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ISSN: 0975-928X

Volume: 10

Number:2

EJPB (2019) 10(2):732-735

DOI:10.5958/0975-928X.2019.00095.4



Research Article

Assessment of variability for seed yield, component characters and MYMV disease resistance in segregating populations of blackgram [*Vigna mungo* (L.) Hepper]

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(Received: 28 Apr 2019; Revised: 30 May 2019; Accepted: 30 May 2019)

Abstract

Magnitude of variability in two F₂ populations involving Mungbean Yellow Mosaic Virus (MYMV) disease susceptible (MDU 1) and resistance (Mash 114 and Mash 1008) parents *viz.*, MDU 1 x Mash 114 and MDU 1 x Mash 1008 of blackgram was studied. Magnitude of GCV was high for number of branches per plant, number of clusters per plant, number of pods per plant, MYMV disease score at 45 DAS, MYMV disease score at 60 DAS and seed yield per plant in both populations. High heritability coupled with high genetic advance as percent of mean was recorded number of branches per plant, number of pods per plant, MYMV disease score at 60 DAS and seed yield per plant in the both the populations. These characters might be controlled by additive gene effects and hence selection will be effective for this character. Skewness revealed that distribution of population was negatively skewed for 100-seed weight in both populations. Kurtosis revealed that platykurtic curve was observed for number of seeds per pod in the F₂ population of both crosses. Hence, these traits can be improved by directional selection in both populations. Considering the kurtosis for MYMV disease score at 45 DAS and 60 DAS, the cross MDU 1 x Mash 1008 had platykurtic nature. Hence selection may be effected in this cross to evolve high yielding MYMV disease resistant variety in blackgram.

Keywords

Blackgram, variability, selection, seed yield, MYMV.

Introduction

Blackgram (*Vigna mungo* (L.) Hepper) is an important food legume crop of Indian sub-continent. It is an important short duration crop and widely cultivated in India. It gives us an excellent source of easily digestible good quality protein and ability to restore the fertility of soil through symbiotic nitrogen fixation. Seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. In India, the blackgram is grown over an area of about 4.50 million hectares with the production of 3.23 million tonnes (Anonymous, 2018). Yellow Mosaic Disease (YMD) is a significant biotic stress causing profound yield loss in blackgram. Mungbean Yellow Mosaic Virus (MYMV) belongs to the genus *Begomovirus* and transmitted by the vector whitefly, *Bemisia tabaci*. Yield loss due to this disease varies from 5 to 100 per cent depending upon disease severity, susceptibility of cultivars and population of whitefly (Nene, 1972). The major constraints in achieving higher yield are the lack of genetic variability, poor harvest index, suitable varieties and genotypes with adaptation to local

condition. Yield is a complex trait controlled by polygenes and highly sensitive for environmental factors. The efficacy of selection depends upon the existence and magnitude of genetic variability for yield and yield contributing traits. Assessment of genetic variation available for yield components, their heritability and genetic advance are of great significance for the breeders in order to plan appropriate selection procedure for crop improvement (Degefa *et al.*, 2014). With this background, the present investigation was carried out to assess the variability for seed yield, yield components and MYMV disease scores in the two crosses involving MYMV disease resistant and susceptible parents in blackgram.

Material and Methods

The experiment was conducted at National Pulses Research Centre, Vamban during *kharif* 2018 in two F₂ populations of blackgram *viz.*, MDU 1 x Mash 114 (Cross 1), MDU 1 x Mash 1008 (Cross 2). MDU 1 is a high-yielding blackgram variety grown in Tamil Nadu, but highly susceptible to Mungbean Yellow Mosaic Virus (MYMV) disease. The

variety was developed and released by Agriculture College and Research Institute, Tamil Nadu Agricultural University, Madurai during 2014 for commercial cultivation in Tamil Nadu. Mash 114 and Mash 1008 are varieties released by Punjab Agricultural University, Ludhiana and resistant to MYMV disease. F_2 populations were screened for MYMV disease resistance through infector row method. Susceptible variety CO 5 was used in the infector row. Recommended agronomic practices were followed to raise the crop. No pesticides were sprayed on the crop to allow the disease infection. Observations were recorded on each individual plants in respect of plant height (cm), number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and seed yield per plant (g), MYMV disease was scored at 45 DAS and 60 DAS (Bag *et al.*, 2014). Average of the parental variance was considered as environmental variance for each cross (Mather, 1949). Statistical method suggested by Burton (1952) for variability, Lush (1940) for heritability, Johnson *et al.* (1955) for genetic advance as percent of mean (GAM) were adopted. Further, characterizations of estimates were made based on the suggestions of Sivasubramanian and Mathavamenon (1973) for variability (< 10% low, 10-20% moderate, > 20% high), Johnson *et al.* (1955) for heritability (< 30% low, 30-60% moderate, > 60% high) and Johnson *et al.* (1955) for genetic advance as percent of mean (< 10% low, 10-20% moderate, > 20% high). The skewness and kurtosis were calculated by adopting the statistical procedure given by Kapur, (1981).

Results and Discussion

Mean and variability of populations for various traits in two crosses are represented in Table 1 and 2. The results indicated that the estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters studied indicating the environmental influence over the traits. The high or moderate estimates of GCV were observed for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, MYMV disease score at 45 DAS, MYMV disease score at 60 DAS and seed yield per plant in both crosses. These results are in accordance with findings of Arulbalachandran *et al.* (2010) and Hemalatha *et al.* (2017). Pod length and 100-seed weight recorded low GCV in both crosses. This is in accordance with the finding of Pushpa Reni *et al.* (2013) and Panigrahi *et al.*, (2014). Number of seeds per pod had low or moderate in both crosses. Selection based on these

characters with high / moderate GCV will be effective for improvement of these traits.

High / moderate heritability and GAM were observed for all traits in both crosses except pod length. The present findings were in agreement with the finding of Sowmini and Jayamani (2013); Kumar *et al.* (2015); Sohel *et al.* (2016); Usharani and Anandakumar (2016) and Bishnoi *et al.* (2017). High heritability and genetic advance as per cent indicated that prevalence of additive gene action in their inheritance. Hence early generation selection may be effective to improve these traits due to the presence of additive gene action.

Normal distribution / noskewness were recorded for plant height, number of pods per cluster and number of pods per plant in both crosses. All other traits had positive or negative skewness in both the crosses. Hundred seed weight had significant and negative skewness in both crosses indicating the evaluating of more proportion of segregants with higher 100- seed weight. In case of MYMV disease scores at 45 DAS and 60 DAS, MDU 1 x Mash 114 had significant and positive while other cross had no significance skewness. It indicated the presence of more proportion of resistant parents in MDU 1 x Mash 114. In case of seed yield per plant both crosses had significant and positive skewness indicating lesser proportion of high yielding parents. Mesokurtic and platykurtic nature of distribution was observed for plant height and number of seeds per pod in both crosses respectively. This indicated the existence of adequate variability for these traits in both crosses. Number of cluster per plant, 100- seed weight and seed yield per plant had leptokurtic nature in both crosses indicating the narrow level of variability for these traits in both crosses. Number of pods per cluster in MDU 1 x Mash 114 and MYMV disease scores at 45 DAS and 60 DAS in MDU 1 x Mash 1008 recorded platykurtic nature. It indicated the availability of adequate variation for these traits in these crosses. Other traits had either leptokurtic or mesokurtic nature in both the crosses.

The present study revealed high / moderate heritability coupled with high / moderate genetic advance as percent of mean recorded for plant height, number of branches per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, MYMV disease score at 60 DAS and seed yield per plant in both F_2 populations. Therefore, these traits should be taken into account while selecting superior and desirable plants that would offer scope for developing high yielding in blackgram breeding programme. Considering the



skewness, the trait 100-seed weight in the both crosses recorded negative skewness. Similarly, kurtosis revealed that the platykurtic nature of curve was recorded for number of seeds per pod in both F₂ populations- which indicated the presence of widervariability for these characters. Hence, directional selection for the characters such as number of branches per plant, number of pods per plant, number of seeds per pod, MYMV disease score at 60 DAS and seed yield per plant, number of seeds per pod will efficiently improve the *per se* performance of these traits. The cross MDU 1 x Mash 1008 recorded platykurtic nature for MYMV disease scores *viz.*, both MYMV disease score at 45 DAS and 60 DAS. Hence selection of MYMV resistant plants can be attempted in this cross to evolve high yielding MYMV disease resistant variety in blackgram.

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Table 1. Mean, Range, variability, skewness and kurtosis of MDU 1 x Mash 114 in F₂ population for various characters

Character	Mean	Range	PCV (%)	GCV (%)	h ² (%)	GAM %	Skewness	Kurtosis
Plant height (cm)	28.43	6.00-56.00	36.53	26.70	53.42	42.34	0.27	0.04
Number of branches per plant	1.92	0.00-6.00	46.38	37.24	64.48	64.90	1.29**	3.99**
Number of clusters per plant	10.03	3.00-38.00	59.52	49.39	68.86	88.94	1.63*	4.48**
Number of pods per cluster	2.70	1.00-4.00	30.49	22.29	53.45	35.37	0.14	-0.76**
Number of pods per plant	28.66	4.00-110.00	71.33	61.81	75.09	116.23	1.53	3.11
Pod length (cm)	5.27	4.20-7.10	10.20	1.30	1.62	0.36	0.08	0.53**
Number of seed per pod	6.85	6.00-8.00	10.37	7.64	54.32	12.22	0.23*	-0.98**
100-seed weight (g)	4.20	2.90-5.00	7.90	7.48	89.57	15.35	-0.45**	2.19**
MYMV disease score at 45 DAS	1.21	1.00-6.00	79.02	37.10	22.04	37.80	3.48**	10.97**
MYMV disease score at 60 DAS	1.68	1.00-8.00	61.60	52.41	72.40	96.79	1.53**	2.76**
Seed yield per plant (g)	6.36	0.50-24.78	80.03	68.51	73.29	127.28	1.53*	2.74**

*, ** significant at 5 % and 1 % levels, respectively

Note: Min= Minimum; Max= Maximum; PCV= Phenotypic coefficient of variation; GCV = Genotypic coefficient of Variation; h²=Heritability(%); GAM = Genetic advance as per cent of mean; MYMV disease score = (1 - 9).

Table 2. Mean, Range, variability, skewness and kurtosis of MDU 1 x Mash 1008 in F₂ population for various characters

Character	Mean	Range	PCV (%)	GCV (%)	h ² (%)	GAM %	Skewness	Kurtosis
Plant height (cm)	35.30	8.00-65.00	30.41	19.22	39.94	26.36	0.37	-0.08
Number of branches per plant	1.96	0.00-8.00	64.32	59.03	84.22	117.56	0.97**	3.51
Number of clusters per plant	9.99	2.00-36.00	49.13	32.50	43.76	46.65	1.38	4.20**
Number of pods per cluster	3.20	1.00-33.00	25.01	14.82	35.11	19.06	-0.20	0.20
Number of pods per plant	31.40	3.00-128.00	62.20	48.78	61.52	83.03	1.60	4.11**
Pod length (cm)	5.40	3.30-6.50	11.82	6.95	34.61	8.88	-0.66**	0.35
Number of seed per pod	7.00	5.00-8.00	12.50	10.46	70.09	19.01	-0.50**	-0.52**
100-seed weight (g)	4.28	2.65-4.95	8.37	7.60	82.36	14.96	-1.31**	4.10**
MYMV disease at 45 DAS	2.99	1.00-7.00	52.20	42.57	66.51	75.33	0.23	-0.87**
MYMV disease at 60 DAS	3.84	1.00-7.00	38.70	33.10	73.14	61.42	0.03	-0.88**
Seed yield per plant (g)	7.00	0.30-38.42	69.96	56.93	66.21	100.52	2.29**	10.08**

*, ** significant at 5 % and 1 % levels, respectively

Note:

Min= Minimum; Max= Maximum; PCV= Phenotypic coefficient of variation; GCV = Genotypic coefficient of Variation; h²=Heritability(%); GAM = Genetic advance as per cent of mean; MYMV disease score = (1 - 9).

