Original Research Article

Genetic variability, Correlation and Path analysis in Mung bean Genotypes (*Vigna radiata* L. Wilczek)

Abstract

Mungbean (*Vigna radiata* L. Wilczek) is one of the most important pulse crops due to the high content of protein as well as the ability to nitrogen fixation in soil. Seed yield is the most complex trait which highly influenced by other traits and also the environment. In this view, the study was aimed to evaluate the relationship between yield and yield attributing traits of sixty genotypes of Mung bean. The genotypes exhibited significant variability in respect to all the fourteen quantitative characters studied. Genetic variability studies showed presence of good amount of variation among the sixty genotypes. Highest PCV and GCV was recorded by seed yield followed by number of seeds per plant and primary branch length. The characters, seed yield per plant, number of seeds per plant, primary branch length, biological yield, harvest index, 100 seed weight, number of pods per plant, number of clusters per plant, plant height and number of primary branches had shown high heritability coupled with high genetic advance as percent mean.Seed yield per plant had shown highly significant and positive correlation with number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, number of seeds per plant, biological yield and harvest index at both phenotypic and genotypic levels. Path analysis showed that biological yield and harvest index were the most important characters for yield improvement.

Keywords: Mung bean, genetic variability, heritability, correlation, path analysis

Introduction

The mung bean (*Vigna radiata* L. Wilczek) is a short-lived, significant legume crop that is grown in Asia and America's tropical and subtropical regions. The Indian subcontinent relies on it as the third-most significant pulse crop. Mungbean plant roots have the ability to fix atmospheric nitrogen with a symbiotic relationship with nitrogen-fixing rhizobia. For any yield improvement programme selection of superior parents is a pre requisite. The yield is connected to different characters that are interconnected to one another and are complex characters. The knowledge of genetic variability in the available germplasm is extremely important and vital for the development of new, higher producing varieties. Knowing the associations between different characters and path coefficients is crucial for accumulating the best possible contribution from characters that contribute to yield. The primary goals of the current study were to investigate the kind, extent, and associations of genetic diversity among mungbean features.

Materials and Methods

The experiment was carried out on 60 genotypes of mung bean, at Genetics and Plant Breeding (GPB) Farm, College of Agriculture, Central Agricultural University, Imphal, Manipur during Kharif 2021, following Randomized Block Design with three replications. Each row was 4 m × 30 cm size with a spacing of 30 cm x 10 cm between and within rows. The research farm is situated geographically at 248 11' N and 938 91' E, at an elevation of 781.8 metres above mean sea level.All the other recommended package of practices were followed during the study for a good crop growth and the genotypes are harvested as and when pods matured. Ten plants were selected at random from each genotype in each replication for recording data.

It is necessary for the authors to make a brief description of the physical environment of the study area (type of climate, temperature, average annual rainfall, seasons, etc.)

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The different characters which were studied *viz*., days to 50 % flowering, days to maturity, plant height (cm), number of primary branches, primary branch length (cm), number of clusters per plant, number of pods per plant, Pod length (cm), number of seeds per pod, number of seeds per plant, 100 seed weight (g), biological yield (g), harvest index (%) and seed yield per plant (g). Genotypic coefficients of variation (GCV) and Phenotypic coefficients of variation (PCV) were computed according to Burton and DeVane(1953). The percentage of heritability (H) was estimated as per the formula given by Allard (1960). The expected genetic advance (GA) as percentage of mean was computed according to the formula suggested by Johnson *et al.* (1955). The genotypic and phenotypic correlations were computed according to formulasuggestedbyFalconer(1967).While path analysis was done by assuggestedbyDeweyandLu(1959).

Results and Discussion

Analysis of variance (ANOVA) was carried out for all the 14 characters under study. The analysis of variance revealed that there was a significant difference among all the genotypes, indicating presence of genetic variability at 0.01 level of significance (Table 1). The estimated variance components, broad-sense heritability and genetic advance of all the characters studied were shown in the Table 2.

PCV and GCV

The maximum PCV (48.45) and GCV (48.41) were recorded for the trait seed yield per plant followed by number of seeds per plant with PCV (47.89) and GCV (47.84); primary branch length PCV (46.33) and GCV (45.41). While the minimum PCV (4.54) and GCV (4.49) values were shown by days to maturity. In the present investigation,the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the 14 traits under study. This indicates the effect of environment on the expression of traits. Similar results were given byRaturi*et al.* (2015), Jeberson*et al.* (2017) and Sabatina*et al.* (2021) in mungbean.

Heritability and Genetic advance

In the present investigation highest heritability was shown by all the characters in the present study *viz.*, days to 50 % flowering, days to maturity, plant height, number of primary branches, primary branch length, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, number of seeds per plant, 100 seed weight, biological yield, harvest index and seed yield per plant (Table 2). Similar results for seed yield and number of pods per plant were shown by Singh *et al.* (2022) in mung bean. The characters seed yield per plant, number of seeds per plant, primary branch length, biological yield, harvest index, 100 seed weight, number of pods per plant, number of clusters per plant, plant height and number of primary branches had shown high heritability coupled with high genetic advance as percent mean. The direct selection of these characters may improve yield. Similar results were produced by Mishra *et al.* (2008), Vadivel *et al.* (2020) Sineka*et al.* (2021) and Salman *et al.* (2021) in mung bean. High heritability with moderate genetic advance as percent mean was shown by characters days to 50 % flowering, pod length and number of seeds per pod. Whereas, days to maturity exhibited high heritability coupled with low genetic advance as percent mean.

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Correlation studies

Association analysis provides the estimates of degree of association among the various components of yield which help in direct selection of associated characters for the improvement of desirable traits like yield.

The estimated values of correlation coefficients between different pairs of characters under investigation were shown in Table 3. Seed yield per plant had shown highly significant and positive correlation with number of clusters per plant, number of pods per plant (similar findings with Srivastava and Singh (2012) and Sandhiya and Shanmugavel (2018), pod length, number of seeds per pod, number of seeds per plant, biological yield and harvest index at both phenotypic and genotypic levels. The results are in concurrence with Prasanna *et al.* (2013), Hemavathy*et al.* (2015), Kaur *et al.* (2017) and Gupta *et al.* (2021) in mung bean. In the present investigation, the genotypic correlations are in agreement with the phenotypic correlations, though the magnitude of the values were higher in the former case for all the traits under study.

Path analysis

The efficiency of selection in any breeding programme mainly depends upon the knowledge of association of characters. The coefficient of correlation simply identifies the relationship between any two variables; it does not reveal how much a change in one variable will affect a change in another, but the Path coefficient analysis is helpful in partitioning the correlation coefficient into direct and indirect effects so as to measure the relative importance of causal factors involved. In the present study, the path analysis showing the direct and indirect effects of the different traits were shown in Table 4. Positive direct effect on seed yield per plant was exhibited by biological yield (0.5863) followed by harvest index (0.4267), number of seeds per plant (0.3058), 100 seed weight (0.0516), number of clusters per plant (0.0442), number of primary branches (0.0405), number of seeds per pod (0.0369) and days to 50% flowering (0.0147). Number of pods per plant, pod length, plant height and days to maturity were indirectly influencing the seed yield per plant through other characters. Based on the path analysis biological yield and harvest index were the most important characters for yield improvement. Harvest index had shown highest positive direct effect in case of Prasanna *et al.* (2013), maximum direct effect of harvest index and biological yield was reported by Gadakh*et al.* (2013)

Table 1. Analysis of variance of different characters in Mungbean (*Vigna radiata* L.Wilczek)

S. No	Characters	Mean sum of squares		
		Replication	Genotypes	Error
1	Days to 50 % flowering	0.039	31.74**	0.146
2	Days to Maturity	0.57	25.98**	0.18
3	Plant height	5.42	203.79**	3.79
4	Number of Primary branches	0.001	0.23**	0.01
5	Primary branch length	5.00	195.99**	2.62

6	Number of Clusters per plant	0.04	0.4**	0.33
7	Number of Pods per plant	0.027	1.80**	0.92
8	Pod length	0.55	1.83**	0.19
9	Number of Seeds per pod	0.01	0.14**	0.21
10	Number of Seeds per plant	25.77	14565.14**	11.16
11	100 Seed weight	0.027	1.21**	0.026
12	Biological yield	0.54	49.37**	0.37
13	Harvest index	5.79	494.16**	6.94
14	Seed yield per plant	0.01	14.85**	0.01

*,** Significance at 5% and 1% respectively

Table 2: Estimate of Mean, range, GCV, PCV, Heritability (broad sense) and genetic advance as percentage of mean

S. No	Character	Mean	Minimum	Maximum	Coefficient of Variation		Heritability (%) Broad sense	Genetic advance	Genetic advance as percentage of Mean
					GCV	PCV			
1	DF	35.21	32.00	45.66	9.21	9.28	98.63	6.64	18.85
2	DM	65.37	61.66	78.00	4.49	4.54	97.86	5.97	9.14
3	PH	34.94	22.3	52.76	23.37	24.02	94.62	16.35	46.83
4	PB	1.87	1.00	3.43	18.2	18.4	98.00	0.6	37.00
5	PBL	17.79	6.46	42.33	45.41	46.33	96.09	16.21	91.71
6	NC	4.58	2.06	8.13	16.5	17.3	88.88	0.69	31.37
7	NPP	11.68	5.16	25.66	22.64	22.97	97.05	1.56	45.93
8	PLN	7.33	5.54	9.99	10.06	11.73	73.44	1.30	17.75
9	SPP	10.99	6.4	13.73	6.24	6.54	91.03	0.418	12.26
10	SPPL	145.61	43.53	285.46	47.84	47.89	99.77	143.3	98.42
11	TW	3.14	2.01	5.32	20.81	20.85	99.64	1.34	42.79
12	BY	9.95	2.86	21.26	40.67	41.34	96.77	8.19	82.40
13	HI	47.98	31.09	68.89	35.13	35.65	97.09	34.17	71.23
14	SY	4.59	0.93	10.26	48.41	48.45	99.81	4.57	99.63

DF-Days to 50% flowering, DM- days to maturity, PH-plant height, PB-number of primary branches, PBL-primary branch length, NC-number of clusters per plant, NPP-number of pods per plant, PLN-Pod length, SPP-number of seeds per pod, SPPL-number of seeds per plant, TW-100 seed weight, BY-biological yield, HI-harvest index and SY-seed yield per plant.

Table 3: phenotypic correlation coefficient (upper diagonal) and genotypic correlation coefficient (lower diagonal) among yield and its attributing traits in 60 genotypes of mungbean

Character	DF	DM	PH	PB	PBL	NC	NPP	PLN	SPP	SPPL	TW	BY	HI	SY
DF	1	0.887**	0.312*	0.070	0.316*	0.355**	0.124	-0.040	-0.140	0.180	-0.080	0.225	-0.072	0.152
DM	0.902**	1	0.211	0.154	0.256*	0.152	-0.090	-0.100	-0.24	-0.034	-0.097	0.024	-0.117	-0.050
PH	0.324*	0.219*	1	-0.053	0.519**	0.535**	0.4967**	0.279*	0.124	0.380**	0.024	0.442**	-0.099	0.306*
PB	0.072	0.158	-0.058	1	0.043	-0.175	-0.151	-0.221*	-0.328*	-0.216*	-0.084	-0.180	0.070	-0.112
PBL	0.323*	0.267*	0.556**	0.047	1	0.337**	0.272*	-0.019	-0.253	0.087	0.073	0.068	-0.047	0.036
NC	0.374**	0.166	0.580**	-0.191	0.368**	1	0.748**	0.335**	0.277*	0.598**	0.111	0.648**	-0.055	0.534**
NPP	0.128	-0.089	0.516**	-0.155	0.284*	0.804**	1	0.340**	0.256*	0.742**	0.138	0.749**	0.069	0.678**
PLN	-0.046	-0.110	0.303*	-0.252	-0.008	0.412**	0.405**	1	0.411**	0.275*	0.496**	0.367**	0.125	0.361**
SPP	-0.155	-0.261*	0.144	-0.346**	-0.280*	0.306*	0.283*	0.512**	1	0.350**	0.167	0.463**	-0.096	0.350**
SPPL	0.181	-0.034	0.393**	-0.219	0.089	0.635**	0.752**	0.323*	0.367**	1	0.127	0.814**	0.321*	0.912**
TW	-0.080	-0.095	0.026	-0.091	0.077	0.115	0.150	0.630**	0.191	0.133	1	0.230	0.215	0.305*
BY	0.229*	0.026	0.460**	-0.183	0.078	0.692**	0.766**	0.437**	0.496**	0.822**	0.236	1	-0.065	0.804**
HI	-0.076	-0.026	-0.103	0.074	-0.057	-0.05	0.074	0.417**	-0.116	0.328*	0.237	-0.041	1	0.498**
SY	0.153	-0.050	0.316*	-0.113	0.038	0.566**	0.687**	0.423**	0.367**	0.913**	0.318*	0.812**	0.508**	1

DF-Days to 50% flowering, DM- days to maturity, PH-plant height, PB-number of primary branches, PBL-primary branch length, NC-number of clusters per plant, NPP-number of pods per plant, PLN-Pod length, SPP-number of seeds per pod, SPPL-number of seeds per plant, TW-100 seed weight, BY-biological yield, HI-harvest index and SY-seed yield per plant.

Table 4: Direct (diagonal) and indirect effects of yield component traits on seed yield in mungbean genotypes

Variables	DF	DM	PH	PB	PBL	NC	NPP	PLN	SPP	SPPL	TW	BY	HI
DF	**0.0147**	0.0133	0.0048	0.0011	0.0047	0.0055	0.0019	-0.0007	-0.0023	0.0027	-0.0012	0.0034	-0.0011
DM	-0.0155	**-0.0171**	-0.0038	-0.0027	-0.0046	-0.0028	0.0015	0.0019	0.0045	0.0006	0.0016	-0.0005	0.0021
PH	-0.0111	-0.0075	**-0.0343**	0.0020	-0.0191	-0.0199	-0.0177	-0.0104	-0.0049	-0.0135	-0.0009	-0.0158	0.0035
PB	0.0030	0.0064	-0.0024	**0.0405**	0.0019	-0.0078	-0.0063	-0.0102	-0.0140	-0.0089	-0.0037	-0.0074	0.0030
PBL	0.0035	0.0029	0.0060	0.0005	**0.0109**	0.0040	0.0031	-0.0001	-0.0030	0.0010	0.0008	0.0009	-0.0006
NC	0.0166	0.0073	0.0257	-0.0085	0.0163	**0.0442**	0.0356	0.0182	0.0136	0.0281	0.0051	0.0306	-0.0025
NPP	-0.0064	0.0045	-0.0258	0.0078	-0.0142	-0.0401	**-0.0499**	-0.0202	-0.0141	-0.0376	-0.0075	-0.0382	-0.0037
PLN	0.0011	0.0027	-0.0074	0.0061	0.0002	-0.0100	-0.0098	**-0.0242**	-0.0124	-0.0078	-0.0153	-0.0106	-0.0036
SPP	-0.0057	-0.0096	0.0053	-0.0128	-0.0104	0.0113	0.0105	0.0189	**0.0369**	0.0136	0.0071	0.0183	-0.0043
SPPL	0.0554	-0.0106	0.1203	-0.0671	0.0274	0.1943	0.2302	0.0989	0.1123	**0.3058**	0.0410	0.2516	0.1005
TW	-0.0042	-0.0049	0.0014	-0.0047	0.0040	0.0060	0.0078	0.0326	0.0099	0.0069	**0.0516**	0.0122	0.0122
BY	0.1348	0.0155	0.2702	-0.1074	0.0459	0.4058	0.4492	0.2564	0.2911	0.4823	0.1383	**0.5863**	-0.0244
HI	-0.0326	-0.0530	-0.0439	0.0316	-0.0247	-0.0238	0.0316	0.0628	-0.0496	0.1403	0.1010	-0.0177	**0.4267**

DF-Days to 50% flowering, DM- days to maturity, PH-plant height, PB-number of primary branches, PBL-primary branch length, NC-number of clusters per plant, NPP-number of pods per plant, PLN-Pod length, SPP-number of seeds per pod, SPPL-number of seeds per plant, TW-100 seed weight, BY-biological yield, HI-harvest index and SY-seed yield per plant.

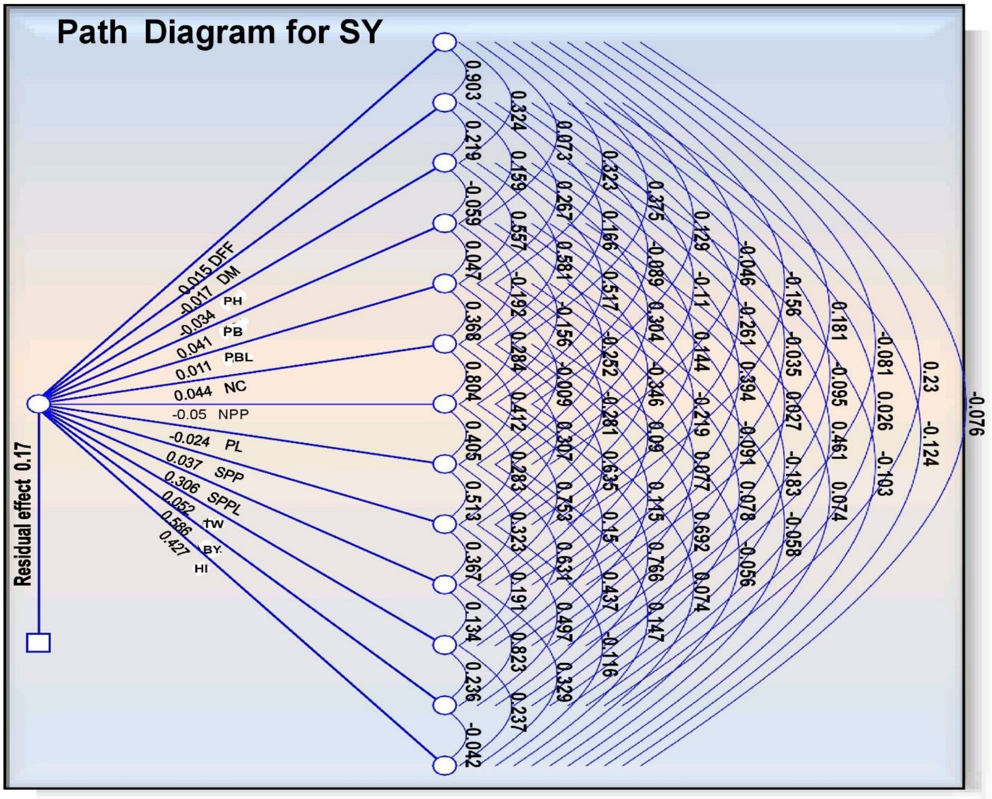

Fig 1: Direct and indirect effects of 13 characters on the seed yield per plant

The manuscript has a poor scientific quality related to the discussion of the results; therefore, I suggest that the authors increase the scientific quality by discussing the results with scientific research already published. I suggest adding a couple of paragraphs like this:

The advantage of using exotic Mung bean germplasm to improve the tolerance of cultivated grains to environmental stress has been defended by several authors (Ranawake et al. 2011). To do this, an understanding of the qualities that contribute to increased tolerance is necessary. Despite the demonstrated ability of mung bean to produce high yields in rainfed agriculture, there is a paucity of information on the characteristics that give rise to its tolerance to drought (Olivares and Hernández, 2019a; Olivares et al. 2018a).

There are two general methods by which plants cope with a dry environment. The first is dehydration tolerance that can withstand water loss and still allow plant growth and photosynthesis to occur at low water potentials. The second is that dehydration cannot be postponed by supporting

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low tissue water potentials, but it has characteristics that prevent or postpone tissue water loss and maintain high leaf water potentials and turgor.

Water deficit continues to be one of the most significant problems of crops of agricultural importance, affecting growth, development, and yield (Cortez et al. 2018; Olivares and Zingaretti, 2018; 2019). Plants adapted to arid and semi-arid regions have developed mechanisms to survive and succeed in these adverse conditions (Olivares et al. 2016; Olivares et al. 2017; Olivares et al. 2018b; Cortez et al. 2019). The response of plants to this environmental stress depends on several factors, including the stage of plant development and the length and severity of the stress (Olivares et al. 2018c, 2018d; Olivares et al. 2021a). In the leaf tissues, the perception of drought stress causes the closing of the stomata to reduce transpiration and therefore limits the absorption of carbon dioxide and reduces the rates of photosynthesis (Olivares et al. 2021b). As a result of the water deficit there may also be greater root growth (Olivares, 2018). This increases the volume of soil explored by the plant to have greater water availability (Olivares et al. 2020a). Plants also synthesize compounds that function as osmolytes to maintain water potential and other proteins that they use to protect cells from damage (Olivares et al. 2022a; 2022b). All these responses are controlled by complex mechanisms that involve changes in gene expression (Olivares et al. 2020b; Olivares and Hernández, 2019b).

Some gene products are directly involved in protective mechanisms, such as abundant end-embryogenesis proteins (EAPs), osmolyte synthesis, and ion transport functions; other gene products, for example, transcription factors or kinases, that participate in signal transduction pathways that mediate cellular responses to external stimuli (Jiménez and Acosta, 2013).

Conclusion

In this study, all the characters viz., days to 50 % flowering, days to maturity, plant height, number of primary branches, primary branch length, number of clusters per plant, number of Pods per plant, Pod length, number of seeds per pod, number of seeds per plant, 100 seed weight, biological yield, harvest index and seed yield per plant showed high heritability indicating low environmental effects. The characters seed yield per plant, number of seeds per plant, primary branch length, biological yield, harvest index, 100 seed weight, number of pods per plant, number of clusters per plant, plant height and number of primary branches had shown high heritability coupled with high genetic advance as percent mean indicating the substantial contribution of additive gene action. The direct selection of these characters may improve yield. High heritability with moderate genetic advance as percent mean was shown by characters days to 50 % flowering, pod length and number of seeds per pod which specified equal influence of additive and non-additive gene action in the expression of these characters. Days to maturity exhibited high heritability coupled with low genetic advance as percent mean which indicate the influence of non-additive gene action in the character expression. The seed yield per plant was significantly correlated with all the characters except days to 50 % flowering, days to maturity, number of primary branches and primary branch length. Based on the path analysis biological yield and harvest index were the most important characters for yield improvement. In-direct selection on number of pods per plant, pod length, plant height and days to maturity had to be practiced for improvement in the yield.

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I suggest adding the following scientific publications that will improve the scientific quality of the manuscript.

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