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Genetic Variability for Yield and Yield Related Traits in Mung bean Genotypes and its Response to Mung bean Yellow Mosaic Virus (MYMV) Resistance Under Natural Conditions

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Abstract

Mungbean is an important pulse crop growing through out the Asian and African countries. It is nutritionally valued for digestible protein of 24 per cent contributing immensely to the national nutritional security. In India, productivity of mung bean is low compared to global average productivity. Among all other biotic and abiotic stresses, mung bean yellow mosaic diseaseis one of the major devastating disease causing yield losses upto 85 per cent. Hence a study was initiated with 302 mung bean genotypes including advanced breeding lines (ABLs) and germplasm accessions to assess the genetic variability for yield and yield contributing traits and to screen for host resistance to mung bean yellow mosaic virus (MYMV) under natural conditions. Analysis of variance for eight yield and yield contributing traits revealed significant difference among genotypes for all the traits except 50 per cent flowering indicating the presence of genetic variability. Presence of narrow difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicatedlow environmental influence on these traits. Highest magnitude of PCV and GCVwas observed for seeds per pod. PCV and GCV of seed yield per plant were 62.41 per cent and 62.21 per cent, respectively. Lowest magnitude of PCV and GCV was observed for days to 50 per cent flowering and days to maturity. High broad sense heritability coupled with high genetic advance as per cent mean (GAM) was observed for all the characters like seed yield per plant, pod length, plant height, seed index, pods per plant except for days to 50 per cent flowering. Hence such of these characters can be used as anindirect selection criteria for yield improvement in mung bean. Further, the genotypes were screenedfor MYMV which grouped the genotypes under study into three categories according to their responses for MYMV. Out of 302 genotypes, 25 found to be resistant with the score of 2 and having lowest percent disease index (PDI) which ranged from 19.92 to 24.90 per cent, 222 were moderately resistant with the score of 3 and 53 were moderately susceptible with the score of 4 when scored under natural conditions for MYMV. Highest PDI was recorded for both susceptible checks china mung (73.04 %) and LM-1668 (78.02 %) and Lowest PDI (19.92 %) was observed in GG-ABL-149, GG-ABL-151, GG-ABL-196, GG-ABL-213 and HUM 12 with 5.9, 5.3, 6.9, 6.6 and 5.4 gram of seed yield per plant. This experiment concluded 25 resistant genotypes as the mostsuitable resistant cultivarsand could be used as resistant source for improving thelocal cultivars which enhances production and productivity of mung bean.

Keywords : Mungbean, Mungbean yellow mosaic virus, Genetic variability, Percent disease index

Mung bean (*Vigna radiata* (L.) Wilczek) is one of the most important *kharif* pulse crop contributing a sizeable share to the global economy. It belongs to the family Fabaceae and grown extensively in major tropical and subtropical countries of the world. It is estimated that India is the largest producer of mungbean with 54 per cent of the world's production and 65 per cent of the global acreage, which meets both domestic needs and imports from Asian and African countries. (Anonymous, 2020). Mung bean production trend in India has been increasing for the past few years and this is attributed to its short maturity period, tolerance to drought and adaptability to a wide range of soils (Esimu *et al*., 2020). Mung bean is rich in protein with extra nutritional values. It mainly contains 24 per cent of digestible protein, 0.6 per cent of fat, 0.9 per cent of fiber and 3.7 per cent of ash. It plays an essential role in soil enrichment by fixing

atmospheric nitrogen through symbiosis (Parimala *et al*., 2020). It not only fetches high value in Indian market, but contributes immensely to national nutritional security especially in countries like India, where child mortality ratiois high according to WHO (Tang *et al*., 2014). However, its productivity in India is 400 kg ha^{-1}as against global average productivity of 730 kg ha^{-1}. This low productivity of greengram is due to lack of genetic variability, low harvest index and its susceptibility to many biotic and abiotic stresses.

Among the several biotic factors Mung bean yellow mosaic disease (MYMD) is one of the major devastating diseases causing severe yield losses in mung bean. The MYMD caused by mung bean yellow mosaic virus (MYMV) was first reported in India during 1955 (Nariani, 1960). MYMV is a member of the family Gemini viridae, belongs to the genus begomovirus (Bos, 1999) and is known to be transmitted by whitefly (*Bemisia tabaci* Genn.) in a persistent, circulative manner (William *et al*., 1968). It has long been a great threat to legume crops. These are plant infecting single stranded DNA viruses composed of either monopartite (a single DNA) or bipartite (with two DNA components : DNA-A and DNA-B) based on their genome organization (Mansoor *et al*., 2003 and Jeske 2009). It is wide spread in most of the South East Asian countries. Resistant cultivars exhibiting stable yields are rarely found (Dharajiya *et al*., 2018). Greengram plants infected with MYMV generally show yellowing or chlorosis of leaves followed by necrosis, shortening of internodes and severe stunting of plants with no yield or few flowers and deformed pods produced with small, immature and shrivelled seeds (Akhtar*et al*., 2009). MYMV reduce the yield upto 85 per cent depending on the severity of the infection and plant growth stage (Naimuddin, 2001). To overcome this vector borne viral disease, different strategies are formed, but no breakthrough is found for cost effective management. Though chemical management of vector is seen as a simple measure, it is not cost-effective, since numerous sprays of insecticides are required to control whitefly. Recurrent sprayings also lead to health hazard and ecological imbalance of living organisms. On the contrary, use of virus resistant varieties is the best approach to alleviate occurrence of MYMV in areas where the infection is a recurring constraint (Meti *et al*., 2017). Use of resistant crop varieties is considered as the reasonable, robust and perfect method of controlling viral diseases.

A good quality research directed towards screening mungbean cultivars against MYMV for the identification of resistant sources is way forward. Therefore, the present study was investigated to assess variability existing among the genotypes and the genetic behaviour of mungbean genotypes against MYMV under natural environment conditions in the semiarid tracts of Karnataka.

Material and Methods

In the present study two experiments were conducted.

Experiment 1

Field experiment was carried out during *kharif* 2019, at the research plot of Department of Genetics and Plant Breeding, GKVK, Bengaluru. 302 mungbean genotypes including 250 advanced breeding lines (ABLs) procured from UAS, Dharwad and 50 germplasm accessions procured from IIPR, Kanpur along with 2 checks (China mung and LM 1668) were evaluated for various agronomic traits.

The seeds of each treatment were sown in a single row with a spacing of 30 x 10 cm spacing in augmented design. Ten days after sowing, seedlings were thinned-out to maintain a spacing of 0.10 m between plants and 0.30 m between rows. Recommended crop production practices were followed to raise a good crop. All recommended agronomic and cultivation practices of mung bean were followed with basal fertilizer application of N - 0.5 kg : P - 6.5 kg : K - 0.3 kg.

Observations on yield and its related characters like Days to 50 per cent flowering (DFF), Days to maturity (DTM), Plant height(cm) (PH), Number of pods per plant (PP), Number of seedsper pod (SP), Seed yield per plant (gm) (SYP) and Seed index (SI) were recorded and subjected for statistical analysis.

Experiment 2

In the second experiment, another set of genotypes including all the 302 genotypes were screened for their response to MYMV disease at the research plot of Department of Genetics and Plant Breeding, GKVK, Bengaluru under natural infection conditions in *summer*, 2020 and the same agronomic practices were followed as mentioned in the experiment I. Susceptible checks were sown as infector rows after every three rows of treatment genotypes all around the experimental plot to provide uniform disease inoculum to the test genotypes.

The genotypes were examined for the appearance of first typical symptoms of MYMV disease and disease severity in each of the genotypes was scored at 30, 45 and 55 days after sowing (DAS) using 1-6 scale developed by world vegetable center and modified by Akhtar *et al*. (2009) (Table 1). Based on the average disease scale, the per cent disease index (PDI) was calculated as the ratio of sum of numerical observations to the product of maximum disease scale and number of observations and expressed in per cent.

$$\text{per cent Disease Indeex} = \frac{\text{Summation of all ratings}}{\text{Total No. of ratings x Maximum disease grade}} \times 100$$

Results and Discussion

Analysis of Variance

Analysis of variance (ANOVA) was carried out for eight yield and yield related traits to test the significance of differences among the green gram genotypes under study (Table 2). The analysis of variance revealed statistical significant differences among the genotypes, indicating the presence of genetic variability for almost all the traits studied except for days to 50 per cent flowering. Similar findings were obtained by Esimu *et al*. (2020) for all other characters except days to 50 per cent flowering. Among the characters, seeds per pod exhibited significant differences at 5 per cent andthe remaining traitsshowed highly significant differences.

Genetic Variability Studies

An assessment of heritable and non-heritable components from the total variability is indispensable in adopting suitable breeding procedure. The extent of variability was also assessed by computing the Phenotypic Coefficient of Variation(PCV) and Genotypic Coefficient of Variation (GCV). The results demonstrating range, mean, PCV and GCV, heritability and genetic advance estimates for eight characters in the study are presented in Table 3. Similar to the findings of Ramakrishnan *et al*. (2018), in this study presence of narrow gap between PCV and GCV for all the characters except seeds per pod suggested that expression of these traits had low environmental influence. However, seeds per pod exhibited high PCV and moderate GCV.

The highest estimates of PCV and GCV value were observed for seed yield per plant. Estimates of GCV were found to be moderate for plant height, pod length, seeds per pod and seed index. Likewise, moderate PCV values were found for the same characters

Table 1

Disease scoring for MYMV

Symptom description	Per cent Disease Index (PDI) (%)	Response
No visible symptoms on leaves	0.01 - 10.00	Highly resistant (HR)
Small yellow specks with restricted spread covering up to 5 % leaf area	10.01 - 25.00	Resistant (R)
Yellow mottling covering 5.1-15 % leaf area	25.01 - 40.00	Moderately resistant (MR)
Yellow mottling and discoloration of 15.1-30 % leaf area	40.01 - 60.00	Moderately susceptible (MS)
Pronounced yellow mottling and discoloration of leaves (covering 30.1-75 % of area) and pods, reduction in leaf size and stunting of plants	60.01 - 80.00	Susceptible (S)

(Akhtar *et al*. (2009)

TABLE 2
Analysis of variance for yield and yield contributing characters

Source	Df	DFF	DTM	PH	PL	PP	SP	SYP	SI
Block (ignoring Treatments)	20	7.52 *	4.69 *	408.51 **	1.51 **	54.78 **	2.83	10.99 **	0.37 **
Treatment (eliminating Blocks)	301	4.28	5.17 **	67.9 **	1.99 **	25.78 **	3.68 *	11.09 **	0.39 **
Treatment: Check	1	0.02	18.67 **	2.47	0.52 **	14.88	1.97	0.44 *	0.07
Treatment: Test and Test vs. Check	300	4.29	5.13 **	68.11 **	2 **	25.82 **	3.68 *	11.12 **	0.39 **
Residuals	20	2.87	1.77	3.57	0.04	6.88	1.79	0.08	0.06
CD @ 5%		4.43	3.48	4.94	0.51	6.86	3.5	0.72	0.66

*Significant @ P =0.05 ; **Significant @ P = 0.01; ***Significant @ P = 0.001; Df: Degrees of freedom; DFF: Days to 50% flowering; DTM: Days to maturity; PH: Plant height (cm); PL: Pod length; PP: Pods per plant; SP: Seeds per pod; SYP: Seed yield per plant; SI: Seed index

except seeds per pod. Moderate GCV and PCV values suggested that these characters were under the influence of additive gene action. Lowest magnitude of PCV and GCV was recorded for days to maturity and days to 50 per cent flowering. Similar findings were earlier reported by Ramakrishnan *et al*. (2018).

High GCV estimates recorded for pods per plant, seed yield per plant and high PCV estimates recorded for pods per plant, seeds per pod and seed yield per plant, which suggested the possibility of improvement through phenotypic selection. These findings are in confirmation with Esimu *et al*. (2020).

The magnitude of range for characters studied was wide, indicating the possibilities of exploiting the available variability for further genetic improvement programmes. One way to achieve this is to explore the largely untapped reservoir of allelic diversity that remains hidden within existing population of germplasm.

Similar to the results with Esimu *et al*. (2020), in the present study broad sense heritability for different characters showed highest heritability for all the characters except days to 50 per cent flowering and seeds per pod where both showed moderate heritability. Heritability which is an index of transmissibility is primarily of interest to a plant breeder. Higher the heritability value of a character less will be the environmental influence for expression of that

TABLE 3
Estimates of mean, variability, heritability, genetic advance for eight yield characters

Trait	Mean ± SE	Range		CV		Broad sense heritability (%)	GAM (%)
		Min	Max	PCV (%)	GCV (%)		
DFF	39.8 ± 0.13	33.48	44.98	5.14	2.88	31.42	3.33
DTM	59.39 ± 0.14	36.19	64.19	3.84	3.12	66.09	5.24
PH	57.88 ± 0.51	37.35	80.53	15.24	14.89	95.42	30
PL	8.02 ± 0.08	3.8	15.38	17.69	17.52	98.11	35.81
PP	19.24 ± 0.32	7.72	36.62	27.85	24.29	76.04	43.69
SP	8.85 ± 0.11	3.85	14.05	21.28	14.97	49.46	21.72
SYP	5.43 ± 0.19	1.26	48.05	62.41	62.21	99.33	127.9
SI	3.67 ± 0.04	1.83	6.05	17.19	15.76	84	29.79

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character, thereby indicating better opportunity for selecting a genetically good individual. In the present experiment, very high to high heritability was observed suggesting that these characters might be highly heritable and less influenced by environment and selecting genotypes on the basis of such characters would be rewarding.

Heritability values coupled with genetic advance as per cent of mean (GAM) would be more reliable and useful in formulating selection procedure. In the present study, high heritability estimates in broad sense coupled with high GAM recorded for almost all the characters except days to 50 per cent flowering. Low GAM was recorded for days to 50 per cent flowering and days to maturity and highest GAM was recorded for seed yield per plant coupled with highest broad sense heritability. Similar findings were reported by Esimu *et al*. (2020). Hence, selection for these characters would be rewarding as they were least influenced by environment.

Responses of Genotypes to MYMV under Natural infection

Three hundred and two mung bean genotypes were evaluated under field condition for their response against the MYMD by raising infector rows in between test entries. The genotypes differed for their responses to infection by MYMV under natural infection conditions.

Lowest PDI was recorded in 25 genotypes which ranged from 19.92 to 24.90 per cent and they were at least lower by 48 per cent compared with those of susceptible check China mung (73.04%) (Table 4). Highest PDI was recorded in susceptible check LM-1668 (78.02 %) and yellow specks, the typical initial symptoms of MYMV disease, appeared earlier in both the susceptible checks, compared with those in other genotypes under natural infection conditions. In those resistant lines, appearance of the initial symptoms delayed and also estimates of PDI remained lower than the other genotypes in the experiment.

Number and percentage of genotypes under resistant, moderately resistant and moderately susceptible in

TABLE 4

Disease reaction of different mung bean genotypes against MYMV

Genotypes	Per cent Disease Index	Disease score	Disease grade
GG-ABL-1	31.54	3	MR
GG-ABL-2	29.88	3	MR
GG-ABL-3	36.52	3	MR
GG-ABL-4	28.22	3	MR
GG-ABL-5	36.52	3	MR
GG-ABL-6	38.18	3	MR
GG-ABL-7	39.84	3	MR
GG-ABL-8	28.22	3	MR
GG-ABL-9	34.86	3	MR
GG-ABL-10	33.20	3	MR
GG-ABL-11	39.84	3	MR
GG-ABL-12	38.18	3	MR
GG-ABL-13	39.84	3	MR
GG-ABL-14	39.84	3	MR
GG-ABL-15	29.88	3	MR
GG-ABL-16	36.52	3	MR
GG-ABL-17	54.78	4	MS
GG-ABL-18	36.52	3	MR
GG-ABL-19	38.18	3	MR
GG-ABL-20	39.84	3	MR
GG-ABL-21	39.84	3	MR
GG-ABL-22	38.18	3	MR
GG-ABL-23	36.52	3	MR
GG-ABL-24	51.46	4	MS
GG-ABL-25	33.20	3	MR
GG-ABL-26	34.86	3	MR
GG-ABL-27	31.54	3	MR
GG-ABL-28	21.58	2	R
GG-ABL-29	46.48	4	MS
GG-ABL-30	46.48	4	MS
GG-ABL-31	44.82	4	MS
GG-ABL-32	51.46	4	MS
GG-ABL-33	51.46	4	MS
GG-ABL-34	29.88	3	MR
GG-ABL-35	29.88	3	MR
GG-ABL-36	34.86	3	MR
GG-ABL-37	21.58	2	R
GG-ABL-38	34.86	3	MR
GG-ABL-39	34.86	3	MR
GG-ABL-40	36.52	3	MR

Genotypes	Per cent Disease Index	Disease score	Disease grade
GG-ABL-41	38.18	3	MR
GG-ABL-42	48.14	4	MS
GG-ABL-43	31.54	3	MR
GG-ABL-44	34.86	3	MR
GG-ABL-45	36.52	3	MR
GG-ABL-46	38.18	3	MR
GG-ABL-47	29.88	3	MR
GG-ABL-48	38.18	3	MR
GG-ABL-49	29.88	3	MR
GG-ABL-50	29.88	3	MR
GG-ABL-51	36.52	3	MR
GG-ABL-52	38.18	3	MR
GG-ABL-53	34.86	3	MR
GG-ABL-54	44.82	4	MS
GG-ABL-55	31.54	3	MR
GG-ABL-56	33.20	3	MR
GG-ABL-57	29.88	3	MR
GG-ABL-58	33.20	3	MR
GG-ABL-59	34.86	3	MR
GG-ABL-60	44.82	4	MS
GG-ABL-61	53.12	4	MS
GG-ABL-62	31.54	3	MR
GG-ABL-63	51.46	4	MS
GG-ABL-64	51.46	4	MS
GG-ABL-65	56.44	4	MS
GG-ABL-66	53.12	4	MS
GG-ABL-67	34.86	3	MR
GG-ABL-68	33.20	3	MR
GG-ABL-69	34.86	3	MR
GG-ABL-70	48.14	4	MS
GG-ABL-71	48.14	4	MS
GG-ABL-72	36.52	3	MR
GG-ABL-73	38.18	3	MR
GG-ABL-74	44.82	4	MS
GG-ABL-75	38.18	3	MR
GG-ABL-76	49.80	4	MS
GG-ABL-77	49.80	4	MS
GG-ABL-78	51.46	4	MS
GG-ABL-79	36.52	3	MR
GG-ABL-80	39.84	3	MR
GG-ABL-81	39.84	3	MR
GG-ABL-82	34.86	3	MR
GG-ABL-83	48.14	4	MS
GG-ABL-84	51.46	4	MS
GG-ABL-85	51.46	4	MS
GG-ABL-86	53.12	4	MS
GG-ABL-87	31.54	3	MR
GG-ABL-88	33.20	3	MR
GG-ABL-89	44.82	4	MS
GG-ABL-90	36.52	3	MR
GG-ABL-91	44.82	4	MS
GG-ABL-92	36.52	3	MR
GG-ABL-93	51.46	4	MS
GG-ABL-94	43.16	4	MS
GG-ABL-95	44.82	4	MS
GG-ABL-96	51.46	4	MS
GG-ABL-97	29.88	3	MR
GG-ABL-98	49.80	4	MS
GG-ABL-99	29.88	3	MR
GG-ABL-100	31.54	3	MR
GG-ABL-101	53.12	4	MS
GG-ABL-102	51.46	4	MS
GG-ABL-103	51.46	4	MS
GG-ABL-104	29.88	3	MR
GG-ABL-105	46.48	4	MS
GG-ABL-106	31.54	3	MR
GG-ABL-107	34.86	3	MR
GG-ABL-108	46.48	4	MS
GG-ABL-109	36.52	3	MR
GG-ABL-110	36.52	3	MR
GG-ABL-111	34.86	3	MR
GG-ABL-112	29.88	3	MR
GG-ABL-113	31.54	3	MR
GG-ABL-114	34.86	3	MR
GG-ABL-115	36.52	3	MR
GG-ABL-116	38.18	3	MR
GG-ABL-117	38.18	3	MR
GG-ABL-118	39.84	3	MR
GG-ABL-119	36.52	3	MR
GG-ABL-120	33.20	3	MR
GG-ABL-121	26.56	3	MR
GG-ABL-122	34.86	3	MR
GG-ABL-123	34.86	3	MR
GG-ABL-124	33.20	3	MR
GG-ABL-125	31.54	3	MR
GG-ABL-126	31.54	3	MR
GG-ABL-127	29.88	3	MR
GG-ABL-128	28.22	3	MR

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Genotypes	Per cent Disease Index	Disease score	Disease grade
GG-ABL-129	29.88	3	MR
GG-ABL-130	29.88	3	MR
GG-ABL-131	23.24	2	R
GG-ABL-132	33.20	3	MR
GG-ABL-133	38.18	3	MR
GG-ABL-134	39.84	3	MR
GG-ABL-135	44.82	4	MS
GG-ABL-136	31.54	3	MR
GG-ABL-137	39.84	3	MR
GG-ABL-138	38.18	3	MR
GG-ABL-139	34.86	3	MR
GG-ABL-140	33.20	3	MR
GG-ABL-141	33.20	3	MR
GG-ABL-142	29.88	3	MR
GG-ABL-143	31.54	3	MR
GG-ABL-144	24.90	2	R
GG-ABL-145	38.18	3	MR
GG-ABL-146	36.52	3	MR
GG-ABL-147	33.20	3	MR
GG-ABL-148	33.20	3	MR
GG-ABL-149	19.92	2	R
GG-ABL-150	34.86	3	MR
GG-ABL-151	19.92	2	R
GG-ABL-152	33.20	3	MR
GG-ABL-153	34.86	3	MR
GG-ABL-154	34.86	3	MR
GG-ABL-155	38.18	3	MR
GG-ABL-156	34.86	3	MR
GG-ABL-157	38.18	3	MR
GG-ABL-158	38.18	3	MR
GG-ABL-159	39.84	3	MR
GG-ABL-160	36.52	3	MR
GG-ABL-161	33.20	3	MR
GG-ABL-162	31.54	3	MR
GG-ABL-163	33.20	3	MR
GG-ABL-164	29.88	3	MR
GG-ABL-165	33.20	3	MR
GG-ABL-166	36.52	3	MR
GG-ABL-167	46.48	4	MS
GG-ABL-168	38.18	3	MR
GG-ABL-169	33.20	3	MR
GG-ABL-170	36.52	3	MR
GG-ABL-171	38.18	3	MR
GG-ABL-172	36.52	3	MR
GG-ABL-173	38.18	3	MR
GG-ABL-174	31.54	3	MR
GG-ABL-175	31.54	3	MR
GG-ABL-176	33.20	3	MR
GG-ABL-177	28.22	3	MR
GG-ABL-178	31.54	3	MR
GG-ABL-179	38.18	3	MR
GG-ABL-180	39.84	3	MR
GG-ABL-181	39.84	3	MR
GG-ABL-182	39.84	3	MR
GG-ABL-183	38.18	3	MR
GG-ABL-184	33.20	3	MR
GG-ABL-185	31.54	3	MR
GG-ABL-186	34.86	3	MR
GG-ABL-187	36.52	3	MR
GG-ABL-188	36.52	3	MR
GG-ABL-189	21.58	2	R
GG-ABL-190	48.14	4	MS
GG-ABL-191	33.20	3	MR
GG-ABL-192	21.58	2	R
GG-ABL-193	34.86	3	MR
GG-ABL-194	39.84	3	MR
GG-ABL-195	39.84	3	MR
GG-ABL-196	19.92	2	R
GG-ABL-197	38.18	3	MR
GG-ABL-198	33.20	3	MR
GG-ABL-199	31.54	3	MR
GG-ABL-200	23.24	2	R
GG-ABL-201	38.18	3	MR
GG-ABL-202	38.18	3	MR
GG-ABL-203	31.54	3	MR
GG-ABL-204	34.86	3	MR
GG-ABL-205	28.22	3	MR
GG-ABL-206	26.52	3	MR
GG-ABL-207	33.20	3	MR
GG-ABL-208	33.20	3	MR
GG-ABL-209	34.86	3	MR
GG-ABL-210	39.84	3	MR
GG-ABL-211	33.20	3	MR
GG-ABL-212	26.56	3	MR
GG-ABL-213	19.92	2	R
GG-ABL-214	36.52	3	MR
GG-ABL-215	33.20	3	MR
GG-ABL-216	31.54	3	MR

Genotypes	Per cent Disease Index	Disease score	Disease grade
GG-ABL-217	23.24	2	R
GG-ABL-218	38.18	3	MR
GG-ABL-219	29.88	3	MR
GG-ABL-220	21.58	2	R
GG-ABL-221	33.20	3	MR
GG-ABL-222	34.86	3	MR
GG-ABL-223	36.52	3	MR
GG-ABL-224	36.52	3	MR
GG-ABL-225	29.88	3	MR
GG-ABL-226	31.54	3	MR
GG-ABL-227	28.22	3	MR
GG-ABL-228	29.88	3	MR
GG-ABL-229	36.52	3	MR
GG-ABL-230	36.52	3	MR
GG-ABL-231	33.20	3	MR
GG-ABL-232	23.24	2	R
GG-ABL-233	33.20	3	MR
GG-ABL-234	38.18	3	MR
GG-ABL-235	34.86	3	MR
GG-ABL-236	31.54	3	MR
GG-ABL-237	29.88	3	MR
GG-ABL-238	33.20	3	MR
GG-ABL-239	38.18	3	MR
GG-ABL-240	38.18	3	MR
GG-ABL-241	24.90	2	R
GG-ABL-242	33.20	3	MR
GG-ABL-243	36.52	3	MR
GG-ABL-244	49.80	4	MS
GG-ABL-245	34.86	3	MR
GG-ABL-246	36.52	3	MR
GG-ABL-247	24.90	2	R
GG-ABL-248	36.52	3	MR
GG-ABL-249	33.20	3	MR
GG-ABL-250	31.54	3	MR
SML 1082	36.52	3	MR
HUM 12	19.92	2	R
PUSA VISHAL	36.52	3	MR
ML 1452	34.86	3	MR
VRM (Gg-1)	34.86	3	MR
MG-331	38.18	3	MR
TMB 96-2	59.76	4	MS
PM-2	58.10	4	MS
PUSA BOLD- 2	54.78	4	MS
Co GG- 912	31.54	3	MR

Genotypes	Per cent Disease Index	Disease score	Disease grade
CHINA MUNG -1	39.84	3	MR
BM- 64	56.44	4	MS
PDM- 178	39.84	3	MR
SML- 832	53.12	4	MS
PUSA- 0891	39.84	3	MR
AKP/ NP/8/9	21.58	2	R
ML- 5	31.54	3	MR
EC- 396399	39.84	3	MR
IC- 121220	34.86	3	MR
EC- 520034- 1	34.86	3	MR
EC 496839	23.24	2	R
OMG- 1030	21.58	2	R
COPERGAAM	34.86	3	MR
SHALIMAR-1	53.12	4	MS
IC- 417873	29.88	3	MR
IC- 540483	38.18	3	MR
PS- 16	21.58	2	R
EC- 396103	51.46	4	MS
OMG- 1045 (PMR)	36.52	3	MR
EC 496839	58.10	4	MS
SML- 1455	51.46	4	MS
LM- 258	39.84	3	MR
IC- 314419	43.16	4	MS
UPM- 98-1	36.52	3	MR
EC- 520016	39.84	3	MR
EC- 520014	58.10	4	MS
BM- 64	54.78	4	MS
IC- 11443-1	39.84	3	MR
EC- 398925	38.18	3	MR
EC- 391178 (4)	38.18	3	MR
EC- 550831	21.58	2	R
TJM- 3	23.24	2	R
EC- 398131	23.24	2	R
IC- 314851	36.52	3	MR
IC- 121237	36.52	3	MR
RMG- 353	21.58	2	R
IPM- 302-2	36.52	3	MR
EC- 426841	39.84	3	MR
TM- 9-2	38.18	3	MR
IC- 314854	39.84	3	MR
CHINA MUNG	73.04	5	S
LM- 1668	78.02	5	S

PDI- Percent Disease Index; DS- Disease Score;
DG- Disease Grade

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ABLs, Germplasm and both are presented in Table 5. Out of three hundred genotypes, 25 genotypes (8.33 %) were characterized as resistant (2), 222 genotypes (74 %) were moderately resistant (3) and 53 genotypes (17.66 %) were under moderately susceptible (4). It was recorded that, out of 250 ABLs 16 were resistant (6.4 %), 193 under moderately resistant (77.2 %) and 41 under moderately susceptible (16.4 %) category. Out of 50 germplasms 9 under resistant (18 %), 29 under moderately resistant (58 %) and 12 under moderately susceptible (24 %) category. No genotypes characterized were under remaining category *viz.,* highly resistant, susceptible and highly susceptible. The results of present screening were in accordance with some other findings. Screening of mungbean entries against MYMV was also carried by Ahmad *et al*. (2017) who failed to find any entry under the category of highly resistant.

PDI of ABLs ranged from 19.92 to 56.44 per cent. Lowest PDI in ABLs was recorded in GG-ABL-149, GG-ABL-151, GG-ABL-196, GG-ABL-213 and highest PDI in ABLs was recorded in GG-ABL- 65. PDI of germplasm ranged from 19.92 to 59.76 per cent. Lowest and highest PDI in germplasm was recorded in HUM 12 and TMB 96-2, respectively.

The study revealed that 25 genotypes including 16 ABLs and 9 germplasm have recorded lowest PDI and possess resistance to MYMV under field conditions (Table 6).

High to moderate magnitude of PCV and GCV and high broad sense heritability coupled with GAM was recorded for the characters like seed yield per plant, pods per plant and pod length. Hence these characters can be used as an indirect selection criteria for yield improvement in mung bean. Host resistance is considered as a novel and cheapest way of mitigating pests and diseases. Hence, the outcome of the current experiment paves way for utilizing the identified

TABLE 6
List of 25 genotypes resistant to MYMV

Genotypes	Percent Disease Index	Disease score	Disease grade
GG-ABL-28	21.58	2	R
GG-ABL-37	21.58	2	R
GG-ABL-131	23.24	2	R
GG-ABL-144	24.9	2	R
GG-ABL-149	19.92	2	R
GG-ABL-151	19.92	2	R
GG-ABL-189	21.58	2	R
GG-ABL-192	21.58	2	R
GG-ABL-196	19.92	2	R
GG-ABL-200	23.24	2	R
GG-ABL-213	19.92	2	R
GG-ABL-217	23.24	2	R
GG-ABL-220	21.58	2	R
GG-ABL-232	23.24	2	R
GG-ABL-241	24.9	2	R
GG-ABL-247	24.9	2	R
HUM 12	19.92	2	R
AKP/ NP/8/9	21.58	2	R
EC 496839	23.24	2	R
OMG- 1030	21.58	2	R
PS- 16	21.58	2	R
EC- 550831	21.58	2	R
TJM- 3	23.24	2	R
EC- 398131	23.24	2	R
RMG- 353	21.58	2	R

TABLE 5
Percentage of resistant, moderately resistant and moderately susceptible cultivars against MYMV disease

Category	Advanced Breeding Lines (ABLs)		Germplasm		Advanced Breeding Lines + Germplasm Total = 300	
	Numbers	Percentage	Numbers	Percentage	Numbers	Percentage
Resistant [2]	16	6.4	9	18	25	8.33
Moderately resistant [3]	193	77.2	29	58	222	74
Moderately susceptible [4]	41	16.4	12	24	53	17.66

resistant sources in breeding progamme to improve local cultivars for developing MYMV resistant varieties, thereby enhancing the production and productivity of mung bean.

Future Line of Work

Viruses such as the single-stranded DNA begomoviruses are emergent problems worldwide (Rojas and Gilbertson, 2008 and Seal *et al*., 2006) as they have higher mutation rates, recombination and re-assortment than other pathogens and distinct evolutionary dynamics compared to bacterial and fungal phytopathogens. Therefore, breeding and screening of mung bean for resistance against MYMV should be carried out regularly and regionally for identification and exploitation of new sources of resistance.

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