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Genetic variability, heritability and character association for yield traits in F_2 and F_3 generations of mungbean [Vigna radiata (L.) Wilczek]

[1]Nikita B Biradar, [2]Nandini R
[1]*Corresponding author Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bengaluru 560 065, Karnataka, India*
[2]*Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, GKVK, Bengaluru 560 065, Karnataka, India*

***Abstract*—Genetic variability for yield and its components was studied in the F_2 (96 plants) and F_3 (96 families) generations of the mungbean cross GG-ABL-449 × GG-ABL-265 at UAS, GKVK, Bengaluru during kharif 2022 and summer 2023. Nine traits were recorded, and the F_3 was evaluated in an augmented design. The F_3 families differed significantly for all traits. Skewness lay within ±1 in both generations, consistent with polygenic control. In F_2, pods per plant and seed yield per plant showed high GCV and PCV while in F_3, , showed high values of PCV and GCV. Plant height, primary branches per plant, pods per plant, seed yield per plant and recorded high heritability (> 67%) with high genetic advance as per cent of mean (> 20%) in both generations, indicating additive gene action. Pods per plant, seeds per pod and pod length were significantly and positively correlated with seed yield in both generations. Selection focused on pods per plant, seeds per pod and pod length in early segregating generations should therefore raise seed yield in this cross.**

***Index Terms*—Mung bean, Variability, heritability, association studies, F_2, F_3**

I. INTRODUCTION

Mungbean [Vigna radiata (L.) Wilczek] is a short-duration grain legume grown widely in India, valued for its protein-rich seed and its fit in cereal-based cropping systems. Average yields remain low, largely because cultivars come from a narrow genetic base and the crop is grown on marginal, rainfed land. Raising yield potential depends on finding and using heritable variation for yield and its components.

Seed yield is a complex trait that depends on several components, each influenced by the environment. Partitioning the observed variation into genetic and environmental parts tells the breeder how much of it can be fixed by selection. The genotypic and phenotypic coefficients of variation (GCV and PCV) measure the extent of variability (Burton and De Vane 1953). Heritability and genetic advance together show how much gain can be achieved through selection (Johnson et al. 1955). Correlations between yield and its components identify traits that can serve as indirect selection criteria.

Most variability studies in mungbean have been made on germplasm or fixed varieties (Hemavathy et al. 2015; Ahmad et al. 2014). Estimates from segregating generations are more directly useful, because that is where selection is practiced, and they show how the genetic parameters change from one generation to the next (Shiv et al. 2017). The present study estimated variability, heritability, genetic advance and character association for nine yield traits in the F_2 and F_3 generations of a cross between two diverse advanced breeding lines.

II. MATERIALS AND METHODS

Plant material and field trials: The cross was made between GG-ABL-449 (DGGV-2 × IPM-2-14), a high-yielding line, and GG-ABL-265, a mutant of SM-17, in the garden of the e Department of Genetics and Plant Breeding, UAS, GKVK, Bengaluru during kharif 2022 (August to November).The 96 F_2 plants were grown with the two parents and two checks viz., China mung and LM 1668. During summer 2023 (February to May), 96 F_3 families, the parents and the checks were grown in an augmented design (Federer 1961) with 12 blocks. Each entry was sown in a single row at 30 × 10 cm spacing and thinned 10 days after sowing. The recommended package of practices was followed, with protective irrigation at critical stages.

Observations: Ten plants per entry were chosen at random and tagged. Data were recorded on days to 50% flowering, plant height (cm, ground level to the tip of the uppermost leaf), primary branches per plant, clusters per plant, pods per plant, pod length (cm, mean of ten pods), seeds per pod (mean of ten pods), seed yield per plant (g) and 100 seed weight(g).

Statistical analysis: For the F_3, analysis of variance followed the augmented design (Federer 1961). For the F_2, the phenotypic variance was the total variance among F_2 plants, and the environmental variance was the mean of the two parental variances (Weber and Moorthy 1952). Genotypic variance was the difference between the two. GCV and PCV were estimated after Burton and De Vane (1953) and classed as low (< 10%), moderate (10–20%) or high (> 20%). Broad-sense heritability was estimated as the ratio of genotypic to phenotypic variance and classed as low (< 30%), moderate (30–60%) or high (> 60%) (Robinson et al. 1949). Genetic advance as per cent of mean (GAM) was computed at 5% selection intensity (k = 2.06) and classed as low (< 10%), moderate (10–20%) or high (> 20%) (Johnson et al. 1955). Skewness was computed for each trait. Phenotypic correlation coefficients were estimated after Al-Jibouri et al. (1958) and tested at n − 2 degrees of freedom. Analyses were done in MS Excel and R version 4.6.2.

The formulae used were:

$$\text{a. Phenotypic coefficient of variaion (PCV \%)} = \frac{\sigma^2 p}{\bar{x}} \times 100$$

$$\text{b. Genotypic coefficient of variaion (GCV \%)} = \frac{\sigma^2 g}{\bar{x}} \times 100$$

$$h^2\% = \frac{\sigma 2g}{\sigma 2p} \times 100$$

Heritability in broadsense (h^2_{BS}):

Where,

h^2_{BS} = Heritability (broad sense) expressed in per cent

σ^2_g = Genotypic variance of F_2 population

σ^2_p = Phenotypic variance of F_2 population

The heritability percentage was categorized as low, moderate and high as suggested by Robinson et al. (1949) and is given below.

0-30% = Low; 30-60% = Medium; Above 60% = High

Genetic Advance (GA): This was calculated as per the formula given by Johnson et al.,(1955)
$GA=h^2\times K\times\sigma_p$
Where,
h^2= broad sense heritability,
σ_p = phenotypic standard deviation,
K= selection differential at 5% intensity selection. This is usually 2.06 (Lush, 1949).

III. RESULTS AND DISCUSSION

Analysis of variance and distribution of traits: The F_3 families differed significantly ($P \leq 0.01$) for all nine traits, and the two checks also differed for every trait (Table 1). Wide variation was present in both F_2 and F_3 generations (Table 2). Seed yield per plant ranged from 2.19 to 9.19 g in F_2 and from 7.50 to 11.30 g in F_3. Pods per plant ranged from 5 to 18 in F_2.

Skewness lay between −0.37 and +0.76 in F_2 and between −0.16 and +0.24 in F_3. All traits were therefore close to normal distribution, as expected for quantitative traits governed by many genes. In F_2, distributions were slightly positively skewed for days to 50% flowering, plant height, primary branches, clusters per plant, seeds per pod and 100 seed weight. They were slightly negatively skewed for pods per plant, pod length and seed yield per plant. Negative skew in yield traits shows that more plants fell above the mean than below it, which favors selection for higher values.

Coefficients of variation: In F_2, GCV and PCV were high for seed yield per plant (31.15% and 32.13%) and pods per plant (25.38% and 25.98%) (Table 2). They were moderate for plant height, primary branches, pod length and 100 seed weight, and low for days to 50% flowering and seeds per pod. In F_3, 100 seed weight had high GCV and PCV (24.30% and 24.31%), and the other traits were moderate.
For most traits GCV was close to PCV, so most of the observed variation was genetic. The gap was wide for clusters per plant (GCV 13.29%, PCV 26.97%), pod length and 100 seed weight in F_2, and for pod length in F_3. The environment therefore had a larger influence on these traits, and selection on single plants would be less reliable for them. High variability for pods per plant and seed yield has also been reported in mungbean by Ahmad et al. (2014) and Hemavathy et al. (2015).

GCV for seed yield and pods per plant fell sharply from F_2 to F_3 (from 31.15% to 10.78% for yield). Two factors may explain this. Variance among F_3 family means is lower than among single F_2 plants, and the two generations were grown in different seasons. The F_3 trial was grown

in summer, when plants were shorter (mean 24.0 cm against 34.3 cm in F_2) but yields per plant were higher.

Heritability and genetic advance: Heritability was high for six of the nine traits in F_2 and for all nine in F_3 (Table 2). In F_2 it was moderate for pod length (45.29%) and low for clusters per plant (24.30%) and seeds per pod (9.46%). High heritability shows that a trait is little affected by the environment, but it does not by itself predict gain from selection. Heritability was therefore read together with GAM (Johnson et al. 1955).

Plant height, primary branches per plant, pods per plant, seed yield per plant and 100 seed weight combined high heritability with high GAM in both generations. GAM was highest for seed yield per plant (62.20%) and pods per plant (51.09%) in F_2 and for 100 seed weight (50.10%) in F_3. These traits are probably controlled mainly by additive genes, and simple selection should improve them. Similar results for pods per plant, seed yield and 100 seed weight were reported by Hemavathy et al. (2015) and Yusufzai et al. (2017).
Days to 50% flowering in F_2 showed high heritability with low GAM (9.95%), and pod length in F_3 showed high heritability with moderate GAM (16.96%). Non-additive gene action may contribute in the expression of these traits, so selection for them is better delayed to later generations. Seeds per pod in F_2 had both low heritability and low GAM, but in F_3 it showed high values for both. Heritability estimates were generally higher in F_3 than in F_2. This is expected because averaging over a family reduces within-family segregation and environmental error. This was also opined by Shiv et al. (2017).

Character association: Pods per plant, seeds per pod and pod length were significantly and positively correlated with seed yield per plant in both generations (Table 3). Pods per plant had the strongest association ($r = 0.792$ in F_2 and 0.451 in F_3). Pods per plant was also positively correlated with seeds per pod (0.544 and 0.366) and with pod length (0.361 and 0.363). Selection for one of these traits should therefore improve the others as well. These associations agree with the reports of Pandey et al. (2007), Raturi et al. (2015) and Kaur et al. (2017).
Associations among other traits were stronger in F_3. Plant height (0.433), clusters per plant (0.429) and 100 seed weight (0.200) were positively correlated with seed yield. Days to 50% flowering (−0.336) and primary branches (−0.327) were negatively correlated with it. Late flowering was associated with fewer clusters, fewer pods and shorter pods. Early-flowering families thus tended to yield more under summer conditions, which favors selection for earliness in this season.

IV. CONCLUSION

The cross GG-ABL-449 × GG-ABL-265 carries enough heritable variation for yield to support selection from the F_2 onward. Pods per plant, seed yield per plant, 100 seed weight, plant height and primary branches combine high heritability with high genetic advance, and so should respond to pedigree or progeny selection. Pods per plant, seeds per pod and pod length are the most reliable indirect selection criteria for seed yield in this material. Later generations of the cross should be tested over seasons to confirm these estimates.

Table 1. Analysis of variance (mean squares) for yield traits in the F_3 generation (augmented design)

Source	df	DFF	PH	PB	CP	PP	PL	SP	SYP	SI
Blocks (Ignoring treatments)	11	20.57**	0.73**	0.73**	0.40**	5.28**	0.21	0.94**	0.85**	3.16**
Treatments (Eliminating blocks)	97	17.51**	0.29**	0.29**	0.47**	2.57**	0.52**	1.87**	1.19**	3.78**
Checks	1	92.04**	8.20**	8.20**	9.13**	23.01**	4.76**	5.90**	11.48**	0.26**
Test entries and test vs check	96	16.74**	0.20**	0.20**	0.38**	2.35**	0.48**	1.83**	1.08**	3.81**
Error	11	0.95	0.05 [	0.05	0.01	0.38	0.10	0.01	0.01	0.01

**Significant at $P \leq 0.01$. DFF = days to 50% flowering; PH = plant height; PB = primary branches per plant; CP = clusters per plant; PP = pods per plant; PL = pod length; SP = seeds per pod; SYP = seed yield per plant; SI = 100 seed weight.

Table 2. Mean, range, skewness and genetic parameters for yield traits in F_2 (96 plants) and F_3 (96 families) of GG-ABL-449 × GG-ABL-265

Trait	Gen.	Mean ± SE	Range	Skewness	GCV (%)	PCV (%)	h^2(bs) (%)	GAM (%)
Days to 50% flowering	F_2	39.83 ± 0.22	35.00–45.00	0.08	5.06	5.31	92.00	9.95
	F_3	40.30 ± 0.46	32.12–48.63	0.01	10.60	10.87	95.04	21.31
Plant height (cm)	F_2	34.32 ± 0.45	27.00–42.40	0.04	11.90	12.71	87.64	22.95
	F_3	24.00 ± 0.41	13.48–33.07	0.05	14.01	16.59	71.29	24.40
Primary branches per plant	F_2	4.80 ± 0.07	3.00–7.20	0.76	13.70	13.90	97.19	27.83
	F_3	4.36 ± 0.06	3.04–5.48	−0.16	11.02	12.18	81.79	20.56
Clusters per plant	F_2	5.13 ± 0.14	2.40–9.00	0.66	13.29	26.97	24.30	13.50
	F_3	3.74 ± 0.06	2.60–5.20	0.24	15.08	15.13	99.34	31.00
Pods per plant	F_2	12.26 ± 0.33	5.00–18.00	−0.37	25.38	25.98	95.44	51.09
	F_3	12.54 ± 0.17	8.79–16.69	0.09	12.49	13.43	86.42	23.94
Pod length (cm)	F_2	6.08 ± 0.11	4.03–8.01	−0.20	12.18	18.10	45.29	16.89
	F_3	6.77 ± 0.07	5.26–8.53	−0.15	9.22	10.35	79.43	16.96
Seeds per pod	F_2	8.32 ±	7.00–9.96	0.26	2.77	9.02	9.46	1.75

		0.08						
	F_3	9.09 ± 0.14	5.40–12.85	−0.16	15.36	15.37	99.89	31.67
Seed yield per plant (g)	F_2	5.71 ± 0.19	2.19–9.19	−0.15	31.15	32.13	93.96	62.20
	F_3	9.12 ± 0.10	7.50–11.30	−0.04	10.78	10.80	99.64	22.19
100 seed weight (g)	F_2	5.02 ± 0.10	3.20–7.80	0.22	16.54	20.05	67.99	28.09
	F_3	8.38 ± 0.20	4.50–12.65	0.06	24.30	24.31	99.92	50.10

GCV, PCV = genotypic and phenotypic coefficients of variation; h^2(bs) = broad-sense heritability; GAM = genetic advance as per cent of mean at 5% selection intensity.

Table 3. Phenotypic correlation coefficients among yield traits: F_2 below the diagonal, F_3 above the diagonal

	DFF	PH	PB	CP	PP	PL	SP	SI	SYP
DFF	1	0.332**	0.532**	−0.444**	−0.394**	−0.452**	−0.259**	−0.351**	−0.336**
PH	−0.047	1	−0.299**	0.364**	0.131	0.384**	0.195*	0.112	0.433**
PB	−0.120	0.025	1	−0.380**	−0.442**	−0.415**	−0.335**	−0.122	−0.327**
CP	0.002	−0.013	−0.056	1	0.415**	0.393**	0.319**	0.189*	0.429**
PP	0.122	0.016	0.170	−0.021	1	0.363**	0.366**	0.143	0.451**
PL	0.028	−0.003	0.083	−0.114	0.361**	1	0.347**	0.264**	0.386**
SP	0.099	−0.084	0.236*	0.133	0.544**	0.172	1	0.268**	0.446**
SI	0.147	0.117	−0.103	0.024	0.124	−0.041	0.049	1	0.200*
SYP	−0.059	−0.028	0.120	−0.032	0.792**	0.283**	0.552**	0.030	1

*, **Significant at $P \leq 0.05$ and $P \leq 0.01$. Abbreviations as in Table 1.

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