

Original Research Article

Genetic Variability and Correlation Studies in Black Gram (*Vigna mungo* [L.] hepper) with Reference to YMV Resistance

D. V. Sushmitharaj¹, D. Shoba^{2*} and M. Arumugam Pillai²

¹Agricultural College and Research Institute, Madurai, Tamil Nadu, India

²Agricultural College and Research Institute, Killikulam, Vallanad, Tuticorin, Tamil Nadu, India

*Corresponding author

ABSTRACT

The present investigation was carried out during 2016 to estimate the genetic variability parameters and genotypic correlations in thirty two advanced black gram genotypes for nine traits viz., days to 50% flowering, plant height (cm), number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, hundred seed weight (g), single plant yield (g) and incidence of yellow mosaic virus (YMV). Based on the mean performance, the genotypes viz., KKB-14-024, KKB-14-022, KKB-14-18, KKB-14-21 and KKB-14-09, KKB-14-038, KKB-14-027 and KKB-14-007 recorded higher performance for most of the traits studied. From the YMV resistance studies, twenty five genotypes showed resistant (R) reaction. A perusal of genetic parameters revealed that GCV, PCV, heritability and Genetic Advance as per cent of Mean (GAM) were high for the traits viz., number of clusters per plant, number of pods per plant, hundred seed weight and single plant yield. High heritability coupled with high GAM were observed for the traits viz., plant height, number of clusters per plant, number of pods per plant and single plant yield indicating that additive gene action is present and selection would be fruitful for these traits. From the correlation co efficient studies, seed yield per plant showed positive association with the traits viz., plant height, number of pods per plant and number of clusters per plant. Hence, simultaneous selection for the above traits would be more rewarding to bring improvement in black gram.

Keywords

Black gram,
YMV
resistance,
Genetic
Variability,
Correlation
Co-efficient

Introduction

Black gram is an important short duration legume crop belonging to the family Leguminosae, cultivated for its dry beans rich in proteins with high lysine which is deficient in cereal grains. In India, pulses have long been considered as the poor man's major source of protein. Black gram is believed to have originated in India (Chatterjee and Bhattacharya, 1986). India is the world's largest producer as well as consumer of black gram. Black gram is a highly prized pulse, rich in phosphoric acid.

It is an important grain legume with easily digestible protein and low flatulence contents. Black gram grain contains about 25% protein, 56% carbohydrate, 2% fat, 4% minerals and 0.4% vitamins.

The productivity of black gram remains low due to biotic (Mung bean yellow mosaic virus, powdery mildew and cercospora leaf spot) and abiotic stresses (drought, heat and pre harvest sprouting). Among the various diseases limiting the black gram

productivity, Mung bean Yellow Mosaic Virus (MYMV) was given special attention because of its severity and ability to cause yield loss up to 85% (Nene, 1973). Low productivity in this crop is also attributable to its narrow genetic base due to common ancestry of various superior genotypes, poor plant type and their cultivation in marginal and harsh environments. The improvement of crop yield largely depends upon the magnitude of genetic variability and the extent to which the determining characters are heritable from generation to generation.

Correlation coefficients reveal the magnitude and direction of association of yield components. Character association helps in formulating an effective breeding strategy to develop productive genotypes. Thus knowledge of genetic variability, genetic advance and correlation are very essential for breeder to choose good parents and to decide the correct breeding method for crop improvement. Keeping the above points in the view, the present study was undertaken with the following objectives of *a.* to assess the potential black gram genotypes based on mean performance; *b.* to identify the black gram genotypes for YMV resistance under a hot spot region *c.* to study the genetic variability parameters for yield and yield attributing traits; *d.* to assess the correlation among yield and component traits.

Materials and Methods

The field experiment was carried out at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam, during Rabi 2016. A total of thirty two advanced black gram breeding lines along with check variety ADT 3 were used for the present study. The experiment was laid out in a Randomized Block Design replicated twice. Each line was sown in 2

rows with spacing of 30×10 cm. For YMV screening, a separate experiment was laid out at Panpozhi (hot spot region for screening YMV), Tenkasi, during Rabi 2016. Each line was sown in 4 rows with spacing of 30×10 cm; susceptible check variety ADT 3 was used for YMV screening. On the tenth day after sowing the crop was thinned out, leaving one healthy seedling per hill. Recommended agronomic practices and need based plant protection measures were taken.

Data collected on nine characters *viz.*, days to 50% flowering, plant height(cm), number of clusters per plant, number of pods per plant, pod length(cm), number of seeds per pod, 100 seed weight(g), seed yield per plant(g), and incidence of yellow mosaic virus. From each replication five random plants were tagged for observing yield and other quantitative characters. The YMV disease was scored on 1-9 arbitrary scale according to Alice and Nadarajan (2007). The description of the scorings are, 1.No visible symptoms on leaves or very minute yellow specks on leaves; 2. Small yellow specks with restrict spread covering 0.1 -5 % leaf area; 3.Yellow mottling of leaves covering 5.1-10% leaf area; 4.Yellow mottling of leaves covering leaf area 10.1-15%; 5.Yellow mottling and discoloration of 15.1-30% leaf area; 6.Yellow discoloration of 30.1 to 50% leaf area; 7. Pronounced yellow mottling and discoloration of Leaves and pod, reduction in leaf size and stunting of plants covering 50.1 to 75 % foliage; 8.Severe yellow discoloration of leaves covering 75.1 to foliage, stunting of plants and reduction in pod size and 9. Severe yellow discoloration of entries covering above 90.1 of foliage, stunting of plants and no pod formation. The YMV disease reaction ratings are, 0.1 to 2.0: Resistant (R); 2.1 to 4: Moderately resistant (MR); 4.1 to 5: Moderately Susceptible (MS); 5.1 to 7:

Susceptible (S) and 7.1 to 9: Highly susceptible (HS).

The mean value of the five plants was computed and taken for analysis for quantitative characters. The various genetic parameters *viz.*, GCV, PCV, heritability and GAM were calculated by adopting the formulae given by Johnson *et al.*, (1955). The association between yield and other yield attributes would be useful for selecting the better genotypes. Genotypic correlation co-efficient was calculated by using the formulae given by (Al-Jibouri *et al.*, 1958).

Results and Discussion

The mean performance of thirty two advanced black gram lines and check variety ADT 3 are presented in Table 1. Early flowering was observed in the genotypes *viz.*, KKB-14-038, KKB-14-024 and KKB-14-027. For the trait plant height, the genotype KKB-14-007 recorded higher plant height (39.0cm). For the trait, number of pods per plant twenty four genotypes had exceeded the check value. A total of eight genotypes had longer pods as compared to check variety. Twelve genotypes recorded more number of seeds per pod than the check variety. A total of sixteen genotypes registered more hundred seed weight than the check variety. For the trait single plant yield, the advanced genotype KKB-14-024 recorded more yield followed by the genotypes *viz.*, KKB-14-022, KKB-14-18, KKB-14-21 and KKB-14-09.

Evaluation of black gram genotypes for disease resistance is a crucial step in controlling plant diseases through host plant resistance. Yellow mosaic disease caused by yellow mosaic virus (YMV) in black gram is the most destructive viral disease affecting yield potential of black gram both qualitatively and quantitatively. Genes

conferring resistance can be to a certain extent identified through routine screening procedures. In the present investigation, a total of twenty five genotypes showed resistant (R) reaction with a rating of 1.0 to 2.0 *viz.*, KKB-14-019, KKB-14-017, KKB-14-032, KKB-14-015, KKB-14-005, KKB-14-033, KKB-14-012, KKB-14-034, KKB-14-035, KKB-14-016, KKB-14-038, KKB-14-010, KKB-14-022, KKB-14-007, KKB-14-006, KKB-14-018, KKB-14-009, KKB-14-014, KKB-14-011, KKB-14-001, KKB-14-002, KKB-14-037, KKB-14-038, KKB-14-029 and KKB-14-027. The susceptible check ADT 3 showed susceptible reaction with a rating scale of 5.1 to 7.0. Identification of resistant lines is essential in the ambit of integrated disease management which is an upcoming concept in the field of agriculture. Earlier studies indicated that identification of resistant sources to YMV is reliable option for controlling the viral disease. All resistance genotypes observed in the present study along with high yield can be utilized in resistance breeding programme in black gram. Similar type of genotypic evaluations were also previously documented by several workers *viz.*, Ganapathy *et al.*, 2003; Peerajade *et al.*, 2004; Pathak and Jhamaria. 2004 and Rajnish Kumar *et al.*, (2006).

The success of any breeding programme depends upon the extent of genetic variability in base population and it is essential to subject a population for selection to achieve improvement in a particular trait. The estimates of genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), heritability (h^2), and genetic advance over mean (GAM) for different characters are presented in Table 2. The highest estimate variation was registered for single plant yield (GCV: 41.14 % and PCV: 42.37%); for number of pods per plant (GCV: 30.47% and PCV: 31.12%); for

number of clusters per plant (GCV: 28.90% and PCV: 30.60). Moderate PCV and GCV values were observed in the present study for the traits *viz.*, plant height, number of pods per plant and seed yield per plant and the results were in accordance with earlier reports for the traits *viz.*, number of pods per plant (Ramesh Babu, 1998); seed yield per plant (Konda *et al.*, 2009); plant height (Acharya *et al.*, 1993) and number of clusters per plant (Patel and Shah, 1982). However, high GCV for the above traits were obtained by Rameshwari *et al.*, 2011.

In general heritability estimates were observed to be high for all the characters under the study except pod length and number of seeds per pod. Highest heritability was recorded for the trait days to 50 per cent flowering (97.6%) followed by the traits *viz.*, number of pods per plant days (95.9%), single plant yield (94.3) plant height (89.9%) and number of clusters per plant (89.2%). High GAM was registered for the trait single plant yield (82.30%) followed by the traits *viz.*, number of pods per plant (61.46 %), number of clusters per plant (56.21 %) and plant height (33.83 %). Therefore for improving these traits simple selection would be more effective in early generation on the basis of mean performance. In the present investigation, high heritability coupled with high GAM were recorded for the traits *viz.*, number of pods per plant, number of clusters per plant, plant height, hundred seed weight and single plant yield indicated that additive gene action is involved in the genetic control of these traits. This is in agreement with the findings of Veeramani *et al.*, (2005) and Reddy *et al.*, (2011).

The genotypic correlation coefficients between different characters studied are presented in Table 3. From the correlation studies, seed yield per plant had significant

and positive association with plant height (0.41*), number of pods per plant (0.39*) and number of clusters per plant (0.35*). Hence, these traits would be utilized in direct selection so as to improve the seed yield per plant. Similar kind positive association of number of clusters per plant and number of pods per plant with seed yield was reported earlier by Venkatesan *et al.*, (2004), Umadevi and Ganesan (2005), Chauhan *et al.*, (2007) and Reddy *et al.*, (2011). From the inter correlation studies, days to 50% flowering showed positive and significant association with plant height, number of clusters per plant and number of pods per plant. The trait plant height recorded positive and significant association with number of clusters per plant and number of pods per plant. The trait number of clusters per plant had shown positive and significant association with number of pods per plant.

There is a need to develop YMV resistant black gram varieties in order to increase the production and productivity levels. From the results of present investigation, it is inferred that the advanced black gram lines *viz.*, KKB-14-024, KKB-14-022, KKB-14-18, KKB-14-21 and KKB-14-09, KKB-14-038, KKB-14-027 and KKB-14-007 recorded higher performance for most of the traits studied. From the YMV resistance studies, twenty five genotypes showed resistant (R) reaction. Hence, the above promising lines may be selected for YMV resistance breeding in black gram. High heritability coupled with high GAM were observed for the traits *viz.*, plant height, number of clusters per plant, number of pods per plant and single plant yield indicating that additive gene action is present and selection would be fruitful for these traits. From the correlation co efficient studies, seed yield per plant showed positive association with the traits *viz.*, plant height, number of pods

per plant and number of clusters per plant.
Hence, simultaneous selection for the above

traits will be more rewarding to bring
improvement in black gram.

Table.1 Mean performance of advanced lines in black gram

Sl. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of clusters per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	Hundred seed weight (g)	Single plant yield(g)
1	KKB-14-001	35*	18.0	12*	28*	3.7	6	3.2	3.70*
2	KKB-14-002	41	25.2	19*	47*	3.7	6	3.6	3.87*
3	KKB-14-003	33*	24.7	10	33*	3.8	6	2.8	3.20*
4	KKB-14-004	33*	20.7	10	22	4.9	6	4.0	2.97*
5	KKB-14-005	36	23.6	8	24	4.5	6	3.9	2.42
6	KKB-14-006	31*	25.4	14*	42*	4.2	7	3.9	5.38*
7	KKB-14-007	36	39.0*	15*	42*	4.5	6	4.0	6.09*
8	KKB-14-008	35*	21.9	14*	26*	4.4	6	4.2	3.86*
9	KKB-14-009	36	31.5*	17*	46*	4.7	7	4.7*	8.03*
10	KKB-14-010	35*	20.6	13*	26*	3.8	7	3.4	3.77*
11	KKB-14-011	35*	30.1*	9	23	3.9	6	3.5	4.42*
12	KKB-14-012	42	36.7*	16*	42*	4.1	7	3.8	5.92*
13	KKB-14-13	38	27.4*	12*	35*	4.0	6	3.2	5.31*
14	KKB-14-014	35*	28.6*	14*	36*	4.5	7	4.0	4.44*
15	KKB-14-015	35*	30.4*	12*	31*	3.9	5	4.5	5.04*
16	KKB-14-016	34*	20.7	8	22	3.6	6	3.3	3.23*
17	KKB-14-017	32*	25.2	12*	28*	3.7	6	3.8	3.16*
18	KKB-14-018	37	31.5*	13*	36*	4.2	7	3.6	8.17*
19	KKB-14-019	35*	28.0*	15*	39*	4.2	7	4.3	6.17*
20	KKB-14-020	35*	26.4*	9	20	3.6	6	3.8	3.68*
21	KKB-14-021	35*	26.2*	14*	31*	3.5	5	3.4	8.13*
22	KKB-14-022	35*	27.7*	12*	39*	3.8	6	3.1	8.80*
23	KKB-14-024	29*	29.2*	8	17	4.3	7	4.7*	9.32*
24	KKB-14-027	29*	22.1	7	15	4.7	7	3.4	2.02
25	KKB-14-029	30*	26.0	7	16	4.6	7	3.9	3.72*
26	KKB-14-032	42	30.5*	13*	36*	4.9	6	3.8	4.25*
27	KKB-14-033	35*	28.4*	9	26*	4.7	7	3.4	1.85
28	KKB-14-034	35*	25.1	15*	35*	3.9	6	3.5	5.44*
29	KKB-14-035	35*	37.0*	17*	40*	4.0	6	3.5	3.37*
30	KKB-14-036	30*	25.9	6	18	5.1	6	6.0*	5.67*
31	KKB-14-037	31*	23.7	8	23	4.2	6	3.3	4.13*
32	KKB-14-038	29*	27.9*	8	20	4.6	7	4.3	2.84*
ADT 3(C).		35	22.84	9	22	4.5	6	3.7	1.64
SEd		0.51	1.57	1.15	1.89	0.53	0.92	0.46	0.48
CD (5%)		1.03	3.20	2.35	3.86	1.08	1.89	0.93	0.98

Table.2 Magnitude of genetic variance for yield components in black gram

Traits	GCV	PCV	Heritability (%)	GAM
Days to 50% flowering	9.45	9.57	97.6	19.24
Plant height	17.32	18.27	89.9	33.83
No. of clusters per plant	28.90	30.60	89.2	56.21
No. of pods per plant	30.47	31.12	95.9	61.46
Pod length	5.51	13.76	16.0	4.54
No. of seeds per pod	5.99	14.06	-18.1	-5.25
Hundred seed weight	13.39	18.05	55.0	20.46
Single plant yield	41.14	42.37	94.3	82.30

Table.3 Genotypic correlation coefficients among yield components in black gram

Traits	Days to 50% flowering	Plant height	No. of clusters per plant	No. of pods per plant	Pod length	No. of seeds per pod	Hundred seed weight	Single plant yield
Days to 50% flowering	1.00	0.35*	0.70*	0.69*	-0.36*	-0.23	-0.33*	0.12
Plant height		1.00	0.42*	0.52*	0.16	0.18	0.19	0.41*
No. of clusters per plant			1.00	0.94*	-0.56*	-0.04	-0.13	0.35*
No. of pods per plant				1.00	-0.30*	0.19	-0.18	0.39*
Pod length					1.00	-0.38*	1.10	-0.26
No. of seeds per pod						-1.00	0.11	0.00
Hundred seed weight							1.00	0.24
Single plant yield								1.00

* Significant at 5% level

References

- Acharya, R., Gupta, S.K and Jamwal, B.S. 1993. Evaluation of local germplasm of urd bean from Jammu. *Indian Journal of Pulses Research*.12 (2): 72-74.
- Alice D, Nadarajan N 2007. Screening techniques and assessment methods for disease resistance, Department of Pulses, TNAU.
- AL-Jibouri, H.A., Miller, P.A and Robinson, H.F. 1958. Genotypic and environmental variances in upland cotton crosses of inter specific origin. *Agron. J.*, 50: 633-636.
- Chatterjee, B.N. and Bhattacharya, K.K 1986. Principles and Practices of Grain Legumes Production, Oxford and IBH publication company, NewDelhi, p. 434.
- Chauhan, M.P., Mishra, A.C. and Singh, A.K. 2007. Correlation and path analysis in urd bean. *Legumes Res.*, 30(3): 205-208.
- Ganapathy, T., Kuruppiah, R and Gunasekaran, K. 2003. Identifying the source of resistance for mungbean yellow mosaic virus (MYMV), urd bean leaf curl virus disease in urd bean (*Vigna mungo* (L.) Hepper). In: *Annual Meeting and Symposium on recent Developments in the diagnosis and Management of Plant Diseases for Meeting Global Challenges*. December 18-20, 2003, University of Agricultural Sciences, Dharwad, p. 30.
- Johnson, H.W., Robinson H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in Soyabean. *Agron. J.*, 47(3): 14-18.
- Konda, C.R., Salimath, P.H. and Mishra, M.N. 2009. Genetic variability studies for productivity and its components in blackgram (*Vigna mungo* (L.) Hepper) *Legume Res.*, 32(1):59-61.
- Nene, Y.L. 1973. Viral diseases of some warm weather pulse crops in India. *Plant Disease Reporter*. 57: 463-467.
- Patel, S.T and Shah, R.M. 1982. Genetic parameters association and path analysis in black gram (*Vigna mungo* L. Hepper). *Madras Agricultural Journal*. 69 (8): 535-538.
- Pathak, A.K and Jhamaria, S.L. 2004. Evaluation of mungbean (*Vigna radiate* L.) varieties to yellow mosaic virus. *Journal of Mycology Plant Pathology* 34(1): 64-65.
- Peerajade, D.A., Ravikumar, R.L and Rao, M.S.L. 2004. Screening of local mung bean collections for powdery mildew and yellow mosaic virus resistance. *Indian Journal Pulses Research*. 17 (2): 190-191.
- Rajnish Kumar., Shamshad Ali and Rizvi, S.M.A. 2006. Screening of mung bean genotypes for resistance for resistance against whitefly, *Bemisia tabaci* and mung bean yellow mosaic virus. *Indian Journal Pulses Research*. 19(1): 135-136.
- Ramesh Babu. 1998. Studies on genetic divergence by D2 statistic and Metroglyph analysis in black gram (*Vigna mungo* L. Hepper). *M.Sc. (Ag.)Thesis*.
- Rameshwari N.N, C.R., Pandey, R.L and Nanda, H.C. 2011. Estimate the genetic parameters, heritability and genetic advance for seed yield and its components in urdbean (*Vigna mungo* L. Hepper). *Agricultural and Biological Research*. 27 (2): 127-131.
- Reddy, R., Kodanda, D., Venkateswaralu, O., Jyothi, G., Siva, L. and Obaiiah, M. C. 2011. Genetic parametes and intra relationship analysis in black gram (*Vinga munga* (L.) Hepper). *Legume res.*, 34 (2):149.
- Umadevi, M and Ganesan, N.M. 2005. Correlation and path analysis for

- yield and yield components in black gram (*Vigna mungo* L. Hepper). Madras Agricultural Journal, 92 (10-12): 731-734.
- Veeramani, N., M. Venkatesan, P. Thangavel and J. Ganesan. 2005. Genetic variability, heritability and genetic advance analysis in segregating generation of black gram (*Vigna munga* (L.) Hepper). Legume Res., 28(1):49-51.
- Venkatesan, M., Veeramani, N., Anbuselvam, Y and Ganesan, J. 2004. Correlation and path analysis in black gram (*Vigna mungo* L. Hepper). Legume Res., 27 (3): 197-200.