*Original Research Article*

**Genetic Variability and Yellow Vein Mosaic Virus (YVMV) Resistance in Mutant Lines of Blackgram (*Vigna mungo* L. Hepper) under Field Condition.**

**ABSTRACT**

**Background:** The creation of genetic variability in a gene pool is the prerequisite of a breeding program. To introduce a higher degree of variability and to identify favourable recombinants ,a combination of hybridization and mutation methods is employed. Among various diseases infecting and reducing yield of blackgram, yellow mosaic disease caused by Mungbean Yellow Mosaic Virus (MYMV) is the crucial one. Due to non-availability of resistant cultivars, cultivation of blackgram crop land is diverted to other cereal crop cultivation and for MYMV management in urdbean production, breeding with the resistant cultivars is effective which is also ecofriendly

**Methods:** A field experiment was carried out during Kharif 2022 by using 90 F4 M3 laid out in an augmented design at AHRS, Bavikere. Based on seed yield, disease index and incidence, 30 F5 M4 were selected for summer 2023 from the first season and laid out in RCBD design. These lines obtained through the hybridization of PU31 and Rashmi, followed by the treatment of F2 seeds with gamma irradiation (20kr) at IIHR in Bangalore.

**Result:** The research we conducted exhibited significant variations for the majority of traits. For the first season, high PCV, GCV, broad sense heritability and genetic advance as per cent of mean observed for the number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod and seed yield. For the second season, moderate PCV, GCV and high broad sense heritability with genetic advance as per cent mean observed for the number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod. Estimated high values of PCV indicates more variability for the trait seed yield per plant in the population and the narrow range between GCV and PCV which implies lesser influence of the environmental effects on the expression of traits. BLM 9, BLM 20, BLM 29, BLM 44, BLM 51 and BLM 58 in the first season and BLM 30 and BLM 51 in the second season showed resistant reaction to YVMV with the least per cent disease index. Hence, these mutant lines can be used for further crop improvement.

**Key words:** Heritability, Irradiation, Mutant lines, Variability, Yield, YVMV

**INTRODUCTION**

Blackgram (*Vigna mungo* L.) is one of the famous lentils used in southern Asia. It belongs to the family Fabaceae. It is a diploid (2n=22) and autogamous plant. It is originated in India (Vavilov, 1926). The progenitor of the blackgram is believed to be *Vigna* *mungo* var. silvestris (Lukoki *et al*., 1980).

India is the world’s largest producer as well as consumer of blackgram. It produces about 22.29 lakh tonnes of blackgram annually from 41.42 lakh hectares of area, with an average productivity of 538 kg per hectare (INDIASTAT, 2021). Karnataka is one of India's major blackgram growing states, with an area of 0.81 lakh hectares, a production of 0.44 lakh tonnes and a productivity of 821.5 kg ha-1 (Anonymous, 2020). Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Karnataka and Andhra Pradesh are the major producers of blackgram in India*.*

The critical position of pulse production, mainly blackgram against the increased population, poses a challenge for breeders to develop high-yielding, short-duration, bold-grained and disease-resistant varieties. This can be achieved through a planned breeding program and adopting proper agronomic practices.

The creation of genetic variability in a gene pool is the prerequisite of a breeding program. The knowledge of certain genetic parameters is essential for proper understanding and their manipulation in any crop improvement program. Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful biometrical tools for determining genetic variability. The variability available in the breeding material helps in selecting the superior plant types. Heritability indicates the relative success of selection as it measures the relative amount of heritable portion of variability. High heritability combined with high genetic advance is more useful than heritability alone in predicting the resultant effect on selecting the best individual (Johnson *et al*., 1955).

Among various diseases infecting and reducing the yield of blackgram, yellow vein mosaic disease caused by mung bean yellow mosaic virus is crucial. MYMV belonging to the Geminiviridae family can affect crop yield up to 100 *per cent* under higher incidence (Nene, 1972). MYMV in India cannot be transmitted by mechanical means and can easily be transmitted by whitefly *Bemisia* *tabaci* (Bashir and Zubir, 2002). MYMV is highly infectious to legume crops such as blackgram, mung bean, pigeon pea, french bean, and soya bean, causing symptoms like yellow flecks on leaves alternating with green patches. After severe infection, leaves become completely yellow and produce fewer flowers and pods. Due to the non-availability of resistant varieties, cultivation of blackgram cropland is diverted to other cereal crops cultivation (Mohan *et* *al*., 2014) and for MYMV management in urdbean production, breeding with the resistant cultivars is effective, which is also eco-friendly (Tamilzharasi *et al.*, 2020). It is essential to find more resistant varieties that perform well at all growing seasons and hence to identify MYMV resistant urdbean cultivars; researchers have made several attempts (Subedi, 2016). In view of the above facts, the present study was targeted to screen the MYMV resistant blackgram varieties under natural condition.

Therefore, by keeping all these in view, the present study in blackgram was undertaken with mutant lines derived from hybridization of PU31 × Rashmi and mutation by using gamma radiation of 20 Kr dosage, which were selected based on high mean performance for seed yield.

**MATERIALS AND METHODS**

The experiment was conducted during *kharif* 2022 and summer 2023 at the Agricultural and Horticultural Research Station (AHRS), Bavikere, Shivamogga, Karnataka, India which is situated in 13° 42’ North latitude and 75° 51’ East longitude and at an altitude of 695 meters above mean sea level.

The experimental material consisted of 90 F4M3 of cross (PU31 × Rashmi) in blackgram [*Vigna mungo* (L.) Hepper], including five checks (PU31, Rashmi, DBGV5 DU1, LBG-791) for kharif 2022 and laid out in an augmented design. For second season, 30 F5M4 selected from 90 F4M3 from the first season based on seed yield, percent disease incidence and percent disease index and laid out in RCBD design.

YVMV screening, the infector row method was followed for providing MYMV infection to all the test genotypes. Rashmi urdbean was used as a susceptible check and LBG -791 urdbean was used as a resistant check. Two replications were assigned for each genotype and after five genotypes, Rashmi (susceptible check) was planted to ensure more MYMV incidence. No insecticide was sprayed to ensure a natural white fly population. Thirty days after sowing, whiteflies started landing on the plants. The crop was regularly monitored for the presence of whiteflies and the development of MYMV. Infection and disease severity of MYMV progressed in the next six weeks. Each plant was rated on a 0-9 modified scale All India Coordinated Research Project on MULLARP proposed by Alice and Nadarajan, 2007. The disease scoring was recorded when the susceptible check (Rashmi) showed 80 *per cent* disease incidence. The progressive screening was also done in the summer of 2023 with blackgram genotypes, which were resistant and moderately resistant at *kharif* 2022. Intensity of the disease incidence is presented in plate 1.

Statistical analysis was performed on the data of traits means recorded on 15 selected plants for yield and its attributing traits using WINDOWSTAT version 9.2 software and R software. Disease scoring was done by using modified MULLARP (0-9) scale was dipected in table 1.

Percentage disease index and *per cent* disease incidence were calculated by using the formula given by Wheeler.

Percent Disease Index =

DI (%) =

**RESULTS AND DISCUSSION**

The present investigation was carried out during *Kharif* 2022 and summer 2023 at Agricultural and Horticultural Research Station (AHRS), bavikere, Shivamogga, Karnataka, India. The experimental material consisted of 90 F4M3 for the first season and 30 F5M4 for the second season, and four checks (PU31, Rashmi, DBGV5, DU1 and LBG791).

For the first season, the experiment was laid out in an augmented design with ten blocks, each block with 15 lines and a total of 90 F4M3. The genotypes were not replicated, while checks were replicated twice in all the blocks. The second season experiment was laid out in RCBD design with 30 F5M3 with two replications selected from 90 F4M3 from the first season based on seed yield, percent disease incidence and percent disease index. Here, genotypes and checks were both replicated twice. Analysis for variability, heritability, genetic advance and association studies for yield and yield attributing traits and identifying the YVMV resistant lines in black gram was taken up.

The F4M3 and F5M4 generation of cross (PU31 × Rashmi) exhibited a considerable amount of variability for all ten characters individually. For the first season, the range is 38 to 43 for days to 50 per cent flowering, Plant height varies between 25.60 cm and 34.80 cm. The number of branches ranges from 2.40 to 3.80. The count of clusters per plant ranges from 11.20 to 16.80, while the number of pods per cluster varies between 2.40 to 3.80. For the number of pods per plant, the range is from 28.00 to 51.80. Pod length spans from 4.46 cm to 5.00 cm. The number of seeds per pod ranges from 4.60 to 5.60. The 100-seed weight varies between 3.84 g to 5.04 g. Lastly, the total seed yield per plant exhibits a range of 8.60 g to 18.32 g.

For the second season, the range is 39 to 43 for days to 50 per cent flowering, Plant height varies between 27.60 to 33.30cm. The number of branches ranges from 3.20 to 3.90. The count of clusters per plant ranges from 7.30 to 10.00, while the number of pods per cluster varies between 2.60 to 3.70. For the number of pods per plant, the range is from 21.90 to 35.80. Pod length spans from 4.39 to 4.68 cm. The number of seeds per pod ranges from 4.00 to 4.70. The 100-seed weight varies between 3.96 to 4.74g. The total seed yield per plant exhibits a range of 7.34 to 9.74g.

**Genetic Variability Parameters**

Second-degree statistics viz., genotypic co-efficient of variation (GCV), phenotypic coefficient of variation (PCV) and broad sense heritability facilitate in deciphering genetic variability. GCV and PCV estimates are unit independent and enable comparison across traits. However, information on heritable variability is more relevant than total variability for crop improvement. This is measured by broad-sense heritability, the ratio of genetic variance to the total variance expressed *per cent*. The estimate of heritability serves as an indicator for effective selection. Heritability estimates' utility is increased when used in conjunction with the selection differential (Johnson *et al.,* 1955).

The variability available in the progeny population is a key for crop improvement programs. Various characters' direct and indirect effects on yield provide guidelines for effective selection for any crop improvement program.

*Genetic variability for the first season (Autumn 2022)*

Analysis of variance was carried out for yield and its attributes in 90 Mutant lines, along with five checks. Analysis of variance revealed significant differences among the genotypes for all the traits studied, indicating the presence of sufficient genetic variability and that the material for the investigation was appropriate and results are presented in Table 2.

In the results of the current experiment, the PCV values were higher than their corresponding GCV values for all the component traits studied, which indicated the environment's influence on these traits. These findings were in close agreement with the reports of Gandi *et al*. (2018), Surekha *et al*. (2020) and Jamil *et al*. (2023).

For the first season, genetic variability studies revealed that high PCV and GCV values were observed for the number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod and seed yield. High heritability and genetic advance as *per cent* of mean was recorded for days to 50 per cent flowering, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod and seed yield (Table 3). These findings were in close agreement with the reports of Kumar *et* *al*. (2015), Surekha *et* *al*. (2020) and Gomathi *et al*. (2023).

By taking into consideration the above-mentioned selection parameters, it was evident that the traits like number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod and seed yield had the highest values of PCV, GCV, broad-sense heritability and genetic advance. High heritability with low genetic advance observed for days to 50 *per cent* flowering and plant height, which showed the existence of the non-additive gene action, thus confirming the role of the environment in the expression of such traits. Selecting these yield attributing traits helps achieve enhanced production. Parallel results were obtained by Gowsalya *et* *al*. (2016), Gandi *et* *al*. (2018), Sarvani *et* *al*. (2020) and Gomathi *et al.* (2023).

*Genetic variability for the second season (summer 2023)*

Analysis of variance was carried out for yield and its attributes in 30 mutant lines, along with four checks. Analysis of variance revealed significant differences among the genotypes for all the traits studied, indicating sufficient genetic variability and the choice of the material for the investigation was appropriately depicted in (Table 4)

For the second season, results of genetic variability studies showed that moderate PCV and GCV values were observed for the number of branches per plant, number of clusters per plant, number of pods per cluster and number of seeds per pod. High heritability, along with high genetic advance as *per cent* of mean was recorded for the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the number of pods per plant and the number of seeds per pod. These findings were in close agreement with the reports of Rolaniya *et* *al*. (2017) and Aftab *et* *al*. (2018).

By considering above mentioned selection parameters, it is confirmed that traits like the number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and number of seeds per pod have moderate PCV, GCV and high broad-sense heritability with genetic advance (Table 4). This showed that higher values of heritability and genetic gain were principally controlled by additive genes Selecting such yield attributing traits helps increase yield. Parallel results were obtained by Gowsalya *et* *al*. (2016), Priyanka *et* *al*. (2016), Panda *et* *al*. (2017), Blessy *et* *al*. (2018), Gandi *et* *al*. (2018), Patidar *et* *al*. (2018), Shobha *et* *al*. (2018) and Chowdhury *et* *al*. (2020).

**Screening of yellow vein mosaic virus (YVMV) under field condition**

YVMV disease can be effectively controlled by using the resistant varieties. Screening of genotypes against YVMV at field condition is necessary to identify the resistant varieties. Even though several genotypes showing resistance to YVMV have already been identified, a lack of durable resistance is observed. Hence, progressive screening over the year is required for identifying resistance sources against YVMV. In the study, screening was done by using the infector row technique. Observations were recorded after a susceptible check showed 80 per cent disease incidence.

*Screening of YVMV under field condition for the first season (Kharif 2022)*

For the first season, the same set of 90 F4M3, evaluated for yield and its component traits, were subjected to Screening for response to yellow vein mosaic virus (YVMV) in *Kharif* 2022. Observations were recorded only after a susceptible check showed 80 *per cent* disease incidence. Analysis of variance was carried out for the *per cent* disease incidence and results are presented in Table 5.

Analysis of variance revealed a significant mean sum of squares attributable to genotypes and 'genotypes vs. checks.'Thus indicating the presence of variability among the genotypes studied for response to YVMV disease. The PDI varied from 2.22 *per cent* in BLM 44 to 77.78 percent in BLM 16, BLM 22 and BLM 32 with resistant and highly susceptible disease reaction, respectively dipected in Plate 2. Among these 90 mutant lines, 6 mutant lines showed resistant reaction with a 1 to 2 rating scale, 28 mutant lines showed moderately resistant reaction with a 2.1 to 4 rating scale, 19 mutant lines showed moderately susceptible reaction with 4.1 to 5 rating scale, 33 mutant lines were susceptible with 5.1 to 7 rating scale, 4 mutant lines were highly susceptible with 7.1 to 9 rating scale depicted in (Table 6) and grouping of blackgram genotypes based on their disease reaction to YVMV during first season (*Kharif* 2022) depicted in (table 7). Similar results were observed by Bhanu *et al*. (2017); Kakumanu and Gorrepati (2017),Kolakar *et al*. (2018) and Pavishna *et al.* (2021).

*Screening of YVMV under field condition for the second season (summer 2023)*

Based on seed yield and resistant reaction to YVMV disease, the best 30 F5M4 were selected for the second season. Analysis of variance was carried out for the *per cent* disease incidence, *per cent* disease index and seed yield (summer 2023) results are presented in Table 8. The PDI varied from 3.33 percent in BLM 51 to 81.11 percent in BLM 25 with resistant and highly susceptible disease reaction, respectively dipected in Plate 3. Among these 30 mutant lines, 2 mutant lines showed resistant reaction with 1 to 2 rating scale. 8 mutant lines showed a moderately resistant reaction with 2.1 to 4 rating scale, 11 mutant lines showed moderately susceptible reaction with 4.1 to 5 rating scale, 7 mutant lines were susceptible with 5.1 to 7 rating scale, 2 mutant lines were highly susceptible with a 7.1 to 9 rating scale depicted in (Table 9) and grouping of blackgram genotypes based on their disease reaction to MYMV during second season (summer 2023) presented in (Table 10). High incidence of yellow vein mosaic observed in summer season compare to kharif season which may be due combination of factors, such as high white fly population, presence of virus inoculum potential and favourable environmental/ ecological conditions.Similar findings were observed by Raje and Rao (2002); Akhtar *et al*. (2011) and Iqbal *et al*.(2011).

**CONCLUSION**

The present mutant lines had wide genetic variability for most yield-attributing traits, which can be used for selection programs for yield improvement.BLM 12, BLM 20, BLM 27, BLM 36 and BLM 73 in the first season and BLM 30, BLM 33, BLM 51, BLM 85 and BLM 90 in the second season were found to be high-yielding among the genotypes.BLM 9, BLM 20, BLM 29, BLM 44, BLM 51 and BLM 58 in the first season and BLM 30 and BLM 51 in the second season showed resistant reaction to YVMV with the least *per cent* disease index. Hence, these mutant lines can be used for further crop improvement.

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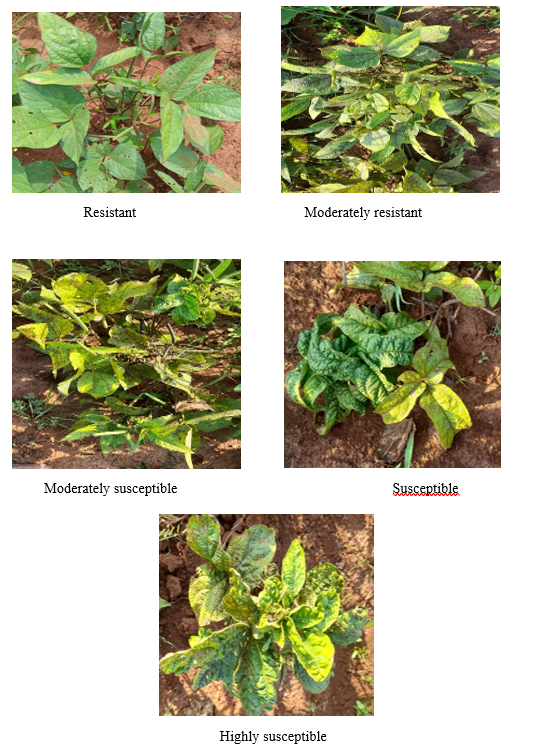
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**Table 1: Modified MULLARP scale (0-9) for YVMV**

|  |  |
| --- | --- |
| **Scale** | **Description** |
| 0 | No visible symptoms on leaves |
| 1 | Very minute yellow specks on leaves |
| 2 | Small yellow specks with restricted spread covering 0.1-5% of the leaf area of the plant |
| 3 | Yellow mottling of leaves covering 5.1-10% of the leaf area of the plant |
| 4 | Yellow mottling of leaves covering 10.1-15% of the leaf area of the plant |
| 5 | Yellow mottling and discoloration of 15.1-30% leaf area of the plant |
| 6 | Yellow discoloration of 30.1-50% leaf area of the plant |
| 7 | Pronounced yellow mottling and discoloration of leaves and pods, reduction in leaf size and stunting of plants covering 50.1-75% foliage of plant |
| 8 | Severe yellow discoloration of leaves covering 75.1-90% of foliage, stunting of plants and reduction in pod size |
| 9 | Severe yellow discolouration of leaves covering above 90.1% of foliage of plants, stunting of plants and no pod formation |

The categories used for assessing the resistant genotypes against yellow mosaic vein virus were given in the following table

|  |  |  |
| --- | --- | --- |
| **Percent Disease Severity** | **Rating** | **Reaction** |
| 0.1-5 | 1 to 2 | Resistant |
| 5.1-15 | 2.1 to 4 | Moderately resistant |
| 15.1-30 | 4.1 to 5 | Moderately susceptible |
| 30.1-75 | 5.1 to 7 | Susceptible |
| 75.1-100 | 7.1 to 9 | Highly susceptible |



**Plate 1: Disease reaction to yellow vein mosaic virus (YVMV) in blackgram**

**Table 2: ANOVA for grain yield and its component traits in blackgram (*Kharif* 2022)**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Source of Variation | DF | Mean Sum of Square | | | | | | | | | |
| DFF | PH | NBP | NCP | NPC | NPP | PL | NSP | TW | SYP |
| Block | 5 | 0.91 | 3.77 | 0.01 | 2.68 | 2.37 | 4.03 | 0.78 | 0.27 | 0.03 | 3.23 |
| Genotypes + Checks | 94 | 39.23\*\* | 32.86\*\* | 0.11\*\* | 47.52\*\* | 10.98\*\* | 79.57\*\* | 2.69\*\* | 3.23\*\* | 0.07\*\* | 11.45\*\* |
| Genotypes | 89 | 41.32\*\* | 34.21\*\* | 0.07\*\* | 45.58\*\* | 10.85\*\* | 31.88\*\* | 2.76\*\* | 3.37\*\* | 0.07\*\* | 10.58\*\* |
| Checks | 4 | 1.12 | 1.97 | 0.76\*\* | 2.57 | 2.04 | 141.33\*\* | 0.60 | 0.37 | 0.02 | 33.22\*\* |
| Checks vs. Genotypes | 1 | 5.88\* | 36.35\*\* | 0.71\*\* | 400.27\*\* | 58.16\*\* | 4077.71\*\* | 4.97\* | 1.97\* | 0.21\*\* | 1.45\* |
| Error | 20 | 1.30 | 1.91 | 0.01 | 1.55 | 0.91 | 1.81 | 0.62 | 0.25 | 0.01 | 2.63 |

\*Significance at 0.05 probability level \*\*Significance at 0.01 probability level

DFF=Days to 50% flowering NPP=Number of pods plant-1

PH=Plant height (cm) PL=Pod length (cm)

NB=Number of branches plant-1 NSP=Number of seeds pod-1

NCP=Number of clusters plant-1 HSW=100 seed weight(g)

NPC=Number of pods cluster-1 TSY=Total seed yield(g)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Mean** | **Minimum** | **Maximum** | **GCV**  **(%)** | **PCV**  **(%)** | **(%)** | **GAM**  **(%)** |
| Days to 50% flowering | 41.18 | 38.00 | 43.00 | 15.37 | 15.62 | 96.86 | 31.22 |
| Plant height(cm) | 30.92 | 25.60 | 34.80 | 18.05 | 18.57 | 94.43 | 36.18 |
| Number of branches per plant | 3.54 | 2.40 | 3.80 | 7.27 | 7.59 | 91.83 | 14.38 |
| Number of clusters per plant | 13.66 | 11.20 | 16.80 | 37.51 | 38.16 | 96.60 | 76.06 |
| Number of pods per cluster | 2.93 | 2.40 | 3.80 | 61.58 | 64.33 | 91.63 | 121.60 |
| Number of pods per plant | 38.74 | 28.00 | 51.80 | 13.90 | 14.31 | 94.33 | 27.85 |
| Pod length | 4.76 | 4.46 | 5.00 | 27.30 | 31.43 | 77.65 | 50.35 |
| Number of seeds per pod | 4.99 | 4.60 | 5.60 | 31.52 | 32.74 | 92.69 | 62.60 |
| 100 seed weight(g) | 4.46 | 3.84 | 5.04 | 5.35 | 5.93 | 81.49 | 9.96 |
| Seed yield(g) | 11.91 | 8.60 | 18.32 | 21.42 | 24.70 | 75.19 | 38.32 |

**Table 3: Estimates of parameters specifying variability for seed yield and its component traits in blackgram (*Kharif* 2022)**

GCV= Genotypic coefficient of variation

PCV= Phenotypic coefficient of variation

h2bs =Broad sense heritability

GAM= Genetic advance as *per cent* mean

**Table 4: ANOVA for grain yield and its component traits in blackgram (summer 2023)**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Source of Variation | DF | Mean Sum of Square | | | | | | | | | |
| DFF | PH | NBP | NCP | NPC | NPP | PL | NSP | TW | SYP |
| Replication | 1 | 0.91 | 0.26 | 0.06 | 0.02 | 0.01 | 0.10 | 0.03 | 0.01 | 0.23 | 0.04 |
| Genotype | 34 | 5.19\*\* | 3.44\*\* | 0.37\*\* | 0.04\*\* | 0.31\*\* | 39.60\*\* | 0.14\*\* | 0.47\*\* | 0.012\*\* | 0.93\*\* |
| Error | 34 | 1.3 | 0.64 | 0.04 | 0.24 | 0.04 | 5.47 | 0.02 | 0.04 | 0.049 | 0.24 |
| CD (5%) |  | 2.31 | 1.63 | 0.39 | 0.99 | 0.40 | 4.75 | 0.28 | 0.40 | 0.45 | 0.99 |
| CD (1%) |  | 3.11 | 2.19 | 0.52 | 1.33 | 0.54 | 4.75 | 0.37 | 0.54 | 0.60 | 1.33 |

\*\*- Significant @1% CD=Critical difference

DFF=Days to 50% flowering NPP=Number of pods plant-1

PH=Plant height (cm) PL=Pod length (cm)

NB=Number of branches plant-1 NSP=Number of seeds pod-1

NCP=Number of clusters plant-1 HSW=100 seed weight(g)

NPC=Number of pods cluster-1 TSY=Total seed yield(g)

**Table 5: Estimates of parameters specifying variability for seed yield and its component traits in blackgram (summer 2023)**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **S.No** | **Characters** | **Mean** | **Minimum** | **Maximum** | **GCV**  **(%)** | **PCV**  **(%)** | **(%)** | **GAM**  **(%)** |
| 1 | Days to 50% flowering | 41.17 | 39.00 | 43.00 | 3.45 | 4.45 | 60.01 | 5.5 |
| 2 | Plant height(cm) | 30.21 | 27.60 | 33.30 | 3.82 | 4.62 | 68.52 | 6.52 |
| 3 | Number of branches plant | 3.59 | 3.20 | 3.90 | 10.77 | 11.88 | 82.19 | 20.12 |
| 4 | Number of clusters plant | 8.60 | 7.30 | 10.00 | 11.46 | 12.66 | 81.91 | 21.36 |
| 5 | Number of pods per cluster | 3.05 | 2.60 | 3.70 | 11.79 | 13.37 | 77.87 | 21.44 |
| 6 | Number of pods per plant | 27.22 | 21.90 | 35.80 | 14.15 | 16.26 | 75.72 | 25.37 |
| 7 | Pod length | 4.56 | 4.39 | 4.68 | 5.58 | 6.38 | 76.57 | 10.06 |
| 8 | Number of seeds pod | 4.34 | 4.00 | 4.70 | 10.76 | 11.71 | 84.52 | 20.39 |
| 9 | 100 seed weight(g) | 4.42 | 3.96 | 4.74 | 6.86 | 8.50 | 65.18 | 11.41 |
| 10 | Seed yield(g) | 8.56 | 7.34 | 9.74 | 6.64 | 8.63 | 59.25 | 10.53 |

GCV= Genotypic coefficient of variation

PCV= Phenotypic coefficient of variation

h2bs =Broad sense heritability

GAM = Genetic advance as per cent of mean

**Table 6: Analysis of variance for the *per cent* disease incidence, *per cent*****disease index and seed yield (*kharif 2022)***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Source of variation** | **Degrees of freedom** | **Mean Sum of square** | | |
| **Percentage disease incidence** | **Percentage disease index** | **Seed yield** |
| Block (eliminating treatments) | 5 | 3.02 | 5.30 | 1.60 |
| Genotypes+Checks (Ignoring blocks) | 94 | 135.50\* | 293.63\*\* | 3.05\*\* |
| Genotypes | 89 | 2.13 | 296.88\*\* | 3.32\*\* |
| Checks | 4 | 169.86 | 899.34\*\* | 2.43 |
| Checks vs.Genotypes | 1 | 8.68\*\* | 26.56\*\* | 0.70 |
| Error | 20 | 0.76 | 2.75 | 1.24 |

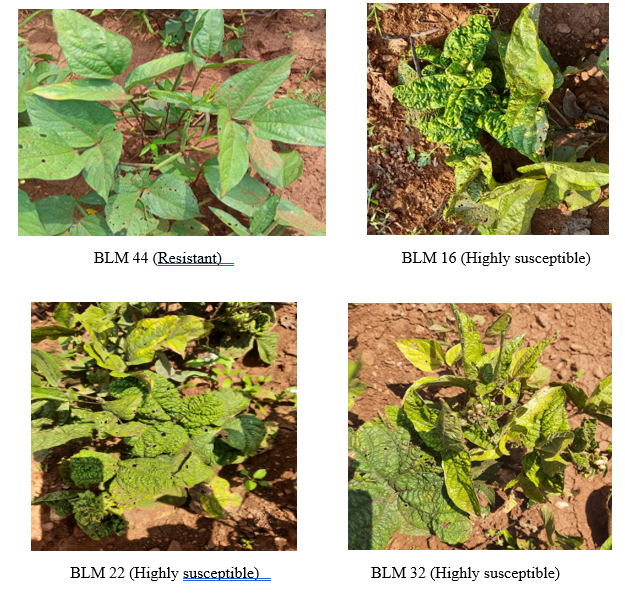
**Table 7: Screening of blackgram mutant lines against YVMV (*Kharif* 2022)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genotypes** | **Percentage of disease incidence** | **Percentage disease index** | **Disease scale** | **Disease reaction** | **Seed yield**  **(g/m)** |
| **BLM 1** | 15.83 | 13.33 | 2 | MR | 9.026 |
| **BLM 2** | 34.23 | 26.67 | 5 | MS | 8.34 |
| **BLM 3** | 35.71 | 23.33 | 5 | MS | 7.95 |
| **BLM 4** | 16.27 | 12.22 | 8 | MR | 7.96 |
| **BLM 5** | 39.32 | 31.11 | 6 | S | 8.46 |
| **BLM 6** | 86.55 | 81.11 | 5 | HS | 8.21 |
| **BLM 7** | 18.75 | 14.44 | 4 | MR | 8.78 |
| **BLM 8** | 82.21 | 76.67 | 6 | HS | 7.53 |
| **BLM 9** | 13.75 | 4.44 | 2 | R | 9.193 |
| **BLM 10** | 23.40 | 15.56 | 5 | MS | 9.74 |
| **BLM 11** | 23.04 | 22.22 | 5 | MS | 8.983 |
| **BLM 12** | 44.13 | 36.67 | 5 | S | 18.32 |
| **BLM 13** | 36.61 | 24.44 | 5 | MS | 8.2 |
| **BLM 14** | 40.83 | 35.56 | 6 | S | 7.44 |
| **BLM 15** | 53.33 | 46.67 | 6 | S | 11.62 |
| **BLM 16** | 73.33 | 77.78 | 8 | HS | 9.28 |
| **BLM 17** | 47.37 | 37.78 | 6 | S | 11.34 |
| **BLM 18** | 52.63 | 37.78 | 6 | S | 11.86 |
| **BLM 19** | 36.84 | 24.44 | 5 | MS | 11.94 |
| **BLM 20** | 8.70 | 4.44 | 2 | R | 15.04 |
| **BLM 21** | 12.50 | 8.89 | 3 | MR | 11.98 |
| **BLM 22** | 82.35 | 77.78 | 8 | HS | 9.82 |
| **BLM 23** | 59.09 | 46.67 | 6 | S | 9.34 |
| **BLM 24** | 28.57 | 13.33 | 4 | MR | 14.18 |
| **BLM 25** | 25.00 | 13.33 | 4 | MR | 13.48 |
| **BLM 26** | 40.00 | 33.33 | 6 | S | 12.22 |
| **BLM 27** | 15.00 | 8.89 | 3 | MR | 15.00 |
| **BLM 28** | 44.44 | 28.89 | 5 | S | 8.90 |
| **BLM 29** | 10.53 | 4.44 | 2 | R | 12.88 |
| **BLM 30** | 17.65 | 8.89 | 3 | MR | 12.06 |
| **BLM 31** | 45.45 | 33.33 | 6 | S | 11.16 |
| **BLM 32** | 54.55 | 77.78 | 8 | HS | 9.96 |
| **BLM 33** | 13.04 | 8.89 | 3 | MR | 12.12 |
| **BLM 34** | 47.06 | 42.22 | 6 | S | 12.06 |
| **BLM 35** | 54.55 | 44.44 | 6 | S | 12.04 |
| **BLM 36** | 26.32 | 13.33 | 4 | MR | 16.12 |
| **BLM 37** | 40.91 | 33.33 | 6 | S | 12.02 |
| **BLM 38** | 43.48 | 33.33 | 6 | S | 12.94 |
| **BLM 39** | 22.73 | 13.33 | 4 | MR | 13.56 |
| **BLM 40** | 19.05 | 13.33 | 4 | MR | 12.06 |
| **BLM 41** | 38.46 | 24.44 | 5 | MS | 10.40 |
| **BLM 42** | 14.29 | 6.67 | 3 | MR | 14.42 |
| **BLM 43** | 18.18 | 6.67 | 3 | MR | 12.28 |
| **BLM 44** | 8.33 | 2.22 | 2 | R | 11.86 |
| **BLM 45** | 15.79 | 11.11 | 4 | MR | 10.04 |
| **BLM 46** | 77.78 | 55.56 | 7 | S | 9.24 |
| **BLM 47** | 40.91 | 33.33 | 6 | S | 10.00 |
| **BLM 48** | 31.58 | 22.22 | 5 | MS | 12.24 |
| **BLM 49** | 38.10 | 26.67 | 5 | MS | 12.02 |
| **BLM 50** | 30.00 | 22.22 | 5 | MS | 11.50 |
| **BLM 51** | 9.09 | 4.44 | 2 | R | 12.02 |
| **BLM 52** | 42.86 | 33.33 | 6 | S | 12.24 |
| **BLM 53** | 30.00 | 20.00 | 5 | MS | 12.06 |
| **BLM 54** | 31.82 | 22.22 | 5 | MS | 10.60 |
| **BLM 55** | 22.73 | 20.00 | 5 | MS | 11.92 |
| **BLM 56** | 19.05 | 11.11 | 4 | MR | 12.18 |
| **BLM 57** | 23.53 | 13.33 | 4 | MR | 12.14 |
| **BLM 58** | 9.09 | 4.44 | 2 | R | 12.10 |
| **BLM 59** | 22.73 | 17.78 | 5 | MR | 11.90 |
| **BLM 60** | 26.09 | 20.00 | 5 | MS | 11.74 |
| **BLM 61** | 28.00 | 17.78 | 5 | MS | 11.92 |
| **BLM 62** | 39.13 | 35.56 | 6 | S | 12.24 |
| **BLM 63** | 16.67 | 13.33 | 4 | MR | 12.88 |
| **BLM 64** | 22.73 | 17.78 | 5 | MS | 11.92 |
| **BLM 65** | 9.09 | 8.89 | 3 | MR | 11.34 |
| **BLM 66** | 37.50 | 33.33 | 6 | S | 11.84 |
| **BLM 67** | 50.00 | 37.78 | 6 | S | 11.70 |
| **BLM 68** | 39.13 | 26.67 | 5 | MS | 11.66 |
| **BLM 69** | 45.45 | 44.44 | 6 | S | 12.30 |
| **BLM70** | 21.74 | 13.33 | 4 | MR | 13.80 |
| **BLM71** | 23.81 | 13.33 | 4 | MR | 12.17 |
| **BLM72** | 52.94 | 26.67 | 5 | MS | 11.52 |
| **BLM73** | 18.18 | 11.11 | 4 | MR | 14.66 |
| **BLM74** | 13.64 | 13.33 | 4 | MR | 12.14 |
| **BLM75** | 47.83 | 40.00 | 6 | S | 11.50 |
| **BLM76** | 54.55 | 42.22 | 6 | S | 10.04 |
| **BLM77** | 52.38 | 51.11 | 6 | S | 10.76 |
| **BLM78** | 54.55 | 60.00 | 7 | S | 10.60 |
| **BLM79** | 56.52 | 35.56 | 6 | S | 10.04 |
| **BLM80** | 48.00 | 40.00 | 6 | S | 11.86 |
| **BLM 81** | 32.00 | 13.33 | 4 | MR | 11.86 |
| **BLM 82** | 56.52 | 37.78 | 6 | S | 10.04 |
| **BLM 83** | 50.00 | 31.11 | 6 | S | 10.98 |
| **BLM 84** | 50.00 | 20.00 | 5 | MS | 11.60 |
| **BLM 85** | 21.74 | 13.33 | 4 | MR | 12.19 |
| **BLM 86** | 62.50 | 48.89 | 6 | S | 11.38 |
| **BLM 87** | 22.73 | 13.33 | 4 | MR | 14.34 |
| **BLM 88** | 47.83 | 40.00 | 6 | S | 11.34 |
| **BLM 89** | 18.18 | 13.33 | 4 | MR | 12.28 |
| **BLM 90** | 17.39 | 11.11 | 4 | MR | 12.19 |
| **Rashmi** | 78.76 | 73.33 | 7 | S | 13.88 |
| **LBG -791** | 8.90 | 2.96 | 2 | R | 14.31 |
| **PU-21** | 11.99 | 4.44 | 2 | R | 14.71 |
| **DU-1** | 32.14 | 28.89 | 5 | MS | 15.04 |
| **DBGV-5** | 30.37 | 27.41 | 5 | MS | 15.53 |

**Table 8: Grouping of blackgram mutant lines based on their disease reaction to**

**MYMV (*Kharif* 2022)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Grade** | **Rating** | **Reaction** | **Number of genotypes** | **Name of the genotypes** |
| 0 | 1 to 2 | Resistant | 6 | BLM 9, BLM 20, BLM 29, BLM 44, BLM 51, BLM 58 |
| 1 |
| 2 |
| 3 | 2.1 to 4 | Moderately resistant | 28 | BLM 1, BLM 4, BLM 7, BLM 21, BLM 24, BLM 25, BLM 30, BLM 33, BLM 36, BLM 39, BLM 40, BLM 42, BLM 43, BLM 45, BLM 56, BLM 57, BLM 59, BLM 63, BLM 65, BLM 70, BLM 71, BLM 73, BLM 74, BLM 81, BLM 85, BLM 87, BLM 89, BLM 90 |
| 4 |
| 5 | 4.1 to 5 | Moderately susceptible | 19 | BLM2, BLM3, BLM 10, BLM 11, BLM 13, BLM 19, BLM 41, BLM 48, BLM 49, BLM 50, BLM 53, BLM 54, BLM 55, BLM 60, BLM 61, BLM 64, BLM 68, BLM 72, BLM 84 |
| 6 | 5.1 to 7 | Susceptible | 33 | BLM 5, BLM 12, BLM 14, BLM 15, BLM 17, BLM 18, BLM 23, BLM 26, BLM 28, BLM 31, BLM 34, BLM 35, BLM 37, BLM 38, BLM 46, BLM 47, BLM 52, BLM 62, BLM 66, BLM 67, BLM 69, BLM 75, BLM 76, BLM 77, BLM 78, BLM 79, BLM 80, BLM 82, BLM 83, BLM 86, BLM 88 |
| 7 |
| 8 | 7.1 to 9 | Highly susceptible | 4 | BLM 6, BLM 8, BLM 16, BLM 32 |
| 9 |



**Plate 2: Symptomatic expression of yellow vein mosaic virus (YVMV) of blackgram (*Kharif* 2022)**

**Table 9: Analysis of variance for the *per cent*****disease incidence, *per cent* disease index and seed yield (summer 2023)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Source of variation** | **Degrees of freedom** | **Mean Sum of square** | | |
| **Percentage disease incidence** | **Percentage disease index** | **Seed yield** |
| Replication | 1 | 2.01 | 91.48 | 1.05 |
| Genotype | 34 | 120.30 | 299.28 | 1.15 |
| Error | 34 | 50.19 | 112.14 | 0.46 |
| CD (5%) |  | 14.40 | 21.52 | 1.38 |
| CD (1%) |  | 19.33 | 28.89 | 1.85 |

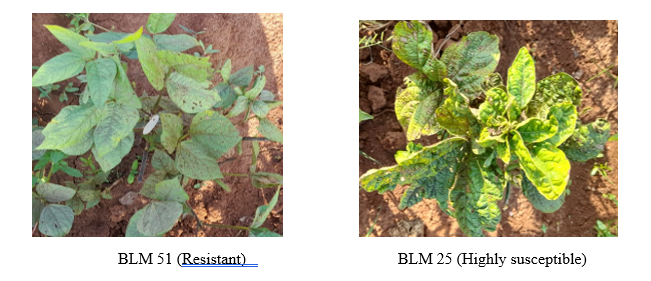
**Table 10: Screening of blackgram mutant lines against MYMV (summer 2023)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genotypes** | **Percentage of disease incidence** | **Percentage of disease index** | **Disease scale** | **Disease reaction** | **Seed yield**  **(gm)** |
| **BLM 9** | 15.83 | 13.33 | 2 | MR | 9.026 |
| **BLM 11** | 34.23 | 26.67 | 5 | MS | 8.34 |
| **BLM 12** | 35.71 | 23.33 | 5 | MS | 7.95 |
| **BLM 20** | 16.27 | 12.22 | 8 | MR | 7.96 |
| **BLM 24** | 39.32 | 31.11 | 6 | S | 8.46 |
| **BLM 25** | 86.55 | 81.11 | 5 | HS | 8.21 |
| **BLM 27** | 18.75 | 14.44 | 4 | MR | 8.78 |
| **BLM 29** | 82.21 | 76.67 | 6 | HS | 7.53 |
| **BLM 30** | 13.75 | 4.44 | 2 | R | 9.193 |
| **BLM 33** | 23.40 | 15.56 | 5 | MS | 9.74 |
| **BLM 36** | 23.04 | 22.22 | 5 | MS | 8.983 |
| **BLM 39** | 44.13 | 36.67 | 5 | S | 8.61 |
| **BLM 40** | 36.61 | 24.44 | 5 | MS | 8.2 |
| **BLM 42** | 40.83 | 35.56 | 6 | S | 7.44 |
| **BLM 43** | 50.48 | 43.33 | 6 | S | 7.552 |
| **BLM 44** | 45.83 | 42.22 | 6 | S | 8.23 |
| **BLM 51** | 11.11 | 3.33 | 2 | R | 9.38 |
| **BLM 53** | 13.10 | 12.22 | 4 | MR | 9.188 |
| **BLM 56** | 17.42 | 10.00 | 8 | MR | 7.99 |
| **BLM 57** | 38.57 | 35.56 | 6 | S | 7.74 |
| **BLM 58** | 52.78 | 10.00 | 8 | MR | 7.34 |
| **BLM 63** | 9.90 | 20.00 | 5 | MS | 8.905 |
| **BLM 70** | 30.56 | 27.78 | 5 | MS | 8.96 |
| **BLM 71** | 29.02 | 24.44 | 5 | MS | 9.14 |
| **BLM 73** | 29.91 | 28.89 | 5 | MS | 8.97 |
| **BLM 74** | 23.21 | 20.00 | 5 | MS | 9.2 |
| **BLM 85** | 33.89 | 38.89 | 6 | S | 9.292 |
| **BLM 87** | 20.19 | 12.22 | 4 | MR | 8.916 |
| **BLM 89** | 31.75 | 23.33 | 5 | MS | 9.03 |
| **BLM 90** | 17.79 | 11.11 | 2 | MR | 9.3 |
| **Rashmi** | 80.30 | 78.89 | 8 | HS | 9.70 |
| **LBG -791** | 11.07 | 3.33 | 2 | R | 10.02 |
| **PU-21** | 11.81 | 4.44 | 2 | R | 9.91 |
| **DU-1** | 28.64 | 26.67 | 5 | MS | 8.98 |
| **DBGV-5** | 25.66 | 25.56 | 5 | MS | 9.49 |

**Table 11: Grouping of blackgram mutant lines based on their disease reaction to**

**MYMV (summer 2023)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Grade** | **Rating** | **Reaction** | **Number of genotypes** | **Name of genotypes** |
| 0 | 1 to 2 | Resistant | 2 | BLM 30, BLM 51 |
| 1 |
| 2 |
| 3 | 2.1 to 4 | Moderately Resistant | 8 | BLM 9, BLM 20, BLM 27, BLM 53, BLM 56, BLM 58, BLM 87, BLM 90 |
| 4 |
| 5 | 4.1 to 5 | Moderately susceptible | 11 | BLM 11, BLM 12, BLM 33, BLM 36, BLM 40BLM 63, BLM 70, BLM 71, BLM 73, BLM 74, BLM 89 |
| 6 | 5.1 to 7 | Susceptible | 7 | BLM 24, BLM 39, BLM 42, BLM 43, BLM 44, BLM 57, BLM 85 |
| 7 |
| 8 | 7.1 to 9 | Highly susceptible | 2 | BLM 25, BLM 29 |
| 9 |



**Plate 3: Symptomatic expression of yellow vein mosaic virus (YVMV) of blackgram (*summer* 2023)**