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Association and Multivariate Analysis of Yield and Yield Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

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Magnitude of the genetic variability present in a population and divergence among the accessions are of paramount importance to a plant breeder for development of improved variety. In the present study correlation and path coefficient analysis, principal component analysis (PCA) and some selection parameters were computed for yield and its contributing characters in 51 mungbean genotypes. Significant variations among the genotypes were observed for all the characters. High heritability (broad-sense) along with high genetic advance was observed for all the characters except days to maturity. Pods/plant showed very high positive direct effect and significant positive genotypic correlation with seed yield/plant. The PCA segregated the 51 accessions into eight clusters in the scatter diagram. Eigen value more than one of the first four principal components contributed 79.18% of the total variability among 51 genotypes evaluated for 10 quantitative traits. Cluster VII had high mean value for plant height, primary branches/plant, secondary branches/plant, pods/plant, seeds/pod and seed yield/plant. Therefore, genotypes of cluster VII (ML-515, PUSA-105, T-44, and RMG-991) could be directly selected and utilized for improvement of these traits.

Key Words: Correlation, Mungbean, Path coefficient, Principal component analysis

Introduction

Green gram or mungbean [*Vigna radiata* (L.) Wilczek] is one of the important food legumes of many tropical and sub-tropical parts of the world. Among the pulse crops in India, mungbean is a highly valuable short duration crop with many desirable characters like high protein content, wide adaptability, low-input requirement and ability to improve soil fertility. The area under this crop is 3.55 million ha with an annual production of 1.82 million tonnes and productivity 512 kg/ha during 2010-11 (AICRP-MULLaRP, 2014). This low yield cannot meet the demand of our rising population. Development of high yielding varieties is one approach to overcome this problem and it is largely depend on the presence of heritable genetic variation in the base population. The estimation of genetic parameters like genotypic and phenotypic variability, genotypic and phenotypic coefficient of variation, heritability and genetic advance are useful for the effective selection and improvement of the base population. The study of correlation and path analysis for yield and its attributing traits will be helpful in improving the grain yield. Breaking the yield plateau which generally is due to narrow genetic base is achieved through diversification of parents. The present study was undertaken to assess the genetic variability, heritability, genetic advance, correlation, path coefficient and multivariate analysis of various desirable characters in 51 genotypes of mungbean, to identify promising lines for hybridization programmes and to explore yield potential and quality of mungbean.

Materials and Methods

The study was undertaken at Agricultural Research Farm, Banaras Hindu University, Varanasi during *kharif* and summer season of 2010-11. The experiment was laid out in a randomized complete block design with three replications in 51 mungbean genotypes. All the genotypes were collected from All India Coordinated Research Project of Pulses, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU, Varanasi. Each plot consisted of 3 m length with row-to-row and plant-to-plant distances being 45 and 10 cm, respectively. All cultural operations were carried out as per the package and practices recommended for raising a good crop. 15 plants were randomly selected from each genotype per replication for recording the data of 10 characters *viz* days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of secondary branches/plant, clusters/plant, pods/plant, seeds/pod, 100-seed weight and seed yield/plant. The pooled mean values over replications were

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subjected to computation for various genetic parameters. The genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation and heritability were estimated (Singh and Choudhary, 1985). Genetic advance was computed by the procedure of Johnson *et al.* (1955). The data were also analyzed for estimating the correlation coefficient (Al-Jibouri *et al.*, 1958) and path analysis (Dewey and Lu, 1959) for grain yield and its component characters. Cluster and PCA was computed by Windostat Version 9.1.

Results and Discussion

Genetic Variability, Heritability and Genetic Advance

Analysis of variance revealed that there was significant variability for all the characters among the genotypes studied (Table 1). Range of variation was highest for plant height followed by pods/plant and clusters/plant, indicating maximum scope for the selection to improve these characters. Similar findings are reported by Gupta *et al.* (2004) and Kumar *et al.* (2010). The magnitude of phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) for all the traits, indicating that significant role of environmental interaction for the expression of all the traits studied. Secondary branches/plant showed high difference between PCV and GCV in comparison to other characters indicating more environmental influence on this character.

The estimated values of broad sense heritability were high (>50%) for all the traits. Estimation of heritability along with genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. High heritability associated with high genetic advance as percent of mean (>20%) was obtained for all the characters except days to maturity. It indicates that probably heritability is due to additive gene effect and selection may be effective. Rahim *et al.* (2008) also reported high heritability coupled with high genetic advance for number of pods/plant, seed yield/plant and plant height in mungbean. Days to maturity had high heritability along with low genetic advance indicating non-additive type of gene action where genotype x environment interaction plays a significant role in the expression of this trait. Rao *et al.* (2006) also reported similar findings in mungbean.

Correlation and Path Coefficient Analysis

Genotypic and phenotypic correlations were estimated among 10 characters in 51 genotypes and these indicated inherent relations between any two traits were due to linkage or pleiotropic action of genes or both. The genotypic correlation coefficients were slightly higher in magnitude than the phenotypic correlation coefficients indicating the genetic variance is predominant in expression of characters (Table 2). Seed yield/plant showed significant positive genotypic and phenotypic correlation with pods/plant, 100-seed weight, primary branches/plant, seeds/pod, plant height and clusters/plant indicating these characters were strongly associated and positive correlation occurs due to coupling phase of linkage of genes controlling the characters. Rohman *et al.* (2003) also reported that seed yield showed strong

Table 1. Analysis of variance and estimates of genetic parameters for ten characters in 51 mungbean genotypes

Traits	Mean sum of squares (genotype)	Mean±S.E.	Range of variation	Coefficient of variation		Heritability (in broad sense %)	Genetic advance (% of mean)
				GCV	PCV		
Days to 50% flowering	64.52**	34.97±0.370	27.00-43.66	13.22	13.35	98.0	34.56
Days to maturity	80.46**	69.27±0.405	62.00-82.00	7.45	7.52	98.1	19.49
Plant height (cm)	418.56**	63.05±.963	42.66-91.00	18.67	18.86	97.9	48.79
Primary branches/plant	10.66**	5.92±.350	1.66-11.00	31.27	32.94	90.1	78.36
Secondary branches/plant	13.39**	4.57±.351	1.66-10.66	45.59	47.53	92.1	115.44
Pods/plant	116.03**	23.25±.696	9.66-41.66	26.57	27.08	96.2	68.82
Seeds/pod	4.01**	10.79±.352	8.00-15.00	10.20	11.69	76.1	23.50
Clusters/plant	73.78**	12.14±.667	3.66-26.66	40.48	41.61	94.6	103.98
100-seed weight (g)	1.67**	4.42±.056	3.30-6.16	16.83	16.98	98.2	44.05
Seed yield/plant (g)	18.11**	10.69±.276	3.83-6.16	22.84	23.29	96.2	59.15

*, **Significant at 5% and 1% level of significance, respectively

Table 2. Genotypic (G) and Phenotypic (P) correlation coefficients among seed yield and component traits in 51 mungbean genotypes

Traits		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Seeds/ pods	Clusters/ plant	100-Seed weight (g)	Seed yield/ plant (g)
Days to 50% flowering	**G**	**1.000**	0.810**	0.201*	0.099	0.072	0.082	-0.023	-0.010	-0.056	0.033
	P	**1.000**	0.804**	0.200*	0.093	0.064	0.079	-0.030	-0.0048	-0.055	0.029
Days to maturity	G		**1.000**	0.013	-0.035	-0.057	0.078	-0.079	-0.072	0.123	0.090
	P		**1.000**	0.014	-0.033	-0.052	0.074	-0.073	-0.067	0.119	0.083
Plant height (cm)	G			**1.000**	0.562**	0.387**	0.333**	-0.087	0.462	-0.114	0.257**
	P			**1.000**	0.544**	0.366**	0.320**	-0.081	0.452**	-0.109	0.246**
Primary branches/ plant	G				**1.000**	0.569**	0.363**	-0.059	0.637	-0.044	0.338**
	P				**1.000**	0.540**	0.338**	-0.076	0.605**	-0.035	0.310**
Secondary branches /plant	G					**1.000**	0.374**	-0.199*	0.540	-0.369	0.059
	P					**1.000**	0.342**	-0.159*	0.490**	-0.347**	0.055
Pods/plant	G						**1.000**	-0.334**	0.453	-0.440**	0.574**
	P						**1.000**	-0.329**	0.432**	-0.431**	0.555**
Seeds/pods	G							**1.000**	-0.203*	0.256**	0.305**
	P							**1.000**	-0.177*	0.212**	0.320**
Clusters/plant	G								1.000	-0.160*	0.255**
	P								1.000	-0.158*	0.242**
100-seed weight (g)	G									**1.000**	0.339**
	P									**1.000**	0.336**

*, **Significant at 5% and 1% level of significance, respectively

positive genotypic and phenotypic correlation with pods/plant, 100-seed weight and seeds/pod. Days to 50% flowering, days to maturity and secondary branches/plant showed non-significant correlation with seed yield/plant indicating these characters were independent and genes controlling these traits are located distantly on the same chromosome or located on different chromosomes.

Path analysis measures the direct and indirect contribution of various independent characters on a dependent character. The genotypic correlation coefficients were partitioned into direct and indirect effects by various yield contributing characters. Path coefficient analysis showed that pods/plant showed very high (>1) while 100-seed weight and seeds/ pod showed high (0.3-1) positive direct effect with seed yield/plant, as also reported by Gupta *et al*. (1982) and Rao *et al*. (2006). In contrast, days to 50% flowering, plant height, secondary branches/plant and primary branches/plant showed very low (0.0-0.09) positive direct effect with seed yield/plant while, days to maturity and clusters/plant showed very low negative direct effects with seed yield/plant indicating that these characters are less important for yield improvement. Highly positive and indirect effect on seed yield/plant *via* clusters/plant, secondary branches/plant, primary branches/plant and plant height were exhibited by pods/plant which also showed high order negative indirect effect via 100-seed weight and seeds/pod. Seeds/pod exhibited high positive effect on 100-seed weight and negative indirect effect on seed yield *via* pods/plant, respectively. 100-seed weight showed low to high negative indirect effect on seed yield/plant through pods/plant, secondary branches/plant and clusters/plant while, low positive indirect effect through seeds/pod. Thus, path coefficient analysis indicates that pods/plant, 100-seed weight and seeds/pod are important direct yield contributing traits and selection for these traits would be useful for yield improvement. Pods/plant, seeds/pod and 100-seed weight exhibited positive indirect effect *via* some characters on seed yield along with considerable negative indirect effect of some other characters, indicating that one character inhibits the effect of other character and is required to attain a proper balance of yield related traits for determining the ideotype for high seed yield in mungbean.

Principal Component Analysis

The PCA is a measure of the divergence between genotypes in terms of spatial distance. Fig. 1 gives the two-dimensional scatter diagram using principal component score II as X-axis and principal component score I as Y-axis wherein the 51 genotypes were distributed into eight clusters. Maximum number of genotypes grouped in cluster III and minimum in cluster IV. The maximum inter-cluster distance was observed between cluster VII and VIII (893.67), demonstrating maximum genetic diversity between these groups (Table 4). Hybridization between genotypes selected from these clusters are likely to produce most variable progeny and produce high heterotic response. The cluster mean values are presented in Table 5. Cluster VII had high mean value for plant height, primary branches/plant, secondary branches/plant, pods/plant, seeds/pod and seed yield/plant. This indicates that genotypes of cluster VII (ML-515, PUSA-105, T-44, and RMG-991) could be directly selected and utilized for improvement of these traits (Table 4).

Eigen value more than one of the first four principal components, contributed 79.18% of the total variability present among the 51 genotypes evaluated for 10 quantitative traits (Table 6). Rahim *et al.* (2008) have also observed that principal components which have eigen value more than one mostly contribute towards variability among the genotype. Eigen vector value of days to 50% flowering was positive for the all four principal components indicating this trait contributes maximum towards divergence. In the present study each principal

Table 3. Genotypic path coefficient matrix of seed yield vs. yield components of 51 mungbean genotypes

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/plant	Seeds/ pods	Clusters/ plant	100-Seed weight (g)	Correlation with seed yield /plant (g)
Days to 50% flowering	**0.0686**	0.0556	0.0138	0.0068	0.0049	0.0056	-0.0016	-0.0007	-0.0039	0.0331
Days to maturity	-0.0791	**-0.0976**	-0.0013	0.0034	0.0057	-0.0076	0.0078	0.0070	-0.0120	0.0901
Plant height (cm)	0.0051	0.0003	**0.0253**	0.0142	0.0098	0.0084	-0.0022	0.0117	-0.0029	0.2575
Primary branches/plant	0.0013	-0.0005	0.0076	**0.0135**	0.0077	0.0049	-0.0008	0.0086	-0.0006	0.3386**
Secondary branches/plant	0.0011	-0.0008	0.0057	0.0083	**0.0146**	0.0055	-0.0029	0.0079	-0.0054	0.0590
Pods/plant	0.0857	0.0813	0.3469	0.3785	0.3898	**1.0403**	-0.3479	0.4713	-0.4587	0.5745**
Seeds/pods	-0.0107	-0.0370	-0.0408	-0.0277	-0.0929	-0.1558	**0.4659**	-0.0947	0.1195	0.3058**
Clusters/plant	0.0005	0.0031	-0.0200	-0.0275	-0.0234	-0.0196	0.0088	**-0.0432**	0.0070	0.2559**
100-seed weight (g)	-0.0393	0.0857	-0.0797	-0.0310	-0.2573	-0.3073	0.1788	-0.1121	**0.6969**	0.3399**

*, **Significant at 5% and 1% level of significance, respectively

Table 4. Cluster distances and distribution of 51 mungbean genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	No. of genotypes	Genotypes
I	**58.90**	140.47	192.56	204.31	169.20	251.33	400.52	226.10	10	ML-1465,HUM-12, ML-1451, MH-521,MH-318, DBG-1030,ML-713,ML-717,PDM-11, K-851
II		**134.76**	288.83	211.77	267.38	277.62	306.59	363.51	6	HUM-8, HUM-9, HUM-7, PUSA-0672, PUSA-9531, P-16
III			**210.84**	366.05	382.64	584.72	361.47	509.57	11	HUM-1, HUM-2, HUM-16, HUM-26, PUSA-0871, PUSA VISHAL, ML-1294, TM-96-2, HUM-15, SML-668, IPM- 02-17-3
IV				**0.00**	202.07	381.38	517.88	313.08	2	TARM-18, UPM-98-1
V					**0.00**	377.16	648.16	292.60	8	ML-1296, IPM-02-17,BDYR-1, DBG-1045, UPM-98-1, IPM- 02-17-19, T-9, DPM-90-1
VI						**0.00**	677.35	153.42	3	ML-5, PUSA RATNA, VRMGG-1/ V. Silvestris
VII							**0.00**	893.67	4	ML-515, PUSA-105, T-44, RMG-991
VIII								**0.00**	7	HUM-6, PDM-54,COGG-912,AKM-9904, TARM-1, VRMGG-1/V. trilogata,TM-2000-1

Table 5. Cluster means for different characters in 51 mungbean genotypes

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/plant	Seeds/pods	Clusters/ plant	100-seed weight (g)	Seed yield/ plant (g)
I	38.58	70.58	46.42	4.83	4.67	20.25	10.33	9.00	3.85	7.80
II	35.58	67.58	68.50	5.92	4.25	13.83	10.50	12.08	4.40	6.51
III	30.71	65.24	57.83	5.19	4.50	23.90	10.69	10.57	4.10	10.27
IV	40.40	76.00	61.37	5.43	3.77	25.57	10.67	10.97	4.52	11.73
V	32.38	68.52	60.62	5.95	3.52	20.38	11.43	10.43	5.64	12.93
VI	35.17	74.83	50.17	4.33	2.17	13.17	11.33	11.17	5.62	8.37
VII	40.00	71.53	87.13	8.40	7.53	28.60	12.93	16.07	4.89	14.88
VIII	31.13	64.00	74.47	7.93	6.00	29.47	10.67	20.27	3.91	12.00

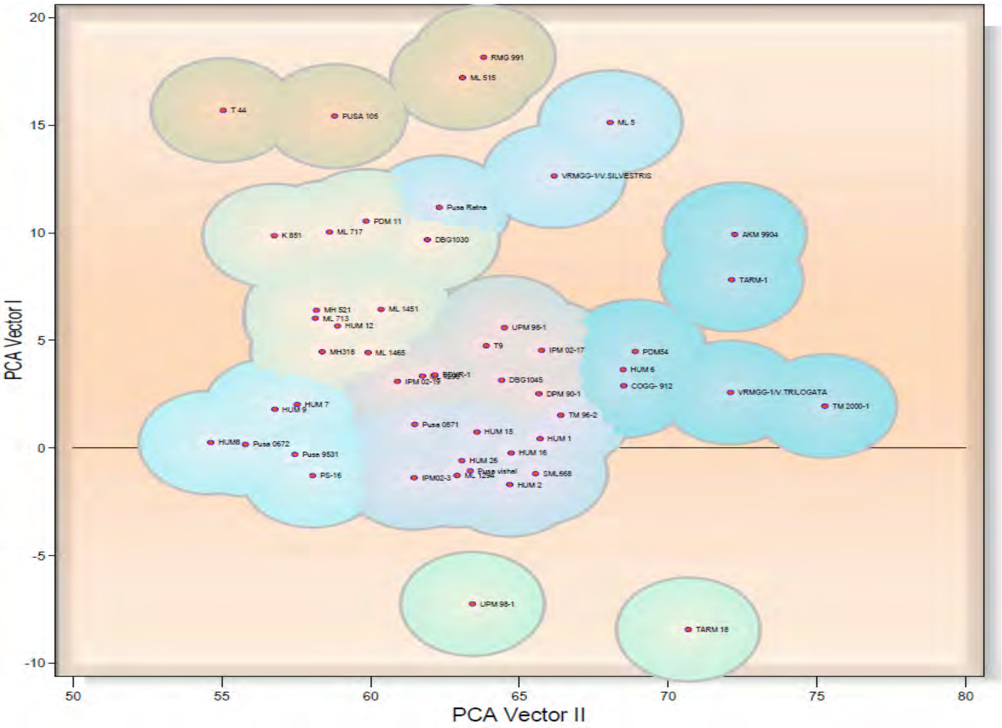

Fig. 1. Scatter diagram of 51 mungbean genotypes

component with traits having coefficient value greater than 0.3 are considered to be important on the overall variation. The first principal component contributes 36.40% of total variance and is determined by traits of pods/plant, seed yield/plant, seeds/pod, secondary branches/plant and plant height. Second principal component, accounting for 19.89% of the total variation, was determined by days to maturity, days to 50% flowering and seeds/pod. Third and fourth principal components contributed 12.53% and 10.34%, respectively, of the variability present among the genotypes for the characters used in the present study. The variation present in third principal component was positively associated with plant height and negatively associated with primary branches/plant and clusters/plant whereas, fourth principal component was positively associated with days to 50% flowering and secondary branches/plant while negatively correlated with 100-seed weight and yield/plant. These results suggest that traits such as pods/plant, seed yield/plant, seeds/pod, secondary branches/plant, plant height, days to 50% flowering and maturity were the principal discriminatory characteristics.

On the basis of finding of present study, it can be concluded that pods/plant, 100-seed weight, primary branches/plant, seeds/pod, plant height and clusters/plant were identified as major components of seed yield

Table 6. Weighting coefficient (eigen vector), eigen values, variance (%) and cumulative variance (%) of first four principal components

Traits	Principal component			
	I	II	III	IV
Days to 50% flowering	0.073	0.559	0.169	0.468
Days to maturity	-0.082	0.583	0.015	-0.045
Plant height (cm)	0.362	-0.115	0.344	-0.110
Primary branches/plant	0.011	0.196	-0.788	0.137
Secondary branches/plant	0.374	-0.142	-0.057	0.464
Pods/plant	0.477	0.116	-0.025	-0.148
Seeds /pods	0.400	0.362	-0.003	-0.100
Clusters/plant	0.294	-0.252	-0.460	-0.066
100-seed weight (g)	-0.244	0.247	-0.127	-0.564
Seed yield /plant (g)	0.428	0.077	0.028	-0.422
Eigen value (root)	3.64	1.99	1.254	1.034
Variance (%)	36.402	19.899	12.539	10.341
Cumulative variance (%)	36.402	56.301	68.84	79.181

and should be given top priority for determining the ideotype for high seed yield in mungbean.

References

AICRP-MULLaRP (2014) Data published in *http://www.aicrpmullarp.res.in.* Accessed 15 September 2014.

Al-Jibouri HA, PA Miller and HF Robinson (1958) Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. *Agron. J.* **50**: 633-637.

Dewey DR and KHA Lu (1959) Correlation and path coefficient analysis of components of crested wheat grass and seed production. *Agron. J.* **51**: 515-518.

Gupta SN, S Lal and L Rai (1982) Correlation and path analysis in mungbean (*Vigna radiata* L. Wilczek). *Haryana Agric. Univ. J. Res.* **12**:287-291.

Gupta SK, P Rathore and K Singh (2004) Genetic variability in mungbean (*Vigna radiata* L. Wilczek). *Agric. Sci. Digest.* **24**:136-138.

Johnson HW, HF Robinson and RE Comstock (1955) Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-318.

Kumar NV, GR Lavanya, SK Singh and P Pandey (2010) Genetic association and path coefficient analysis in mungbean *Vigna radiata* L. Wilczek. *AAB Bioflux* **2**:251-257.

Rahim MA, AA Mai, F Mahmud and KS Afrin (2008) Multivariate analysis in some mungbean (*Vigna radiata* L. Wilczek) accessions on the basis of agronomic traits. *American-Eurasian J. Scientific Res.* **3:** 217-221.

Rao CM, YK Rao and M Reddy (2006) Genetic variability and path analysis in mungbean. *Legume Res.* **29**: 216-218.

Rohman MM, ASMI Hussain, MS Arifin, Z Akhter and M Hasanuzzaman (2003) Genetic variability, correlation and path analysis in mungbean. *Asian J. Plant Sci.* **2**: 1209-1211.

Singh RK and BD Choudhary (1985) *Biometrical Methods in Quantitative Genetics Analysis*. Kalyani Publishers, New Delhi, India, 303 p.