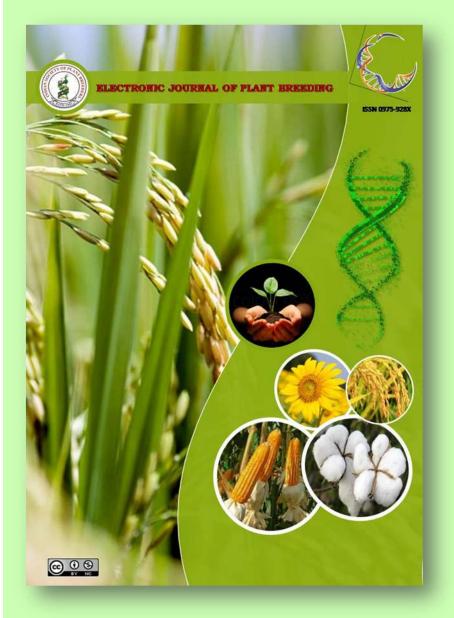# Correlation analysis for yield, yield components and MYMV disease scores in blackgram (*Vigna mungo* (L.) Hepper)

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Research Article

Correlation analysis for yield, yield components and MYMV disease scores in blackgram (*Vigna mungo*(L.) Hepper)

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Abstract
The present study was carried out to find the correlation for yield, its attributes and mungbean yellow mosaic virus (MYMV) disease scores in F_2 populations derived from two crosses of blackgram *viz.,* MDU 1 × Mash 114 and MDU 1×Mash 1008 and parent MDU 1. F_2 populations had MYMV disease score ranged between 1- 9 scale, while the parent MDU 1had 6-9 scale. Correlation studies showed that the trait seed yield per plant (g)had significant and positive correlation with the traits *viz.,* plant height (cm), number of branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, pod length (cm) and 100-seed weight (g). Hence, it may be concluded that these characters may be considered as selection index for seed yield per plant in blackgram in both crosses. MYMV disease score had no association with seed yield and component traits in MYMV susceptible parent MDU 1 as well as F_2 population. Even though the parent MDU 1 has highly susceptible reaction for MYMV disease, there was no association between disease score and seed yield or yield components. Hence it may be concluded that the susceptible parent MDU 1 has tolerance towards MYMV disease incidence.

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. The seeds are highly nutritious with protein (24-26%), carbohydrates (60%), fat (1.5%), minerals, amino acids and vitamins. The biological value improves greatly, when wheat or rice is combined with blackgram because of the complementary relationship of the essential amino acids such as arginine, leucine, lysine, isoleucine, valine and phenylalanine, etc., (Mehra *et al*., 2016). In India, the area comes under blackgram is about 4.50 million hectares with the production of 3.23 million tonnes (Annonymous, 2018). Yellow Mosaic Disease (YMD) is a significant biotic stress causing profound yield loss in blackgram. Yellow Mosaic Virus (YMV) belongs to the genus Begomo virus 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 highly complex trait which controlled by polygenes and interlinked with other yield components. Hence it is often very difficult to improve yield directly. It can be achieved by improving closely related traits (Roopalakshmi *et al*., 2003). The knowledge on interrelationship of component characters with seed yield and among themselves is of paramount importance to the breeder for making improvement in complex character like seed yield per plant, for which direct selection is not much effective. Hence, the present investigation was undertaken to assess the nature and magnitude of association of seed yield and yield attributes with MYMV disease score in segregating populations.

Material and Methods

The present research work was carried out at National Pulses Research Centre, Vamban during the kharif 2018. The experimental material consist of two crosses viz., MDU 1 × Mash 114 (cross 1), MDU 1 × Mash 1008 (cross 2) and their parents. Among parents, MDU 1 is susceptible to mungbean yellow mosaic virus (MYMV) disease. Other parents viz., Mash 114 and Mash 1008 are MYMV disease resistant parents. Data on resistant parents were not

included as it has not shown variation for MYMV disease scores. Hence, data on F2 populations and susceptible parent MDU 1 alone were presented in this article. F2 populations were screened for MYMV disease resistance through infector row method. Susceptible variety CO 5 was used in the infector row. Recommended agronomic packages of practices were followed to raise the crop. Data on 11 quantitative characters viz., 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), seed yield per plant (g), MYMV disease score at 45 DAS and 60 DAS were collected in all plants in each cross. (92 and 163 plants in cross 1 and 2 respectively) and 40 plants in MDU 1. The method of scoring was enclosed in Table 1. The simple correlation coefficients among traits were calculated for individual crosses and parents as per the method suggested by Johnson *et al*. (1955). The data analysis was done using TNAUSTAT (Manivannan, 2014).

Results and Discussion

The F2 populations had very wide range of MYMV disease incidence ranged from 1-7 score at 45 and 1-8 at 60 DAS. The susceptible parent MDU 1 has MYMV disease score ranged from 5-9 at 45 and 6-9 at 60 DAS (Table 2). The correlation coefficient among yield, yield components and MYMV disease scores were presented in Table 3.

Among the 11 characters studied from the two crosses, seed yield per plant had significant and positive association with plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length and 100-seed weight in F2 populations of both crosses viz., MDU 1 × Mash 114 and MDU 1 × Mash 1008. However, the F2 populations of MDU 1 × Mash 114 alone showed significant and positive correlation between seed yield per plant and number of seeds per pod. Seed yield per plant had significant and positive association with number of clusters per plant, number of pods per plant and number of seeds per pod in the female parent MDU 1.

Plant height had showed significant and positive correlation with number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and 100-seed weight in both crosses. Plant height had positive and significant correlation with number of branches per plant, number of cluster per plant, number of pods per plant and number of seeds per pod in MDU 1.This finding is in accordance with the reports of Mehra *et al*. (2016) and Keerthiga *et al*. (2018). However, the F2 population of MDU 1× Mash 114 showed significant and positive correlation between

plant height and number of pods per cluster which is in accordance with Keerthiga *et al*. (2018).

Number of branches per plant had showed positive and significant with number of clusters per plant, number of pods per plant, pod length and number of seeds per pod in both crosses MDU 1 × Mash 114 and MDU 1 × Mash 1008. In addition, number of branches per plant had significant and positive correlation with number of pods per cluster and 100-seed weight in the F2population of MDU 1× Mash 114 cross alone. Number of branches per plant had significant and positive relation with number of cluster per plant and number of pods per plant in MDU 1.

Number of clusters per plant showed positive and significant correlation with number of pods per plant, number of seeds per pod and 100-seed weight in the F2 population from both crosses. This trait showed positive and significant correlation with number of pods per cluster and pod length in the F2populations of crosses MDU 1 ×Mash 114and MDU 1 × Mash 1008 had respectively. In the parent MDU 1, number of clusters per plant had positive and significant correlation with number of pods per plant and number of seeds per pod. The similar reports of Parveen *et al*. (2011), Shivade *et al*. (2011), Mathivathana *et al*. (2015), Suguna *et al*. (2017) and Bandi *et al*. (2018).

Number of pods per cluster had showed positive and significant correlation with number of pods per plant in the F2 population of both crosses MDU 1 × Mash 114 and MDU 1 × Mash 1008. Similar findings were reported by Baudh *et al*. (2014) and Mathivathana *et al*. (2015). This trait had positive and significant correlation with pod length, number of seeds per pod and 100-seed weight in While among the F2 population from a cross MDU 1 ×Mash 114 alone.

Number of pods per plant had positive and significant correlation with pod length, number of seeds per pod and 100-seed weight in the F2 populations of both crosses MDU 1 × Mash 114 and MDU 1 × Mash 1008. Number of pods per plant had positive and significant relation with the trait number of seeds per pod in MDU 1. These results were in accordance with Hemalatha *et al*. (2017) and Suguna *et al*. (2017).

Pod length showed positive and significant correlation with number of seeds per pod in both the crosses MDU 1 × Mash 114 and MDU 1 × Mash 1008. The results are similar to the reports of Sohel *et al*. (2016) and Suguna *et al*. (2017).In addition the parent MDU 1 had negative and significant correlation on MYMV disease score at 45 DAS.

Among the crosses MDU 1 × Mash 114 alone had positive and significant correlation between number of seeds per pod and100-seed weight. Similar results were reported by Suguna *et al.* (2017) and Bandi *et al.* (2018). In the parent MDU 1, number of seeds per pod had negative and significant correlation on MYMV disease score at 45 DAS and 60 DAS respectively.

In the cross MDU 1 × Mash 1008 alone 100-seed weight had positive and significant correlation with MYMV disease score at 45 DAS and MYMV disease score at 60 DAS.MYMV disease score at 45 DAS and 60 DAS had significant association in F2 population of both crosses MDU 1 × Mash 114 and MDU 1 × Mash 1008.In addition the parent MDU 1, MYMV disease score at 45 DAS had positive and significant correlation on MYMV disease score at 60 DAS.

Based on the results of the present investigation, it is clear that yield component traits viz., plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length and 100-seed weight were correlated with seed yield per plant. Hence these traits can be considered as selection indices for improvement of seed yield per plant. MYMV disease scores at 45 DAS and 60 DAS had no association with seed yield per plant and component traits. It is surprising to note that even through the F2 populations had very wider range of MYMV disease score between 1 and 8, the MYMV disease has no influence on the seed yield and component traits. Even though the parent MDU 1 has highly susceptible reaction for MYMV disease, there was no association between disease score and seed yield or yield components. Hence it may be concluded that the susceptible parent MDU 1 has tolerance mechanism towards MYMV disease incidence.

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Table 1. MYMV disease scoring method

Grade	Description	Reaction
1	No visible symptoms on leaves	Free
2	Small yellow specks with restricted spread covering 0.1-5% leaf area	Highly Resistant (HR)
3	Mottling of leaves covering 6-10% leaf area	Resistant (R)
4	Yellow mottling covering 11-15% leaf area	Moderately resistant (MR)
5	Yellow mottling and discolouration of 15-20% leaf area	Moderately susceptible MS)
6	Yellow coloration of 21-30% leaves and yellow pods	Susceptible (S)
7	Pronounced yellow mottling and discoloration of leaves and pods, reduction in leaf size and stunting of plants covering 30-50% of foliage	Susceptible (S)
8	Severe yellow discoloration of leaves covering 50-75% of foliage, stunting of plants and reduction in pod size	Highly susceptible (HS)
9	Severe yellowing of leaves covering above of foliage, stunting of plants and no pod formation	Highly susceptible (HS)

Table 2. Mean and range for MYMV disease scores in parent MDU 1 and F_2 populations

Characters	MDU 1		MDU 1 × Mash 114		MDU 1 × Mash 1008	
	Mean	Range	Mean	Range	Mean	Range
MYMV disease score at 45 DAS	7.35	5-9	1.21	1-6	2.99	1-7
MYMV disease score at 60 DAS	8.25	6-9	1.68	1-8	3.84	1-7

Table 3. Simple correlation coefficients among yield, yield components and MYMV disease scores in parent MDU 1 and F_2 populations

Characters	Crosses/Parent	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)	MYMV Disease Score at 45 DAS	MYMV Disease Score at 60 DAS	Seed yield per plant (g)
Plant height (cm)	P_1	0.36*	0.42**	-0.05	0.32*	0.21	0.48**	-0.09	-0.20	-0.11	0.24
	C_1	0.38**	0.57**	0.38**	0.57**	0.21*	0.33**	0.34**	0.17	0.11	0.58**
	C_2	0.23*	0.30**	0.09	0.37**	0.38**	0.37**	0.27**	0.05	0.11	0.36**
Number of branches per plant	P_1		0.72**	-0.08	0.53**	-0.08	0.22	0.11	-0.06	-0.02	0.26
	C_1		0.71**	0.36**	0.66**	0.37**	0.33**	0.23*	-0.04	0.06	0.63**
	C_2		0.66**	0.06	0.58**	0.32**	0.30**	0.04	-0.09	-0.11	0.56**
Number of clusters per plant	P_1			-0.09	0.78**	-0.12	0.46**	0.16	-0.12	-0.12	0.42**
	C_1			0.52**	0.92**	0.19	0.29**	0.25*	0.02	0.03	0.87**
	C_2			0.14	0.88**	0.29**	0.26**	0.15*	-0.07	-0.12	0.69**
Number of pods per cluster	P_1				0.30	-0.13	0.20	-0.05	0.13	0.10	0.27
	C_1				0.69**	0.28**	0.37**	0.25*	-0.01	-0.08	0.67**
	C_2				0.16*	0.07	0.05	0.08	-0.04	-0.03	0.22**
Number of pods per plant	P_1					-0.23	0.45**	0.11	-0.11	-0.16	0.45**
	C_1					0.24*	0.35**	0.27**	-0.01	0.02	0.94**
	C_2					0.28**	0.28**	0.23**	-0.07	-0.09	0.77**
Pod length (cm)	P_1						0.01	-0.12	-0.32*	-0.22	-0.18
	C_1						0.73**	0.14	0.01	-0.01	0.27**
	C_2						0.78**	0.03	0.00	0.06	0.21**
Number of seeds per pod	P_1							-0.04	-0.38*	-0.46**	0.45**
	C_1							0.22*	0.09	-0.03	0.37**
	C_2							0.05	-0.07	0.00	0.20
100-seed weight(g)	P_1								0.09	0.08	-0.02
	C_1								-0.12	-0.08	0.31**
	C_2								0.17*	0.16*	0.33**
MYMV Disease Score at 45 DAS	P_1									0.90**	0.10
	C_1									0.69**	0.04
	C_2									0.90**	-0.11
MYMV Disease Score at 60 DAS	P_1										0.01
	C_1										0.03
	C_2										-0.11

*, ** significant at 5 and 1 levels, respectively,
Note; P_1= MDU 1; C_1 =MDU 1 × Mash 114; C_2 = MDU 1 × Mash 1008