

Genetic Variability and Correlation Studies on Yield and Yield Related Attributes in Mungbean [*Vigna radiata* (L.) Wilczek]

N. K. PARIMALA, K. M. HARINIKUMAR, D. L. SAVITRAMMA, SRITAMA KUNDU AND SHAILJA CHAUHAN
Department of Plant Biotechnology, College of Agriculture, UAS, GKVK, Bengaluru - 560065
e-mail : harinikumarm@gmail.com

ABSTRACT

Genetic variability such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) among different traits is very much important in any crop improvement. Heritability basically measures the phenotypic variance and its effect on genetic causes, so this is also an important consideration in case of successful breeding program. Correlation coefficient analysis explains the extent of relationship within important plant traits and it gives basic standards for selection of genotypes leads to good yield. In the present study the analysis of variance for 12 yield and yield related traits revealed that significant difference was presence among the RILs for all the traits except 50 per cent flowering and days to maturity indicates the presence of genetic variability in this population. The GCV and PCV were found high for cluster/plant, pods/plant, pod yield, seed yield and threshing percentage. Heritability high for plant height, cluster/plant, pods/plant, seeds/pod, threshing percentage and test weight, High level of genetic advance per cent mean found in plant height, clusters/plant, pods/plant, pod yield, seed yield, threshing percentage and test weight. Correlation study shows seed yield was positively associated with all the traits except for 50 per cent flowering and days to maturity. Therefore, more importance should be given to these characters in indirect selection for seed yield improvement in mungbean.

Keywords : Genetic variability, RIL population, Yield, Yield attributes of mungbean

MUNGBEAN [*Vigna radiata* (L.) Wilczek] is an important legume crop in Southeast Asia. It occupies third position among the pulse crops of India (Rishi, 2009). In India, its cultivation is taken mainly in Madhya Pradesh, Maharashtra, Uttar Pradesh, Andhra Pradesh, Karnataka and Rajasthan. Because of the increasing mungbean popularity in Indian ethnic foods and apparent health benefit, its domestic consumption has been increased (Datta *et al.*, 2012).

Mungbean seeds are very digestible and also having extra nutritional values. It mainly contains nearly 24 per cent of protein, 0.6 per cent of fat, 0.9 per cent of fiber and 3.7 per cent of ash. It plays an essential role in soil enrichment by atmospheric nitrogen fixation through symbiosis.

Genetic variability such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) among different traits is very much important in any crop improvement. Heritability basically measures the phenotypic variance and its effect on genetic causes, so this is also an important

consideration in case of successful breeding program. Heritability with genetic advance mean assures in understanding the mode of quantitative traits inheritance.

Correlation coefficient analysis is a convenient technique, which explains the extent of relationship within important plant traits and it gives basic standards for selection of genotypes and leads to good yield and yield attributing components in the field experiments. Consideration of these points, the present study was planned to screen the F₈ RILs, to study available genetic variability, heritability, genetic advance and correlation for yield and yield related traits in mungbean which will help in detaching high yielding and quality traits.

MATERIAL AND METHODS

During the 2018 rabi, the field experiment was cultivated at the 'K' block of the University of Agricultural Sciences, GKVK, Bengaluru. In the rabi season from October, 2018 to January, 2019 the field experiment was conducted in an augmented block

TABLE 1
 Analysis of variance for yield and yield related traits in F₈ mungbean recombinant inbred lines derived from the cross between Chinamung and BL 849

Source of Variation	DF	DFE	DTM	PH	B/P	C/P	P/P	PL	S/P	PY/P	SY	T%	TW
Blocks	4	14.839	2.835	19.354 ***	5.508 ***	2.287 **	1.023 **	2.400 **	1.520 ***	2.736 **	1.876 **	0.129 **	0.052
Enteries (RIL's+Checks)	98	5.795	6.839	10.817 ***	0.938 *	1.182 **	1.656 ***	0.776	0.611 **	0.913 *	0.787 *	0.109 **	0.274 *
Checks	3	1.467	3.65	12.307 **	0.552 *	1.274	1.244 ***	0.335	0.219	0.172	0.116	0.023	0.214
RIL's	94	5.864	7.005	10.684 ***	0.957 **	1.188 *	1.668 **	0.798 *	0.620 **	0.946 **	0.809 *	0.105 **	0.277 *
Checks vs RIL's	1	12.309	0.827	18.933 **	0.321	0.296	1.739 **	0.017	0.923 *	0.001	0.667	0.719 ***	0.104
Error	12	5.258	4.526	1.201	0.422	0.373	0.111	0.338	0.131	0.358	0.318	0.023	0.092
CD @5%	1	6.145	5.7	2.936	1.74	1.637	0.891	1.558	0.97	1.607	1.512	0.409	0.813

Legend: *Significant @ P=0.05 ** Significant @ P=0.01 ***Significant @ P=0.001
 DFF: Days to fifty per cent flowering DTM: Days to maturity PH: Plant height (cm) B/P: Branches per plant
 C/P: Clusters per plant P/P: Pods per plant PL: Pod length(cm) S/P: Seeds per pod
 PY/P: Pod yield per plant (g) T %: Threshing per cent TW: Test weight

TABLE 2
Phenotypic evaluation of F8 RIL population for powdery mildew disease resistance and yield related traits in the cross between Chinamung and BL 849

Traits	Mean \pm SE	Range		CV		Broad sense h^2 (%)	GAM (%)
		Min	Max	PCV (%)	GCV (%)		
Days to 50 % flowering	48.86 \pm 0.24	46	55	4.92	1.47	8.96	0.908
Days to Maturity	74.07 \pm 0.27	67	80	3.48	1.96	31.80	2.285
Plant Height	21.17 \pm 0.33	14.99	27.82	14.41	13.44	87.60	25.84
Branches/plant	5.59 \pm 0.10	3.33	7.8	16.76	12.09	52.04	17.96
Clusters/plant	3.59 \pm 0.11	1.84	6.52	28.76	23.20	65.12	38.58
Pods/plant	4.40 \pm 0.13	2.01	8.25	27.22	26.16	92.33	51.78
Pod length	5.98 \pm 0.91	3.15	7.84	14.29	10.47	53.77	15.83
Seeds/pods	5.29 \pm 0.80	3.00	6.88	13.99	12.20	76.12	21.93
Pod yield	2.22 \pm 0.99	1.02	5.34	41.75	31.90	58.38	50.21
Seed yield	1.61 \pm 0.92	0.12	4.68	53.24	40.15	56.88	62.37
Threshing %	0.60 \pm 0.03	0.12	2.49	50.09	43.34	74.88	77.25
Test weight	3.09 \pm 0.05	1.92	4.57	16.17	12.85	63.21	21.05

Legend: Min: Minimum range.

CV: Co-efficient of Variation (%),

GCV: Genotypic Co-efficient of Variation (%),

GAM: Genetic advance of mean (%).

Max: Maximum range.

PCV: Phenotypic Co-efficient of Variation(%),

Broad sense h^2 : Broad sense heritability(%).

design with five blocks repeated once to investigate the response of recombinant inbred lines population to powdery mildew. The mungbean RILs used were developed from a cross, Chinamung \times BL-849. All the RILs used were collected from the Department of Genetics and Plant Breeding at the University of Agricultural Sciences, Bangalore. The current F_8 RILs were developed from the cross Chinamung \times BL849, the F_1 from this cross was forwarded up to F_5 generation by selfing to attain stability in population, Further, F_6 and F_7 generations were forwarded to the present generation *i.e.*, F_8 (Divya and Savithramma *et al.*, 2018). The parents used to develop these RILs have distant characteristics. Chinamung is high yielding but highly susceptible to powdery mildew disease used as female parent, BL 849 is the low yielding yet highly resistant (HR) to powdery mildew disease with a score of zero in the scale of 1-5 used as male parent. Chinamung, BL 849, KKM 3 and Pusabaisakhi were used in each block which helped

in spreading the disease to RIL's. All the recommended package of practices were followed. Standard statistical procedure was used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952). The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and covariance.

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance revealed the presence of significant difference among the RILs for all the traits except at 50 per cent flowering and days to maturity indicating the presence of genetic variability in this population Table 1.

Genetic variability studies

The GCV and PCV were found high for cluster/plant, pods/plant, pod yield, seed yield and threshing percentage. GCV and PCV are low for 50 per cent

TABLE 3
Phenotypic correlation for yield and yield attributing traits of F₈ mungbean RIL population.

	DFE	DTM	PH	B/P	C/P	P/P	PL	S/P	PY/P	T%	TW
DFE	1.00										
DTM	0.82 ***	1.00									
PH	-0.20 *	-0.04	1.00								
B/P	-0.10	0.02	0.62 ***	1.00							
C/P	-0.14	-0.01	0.47 ***	0.57 ***	1.00						
P/P	-0.17	0.00	0.62 ***	0.43 ***	0.43 ***	1.00					
PL	-0.16	-0.06	0.10	0.19	0.22 *	0.06	1.00				
S/P	-0.03	0.06	0.23 *	0.30 **	0.30 **	0.23 *	0.67 ***	1.00			
PY/P	-0.33 ***	-0.22 *	0.22 *	0.36 ***	0.32 **	0.27 **	0.34 ***	0.41 ***	1.00		
T%	-0.20 *	-0.11	0.16	0.23 *	0.12	0.14	0.20 *	0.23 *	0.38 ***	1.00	
TW	-0.01	-0.00	0.08	0.06	0.21 *	0.16	0.05	0.13	0.35 ***	0.14	1.00
SY	-0.28	-0.19	0.18	0.30	0.29	0.24	0.30	0.36	0.94	0.05	0.32

Legend : *** Significance at P < 0.05% ** Significance at P < 1% * Significance at P < 5%
 DFE: Days to fifty per cent flowering, DTM: Days to maturity PH: Plant height (cm) C/P: Clusters per plant
 B/P: Branches per plant PL: Pod length S/Y: Seed yield per plant S/Y: Seed yield per plant
 P/P: Pods per plant, PY/P: Pod yield per plant (g) S/P: Seeds per pod T%: Threshing per cent
 TW: Test weight,

flowering and also in days to maturity. GCV and PCV observed moderate for plant height, branches/plant, and pod length, seeds/pod and test weight. Improvement in the traits with high range of GCV and PCV for through simple selection is effective. Presence of low GCV and PCV shows lesser genetic variability. So, difficult to select for breeding. The result showed high heritability for plant height, cluster/plant, pods/plant, seeds/pod, threshing percentage and test weight. Heritability at moderate level was observed in days to maturity, branches/plant, pod length, pod yield and seed yield. Heritability was noticed low in 50 per cent flowering, In case of Genetic advance *per cent* mean for 50 per cent flowering and days to maturity showed low. But moderate level of genetic advance *per cent* mean was found in branches/plant and pod length. High level of genetic advance *per cent* mean was found in plant height, clusters/plant, pods/plant, pod yield, seed yield, threshing percentage and test weight. Higher heritability indicated the presence of additive gene effects and when united with the more genetic advance it provides more priority for selection in the next generations (Table 2). The findings are in confirmation with Divya *et al.* (2018).

Correlation studies

The seed yield is most important trait among all the phenotypical traits. Seed yield in the mungbean crop can be increased by selecting constituent characters. In present study seed yield was positively correlated with all the traits such as plant height, number of branches / plant, number of cluster / plant, number of pods / plant, pod length, number of seeds / plant, pod yield / plant, threshing percentage and test weight of 100 seeds except two traits *i.e.*, 50 per cent flowering and days to maturity. The similar results reported in mungbean by Raje *et al.*, 2000; Divya *et al.*, 2018 explained significant positive correlation of seed yield with the seeds / pod and height of the plant contributed for good yield. Thus, this trait can be used in the breeding program under prevailing environmental condition for yield (Table 3).

(Received : August, 2019 Accepted : September, 2019)

REFERENCES

- BURTON, G. W. AND DE VANE, E. M., 1953, Estimating heritability in tall fescue (*Festuca circuncilnaceae*) from replicated clonal material. *Agron. J.*, **45** : 478-481.
- DATTA, S., GANGWAR, S., SHIV KUMAR, GUPTA, S., RAI, R., K AASHYAP, M., SINGH, P., CHATURVEDI, S. K., SINGH, B. B. AND NADARAJAN, N., 2012, Genetic diversity in selected Indian greengram [*Vigna radiata* (L.) Wilczek] cultivars using RAPD markers. *American J. Pl. Sci.*, **3** : 1085-1091.
- DIVYA RAMAKRISHNAN AND SAVITHRAMMA, D. L., 2018, Screening of mungbean germplasm for powdery mildew disease resistance. *Int. J. Agronomy and Agric. Res.*, **6** (4): 16-21.
- RAJE, R. S. AND RAO, S. K., 2002, Screening of mungbean (*Vigna radiata* L. Wilczek) germplasm for yellow mosaic virus, Cercospora leaf spot and powdery mildew. *Legume Res.*, **25** (2): 99-104.
- RISHI, N., 2009, Significant plant virus diseases in India and a glimpse of modern disease management technology. *J. General Pl. Pathol.*, **75** : 1-18.