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Genetic Variability, Character Association, Path Analysis and Genetic Diversity in Mungbean (*Vigna radiata* L.) Genotypes

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Abstract

Mungbean (*Vigna radiata* L.) is an important pulse crop and improvement of its yield depends on the availability of useful genetic variability. The present study was carried out to assess genetic variability, heritability, genetic advance, character association, path analysis and genetic diversity in mungbean. Eight genotypes were evaluated during the kharif season at G H Raison University, Saikheda, Madhya Pradesh, using a randomized block design with three replications. Nine quantitative characters were recorded, namely plant height, leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pods cluster⁻¹ plant⁻¹, pod length, seeds pod⁻¹, 1000-seed weight and yield plant⁻¹. Phenotypic variance was higher than genotypic variance for all the characters. Relatively high GCV and PCV were recorded for branches plant⁻¹, pods plant⁻¹, 1000-seed weight and yield plant⁻¹. High heritability together with high genetic advance as percentage of mean was observed for plant height, leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pod length, seeds pod⁻¹, 1000-seed weight and yield plant⁻¹. Yield plant⁻¹ showed significant positive association with leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pods cluster⁻¹ plant⁻¹, pod length, seeds pod⁻¹ and 1000-seed weight at both genotypic and phenotypic levels. Path analysis showed positive direct effects of plant height, leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, seeds pod⁻¹ and 1000-seed weight on yield. Seeds pod⁻¹ had the highest positive direct effect. The multivariate analysis also indicated the presence of genetic divergence among the genotypes. The results suggest that seeds pod⁻¹, pods plant⁻¹, branches plant⁻¹ and other positively associated traits can be considered during selection for higher yield in mungbean.

Keywords: Mungbean, genetic variability, heritability, genetic advance, correlation, path analysis, genetic diversity

Introduction

Mungbean (*Vigna radiata* L.) is an important pulse crop grown in many parts of India. It is valued for its protein-rich seed, short duration and suitability in different cropping systems. Yield in mungbean is a complex character and is influenced by several component characters. Therefore, information on variability and association among yield and yield-related characters is useful for crop improvement.

Genetic variability provides the basic material for selection. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance help to understand the amount and nature of variability present in a population. Correlation analysis is useful for studying the association between characters, whereas path coefficient analysis helps to understand the direct and indirect contribution of different characters to yield.

Several studies in mungbean have reported useful variability for pods plant⁻¹, branches plant⁻¹, seed weight and seed yield, and have emphasized the importance of these characters in selection. Recent mungbean studies have also used variability, correlation and path analysis together for identifying important yield components.

The present investigation was therefore undertaken to study genetic variability, character association, direct and indirect effects of yield-related characters and genetic diversity among selected mungbean genotypes.

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Materials and Methods

Experimental material and design

The experiment was conducted at the research farm of G H Raisoni University, Saikheda, Pandhurna, Madhya Pradesh, during the kharif season. Eight mungbean genotypes were evaluated in a randomized block design with three replications.

Table 1: List of Mungbean (*Vigna radiata* L.) Genotypes Evaluated in the Study

Code	Genotype
G1	BPMR-145
G2	BM-2003-2
G3	BM-2002-1
G4	BM-4
G5	PM-707-5
G6	KM 11-584
G7	M-9339
G8	NMK-15-08

Characters recorded: Observations were recorded on ten randomly selected plants from each genotype in each replication. The characters studied were plant height (cm), number of leaves plant⁻¹, number of branches plant⁻¹, number of pods plant⁻¹, number of pods cluster⁻¹ plant⁻¹, pod length (cm), number of seeds pod⁻¹, 1000-seed weight (g) and yield plant⁻¹ (g).

Statistical analysis: Analysis of variance was carried out to test the significance of differences among genotypes. Genotypic and phenotypic variances, GCV, PCV, broad-sense heritability and genetic advance were estimated using standard procedures. Genotypic and phenotypic correlation coefficients were calculated to determine the association among characters. Path coefficient analysis was carried out at the genotypic level following Dewey and Lu (1959). Principal component, principal coordinate and cluster analyses were used to study multivariate diversity.

Results and Discussion

Genetic variability: The analysis showed significant differences among the genotypes for the characters studied, indicating the presence of genetic variability. For all characters, phenotypic variance was slightly higher than genotypic variance. The difference between PCV and GCV was comparatively small for most traits, suggesting that environmental influence was not very large for many of the characters.

Table 2: Genetic Variability Parameters, Heritability, and Genetic Advance for Quantitative Traits in Mungbean

Character	GCV (%)	PCV (%)	Heritability (%)	GA as % of mean
Plant height	10.609	10.824	96.073	21.421
Leaves plant ⁻¹	15.831	16.160	95.977	31.950
Branches plant ⁻¹	18.309	19.671	86.636	35.107
Pods plant ⁻¹	27.092	27.182	99.335	55.623
Pods cluster ⁻¹ plant ⁻¹	8.194	14.716	31.007	9.400
Pod length	14.415	14.533	98.389	29.455
Seeds pod ⁻¹	16.857	17.540	92.371	33.375
1000-seed weight	25.254	25.339	99.331	51.848
Yield plant ⁻¹	32.220	32.480	98.427	65.850

The highest variability was observed for yield plant⁻¹, followed by pods plant⁻¹ and 1000-seed weight. Branches plant⁻¹ also showed comparatively high GCV and PCV. Similar trends have been reported in mungbean where yield, pods plant⁻¹ and seed weight often show higher variability than other quantitative characters.

Heritability and genetic advance: High heritability was recorded for most of the characters. High heritability together with high genetic advance as percentage of mean was observed for plant height, leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pod length, seeds pod⁻¹, 1000-seed weight and yield plant⁻¹. This combination indicates that a considerable part of the observed variation is heritable and that selection can be useful for these characters. Pods cluster⁻¹ plant⁻¹ showed comparatively lower heritability and genetic advance than the other traits, suggesting a greater influence of environmental factors on its expression. High heritability with high genetic advance has also been reported for several yield-related traits in mungbean.

Correlation analysis: Yield plant⁻¹ showed significant positive genotypic and phenotypic correlations with leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pods cluster⁻¹ plant⁻¹, pod length, seeds pod⁻¹ and 1000-seed weight. The genotypic correlations were generally slightly higher than the corresponding phenotypic correlations.

Table 3: Genotypic (\$r_g\$) and Phenotypic (\$r_p\$) Correlation Coefficients between Seed Yield and Yield-Attributing Traits

Trait associated with yield	Genotypic correlation (rg)	Phenotypic correlation (rp)
Leaves plant ⁻¹	0.697**	0.662**
Branches plant ⁻¹	0.872**	0.799**
Pods plant ⁻¹	0.658**	0.653**
Pods cluster ⁻¹ plant ⁻¹	0.656**	0.405**
Pod length	0.736**	0.722**
Seeds pod ⁻¹	0.878**	0.843**
1000-seed weight	0.541**	0.537**
Plant height	-0.116 NS	-0.108 NS

The highest positive genotypic correlation with yield was recorded for seeds pod⁻¹ (0.878), followed by branches plant⁻¹ (0.872). These results indicate that improvement in these characters may be associated with improvement in yield. Positive associations of branches, pods and seed weight with mungbean yield have also been reported by other workers.

Path coefficient analysis: Path analysis was used to separate the correlation of each character with yield into direct and indirect effects. Seeds pod⁻¹ had the highest positive direct effect on yield (0.689). Pods plant⁻¹, leaves plant⁻¹, branches plant⁻¹ and plant height also showed positive direct effects.

Table 4: Direct Effects of Component Characters on Seed Yield per Plant Obtained Through Path Coefficient Analysis

Character	Direct effect on yield
Plant height	0.160
Leaves plant ⁻¹	0.338
Branches plant ⁻¹	0.196
Pods plant ⁻¹	0.435
Pods cluster ⁻¹ plant ⁻¹	-0.229
Pod length	-0.331
Seeds pod ⁻¹	0.689
1000-seed weight	0.016

Pods cluster⁻¹ plant⁻¹ and pod length showed negative direct effects even though their correlations with yield were positive. This indicates that their positive association with yield was mainly due to indirect effects through other characters. The residual effect was 0.106, showing that most of the variation in yield was explained by the characters included in the analysis. The strong positive correlation and positive direct effect of seeds pod⁻¹ make it an important character for selection. Pods plant⁻¹ also showed a comparatively high positive direct effect and a significant positive correlation with yield.

Principal component analysis: Principal component analysis was used to summarize the variation among the characters. The first four principal components together accounted for 89.82% of the total variation.

Table 5: Eigenvalues, Percentage Variance, and Cumulative Variance Explained by Principal Components

Component	Eigenvalue	Variation (%)	Cumulative (%)
PC I	5.170	57.45	57.45
PC II	1.268	14.09	71.54
PC III	0.903	10.03	81.57
PC IV	0.742	8.25	89.82
PC V	0.517	5.74	95.56
PC VI	0.184	2.05	97.61
PC VII	0.117	1.30	98.91
PC VIII	0.067	0.74	99.65
PC IX	0.032	0.35	100.00

PC I contributed the largest share of variation (57.45%), followed by PC II (14.09%). Thus, a large proportion of the total variation was represented by the first few components. Note: the original thesis states that the first four components had eigenvalues greater than 1. The reported eigenvalues show that only PC I and PC II are greater than 1. Therefore, this statement should be corrected after checking the original PCA output before journal submission.

Genetic diversity and clustering: The multivariate analysis indicated the presence of genetic divergence among the genotypes. The maximum reported inter-genotypic distance was between G1 and G6 (1.288), followed by G2 and G6 (1.270) and G1 and G7 (1.254). The thesis reports four clusters and gives cluster means for the quantitative characters. Cluster II recorded relatively high values for leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pod length and 1000-seed weight. Cluster III recorded a high mean for seeds pod⁻¹ and yield plant⁻¹.

Table 6: Cluster Means of Mungbean Genotypes for Various Quantitative Characters

Character	Cluster I	Cluster II	Cluster III	Cluster IV
Plant height	52.08	43.49	47.25	42.15
Leaves plant ⁻¹	9.53	13.11	13.05	11.16
Branches plant ⁻¹	3.08	3.77	3.39	3.22
Pods plant ⁻¹	10.14	18.33	11.41	13.50
Pods cluster ⁻¹ plant ⁻¹	5.23	5.72	6.18	5.57
Pod length	8.04	10.45	10.02	8.27
Seeds pod ⁻¹	9.25	10.83	12.50	10.44
1000-seed weight	28.58	50.84	39.83	29.11
Yield plant ⁻¹	3.23	5.05	5.10	4.24

An important data issue was found in the original thesis. The main experiment is described as having eight genotypes, whereas the clustering section contains references to G10, G11, G12, G13 and G14 and gives cluster sizes of 4, 2, 2 and 6. These numbers total fourteen genotypes. This cannot be reconciled from the available material, so the cluster membership should be checked against the original statistical output before the paper is submitted.

Nutrient and chlorophyll content

Variation was also recorded for potassium, phosphorus and chlorophyll content among the eight genotypes. G2 recorded the highest potassium content (2.72%) and high phosphorus content (0.11%). G2 and G7 recorded the highest chlorophyll value (0.29 mg g⁻¹) among the reported genotypes.

Table 7: Variation in Potassium (K), Phosphorus (P), and Chlorophyll Content among Mungbean Genotypes

Genotype	K content (%)	P content (%)	Chlorophyll (mg g ⁻¹)
G1	2.61	0.100	0.26
G2	2.72	0.110	0.29
G3	2.31	0.100	0.18
G4	2.38	0.114	0.20
G5	2.33	0.113	0.21
G6	2.35	0.061	0.22
G7	2.47	0.113	0.29
G8	2.38	0.065	0.19

Conclusion

The present study showed useful genetic variation among the mungbean genotypes for yield and yield-related characters. High variability was observed for yield plant⁻¹, pods plant⁻¹ and 1000-seed weight. High heritability together with high genetic advance was observed for most of the important quantitative characters, indicating good scope for selection. Yield plant⁻¹ was positively associated with leaves plant⁻¹, branches plant⁻¹, pods plant⁻¹, pods cluster⁻¹ plant⁻¹, pod length, seeds pod⁻¹ and 1000-seed weight. Path analysis showed that seeds pod⁻¹ had the highest positive direct effect on yield, followed by pods plant⁻¹ and leaves plant⁻¹. Therefore, these traits can receive greater attention while selecting promising mungbean genotypes. The diversity analysis also indicated that the material was genetically variable, with the highest reported distance between G1 and G6. However, the cluster-analysis section of the original thesis needs verification because the reported cluster membership corresponds to fourteen genotype labels although the experiment is described as involving eight genotypes. After verification of this point, the identified divergent genotypes can be considered for further breeding work.

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References

1. Alom KMM, Rashid MH, Biswas M. Genetic variability, correlation and path analysis in mungbean

- (*Vigna radiata* L.). J Environ Sci Nat Resour. 2014;7(1):131-138.
2. Asari T, Patel BN, Patel R, Patil GB, Solanki C. Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mungbean [*Vigna radiata* (L.) Wilczek]. Int J Chem Stud. 2019;7(4):383-387.
 3. Azam MG, Hossain MA, Alam MS, Rahman KS, Hossain M. Genetic variability, heritability and correlation path analysis in mungbean (*Vigna radiata* L. Wilczek). Indian J Agric Res. 2018;43(3):407-416.
 4. Bangar P, Chaudhury A, Umdale S, Kumari R, Tiwari B, Kumar S, *et al.* Detection and characterization of polymorphic simple sequence repeat markers for the analysis of genetic diversity in Indian mungbean (*Vigna radiata* L. Wilczek). Indian J Genet. 2018;78(1):111-117.
 5. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51:515-518.
 6. Narasimhulu R, Naidu NV, Priya MS, Rajarajeswari V, Reddy KHP. Genetic variability and association studies for yield attributes in mungbean (*Vigna radiata* L. Wilczek). J Plant Sci. 2013;2(3):82-86.
 7. Niharika B, Singh DP, Khulbe RK. Genetic variability and correlation studies in advanced inter-specific and inter-varietal lines and cultivars of mungbean (*Vigna radiata* L.). Food Legumes. 2014;27(2):155-157.
 8. Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS. Genetic variability, character association and genetic divergence in mungbean (*Vigna radiata* L. Wilczek). Omics J. 2010;3(1):1-6.