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RESEARCH PAPER

Genetic variability studies for yield and yellow mosaic virus resistance in F_2 population of Mungbean *Vigna radiata* (L.)

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Abstract: An investigation was carried out to assess the genetic variability of nine quantitative characters in F_2 population of the cross DGGV-2 × IPM-2-14 and to study the association of yield and its attributing traits. High to moderate level of PCV and GCV estimates were recorded for single plant yield, number of seeds per plant, coefficient of infection, number of clusters, number of pods per cluster, number of pods per plant, number of seeds per pod and plant height. High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for single plant yield, number of seeds per plant, coefficient of infection, number of pods per cluster, number of clusters, number of pods per plant, height of the plant and number of seeds per pod. Correlation studies for seed yield and its attributing traits revealed significant positive correlation of number of seeds per plant, number of pods per plant, number of clusters, number of pods per cluster and height of the plant with seed yield per plant inferring that these traits strongly influenced seed yield per plant. Coefficient of infection (MYMV disease) exhibited significant negative correlation with yield and yield contributing traits. The present findings could be useful for establishing selection criteria for high seed yield in the mungbean breeding programme.

Keywords: Correlation, Genetic advance over mean, Heritability, Mungbean

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] (2n = 2x = 22) belongs to the family Leguminaceae, is one of the important pulse crops in India and is cultivated in an area of 4.30 million ha with a production of 2.07 million tonnes and average productivity of 481 kg ha^{-1} (Anon., 2017). In India, it is cultivated in *kharif*, *rabi* and summer seasons. The maximum area of its cultivation is under *kharif,* where intercropping with sorghum, pearl millet, maize, cotton, castor, pigeon pea *etc.*, are popular under varied agroconditions.

Important green gram growing states in India are Rajasthan, Punjab, Orissa, Andhra Pradesh, Maharashtra, Karnataka and Bihar. In Karnataka, it occupies an area of 3.54 lakh ha with a total production of 0.66 lakh tonnes and the average productivity is 309 kg ha^{-1} (Anon., 2017). It is less than the national productivity, there by indicating the scope to improve its productivity potential. Mungbean is widely grown in several cropping systems due to its short duration (60-75 days), drought tolerance and ability to fix atmosphere nitrogen through symbiotic relationship with soil bacteria and improve the soil fertility (Rana *et al.,* 2016).

Mungbean seeds contain 26 per cent protein, 51 per cent carbohydrate, 10 per cent moisture, 4 per cent minerals and 3 per cent vitamins (Khan, 1981). Seeds and flour of mungbean are used as major ingredients in several kinds of food. Mungbean sprouts are consumed as a popular vegetable and they contain higher vitamin C and iron levels. Mungbean starch is used to produce noodles, biscuits and cakes. Plant parts are used as fodder and manure.

In a highly self-pollinated crop like mungbean, the breeding strategy for varietal development generally involves selection of potential genotypes from the existing germplasm, utilizing them in the hybridization programme and isolation of superior genotypes in the segregating population. This necessitates a thorough knowledge of genetic variability estimates (genetic variability, heritability and GAM) and association between yield and yield components that can be achieved through selection.

Material and methods

The present study comprised of 260 F_2 individuals derived from a cross DGGV-2 × IPM-2-14. The experiment was conducted during summer 2018 at Main Agricultural Research Station, Dharwad, Karnataka. All the test entries were sown in an augmented design in 5 blocks using 4 checks. The F_2 population along with the parents was screened for mungbean yellow mosaic virus disease resistance, yield and yield contributing traits. Each entry was sown in a single row of four metre length with the spacing of 30 × 10 cm. All the recommended agronomic practices were followed. No insecticidal spray was given in order to allow the vector whitefly population .

To ensure sufficient availability of the insect population, susceptible check was planted in each block and around the experimental layout. Planting of susceptible check DGGV-2 as an infector row (Four rows) was taken up around the experimental layout.

Results and discussion

The mean performance of two parents for nine quantitative traits suggested that variability was observed for all the traits studied (Table 1). The diversity of these two parents for these important traits fully justified their selection for generating the breeding material.

In the study, high PCV and GCV estimates were observed for single plant yield (29.97 % and 27.63 %), number of

Table 1. Mean performances of parents and checks for yield and yield contributing traits and disease resistance (Coefficient of infection)

Parents/checks	PH	NOC	NOPPC	NOP	NSPP	PL	NOS	SPY	CI
DGGV 2 (Susceptible Check)	33.9	5.46	1.7	9.16	6.36	12.32	59.28	2.55	53.51
WGG-42 (Resistant check)	36.9	6.12	1.78	10.84	6.85	11.88	73.52	3.91	17.4
IPM-2-14 (Resistant check)	40.9	7.3	2.77	20.24	5.27	8.00	105.36	4.23	7.66
DGGV 7 (Moderately susceptible check)	31.8	5.56	1.6	8.8	7.55	8.48	66.76	2.85	38.44

PH = Plant height (cm); NOC = Number of clusters; NOPPC = Number of pods per cluster; NOP = Number of pods;
NSPP = Number of seeds per pod; PL = pod length (cm); NOS = Number of seeds; SPY = Single plant yield (g); CI = Coefficient of infection (%)

seeds per plant (27.66 % and 26.33 %), coefficient of infection (23.63 % and 22.20 %), number of clusters (23.34 % and 20.59 %) and number of pods per cluster (22.98 % and 20.52 %). Moderate level of PCV and GCV estimate were observed in number of pods per plant (17.54 % and 16.87 %), number of seeds per pod (15.43 % and 13.91 %) and plant height (14.87 % and 14.17 %) (Table 2). These observations indicated ample scope for improvement of the above traits based on phenotypic values. But Moderate PCV (10.79 %) and low GCV (9.14 %) were observed for pod length.

Phenotypic coefficients of variation were higher than genotypic coefficients of variation for all the traits under study (Table 2) showing higher influence of environment on the traits. These results are in accordance with the findings of Singh *et al.* (2009) and Konda *et al.* (2009).

The heritability in a broader perspective is the proportion of genotypic variability to the total variability. Heritability estimates in the broad sense alone is not a true indicator of effectiveness of selection for the trait since, it is restricted by their interactions with the environment. Hence, heritability values considered along with predicted genetic gain increases the reliability of the parameter as a tool in selection programme. Heritability and genetic advance over mean estimates are presented (Table 2). In the investigation, heritability in broad sense was found to be high in all the traits. High heritability coupled with high GAM was noticed for single plant yield (84.99 and 52.48 %), number of seeds per plant (90.58 and 51.62 %), coefficient of infection (88.26 and 42.97 %), number of pods per cluster (79.70 and 37.74 %), number of clusters (77.82 and 37.42 %), number of pods per plant (92.52 and 33.43 %), height of the plant (90.73 and 27.80 %) and number of seeds per pod (81.29 and 25.84 %) indicating that these traits were controlled by additive genes indicating the availability of sufficient heritable variation that could be made use in the selection programme and can easily be transferred to successive generations. Similar results were found by Arulbalachandran *et al.* (2010), Singh *et al.* (2009) and Konda *et al.* (2009). Pod length recorded a high heritability with moderate level of GAM (71.84 and 15.96 %). This kind of result was observed by Dev *et al.* (2017).

In any crop improvement programme, it becomes necessary to have simultaneous selection of more than one character, especially in the case of complex character like yield, which is influenced by many other contributing traits. Correlation of characters serves as a measure and forms the basis of selection

Table 2. Estimates of components of variability for yield and yield contributing traits in F_2 population

Characters	Mean	S.D	Standard Error	C.D. at 5%	PCV (%)	GCV (%)	h^2 %	GA	GAM
Plant height (cm)	32.96	4.97	1.81	3.95	14.87	14.17	90.73	9.10	27.80
Number of clusters	5.00	1.19	0.66	1.44	23.34	20.59	77.82	1.84	37.42
Number of pods per cluster	2.06	0.49	0.26	0.57	22.98	20.52	79.70	0.78	37.74
Number of pods per plant	10.38	3.77	1.08	2.35	17.54	16.87	92.52	6.14	33.43
Number of seeds per pod	6.45	1.01	0.52	1.14	15.43	13.91	81.29	1.66	25.84
Pod length (cm)	9.10	1.13	0.63	1.37	10.79	9.14	71.84	1.44	15.96
Number of seeds per plant	70.40	19.79	7.02	15.31	27.66	26.33	90.58	34.89	51.62
Single plant yield (g)	2.97	0.91	0.40	0.87	29.97	27.63	84.99	1.48	52.48
Coefficient of infection (%)	31.63	12.61	3.35	7.31	23.63	22.20	88.26	14.53	42.97

Table 3. Correlation coefficients for yield and yield contributing traits

	PH	NOC	NOPPC	NOP	NOSPP	PL	NOS	SPY	CI
Plant height (cm)	1	0.291^{**}	0.284^{**}	0.404^{**}	0.673^{**}	0.101	0.459^{**}	0.425^{**}	-0.319^{**}
Number of clusters		1	0.041	0.736^{**}	0.066	0.113	0.665^{**}	0.660^{**}	-0.222^{**}
Number of pods per cluster			1	0.677^{**}	0.033	-0.030	0.591^{**}	0.559^{**}	-0.281^{**}
Number of pods per plant				1	0.061	0.050	0.856^{**}	0.829^{**}	-0.326^{**}
Number of seeds per pod					1	0.065	0.240^{**}	0.197^{**}	-0.092
Pod length (cm)						1	0.022	0.107	-0.067
Number of seeds per plant							1	0.919^{**}	-0.362^{**}
Single plant yield (g)								1	-0.387^{**}
Coefficient of infection (%)									1

** Correlation is significant at the 0.01 level (2-tailed)

DGGV-2 (Susceptible)P_1 F_1-77 (Resistant) IPM 2-14 (Resistant)P_2

Plate 1. Comparison of F_1 along with the parents for reaction to MYMV disease

as it gives strength and direction of relationship between the characters studied. Selection for yield will be effective, only when it is considered along with its yield components rather than relying on yield alone. When a breeder applies selection pressure for a trait, it also brings about a simultaneous change in all associated characters with it.

The phenotypic correlations estimated among nine characters to determine their nature of relationship in F_2 population of the cross DGGV-2 × IPM-2-14 are presented (Table 3). Seed yield per plant exhibited significant positive correlation with number of seeds per plant (0.919), number of pods per plant (0.829), number of clusters (0.660), number of pods per cluster (0.559) and height of the plant (0.425) in F_2 population of this cross. These results are in agreement with the findings of Alam *et al.* (2014) and Gupta *et al.* (2013).

Coefficient of infection (MYMV disease) is negatively correlating with yield and yield contributing traits. Coefficient of infection exhibited significant negative correlation with single plant yield (-0.387), number of seeds per plant (-0.362), number of pods per plant (-0.326), height of the plant (-0.319), number of clusters (-0.222) and number of pods per cluster (-0.281). These results are in accordance with the findings of Nair *et al.* (2017) and Chen *et al.* (2013).

The important yield attributing traits *viz.*, number of seeds per plant, number of pods per plant, number of clusters, number of pods per cluster and height of the plant also had significant positive correlation among themselves. Hence, selection for any one of these traits will result in the improvement of seed yield.

Thus, the present study suggests that selection for high seed yield should be based on number of seeds per plant, number of pods per plant, number of clusters, number of pods per cluster, height of the plant and MYMV resistance in mungbean. Therefore, due emphasis is to be given on these characters for selecting high yielding superior lines in segregating population of mungbean.

The screening for MYMV disease is invariably carried out during summer when the temperature is high and dry weather prevails. So the current investigation was carried out under summer season . Moreover susceptible check DGGV 2 was planted in each block which served as infector row. The fact is evident from Table 1, where range and Mean performances of resistant and susceptible parents and checks for yield , yield contributing traits and Disease resistance (Coefficient of infection) is indicated. The prevailing weather conditions during the experimental period are given in Table 4.

The parents, checks and all the F_2 plants were evaluated for MYMV infection in the field condition by the disease rating scale suggested by Singh and Singh (2000). In the present study, DGGV-2 having coefficient of infection 53.51 per cent was categorized as susceptible whereas IPM-2-14 was categorized as resistant as it was showing coefficient of infection 7.66 per cent. WGG-42 and DGGV-7 were categorized as moderately resistant and moderately susceptible respectively.

The F_2 plants 77, 160, 183, 191, 207, 228 and 60, 87 have shown highly resistant and resistant reaction to MYMV disease, respectively with reasonable yield .These genotypes can be effectively used in developing MYMV resistant varieties/genotypes by using standard selection methods. Some genotypes produced higher yield but they have shown moderately resistant and moderately susceptible reaction to MYMV disease. These genotypes should be forwarded and can be used in backcross or hybridization programme to impart MYMV disease resistance.

Table 4. The meteorological data for the year 2018 at Main Agricultural Research Station, Dharwad during the crop growth stage

Months	Temperature		RH %	Rainfall (mm)	No. of rainy days
	Maximum °C	Minimum °C			
January	29.8	13.9	66	0.0	0
February	32.1	15.7	46	1.0	0
March	34.9	19.3	47	72.4	3
April	36.2	21.1	58	32.8	3

Table 5. Superior genotypes showing highly resistant and resistant reaction to MYMV disease in F_2 population

Sl. No.	F_2 Plant no.	Plant height (cm)	Number of pods	Number of seeds	Yield per plant (g)	Coefficient of infection (%)	Disease reaction
1	77	32.00	12	94	3.90	2.94	HR
2	160	32.00	13	83	3.59	1.61	HR
3	167	24.00	5	42	1.98	2.08	HR
4	183	42.00	31	204	8.19	4.34	HR
5	191	35.00	10	72	3.65	1.42	HR
6	207	30.00	12	78	3.82	1.04	HR
7	228	40	14	117	6.63	1.66	HR
8	54	35.00	8	49	2.21	9.06	R
9	60	36.00	16	91	4.30	9.12	R
10	87	38.00	14	99	4.27	8.14	R
11	255	30.00	8	60	2.18	5.05	R
12	DGGV2 (Susceptible Check)	43	20	160	7.72	53.51	S
13	IPM-2-14 (Resistant check)	36	16	89	6.2	7.66	R

HR = Highly resistant R = Resistant MYMV: Mungbean Yellow Mosaic Virus

In the present study, the F_2 plant number 183 has recorded lowest coefficient of infection (4.34) and moderate yield of 8.19 grams per plant. This genotype can be used as donor for breeding agronomically superior genotype with MYMV resistance.

Nevertheless, the F_2 plant number 88 and 161 have recorded moderately resistant reaction to MYMV under natural field conditions with yield of 8.28 and 8.25 grams per plant, respectively. These genotypes can be stringently screened for reaction to MYMV under artificial epiphytotic conditions and on confirmation of their resitance reaction, can be utilized in downstream breeding programmes aimed at releasing high yielding mungbean variety with MYMV resistance.

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