

Study on Genetic Diversity and correlation in Mungbean [*Vigna radiata* (L.) Wilczek] Under Arid Zone

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ABSTRACT: The analysis of variance disclosed significance differences among 35 genotypes for all the 13 characters proposing the presence of great inherent genetic variations. The highest magnitudes of GCV and PCV were discovered for number of pods per plant and water absorption capacity. High heritability associated with high genetic advance as per cent of mean altogether spotted for the traits like number of pods per plant, water absorption capacity, seed yield per plant and plant height. Seed yield per plant had significant and positive correlation with number of pods per plant, pod length, 100-seed weight, biological yield per plant, harvest index, germination percentage, seed volume and water absorption capacity. In addition to these traits, positive direct effect to seed yield was detected for days to maturity, plant height, number of pods per plant, 100-seed weight, biological yield per plant, harvest index, germination percentage, seed volume and water absorption capacity. The 35 genotypes were grouped into 10 clusters using Mahalanobis's D² statistics which designates the ample amount of diversity is present.

Keywords: Genotypes, variability, correlation, path coefficient.

INTRODUCTION

Legumes occupy a unique position in sustainable agriculture as they are bestowed with numerous virtues such as biological nitrogen fixation (BNF), soil fertility restoration, nutritious food/ feed/fodder, low-water foot print, negative 'C' foot print and ability to thrive well in harsh climate. Mungbean (*Vigna radiata* (L.) R. Wilczek) is an important legume crop cultivated in the cereal-based farming systems in Asia, Sub Saharan Africa and Australia. Short crop duration, low input requirements and high global demand make mungbean an ideal rotation crop for small holder farmers. It generates a triple benefit: additional income, additional nutrient-rich food and increased soil fertility by nitrogen fixation (Nair *et al.*, 2020).

Being a highly self-pollinated crop, natural variability for yield and yield related traits is very narrow in mungbean making selection ineffective. However, proper evaluation of the extent of genetic variation available for yield components, their heritability values and genetic advance could be of great significance for the breeders in order to choose best genotypes for improvement (Degefa *et al.*, 2014). Estimates of genetic parameters provide an indication of the relative importance of the various types of gene effects affecting the total variation of a plant character.

Correlation evaluation between yield and other components are effective in selecting desired plant characters for constituting an efficient breeding programme. Correlation coefficient calculates the degree of association, and also the genetic or non-genetic association between two or more characters which frame the basis for selection. Path analysis simply breaks the correlation coefficient into the actions of direct and indirect effect of a set of independent variables on the dependent variables.

Multivariate analysis with the aid of Mahalanobis D² statistics is a powerful tool that measures the degree of divergence at genotypic level and determines the relative contribution of each component character to the total divergence (Wesly *et al.*, 2020).

MATERIALS AND METHOD

The experimental material consisted of 35 genotypes of mungbean which were procured from SKN-RARI, Durgapura, Jaipur; Agricultural Research Station, Mandore, Jodhpur; NBPGR-RS Jodhpur; Indian Institute of Pulse Research- Regional Station, Bikaner; and National Seed Project, Bikaner. These genotypes were evaluated in randomized block design with three replications accommodating 4 meter long two rows per replication at 30 cm spacing. Observations were

recorded for 13 quantitative characters *viz.*, field observations *i.e.*, days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, pod length, 100-seed weight, biological yield per plant, harvest index, seed yield per plant; Laboratory observations *i.e.*, germination percentage, seed volume and water absorption capacity to study the genetic variability and character association in the mungbean. So that promising genotype could be identified for breeding programme to develop high yielding varieties of mungbean for the arid zone. Analysis of variance was done by subjecting the data to the statistical method described by Panse and Sukhatme (1985); Singh and Chaudhary (1985). Genotypic variances and phenotypic variances were calculated according to Johnson *et al.*, (1955); Comstock and Robinson (1952), respectively from the expectations of mean squares by using an ANOVA table for each character. Heritability in a broad sense was calculated as suggested by Burton and Devane (1953). The expected genetic advance for each character was calculated as suggested by Johnson *et al.*, (1955).

Phenotypic and genotypic correlation and path coefficients of variation were computed as per the method given by Dewey and Lu (1959). Genetic divergence will be measured as per standard procedure of D^2 analysis given by Mahalanobis, (1928).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among genotypes of mungbean for all the 13 characters, thereby a considerable amount of variability in the materials used in the experiment. Similar findings were earlier reported by Talukdar *et al.* (2020); Wesly *et al.* (2020).

The estimates of GCV and PCV were high for number of pods per plant and water absorption capacity and moderate for seed yield per plant, harvest index, 100-seed weight, biological yield per plant, plant height, number of seeds per pod, seed volume, pod length and germination percentage (Table 1). Results are in agreement with Jeberson *et al.*, (2015); Talukdar *et al.* (2020); Wesly *et al.*, (2020).

Table 1: Estimates of genetic variability parameters for different characters.

Sr. No.	Characters	GCV	PCV	Heritability (%)	Genetic Advance	GA as % of mean
1.	Days to 50% flowering	4.85	5.25	85.64	3.7	9.26
2.	Days to maturity	2.73	2.96	85.13	3.64	5.2
3.	Plant height (cm)	11.81	13.71	74.28	10.45	20.98
4.	No. of pods per plant	27.37	28.24	93.94	14.43	54.66
5.	No. of seeds per pod	10.46	13.09	63.82	1.96	17.21
6.	Pod length (cm)	8.47	10.99	59.47	1.15	13.46
7.	100-Seed weight	12.93	15.96	65.7	0.92	21.6
8.	Biological yield per plant (g)	12.46	15.75	62.53	4.32	20.29
9.	Harvest index	10.48	16.03	42.78	5.19	14.12
10.	Germination percentage	5.19	10.75	23.37	4.72	5.17
11.	Seed volume (μ l/seed)	9.93	11.73	71.71	6.15	17.32
12.	Water absorption capacity	19.17	20.35	88.76	15.39	37.21
13.	Seed yield per plant (g)	15.79	17.92	77.58	2.22	28.65

High heritability coupled with high genetic advance were observed for number of pods per plant, water absorption capacity, seed yield per plant and plant height (Table 1). These results were confined by Manivelan *et al.*, (2019); Wesly *et al.*, (2020). Which shows that these characters were under the control of additive gene action indicating that these characters were less influenced by environment and direct/simple selection for these characters would be effective for future improvement. Therefore, these characters can assist in selection programme.

Seed yield per plant had significant and positive correlation with number of pods per plant, pod length, 100-seed weight, biological yield per plant, harvest

index, germination percentage, seed volume and water absorption capacity at phenotypic level (Table 2). Findings get corroborated with Jadhav *et al.*, (2019); Goyal *et al.*, (2021). Therefore, prominence should be given to these characters in mungbean improvement programme.

Path coefficient analysis revealed that, the characters *viz.* days to maturity, plant height, number of pods per plant, 100-seed weight, biological yield per plant, harvest index, germination percentage, seed volume and water absorption capacity showed positive direct effect at phenotypic level (Table 2). Results are in compliance with Jadhav *et al.* (2019); Goyal *et al.*, (2021).

On the basis of D^2 statistics, 35 genotypes of mungbean have been grouped into 10 clusters. The cluster I and II have the largest 10 genotypes each followed by cluster III with 5 genotypes, cluster IV, VI and X have 2 genotypes each, while cluster V, VII, VIII and IX have one genotype each or monogenotypic. Mathankumar *et al.*, (2020); Talukdar *et al.*, (2020).

The maximum intra cluster distance (64.92) was showed by cluster X afterwards cluster VI (51.87), cluster II (44.76), cluster III (37.89), cluster I (37.81) and cluster IV (36.03). The intra cluster distance was zero for remaining 4 cluster because of solitary

genotype. The highest inter cluster distance was observed between cluster VI and X (418.76) followed by cluster IV and X (402.55), cluster VI and VIII (367.49), cluster III and X (343.52), cluster I and X (300.90) respectively. The greater distance between two cluster shows the presence of wider genetic diversity among the genotypes of those cluster. Maximum inter cluster divergence indicated that good recombinants can be realized by mating between the genotypes. Similar findings were described by Mathankumar *et al.*, (2020); Talukdar *et al.*, (2020).

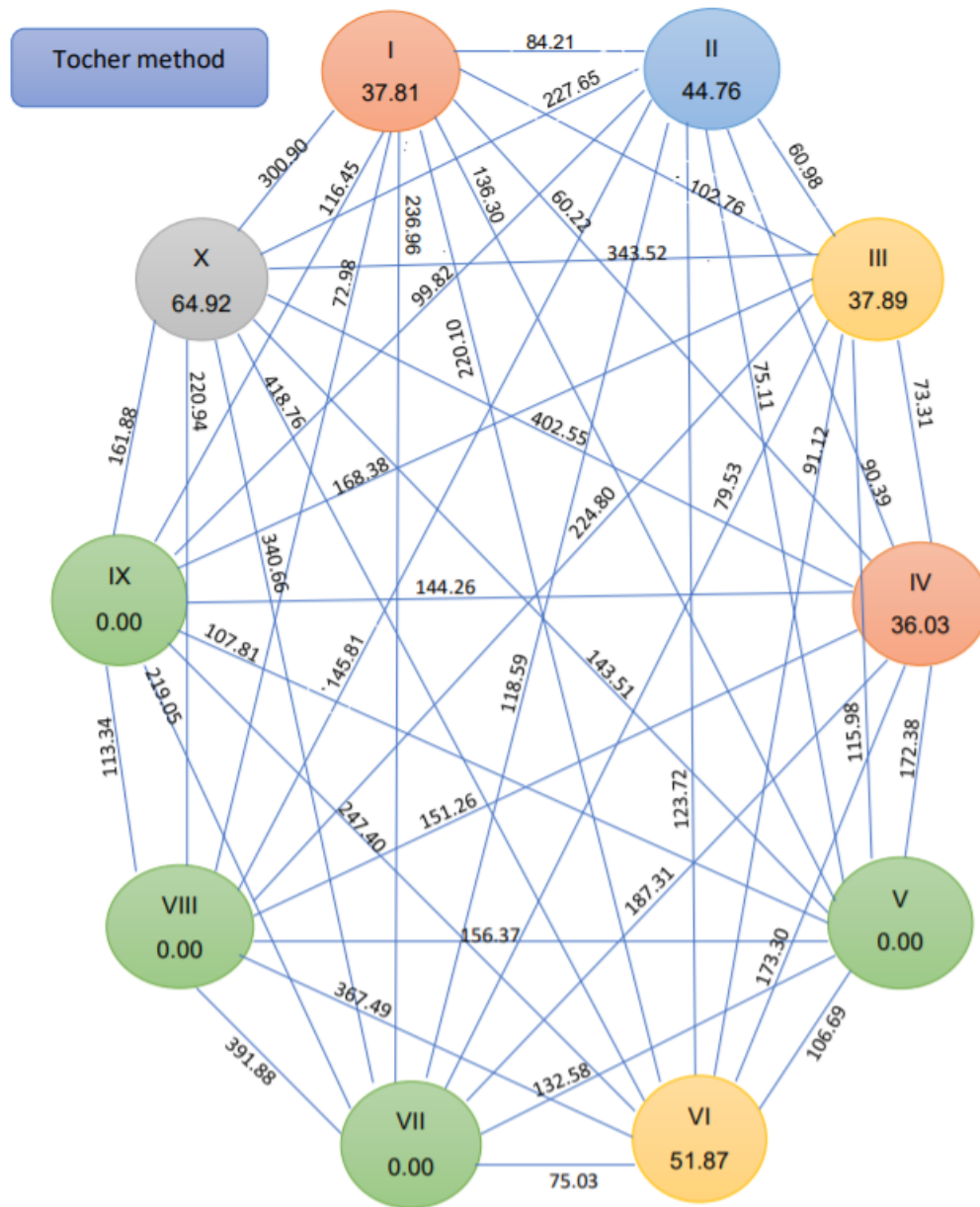


Fig. 1. Mahalanobis Euclidean distance (Not to scale).

Table 2: Phenotypic (P) and Genotypic (G) path coefficient of various characters on seed yield of mungbean.

Characters		D.F	D.M	P.H	P.P	S.P	P.L	T.W	B.Y	H.I	G.P	S.V	WAC	S.Y
D.F	P	-0.3229	0.2810	0.0118	-0.0065	0.0128	0.0054	-0.0066	-0.1578	-0.3376	-0.0114	-0.0060	-0.0004	-0.5379 **
	G	48.5014	-50.6150	-0.7402	-0.9811	1.7594	-1.0909	0.2491	0.3662	0.3680	1.3481	0.1229	0.0746	-0.6376 **
D.M	P	-0.3225	0.2814	0.0119	-0.0065	0.0128	0.0053	-0.0065	-0.1575	-0.3372	-0.0115	-0.0060	-0.0004	-0.5368 **
	G	48.5058	-50.6105	-0.7492	-0.9886	1.7589	-1.0812	0.2443	0.3690	0.3673	1.3488	0.1225	0.0745	-0.6383 **
P.H	P	-0.0964	0.0843	0.0397	0.0018	0.0083	0.0031	-0.0079	0.1587	-0.2194	-0.0103	-0.0057	-0.0003	-0.0441 NS
	G	19.1387	-20.2143	-1.8759	0.2494	1.2767	-0.7605	0.3955	-0.3306	0.3025	1.5184	0.0973	0.0628	-0.1399 NS
P.P	P	0.0949	-0.0838	0.0033	0.0220	-0.0086	-0.0008	0.0007	0.4122	0.1925	0.0081	0.0021	0.0002	0.6427 **
	G	-14.5432	15.2909	-0.1430	3.2721	-1.0886	-0.0812	-0.0130	-0.8934	-0.1795	-0.8476	-0.0390	-0.0339	0.701 **
S.P	P	0.1520	-0.1316	-0.0121	0.0069	-0.0273	-0.0140	0.0095	0.3215	0.1508	0.0139	0.0081	0.0004	0.478 **
	G	-31.3649	32.7197	0.8803	1.3092	-2.7206	2.3868	-0.4680	-0.5587	-0.2999	-0.9991	-0.1428	-0.0926	0.6493 **
P.L	P	0.0618	-0.0531	-0.0043	0.0006	-0.0135	-0.0282	0.0167	0.2519	0.0531	0.0049	0.0094	0.0004	0.2998 **
	G	-14.5587	15.0561	0.3925	-0.0731	-1.7867	3.6343	-0.8182	-0.5763	-0.1395	-0.3822	-0.1889	-0.0932	0.4662 **
T.W	P	0.0665	-0.0574	-0.0098	0.0005	-0.0081	-0.0148	0.0319	0.1903	0.0229	0.0038	0.0096	0.0004	0.2351 *
	G	-12.7535	13.0530	0.7833	0.0448	-1.3441	3.1394	-0.9472	-0.4528	-0.0442	-0.8746	-0.2088	-0.0935	0.3017 NS
B.Y	P	0.0593	-0.0515	0.0073	0.0105	-0.0102	-0.0083	0.0071	0.8600	-0.3532	-0.0019	0.0037	0.0002	0.5227 **
	G	-11.9711	12.5858	-0.4180	1.9701	-1.0244	1.4114	-0.2890	-1.4838	0.0723	0.0300	-0.0853	-0.0427	0.7553 **
H.I	P	0.1231	-0.1072	-0.0098	0.0048	-0.0046	-0.0017	0.0008	-0.3430	0.8855	0.0110	0.0032	0.0002	0.5623 **
	G	-29.6213	30.8552	0.9418	0.9747	-1.3543	0.8416	-0.0695	0.1781	-0.6025	-1.4471	-0.0918	-0.0498	0.555 **
G.P	P	0.1025	-0.0902	-0.0113	0.0049	-0.0106	-0.0039	0.0033	-0.0465	0.2714	0.0359	0.0049	0.0002	0.2608 **
	G	-32.4969	33.9288	1.4157	1.3784	-1.3509	0.6903	-0.4117	0.0221	-0.4334	-2.0120	-0.1229	-0.0850	0.5224 **
S.V	P	0.1096	-0.0950	-0.0129	0.0027	-0.0126	-0.0151	0.0174	0.1803	0.1622	0.0100	0.0176	0.0004	0.3647 **
	G	-24.1518	25.1185	0.7398	0.5164	-1.5737	2.7819	-0.8016	-0.5127	-0.2240	-1.0022	-0.2468	-0.0966	0.5473 **
WAC	P	0.1452	-0.1254	-0.0132	0.0049	-0.0132	-0.0145	0.0159	0.1840	0.1862	0.0096	0.0097	0.0008	0.39 **
	G	-25.1005	26.1479	0.8170	0.7686	-1.7471	2.3478	-0.6138	-0.4394	-0.2081	-1.1857	-0.1653	-0.1442	0.4773 **

Residual effect = 0.0153 at phenotypic level, Residual effect = 0.129 at genotypic level.

Note : D.F= Days to 50% flowering, D.M= Days to maturity, P.H= Plant height, P.P= Pods per plant, S.P= Seeds per pod, P.L= Pod length, T.W= 100-Seed weight, B.Y= Biological yield per plant, H.I=Harvest index, G.P= Germination percentage, S.V= Seed volume, WAC= Water absorption capacity, S.Y= Seed yield per plant

CONCLUSION

The genotypes which produced substantial seed yield and performed better for desirable traits were Keshwanand mung-1, RMG-492, GM-4, SML-668, RMG-62, IPM-2-3, VIRAT, Ganga-8, MEHA and MH-421. Thus, these varieties could be used for cultivation in arid zone as well as used in breeding programme to develop high yielding varieties.

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Conflicts of Interest. Nil.

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