Annals of Phytomedicine 15(1): 835-845, 2026

DOI: http://dx.doi.org/10.54085/ap.2026.15.1.75

Annals of Phytomedicine: An International Journal

http://www.ukaazpublications.com/publications/index.php

Print ISSN : 2278-9839 Online ISSN : 2393-9885

Original Article : Open Access

Genetic analysis for yield components and phytochemicals in recombinant inbred lines of black gram (*Vigna mungo* (L.) Hepper)

R. Latha and S. Ganapathy*◆

Agricultural Research Station, Thirupathisaram-629901, Kanyakumari District, Tamil Nadu, India

** Oilseeds Research Station, Tindivanam-604002, Villupuram District, Tamil Nadu, India*

Article Info

Article history

Received 13 March 2026

Revised 20 April 2026

Accepted 21 April 2026

Published Online 30 June 2026

Keywords

(*Vigna mungo* (L.) Hepper)

Black gram

YMV

Phenols

Tannins

Genetic analysis

Abstract

Black gram is one of the major pulses grown in India and is the world's largest producer and consumer. Low productivity in black gram is due to susceptibility to various biotic and abiotic stresses, lack of genetic variability, poor harvest index and the absence of suitable ideotypes for various cropping systems. A fundamental requirement for crop improvement in desired direction through breeding is genetic variability. Phytochemicals, *viz*., phenols and tannins play important role in free radical scavenging and resistance against pest and diseases. Hence, the present study was carried out with the objectives of analysing the genetic parameters, *viz*., GCV, PCV, genetic advance and heritability for yield and yield attributes and phytochemicals associated with resistance to MYMV. A total of 72 recombinant inbred lines were developed from the cross ADT 3xKKB 15052 through single seed descent method. Genetic analysis for yield attributes and phytochemicals were studied in the RILs. The traits single plant yield, number of pods per plant, number of clusters per plant, and number of primary branches, have high PCV and GCV which results in efficient crop improvement by direct selection of these traits. All the yield and yield contributing traits showed high heritability of more than 90%. High genetic advance was recorded in single plant yield (64.27%), number of clusters per plant (61.35%), number of pods per plant (56.61%), number of primary branches per plant (56.22%), pod length (33.20), and days to 50% flowering (29.10%). These results indicated the possibility of improvement of these yield attributes through selection. The RIL 14 has high total phenol and tannin content of 208 mg 100 g^{-1} and 965 mg 100 g^{-1}, respectively. However, the total phenol and tannin content of VBN8 is 190 mg 100 g^{-1} and 845 mg 100 g^{-1}, respectively. The RILs 42 and 43 with single plant yield of 11.88 g and 11.96, respectively, with moderate resistance to yellow mosaic virus can be developed into new varieties. The RIL s with YMV resistance and moderate yield potential can be used as donors in resistance breeding programme.

1. Introduction

Pulses are important food crops rich in protein and essential nutrients. The most important pulses are black gram (*Vigna mungo* (L.) Hepper), green gram (*Vigna radiate* (L.)), chickpea (*Cicer arietinum* (L.)), cowpea (*Vigna unguiculata* (L.) Walp), and pigeon pea (*Cajanus cajan* (L.) Mill.). In India, pulses are cultivated over an area of 130.76 lakh ha with a production of 80.46 lakh tonnes in 2019-20 (DPD, 2020). Black gram is one of the major pulses grown in India and is the world's largest producer and consumer, followed by neighbouring nations such as Myanmar and Pakistan. About 19% of India's entire pulse acreage and 23% of its total pulse production is monopolized by black gram. Tamil Nadu had 4.02 lakh ha under black gram cultivation, producing 2.25 lakh tonnes with a productivity of 560 kg/ha in 2020-21 (Season and crop report, 2020). Low productivity in black gram is due to susceptibility to various biotic and abiotic stresses, lack of genetic variability, poor harvest index, and the absence of suitable ideotypes for various cropping systems. One of the most important objectives for breeders in case of black gram improvement is to develop high yielding variety with resistance to both biotic and abiotic stresses.

A fundamental requirement for crop improvement in desired directions through breeding is genetic variability. A wide range of genetic variability for the traits to be selected in a population is essential for selection of desirable genotypes. The phenotypic variability is due to genotypic variability and environmental effect. Though the genotypic variability is heritable, the environmental effects influence the yield characteristics. This was evident as the PCV is higher than the GCV. Heritability is another parameter need to be considered during selection. The term "genetic advance" describes an increase in the mean genotypic value of the selected family over the base population. Hence, heritability and genetic advance need to be considered while breeding for improvement of traits. In the present study the variability, GCV, PCV, genetic advance and heritability for yield and yield attributes were studied in 72 recombinant inbred lines (RILs) developed through single seed decent method. The phytochemicals, *viz*., phenols and tannins play a key role in disease resistance. In the present research, the influence of phenol and tannins on YMV resistance in black gram was studied. In addition to disease resistance, phenols enhance free radical scavenging activity. Tannins are polyphenolic metabolites, which are often categorised as anti-nutritional factors due to protein indigestibility and poisoning effects

Corresponding author: Dr. R. Latha

Associate Professor (PBG),Agricultural Research Station, Thirupathisaram-629 901, Kanyakumari District, Tamil Nadu, India

E-mail: latharamaiah@tnau.ac.in

Tel.: +91-9025980619

when present in higher concentration. Presence of tannins in moderate concentrations accounts to disease resistance and does not cause much anti nutritional effect making the crop safe for consumption.

2. Materials and Methods

The experimental materials for this study consisted of 72 RILs derived from the cross ADT3 x KKB 15 052 through Single seed decent method. ADT3 was a high yielding black gram variety susceptible to Mung bean yellow mosaic virus (MYMV), whereas KKB15 052 was a MYMV resistant culture. The study was carried out during kharif 2022 at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam, to investigate the genetics of yield and yield attributes. The details of parental genotypes used in the study are presented in Table 1. The RILs were raised in RBD with two replications. All the agronomic practices were carried out to raise healthy crop without spraying pesticides so as to screen the RILs for resistance to MYMV.

Table 1: Details of parental genotypes

Genotypes	Pedigree	Source	Key features
ADT3 (Female)	Pureline selection from Thirunelveli local	TRRI, Aduthurai, Tamil Nadu	(i) Moderately resistant to Yellow Mosaic Virus, powdery mildew, pod borer (ii) Rice fallow pulses
KKB15052 (Male)	PU 0620 x 2-107	Agricultural College and Research Institute, Killikulam	(i) Resistant to Yellow Mosaic Virus (ii) Resistant to powdery mildew and borers

2.1 Screening for resistance to MYMV

The RILs were raised along with MYMV susceptible variety CO_5 as infector row. After every five plots of RILs, one plot of CO_5 was planted as infector row. The RILs along with the susceptible check CO_5 and resistant check VBN8 were screened for MYMV incidence in the field condition. The disease incidence was estimated by using the following formula:

$$\text{Per cent disease incidence} = \frac{\text{Number of infected plants in the plot}}{\text{Total number of plants in the plot}} \times 100$$

The formula given by Wheeler (1969) was used for calculating per cent disease index:

Per cent disease index

$$= \frac{\text{Sum of all numerial ratings}}{\text{Number of observations} \times \text{Maximum disease rating}} \times 100$$

The severity of the disease was categorized according to Gantait and Das (2009) (Table 2).

Table 2: Categorization of black gram for YMV resistance

Per cent disease incidence	Rating	Reaction
0.1-5	1.0-2.0	Resistant (R)
5.1-15	2.1-4	Moderately resistant (MR)
15.1-30	4.1-5	Moderately susceptible (MS)
30.1-75	5.1-7	Susceptible (S)
75.1-100	7.1-9	Highly susceptible (HS)

2.2 Observation on biometrical traits

2.2.1 Days to 50 per cent flowering

The time taken from the day of sowing to the day of blooming in 50 per cent of plants was recorded.

2.2.2 Plant height

Plant height was measured from ground level to the tip of main stem of the plant at the time of harvest and expressed in centimetre.

2.2.3 Number of primary branches per plant

The number of branches arising from main stem was recorded at the time of harvest.

2.2.4 Number of clusters per plant

The total number of clusters with pods was recorded at the time of harvest.

2.2.5 Number of pods per plant

The total number of healthy and productive pods was recorded at the time of harvest.

2.2.6 Number of seeds per pod

The average number of seeds per pod from five random plants was recorded at the time of harvest.

2.2.7 Hundred seed weight (g)

The mean weight of hundred seed from five random plants was measured and was expressed in gram.

2.2.8 Pod length

The average length of five pods from a single plant was recorded and expressed in centimetre.

2.2.9 Single plant yield (g)

The mean weight of seeds obtained from five random plants was recorded and expressed in gram.

2.3 Statistical analysis

The analysis of variance was carried out according to Panse and Sukhatme (1957) to estimate mean, variance and standard deviation.

2.3.1 Estimation of genetic parameters

Based on the mean and variance the phenotypic and genotypic coefficients of variance was calculated (Burton, 1952).

Phenotypic coefficients of variance = $\frac{\sigma p}{\text{Mean}} \times 100$

Genotypic coefficients of variance = $\frac{\sigma g}{\text{Mean}} \times 100$

2.3.2 Genetic advance and Heritability

2.3.2.1 Heritability

Broad sense heritability was estimated according to Lush (1940).

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

where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

Heritability was categorized as suggested by Sivasubramanian and Madhavamenon (1973).

Low heritability = < 30 %

Moderate heritability =30-60 %

High heritability = > 60 %

2.3.2.2 Genetic advance

Genetic advance was calculated according to Johnson and Bernard (1962).

Genetic advance = $\frac{\sigma^2 g}{\sigma_p^2}$

where,

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

k = selection differential (2.06)

2.3.2.3 Genetic advance as per centage of mean (GAM)

Genetic advance as percentage of mean = $\frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$

GAM was categorized according to Robinson *et al.* (1949).

Low = <10 %

Medium = 10-20 %

High = >20 %

2.4 Biochemical analysis

2.4.1 Estimation of tannins

The tannin content present in the RILs were estimated by Folin-Denis method. Powdered leaf sample of 0.5 g was collected in a 250 ml conical flask containing 75 ml of water. The mixture was then boiled for 30 min and centrifuged for 20 min. The supernatant was collected in a volumetric flask and the volume was made up to 100 ml. Leaf extract of 0.2 ml was taken in a test tube and 0.5 ml of Folin - Denis reagent, 1 ml of sodium carbonate solution were added and the volume was made up to 10 ml with distilled water. The reaction mixture was kept aside for 30 min and the absorbance was measured at 700 nm.

2.4.2 Phenol estimation

The phenol content was estimated by Folin-Ciocalteau method. Fresh leaf sample of one gram was macerated in 5 ml of 80 per cent ethanol and centrifuged. The supernatant was collected, diluted to 25 ml and kept in water bath for 5 min. 6.5 ml of distilled water, 0.5 ml of Folin-Ciocalteau reagentand 2 ml of Sodium carbonate (20%) were added to 1 ml of leaf extract. After 30 min, the absorbance was measured at 660 nm.

Table 3: Categorization of black gram RILs based on disease reaction

Grade	RILs/ Parents/ Check	Rating	Reaction	Number of RILs
0	-	1 to 2	Resistant	7
1	14, 66, 67,			
2	1, 2, 39, 55			
3	4, 6, 10, 11, 13, 22, 35, 37, 46, 49, 51, 64, 65	2.1 to 4	Moderately resistant	22
4	15, 16,19, 24, 31, 32, 42, 43, 58, 69			
5	3, 5, 7, 17, 18, 33, 36, 38, 40, 41, 44, 47, 48, 50, 52, 59, 63, 68, 72	4.1 to 5	Moderately susceptible	19
6	8, 9, 12, 19, 20, 21, 23, 25, 26, 28, 29, 30, 34, 45, 53, 56, 57, 60, 61, 70	5.1 to 7	Susceptible	24
7	27, 54, 62, 71			
8	-	7.1 to 9	Highly susceptible	-
9	-			

3. Results

3.1 Resistance to MYMV in RILs

The resistance of RILs against MYMV as per cent disease incidence and resistance score are presented in Table 3. The RILs 1, 2, 14, 39, 55, 66 and 67 were observed with per cent disease incidence of less than 5.00 and categorized as resistant to MYMV. Similarly, the RILs 4, 6, 10, 11, 13, 15, 16, 19, 22, 24, 31, 32, 35, 37, 42, 43, 46, 49, 51, 58, 64, 65 and 69 with per cent disease incidence of 5.00 to 10.00, were categorized as moderately resistant to MYMV. The RILs 3, 5, 7, 17, 18, 33, 36, 38, 40, 41, 44, 47, 48,50, 52, 59, 63, 68, 72 recorded per cent disease incidence of more than 10.00 and were categorized as moderately susceptible to MYMV. The RILs 8, 9, 12, 20, 21, 23, 25, 26, 27, 28, 29, 30, 34, 45, 54, 56, 57, 60, 61, 62, 70 and 71 were categorized as susceptible to MYMV. The susceptible parent (ADT 3) and susceptible check (CO 5) had recorded per cent disease incidence of 72.33 and 58.17, respectively, whereas the resistant parent (KKB 15052) and resistant check (VBN 8) had recorded per cent disease incidence of 2.31 and 4.87, respectively.

3.2 *Per se* performance

The *per se* performance for yield parameters was analysed for 72 RILs along with parents and checks and are presented in Table 4. The *per se* performance ranged from 20 to 47 days for the trait days to 50 per cent flowering with the mean value of 34.31. For plant height, the *per se* performance ranged from 21.34 cm to 53.56 cm with the mean value of 36.84 cm. For the trait number of primary branches per plant, it ranged from 1 to 5 with the mean value of 3.16. For the trait number of clusters per plant, it ranged from 5 to 33 with the mean value of 15.36. For the trait number of pods per plant, it ranged from 10 to 72 with the mean value of 54.22. For the trait number of seeds per pod, the *per se* performance ranged from 3 to 8 with the mean value of 5.73. The *per se* performance ranged from 2.68 g to 5.69 g for the trait hundred seed weight with mean value of 4.19 g. The *per se* performance ranged from 2.79 cm to 6.12 cm for the trait pod length with the mean performance of 4.50. The *per se* performance ranged from 2.89 g to 19.12 g for the single plant yield with the mean value of 6.39.

Table 4: ***Per se*** **performance for yield and yield attributes**

RILs	DFF	PH	NPBPP	NCPP	NPPP	NSPP	HSW	PL	SPY
1	39.00	32.32	3	16	59	5	4.31	4.46	4.36
2	38.00	29.70	3	5	30	4	3.84	3.56	3.87
3	37.00	27.27	3	8	26	5	3.39	4.43	3.46
4	38.00	34.77	3	7	31	5	3.32	4.49	3.39
5	37.00	40.40	3	16	65	7	4.36	5.08	4.61
6	44.00	35.23	3	17	60	6	3.95	4.92	4.11
7	44.00	39.73	5	18	63	6	4.40	4.07	5.17
8	44.00	46.53	2	14	71	6	4.78	4.98	6.19
9	47.00	42.42	5	16	67	6	4.57	4.93	4.67
10	42.00	41.72	5	19	67	7	4.88	5.10	5.25
11	43.00	43.36	3	16	64	6	4.30	4.46	6.63
12	46.00	47.47	3	19	66	6	4.95	5.05	5.44
13	45.00	38.61	3	13	51	4	4.17	4.46	4.54
14	44.00	40.40	3	15	58	4	4.62	4.75	5.95
15	41.00	41.72	3	13	38	4	4.08	4.57	4.27
16	36.00	38.38	3	13	40	3	4.05	4.55	4.16
17	34.00	37.25	3	14	33	3	4.23	4.03	4.42
18	33.00	38.74	3	12	36	2	3.36	3.97	3.82
19	33.00	41.58	2	16	55	5	4.63	4.95	5.61
20	38.00	44.44	2	18	55	6	4.27	5.05	5.03
21	37.00	38.74	3	16	49	5	4.20	5.17	4.64
22	35.00	51.83	2	16	50	5	4.52	4.98	4.64
23	36.00	38.38	3	15	60	6	4.84	4.55	5.03
24	36.00	34.65	2	17	54	5	4.17	4.46	4.63

25	38.00	35.35	2	23	69	6	3.94	4.55	4.17
26	21.00	26.82	2	9	29	5	3.31	4.47	3.65
27	33.00	29.29	3	12	48	8	3.32	5.56	3.60
28	32.00	37.25	3	20	66	5	4.26	5.03	4.59
29	33.00	42.28	5	18	64	5	4.73	4.97	4.78
30	33.00	21.85	3	20	61	4	4.58	4.46	4.62
31	34.00	23.76	5	12	36	6	4.13	4.04	4.38
32	34.00	35.35	5	9	29	5	3.39	3.68	3.85
33	35.00	29.80	5	15	47	5	3.78	3.99	3.94
34	35.00	40.40	5	23	92	6	4.65	4.04	18.94
35	33.00	34.65	4	19	79	4	4.39	3.47	15.82
36	39.00	30.30	4	24	72	7	4.70	5.05	14.58
37	35.00	39.73	3	32	82	6	4.50	4.97	15.57
38	40.00	37.37	5	20	94	7	5.03	5.56	17.26
39	37.00	34.65	5	25	10	7	2.70	6.04	2.91
40	31.00	37.37	2	21	65	7	3.35	4.97	3.55
41	30.00	41.72	2	23	71	6	4.52	4.95	9.56
42	30.00	32.32	3	27	77	7	4.36	5.56	11.88
43	28.00	30.20	3	14	73	6	4.64	5.96	11.96
44	29.00	46.69	3	17	66	6	4.35	3.99	6.91
45	30.00	30.69	3	25	58	6	4.74	3.96	6.71
46	34.00	44.44	5	19	64	6	4.73	4.07	7.22
47	34.00	24.83	4	12	76	6	4.38	4.92	10.71
48	32.00	49.83	3	16	53	6	4.20	4.98	5.99
49	31.00	40.40	3	23	94	7	4.88	5.08	11.29
50	25.00	41.58	3	9	65	5	3.97	3.93	5.99
51	29.00	48.48	3	19	69	7	4.40	5.08	7.32
52	29.00	44.70	3	18	77	6	5.08	4.98	9.73
53	27.00	47.47	4	12	46	6	5.16	4.44	5.46
54	31.00	34.23	3	11	49	6	5.59	5.10	5.91
55	30.00	37.75	5	16	71	6	4.73	5.94	8.87
56	30.00	46.53	2	18	80	6	4.71	4.95	8.92
57	32.00	29.48	1	17	88	7	4.19	5.39	7.78
58	37.00	31.47	2	9	37	3	3.50	2.95	3.64
59	32.00	26.91	3	10	39	3	3.64	3.49	4.11
60	35.00	30.50	3	11	44	4	3.84	3.05	4.41
61	29.00	32.45	3	6	26	2	3.91	4.92	4.81
62	28.00	34.57	4	9	34	5	3.51	4.07	3.71
63	32.00	25.91	2	8	28	3	3.75	3.89	4.01

64	31.00	29.60	2	7	21	2	3.44	4.93	4.59
65	34.00	36.72	2	6	15	4	3.99	3.57	5.08
66	30.00	36.63	3	8	27	3	3.64	3.27	4.93
67	37.00	38.61	4	11	37	4	3.72	3.86	5.40
68	34.00	43.72	4	12	33	5	3.63	4.17	4.29
69	31.00	31.47	4	14	39	3	3.43	3.15	4.23
70	35.00	33.89	2	10	32	2	3.47	2.99	3.59
71	37.00	33.55	2	10	16	4	3.65	3.05	3.78
72	32.00	34.42	3	8	36	4	4.22	2.95	4.60
VBN 8	38.00	35.58	3	15	83	6	4.88	5.08	13.64
ADT 3	36.00	36.88	3	11	60	4	4.65	4.68	11.85
MEAN	**34.31**	**36.83**	**3.1625**	**15.62**	**54.22**	**5.73**	**4.19**	**4.50**	**6.39**
SE	**0.65**	**0.56**	**0.0568**	**0.27**	**1.03**	**0.10**	**0.07**	**0.08**	**0.11**
CD @5%	**1.84**	**1.54**	**0.1587**	**0.76**	**2.90**	**0.29**	**0.21**	**0.22**	**0.33**

Note: DFF-Days to 50% flowering; PH-Plant height; NPBPP-Number of primary branches per plant; NPPP-Number of pods per plant; NSPP-Number of seeds per pod; HSW-Hundred seed weight; PL-Panicle length; SPY- Single plant yield.

3.3 Variability parameters

The results on variability parameters are presented in Table 5 and Figure 1. The phenotypic coefficient of variation (PCV) ranged from 14.87 (days to 50% flowering) to 56.62. (single plant yield).

The range of the genotypic coefficient of variation (GCV) was 14.49 (days to 50% flowering) to 56.53%. (single plant yield). The PCV and GCV were moderate for days to 50% flowering, plant height, hundred seed weight, and pod length and high for single plant yield, number of pods per plant, number of clusters per plant, and number of primary branches per plant.

Table 5: Variability parameters for RILs

Characters	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Days to 50% flowering	14.87	14.49	94.99	29.10
Plant height	17.90	17.72	97.89	36.11
Number of primary branches/plants	32.44	32.39	99.08	56.22
Number of clusters per plant	34.90	34.77	99.24	61.35
Number of pods per plant	37.48	37.33	99.22	56.61
Number of seeds per pod	23.53	23.31	98.12	47.57
Hundred seed weight	13.61	13.23	94.51	26.50
Pod length	16.70	16.41	94.47	33.20
Single plant yield	56.62	56.53	99.67	64.27

3.4.1 Heritability

Heritability was high for single plant yield (99.67%), clusters per plant (99.24%), pods per plant (99.2%), days to 50% flowering (94.99%), primary branches per plat (99.08%), hundred seed weight (94.51%), seeds per pod (98.12%), pod length (94.47%), and plant height (97.89%).

3.4.2 Genetic advance as per cent of mean (GAM)

The GAM ranged from 29.10% (days to 50% flowering) to 64.27% (single plant yield). High GAM was recorded for the traits single plant yield (64.27%), number of clusters per plant (61.35%), number of pods per plant (56.61%), number of primary branches per plant (56.22%), pod length (33.20), and days to 50% flowering (29.10%).

3.4.3 Phenol and tannin content in RILs

The resistant RILs 14, 66 and 67 contain either high level of phenol or tannin or both. The RIL 14 had a high total phenol and tannin content of 208 mg 100 g^{-1} and 965 mg 100 g^{-1}, respectively. The RILs 66 and 67 recorded 920 mg 100 $g^{-1}$and 944 mg 100 g^{-1} of tannin, respectively. Similarly, the total phenol and tannin content of resistant check VBN8 was 190 mg 100 g^{-1} and 845 mg 100 g^{-1}, respectively. RILs 4, 6, 15, 22, 32, 43, 65, 66 and 67 with high phenol were found to be moderately resistant to MYMV. Moderately susceptible RIL 33 had phenol content of 192 mg 100 g^{-1}. The susceptible RILs had comparatively lower phenol or tannin content or both. The results are presented in Table 6.

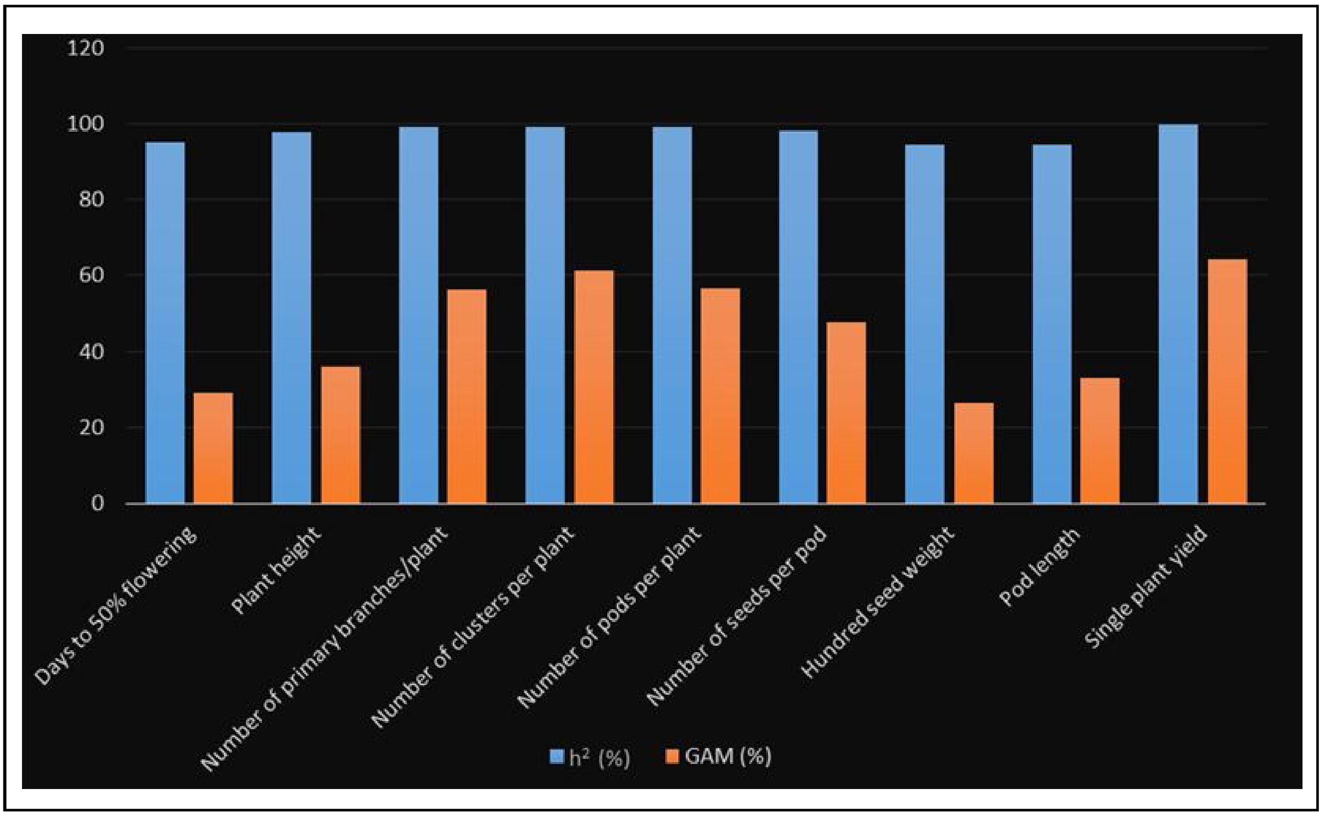

Figure 1: Heritability and genetic advance for yield and yield attributes.

3.4 Heritability and genetic advance

Table 6: Phenol and tannin content and YMV disease reaction of RILs

S.No.	RILs	Disease scale	Phenol content (mg 100 g^{-1})	Tannin content (mg 100 g^{-1})	Disease reaction
1	1	2	180	885	R
2	2	2	198	879	R
3	3	5	166	743	MS
4	4	3	188	792	MR
5	5	5	143	711	MS
6	6	3	162	765	MR
7	7	5	139	787	MS
8	8	6	121	799	S
9	9	6	111	564	S
10	10	3	165	678	MR
11	11	3	173	683	MR
12	12	6	98	495	S
13	13	3	159	498	MR
14	14	1	208	965	R

S.No.	RILs	Disease scale	Phenol content (mg 100 g^{-1})	Tannin content (mg 100 g^{-1})	Disease reaction
15	15	4	189	687	MR
16	16	4	159	654	MR
17	17	5	167	389	MS
18	18	5	154	376	MS
19	19	4	134	399	MS
20	20	6	160	480	MS
21	21	6	135	682	MS
22	22	3	171	678	MR
23	23	6	110	654	S
24	24	4	144	876	MR
25	25	6	130	287	S
26	26	6	156	498	S
27	27	7	133	443	S
28	28	6	98	784	S
29	29	6	144	654	S
30	30	6	151	366	S
31	31	4	166	761	MR
32	32	4	187	670	MR
33	33	5	192	498	MS
34	34	6	123	398	S
35	35	3	178	436	MR
36	36	5	156	388	MS
37	37	3	168	498	MR
38	38	5	172	339	MS
39	39	2	188	769	R
40	40	5	134	382	MS
41	41	5	143	478	MS
42	42	4	127	528	MR
43	43	4	178	686	MR
44	44	5	144	734	MS
45	45	6	138	489	S
46	46	3	128	684	MR
47	47	5	111	546	MS
48	48	5	108	534	MS
49	49	3	152	797	MR
50	50	5	165	638	MS
51	51	3	173	765	MR
52	52	5	147	376	MS

53	53	6	165	746	MS
54	54	7	132	656	S
55	55	2	165	786	MR
56	56	6	156	438	S
57	57	6	176	656	S
58	58	4	119	376	MR
59	59	5	165	387	MS
60	60	6	123	297	S
61	61	6	133	397	S
62	62	7	113	360	S
63	63	5	181	465	MS
64	64	3	167	245	MR
65	65	3	187	286	MR
66	66	1	197	920	R
67	67	1	193	944	R
68	68	5	162	469	MS
69	69	4	177	376	MR
70	70	6	144	498	S
71	71	7	143	485	S
72	72	5	120	530	MS
73	VBN 8	1	190	845	R

4. Discussion

Malnutrition and disorders associated with protein deficiency are mostly caused by poor availability of protein in developing nations. Black gram is considered as one of the best sources of protein for the vegetarian diet. Due to its low production potential and susceptibility to diseases like yellow mosaic virus, black gram is cultivated in limited area. Many breeding techniques including marker assisted breeding were employed for evolving black gram varieties with resistance to MYMV. From this study, seven RILs of ADT3 X KKB 15052 were found to be resistant to MYMV with a score of 1to 2 and 22 RILs were moderately resistant with a score of 2.1to 4. These RILs can either be developed into new varieties with resistance to MYMV or as donor in breeding programmes. These results are in accordance with the findings of Pavishna *et al.* (2019), who reported 28 resistant genotypes. Obaiah *et al.* (2013) and Bhanu *et al.* (2017) reported several genotypes resistant to MYMV and were used as donors in breeding of new black gram varieties resistant to MYMV.

The success of any breeding programme depends on the expression of desirable yield and yield attributes in the selected genotypes. Selection of such genotypes is based on per se performance and the genetic factors, *viz*., PCV, GCV, heritability and genetic advance of yield contributing characters. In the present study, all these genetic parameters along with per se performance were studied so as to determine the breeding methods to be employed for yield improvement in black gram. RIL 34 recorded the highest single plant yield of 18.94 g, followed by RILs 35 and 37 with single plant yield of 15.82 g and 15.57 g, respectively. All these RILs were found to be superior for other yield contributing traits, *viz.,* number of primary branches per plant (3-5), number of cluster per plant (20-32), number of pods per plant (79-94) and hundred seed weight (4.5- 5.03**).** These RILs were found to be moderately resistant to MYMV and can be utilized for development of high yielding genotypes. The traits single plant yield, number of pods per plant, number of clusters per plant, and number of primary branches, had high PCV and GCV which results in efficient crop improvement by direct selection of these traits. Gomathi *et al*. (2020); Kuralarasan and Jayamani (2021) reported similar results of high PCV and GCV for the traits single plant yield, number of pods per plant and number of clusters per pod. Days to 50% flowering, plant height, hundred seed weight, and pod length showed moderate GCV and PCV and are in concordance with the earlier reports (Partap *et al.,* 2019; Chowdhury *et al.,* 2020; Kuralarasan and Jayamani, 2021).

In the present study, all the yield attributes and single plant yield recorded high degree of heritability and genetic advance and hence these traits can be improved by any breeding method with direct selection. Many reports are in corroboration with this finding (Bandi *et al*., 2018; Mohanlal *et al*., 2018 ;Tanveer *et al*., 2018;Partap *et al*., 2019; Chowdhury *et al*., 2020 ;Thirumalai and Murugan, 2020; Chippy *et al*., 2021; Rehman *et al*., 2021).

Association of MYMV resistance with biochemical factors, *viz.,* total phenols and tannins was also studied for indirect selection of black gram genotypes with MYMV resistance. The RILs with high phenol content, 1, 2, 14, 66 and 67, showed resistance to MYMV than the RILs with low phenol, which were either moderately susceptible or susceptible to MYMV. Similar results were reported by Ranjitha *et al.* (2018) in black gram and Prabu and Warade (2009) in wild okra interspecific hybrids. Moderately resistant RILs 4, 15, 32 and 65 and moderately susceptible RIL 33 with higher phenol content indicated that the plants defence mechanism produces high number of phenols under biotic and abiotic stress conditions. Similarly, the results of high tannin content in resistant RILs 14, 66 and 67 were in accordance with the findings of Kanth *et al.* (2021).

5. Conclusion

Among the 72 RILs studied,7 RILs (1, 2, 14, 39, 55, 66 and 67) were resistant and 23 RILs were moderately resistant to MYMV. The resistant RILs 14, 66 and 67 had either high tannin content or high phenol content. Hence phenols and tannins can be considered as traits for indirect selection of MYMV resistance in black gram. 17 RILs out of 72 RILs showed superior performance for the trait, single plant yield along with other yield contributing traits. All the yield and yield attributing traits showed high variability parameters, heritability and genetic advance indicating the presence of additive gene action and low environmental influence, making these traits highly effective for selection. Hence, direct selection of these traits is beneficial for crop improvement programs. The RIL 35 with single plant yield of 15.82 g, phenol content of 178 mg 100 $g^{-1}$and tannin content of 436mg 100 g^{-1} and RIL 37 with single plant yield of 15.57 g, phenol content of 168 mg 100 $g^{-1}$and tannin content of 498 mg 100 g^{-1} were moderately resistant to MYMV. These RILs can be developed into new black gram varieties with high yield potential, resistant to MYMV and with nutraceuticals as these lines has higher phenols and moderate amount of tannins.

Acknowledgements

The authors gratefully acknowledge the financial and technical support provided by Tamil Nadu Agricultural University, Coimbatore.

Conflict of interest

The authors declare no conflict of interest relevant to this article.

References

Bhanu, A. N.; Singh, M. N. and Srivastava, K. (2017). Screening mungbean [*Vigna radiata* (L.) Wilczek] genotypes for mungbean yellow mosaic virus resistance under natural condition. Advances in Plants and Agriculture Research, **7(6):**00276.

Bandi, H.R.K.; Rao, K. N.; Krishna, K.V. and Srinivasulu. K. (2018). Variability, heritability and genetic advance for quantitative characters in rice fallow black gram [*Vigna mungo* (L.) Hepper]. International Journal of Current Microbiology and Applied Sciences, **7(2):**171-176.

Burton, G. W. (1952). Quantitative inheritance in grasses. Proceedings of the Sixth International Grassland Congress pp:277-283.

Chippy, A.; Pillai, M. A. and Shoba, D. (2021). Genetic diversity analysis in black gram [*Vigna mungo* (L.) Hepper]. Electronic Journal of Plant Breeding, **12(1):**37-45.

Choudhary, R. R. (2020). Pulses: Superfood for future. Indian Farmer, **7(10):**899.

Chowdhury, T.; Das, A.; Mandal, G.; Bhattacharya, S. and Chatterjee, S. (2020). Genetic variability, character association and divergence study in urdbean [*Vigna mungo* (L). Hepper]. International Journal of Current Microbiology and Applied Sciences, **9(2):**1726-1734.

DPD. (2020). Kharif Pulses Prospects -2020-21. Directorate of Pulses Development, Ministry of Agriculture and Farmers Welfare. Government of India. Retrieved from.

Gantait, S. and Das, P. K. (2009). Genetic divergence, adaptability and genotypic response to YMV in black gram. Legume Research, **32(2):**79-85.

Gomathi, D.; Shoba, D.; Ramamoorthy, V. and Pillai, M. A. (2020). Genetic variability and association analysis in F3 progenies of IC 436656 x KKB14045 in black gram (*Vigna mungo* L. Hepper) for agro-morphological traits. Electronic Journal of Plant Breeding, **11(04):**1211-1214.

Johnson, H.W. and Bernard. R.L. (1962). Soybean genetics and breeding. Advances in Agronomy, **14:**149-221

Kanth, A.; Goswami, K. and Shukla, P. (2021). Nutritional quality evaluation of improved varieties of black gram (*Phaseolus mungo*). The Pharma Innovation Journal, **10(1):**201-207.

Kuralarasan, V. and Jayamani, P. (2021). Genetic analysis for seed yield and yield component traits in recombinant inbred lines (RIL) population of black gram (*Vigna mungo* (L.) Hepper). Journal of Pharmacognosy and Phytochemistry, **10(1):**811-815.

Lush, J. L. (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Journal of Animal Science, **1940(1):**293-301.

Mohanlal, V.; Saravanan, K. and Sabesan, T. (2018). Regular article studies in genetic correlation and path coefficient analysis of black gram (*Vigna mungo* (L.) Hepper) genotypes under salinity. Journal of Phytology, **10**:09-11.

Obaiah, S.; Bhaskar Reddy, B. V.; Eswara Reddy, N. P. and Siva Prasad, Y. (2013). Screening of some black gram (*Vigna mungo* (L.) Hepper) genotypes for resistance to yellow mosaic virus. Current Biotica, **7(1&2):**96-100.

Panse, V. G. and Sukhatme, P. V. (1957). Genetics of quantitative characters in relation to plant breeding. The Indian Journal of Genetics and Plant Breeding, **17(2):**318-328.

Partap, B.; Kumar, M.; Kumar, V. and Kumar, A. (2019). Genetic variability and correlation studies of seed yield and its components in black gram (*Vigna mungo* (L.) Hepper). Journal of Pharmacognosy and Phytochemistry, **8**:2035-2040.

Pavishna, M.; Kannan, R.; Arumugam Pillai, M. and Rajinimala, N. (2019). Screening of black gram genotypes against mung bean yellow mosaic virus disease. Journal of Pharmacognosy and Phytochemistry, **8(3):**4313-4318.

Prabu, T. and Warade, S. (2009). Biochemical basis of resistance to yellow vein mosaic virus in okra. Vegetable Science, **36(3):**283-287.

Ranjitha, B.; Rajarajeswari, V.; Sudhakar, N.; Naidu, P. and Bhaskara Reddy, B. (2018). biochemical variability and seed yield of resistant and susceptible black gram (*Vigna mungo* (L.) Hepper) genotypes elicited by *Bemisia tabaci* (Gennadius). International Journal of Current Microbiology and Applied Sciences, **7(8):**4422-4426.

Rehman, M. A.; Lal, G. M. and Bhattacharjee, I. (2021). Genetic variability for quantitative traits in F4 generation of black gram [*Vigna mungo* (L.) Hepper]. Journal of Pharmacognosy and Phytochemistry, **10(1):**252-256.

Robinson, H.; Comstock. R.E. and Harvey. P. (1949). Estimates of heritability and the degree of dominance in corn. Agronomy Journal, **41**(8):353-359.

Season and crop report. (2019-2020). Department of Economics and Statistics, Government of Tamil Nadu, Chennai. Retrieved, **40**(1):343-349.

Sivasubramanian, S. and Madhavamenon, P. (1973). Genotypic and phenotypic variability in rice. Madras Agricultural Journal, **60(9):**1093-1096.

Tanveer, H.; Kumar, A.; Singh, R.; Singh, H.; Singh, S. and Singh, R. (2018). Studies on genetic variability, character association and path analysis in black gram (*Vigna mungo* (L.) Hepper) varieties. Trends in Biosciences, **11(42):**4182-4185.

Thirumalai, R. and Murugan, S. (2020). Multivariate analysis in black gram (*Vigna mungo* (L.) hepper) genotypes for mungbean yellow mosaic virus (mymv) resistance. Plant Archives, **20(1):**2473-2480.

Citation **R. Latha and S. Ganapathy (2026). Genetic analysis for yield components and phytochemicals in recombinant inbred lines of black gram (*Vigna mungo* (L.) Hepper). Ann. Phytomed., 15(1):835-845, http://dx.doi.org/10.54085/ap.2026.15.1.75.**