	08.0	39.0	13.48	42.28	16.44	29.12	31.89
Length of pods (cm)	12.29 \pm 1.18	06.0	16.0	1.31	2.72	9.32	13.41	48.30
Number of seeds per pod	12.28 \pm 1.19	04.0	15.0	1.25	2.66	9.12	13.28	47.11
100-seed weight (g)	4.20 \pm 0.13	2.90	5.60	0.21	0.23	10.92	11.35	92.52
Seed yield per plant (g)	11.69 \pm 2.21	5.40	23.90	15.09	19.95	33.23	38.21	75.63

Table 2. Means of 9 morphological traits among the highest yielding accessions of mungbean

Characters/ germplasm	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	Length of pods (cm)	No. of seeds pod ⁻¹	100-seed weight (g)	Seed yield plant ⁻¹ (g)
ANM-1101	41	72	64.20	4.8	32.2	12.8	12.8	4.6	16.8
ANM-1105	39	68	53.40	4.6	28.2	13.8	13.6	4.5	17.2
ANM-1107-2	39	66	28.20	5.2	26.8	13.4	13.4	4.9	17.7
ANM-1108	37	67	42.00	5.4	31.2	12.0	12.0	4.5	17.1
ANM-1111	41	71	56.80	5.6	35.6	14.0	14.0	4.4	16.9
ANM-1112	39	69	52.20	6.0	36.4	14.0	14.0	5.1	23.9
ANM-1138	34	69	51.60	6.0	35.0	12.6	12.6	4.9	18.7
ANM-1144	33	66	34.80	5.0	34.8	12.2	12.2	4.6	16.2
ANM-1146	29	69	41.00	3.8	30.8	12.2	12.2	4.8	18.4
ANM-1147	37	71	48.40	4.2	32.2	11.6	11.6	4.6	17.2
Pusha Vishal (c)	34	64	42.00	4.8	27.2	12.8	12.8	4.8	16.8
ML 818 (c)	33	66	46.20	5.4	27.6	11.4	11.4	4.2	13.1
ML 1165 (c)	39	71	34.80	4.4	28.8	12.6	12.6	4.1	14.6
SML 668 (c)	33	66	35.60	4.2	22.6	12.6	12.6	4.5	12.8
OBGG 66 (c)	34	63	40.20	4.2	24.4	11.6	11.6	4.6	13.1
SE (m)	0.34	0.25	0.69	0.18	0.46	0.21	0.19	0.12	1.38
CD	3.13	3.16	7.23	1.30	5.67	1.46	1.49	0.36	2.74

The hierarchical (UPGMA) cluster analysis classified the 56 genotypes into three main and one minor groups (Table 3). A dendrogram based on average linkage distance was also constructed. In general, indigenous mungbean landraces were included in all the major groups. Cluster III was the largest with 24 indigenous landraces from Andaman and Nicobar group of Islands, a few breeding lines and cultivars/improved varieties from mainland. Cluster I consisting 10 genotypes had taller plant at maturity, late flowering and possessed maximum number of branches per plant, number of pods per plant, length of pods and number of seeds per pod high seed yield per plant. Two distinct genotypes in Cluster IV showed very early flowering and had highest 100 seed weight. The ANM-11-12 was distinct from the other genotypes only for seed yield per plant and number of pods per plant.

The advance breeding lines and recommended cultivars were mostly grouped in Cluster I. Parents with wider genetic base are expected to create longer genetic variation which can increase in genetic gain in selection from segregating populations. Morphological characterizations is an important step in classification of crop germplasm because a breeding program

mainly depends upon the magnitude of genetic variability available in that species [5-7].

The analysis based on standardized data revealed that three principal components (PCs) together accounted for 73.22% of the total phenotypic variability in 56 mungbean accessions including checks. Based on the eigen values and proportion of variation computed, the eigen vectors, associated calculative vectors (Table 4) and cattle scree graph for variation have been scaled in a manner that the largest value in each vector is unity. The results showed that first three principal component and factors with eigen values >1 contributed nearly to 74% of the variability among 56 genotypes evaluated for 9 quantitative traits. Characters contributing more positively to the first principal component (PC1) were length pod, number of seeds/pod, seed yield/plant, number of pods/plant, number of branches/plant, plant height and days to 50% flowering (Table 4). The characters with greatest positive weight on second principal component (PC2) were days to maturity, days to 50% flowering, seed yield/plant and 100-seed weight. Number of seeds per plant and plant height contributed maximum for PC 3.

Table 3. Mungbean landraces/genotypes in clusters

Cluster	Landraces/genotypes in the clusters
I	ANM-11-01, ANM-11-03, ANM-11-05, ANM-11-20-2, ANM-11-09, ANM-11-17, ANM-11-11, ANM-11-38, ANM-11-22, ANM-11-12
II	ANM-11-02, ANM-11-19, ANM-11-36, ANM-11-04, ANM-11-15, ANM-11-18, ANM-11-34, ANM-11-10, ANM-11-16, ANM-11-33, ANM-11-31, ANM-11-32, ANM-11-39, ANM-11-43, ANM-11-13, ANM-11-21-1, ANM-11-21-2, ANM-11-20-1, ANM-11-35, ANM-11-26
III	ANM-11-06, ANM-11-07-1, ANM-11-14, ANM-11-47, ANM-11-30, ANM-11-37, ANM-11-24, ANM-11-29, ANM-11-25, ANM-11-42, ANM-11-28, ANM-11-07-2, ANM-11-08, ANM-11-23 (DMS-08-01), Pusha Vishal, OBGG-66, ML-818, ANM-11-44, ANM-11-45, ANM-11-41, ANM-11-48, ML- 1165, ANM-11-40, SML-668
IV	ANM-11-27, ANM-11-46

Table 4. Principal components (PCs) for morphological traits in mungbean genotypes

Morphological traits	PC 1	PC 2	PC 3
Days to 50% flowering	0.2817	0.3897	0.0613
Days to maturity	0.1779	0.5399	0.2388
Plant height (cm)	0.2833	0.0132	0.3876
Number of branches/plant	0.3716	-0.1744	0.3228
Number of pods/plant	0.3818	-0.2074	0.3122
Length of pods (cm)	0.4079	-0.0344	-0.4452
Number of seeds/pod	0.4073	-0.0337	0.4465
100-seed weight (g)	-0.0009	0.2998	0.3343
Seed yield/plant (g)	0.4031	0.3242	0.2723
Eigen values	3.5404	2.1773	1.6046
Proportion (σ^2)	0.3540	0.2177	0.1605
Cumulative proportion of variation (σ^2)	0.3540	0.5718	0.7322

The principal component analyses could help to identify landraces with suitable and unique traits which can be used in direct selection and hybridization program for improvement of mungbean.

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