

## Assessment of Mungbean [*Vigna radiata* (L.) Wilczek] Genotypes for Genetic Divergence and Yellow Mosaic Disease (YMD) Resistance

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**ABSTRACT:** The experimental material consisting of 106 genotypes were evaluated for 14 yield and its attributing traits during *Kharif* 2021 to ascertain genetic divergence, path coefficients and the MYMV disease resistance. The maximum positive direct effect on seed yield per plant was observed by the biological yield per plant followed by harvest index, days to flowering, plant height and number of branches per plant. Number of clusters per plant and number of seeds per pod apart from their direct effect on seed yield exhibited a positive indirect effect *via* days to maturity, biological yield, harvest index and 100-seed weight. Therefore, these traits should be given higher priority in direct selection for high-yielding mungbean genotypes. No association between MYMV and yield attributing traits was observed. The hierarchical cluster analysis classified mungbean genotypes into ten discrete clusters indicating the presence of substantial genetic diversity in the evaluated genotypes. The most diverse genotypic pairs were Pusa Vishal and EC 393407 followed by VGG-2 & IPM 205-7, ML 1628 & EC 393407, IPM 409-4 & VGG-2, SML 1018 & VGG-2. These genotypes were found to have heterogenic origin and can results into most diverse heterotic combinations among all the genotypes studied. After the field screening of 106 genotypes using the infector row technique against MYMV 23 genotypes were found to be highly resistant, 42 resistant, 33 moderately susceptible, six susceptible and two were found highly susceptible. Based on yield and other morphological traits studied, the genotypes ML 1628, ML 2037, SML 1023, MH 521, MH 560, MH 565, IPM 312-394, IPM 410-3 and EC 581523 were found superior and exhibited sufficient diversity and can be utilized for future mungbean improvement programs.

**Keywords:** Genetic diversity, MYMV, Mungbean.

### INTRODUCTION

Population explosion, malnutrition, narrowing gene pool, climate change, depleting soil health, shrinking water resources, poverty and less resource availability in agriculture sector are major challenges affecting the food and nutritional security worldwide. The best and easiest way to solve this problem is to diversify the agriculture (Gupta *et al.*, 2022). Pulses occupy pivotal position among food grains particularly in India, where the majority of population is vegetarian and depends on them for protein supplement (Sharma *et al.*, 2023). Mungbean (*Vigna radiata* (L.) Wilczek.;  $2n=22$ ) is a native crop of the Indo-Burma region of the Hindustan centre (Vavilov, 1935; Candolle, 1988). Area wise mungbean is second most important legume crop after chickpea (*Cicer arietinum*) in Indian agriculture (Anonymous, 2022). It is highly nutritious and an inexpensive source of easily digestible high-quality protein, amino acids, lipids, fat, fiber, ash, and carbohydrates and provides 334–344 kcal energy (Rohilla *et al.*, 2022). Mungbean has the ability to fix atmospheric nitrogen in symbiotic association with Rhizobium bacteria, which enables them to meet their

own nitrogen requirement and also benefit the succeeding crops (Ali *et al.*, 1992). Besides improving the soil quality, they reduce the burden of nitrogen requirements when grown in rotation with cereals (Yaqub *et al.*, 2010; Sharma *et al.*, 2023). Mungbean seeds are free from anti-nutritional factors such as trypsin inhibitor, phytohaemagglutinin and tannin (Chen *et al.*, 2003). Mungbean sprouts are becoming popular in certain vegetarian diets as sprouting increases thiamine, niacin and ascorbic acid (Kavas and El 1991). The main reason for stagnancy in productivity of mungbean is attributed to poor harvest index, lack of genetic diversity and susceptibility to biotic and abiotic stresses ultimately leading to yield instability (Chauhan *et al.*, 2010; Pratap *et al.*, 2019). The pulse breeding programs emphasized the compulsion of creating variability for yield traits and identifying the lines for new areas. The path analysis assists in differentiating the correlation coefficient of yield attributing components with seed yield into its direct and indirect effects to confirm the actual contribution of an attribute as well as its influence through other traits. Yellow Mosaic Disease (YMD) is the foremost production constraint in Asia (Khattak *et al.* 2000; Selvi *et al.*

2006; Iqbal *et al.*, 2011; Paul *et al.*, 2013) which may lead up to 100% yield losses under severe incidence. Depending on the severity of the MYMV infection, the yield penalty may reach up to 85% (Haq *et al.*, 2010). It is caused by a virus of the *begomovirus* genus belonging to the family *Geminiviridae*, which are transmitted by whitefly (*Bemisia tabaci*), an insect vector, in a continual mode (Selvi *et al.*, 2006; Malathi *et al.*, 2008). Assessing the new germplasm lines to determine variability for yield, its components and YMD resistance is the need of the present-day mungbean breeding program. In this context, study has been planned to identify the accessions with the most potential and valuable traits for yield improvement along with resistance to YMD.

## MATERIALS AND METHODS

**Experimental site.** The field experiment was conducted at the Pulses Research Area of the Department of Genetics and Plant Breeding, Chaudhary

Charan Singh Haryana Agricultural University, Hisar, Haryana.

**Climate:** Weather conditions such as temperature, precipitation, bright sunshine hours and relative humidity according to Standard Meteorological Week (SMW) during the growth period of the crop is given in Figs. 1-4.

**Experimental material:** Experimental material composed of 106 diverse genotypes of mungbean (Table 1). One infector row (SML 1082) was grown after every five test entries and all around the experimental plot in order to enhance infection of yellow mosaic disease under field conditions.

**Experimental design and layout plan:** The experiment was laid out in a Randomized Block Design in two replications. Each genotype was grown in a row of 4m length with row to row 30 cm and plant to plant 10 cm spacing. All the recommended package of practices was adopted to raise healthy crop.

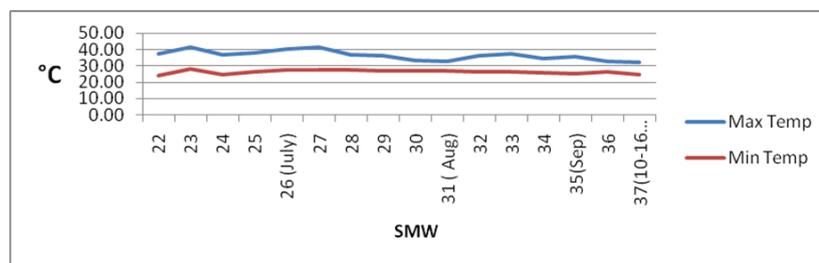


Fig. 1. Maximum and minimum temperature.

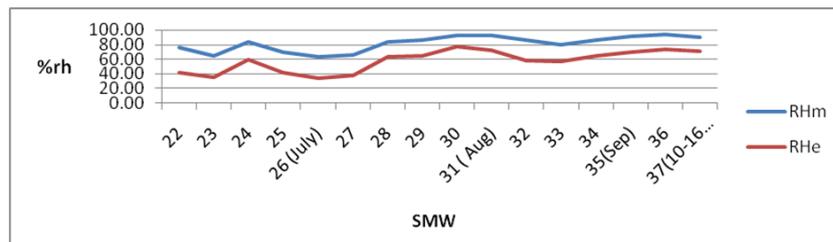


Fig. 2. Relative humidity for morning and evening during the crop growth period.

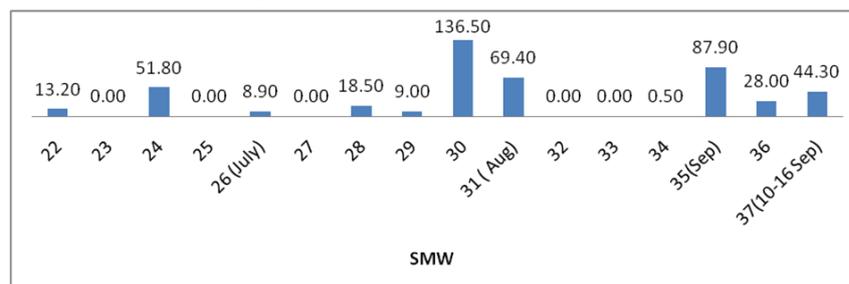


Fig. 3. Rainfall in millimeter during the crop growth period.

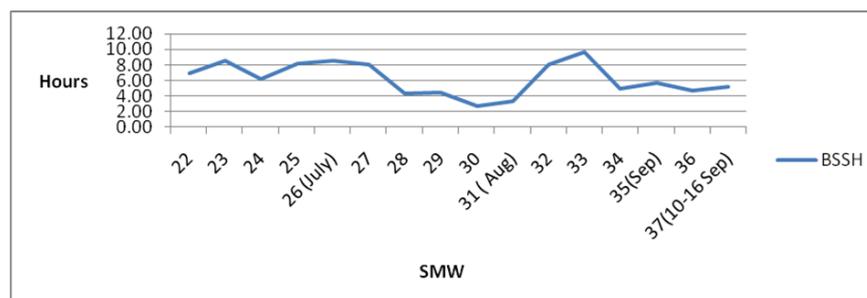


Fig. 4. Bright sun shine hours during the crop growth period.

**Table 1: List of genotypes used in present investigation.**

Sr. No.	Genotype	Sr. No.	Genotype	Sr. no	Genotype
1.	2KM 101	37.	IPM 06-5	73	PDM 96-262
2.	2KM 111	38.	IPM 2-03	74	PLM 24
3.	2KM 112	39.	IPM 205-7	75	PLM 62
4.	2KM 115	40.	IPM 302-2	76	PLM 76
5.	2KM 117	41.	IPM 312-19	77	PM 11-51
6.	2KM 138	42.	IPM 312-394	78	PM 99-3
7.	2KM 216	43.	IPM 409-4	79	Pusa 0672
8.	ADGG 13034	44.	IPM 410-3	80	Pusa 0871
9.	AKM 9904	45.	KM 2211	81	Pusa 1141
10.	Asha	46.	KM 2241	82	Pusa 1142
11.	CH 210-3	47.	KM 2328	83	Pusa 1501
12.	COGG 1102	48.	M 395	84	Pusa 1502
13.	COGG 13-14	49.	M 605	85	Pusa 1542
14.	COGG 13-19	50.	MH 521	86	Pusa 1601
15.	COGG-8	51.	MH 539	87	Pusa 1642
16.	EC 251552	52.	MH 560	88	Pusa 9531
17.	EC 30400	53.	MH 565	89	Pusa Ratna
18.	EC 393407	54.	MH 709	90	Pusa Vishal
19.	EC 393410	55.	MH 729	91	RMG 991
20.	EC 399233	56.	MH 921	92	Samrat
21.	EC 470090	57.	MH 98-1	93	SHIM 12-1
22.	EC 470096	58.	ML 1108	94	SML 1018
23.	EC 581523	59.	ML 1451	95	SML 1023
24.	EC 581523B	60.	ML 1628	96	SML 1082
25.	GANGA 8	61.	ML 1907	97	SML 1115
26.	GM- 9926 YMV	62.	ML 2037	98	SML 1194
27.	HUM 16	63.	ML 735	99	SML 1781
28.	HUM 27	64.	ML 759	100	SML 668
29.	HUM 7	65.	ML 776	101	TMB 131
30.	IC 103196	66.	NBPGR 150	102	TMB 163
31.	IC 15276	67.	NDMZ 13-11	103	TMB 196
32.	IC 39574	68.	NDMZ 13-12	104	TRCM 155-1
33.	IPM 02-14	69.	NDMZ 15-2	105	VGG-1
34.	IPM 02-17	70.	NDMZ 215-1	106	VGG-2
35.	IPM 02-19	71.	OUM 11-5		
36	IPM 03-2	72.	PANT M-5		

**RESULTS AND DISCUSSION**

The direction of direct and indirect effects along with the magnitude of different yields and yield attributing traits decide the overall effect on the seed yield. Table 2 shows the direct and indirect contributions of each trait to seed yield per plant.

**Direct effect.** The path coefficient analysis on genotypic basis revealed that among the 11 traits studied, seven traits exhibited positive direct effect and four showed negative direct effect on seed yield. The maximum positive direct effect on seed yield per plant was exhibited by biological yield per plant (0.966) followed by harvest index (0.738), number of clusters per plant (0.054), days to 50% flowering (0.054), number of seeds per pod (0.021), 100-seed weight (0.012), number of branches per plant (0.007) while MYMV (-0.008), number of pods per plant (-0.011), plant height (-0.020) and days to maturity (-0.060) exhibited negative direct effect. Other traits which were not included in the study cause the residual effect of 0.00596.

**Indirect effect.** Biological yield exhibited positive indirect effect *via* number of clusters per plant, number of pods per plant, number of seeds per pod, plant height and 100-seed weight and negative indirect effect *via* days to 50% flowering, number of branches per plant and harvest index. Likewise, harvest index exhibited positive indirect effect *via* 100-seed weight, number of seeds per pod, number of pods per plant and number of clusters per plant and negative indirect effect *via* days

to maturity, days to 50% flowering, plant height and biological yield.

Clusters per plant exhibited positive indirect effect *via* biological yield per plant, harvest index and days to maturity and negative indirect effect *via* days to 50% flowering and number of pods per plant. Number of seeds per pod exhibited positive indirect effect *via* biological yield per plant, harvest index, days to maturity, number of clusters per plant and 100-seed weight and negative indirect effect *via* days to 50% flowering, days to maturity and number of branches per plant. Similarly, 100-seed weight exhibited positive indirect effect *via* harvest index, biological yield per plant, days to maturity, number of seeds per pod and plant height and negative indirect effect *via* days to maturity, days to 50% flowering, plant height and number of branches per plant. Direct effect of biological yield was positive on seed yield but its overall effect reduced by negative indirect effect of all the traits except number of clusters per plant, number of seeds per pod and 100-seed weight. Similarly, for harvest index sufficient negative indirect effect was exhibited by biological yield (-0.386), days to 50% flowering (-0.032) and number of pods per plant (-0.003). Various path coefficients studies by numerous workers in mungbean have been done by Baisakh *et al.* (2016); Sunayana *et al.* (2017); Garg *et al.* (2017); Muthuswamy *et al.* (2019); Ahmad and Belwal (2020); Singh *et al.* (2021) and these researches revealed the similar kind of results for the various traits.

**Genetic divergence.** Based on 12 quantitative traits, the Unweighted Pair Group method using Arithmetic Averages (UPGMA) of Hierarchical Cluster Analysis was applied with City Block Distances to categorize the one hundred six mungbean genotypes. One hundred six mungbean genotypes were classified into ten clusters as shown in Table 3. Cluster I had the maximum number of genotypes (59 genotypes) followed by cluster VIII (19 genotypes), clusters II and III (7 genotypes each), cluster V (5 genotypes), cluster IV (3 genotypes), cluster VI and IX (2 genotypes each) and cluster VII and cluster X (one genotype each). Wesley *et al.* (2020); Sunayana *et al.* (2017); Gayacharan *et al.* (2020); Win *et al.* (2020) identified genetic divergence in mungbean genotypes and classified them, similarly. Table 4 shows the intra- and inter-cluster distances between ten clusters. The maximum intra-cluster distance was found in Cluster I (30.22) followed by Cluster VIII (29.25), Cluster III (25.19), Cluster II (23.01), Cluster V (19.23), Cluster IX (16.22), Cluster IV (16.08) and Cluster VI (7.56). The maximum inter-cluster distance was found between cluster VII and X (84.01) followed by cluster III and X (82.66) and then cluster II and VII (74.23). The minimum inter-cluster distance was recorded between cluster IX and X (16.22) followed by cluster II and cluster IV (35.83) results are in accordance with Singh *et al.* (2021).

The cluster wise mean values for all the twelve quantitative traits (Table 5) revealed that cluster I hadn't any maximum values for mean of any yield attributing trait. So, on the basis of mean values, cluster I doesn't seem to be superior but on critical evaluation of genotypes in this cluster, some superior genotypes were found which had quite fair seed yield per plant *viz.*, MH 709 (12.024 g), IPM 03-2 (11.716 g), MH 729 (11.461 g), ML 2037 (11.324 g), MH 921 (11.245 g),

MH 98-1 (11.185 g) and MH 539 (11.139 g). Cluster II genotypes exhibited the second-highest mean values for the days to maturity (75), plant height (79 cm) and biological yield per plant (55.67 g) while occupying the first position in the number of branches per plant (4.01). Genotypes in cluster III (CH 210-3, EC 251552, EC 30400, EC 393407, EC 393410, EC 399233, EC 470090) showed highest mean for days to 50% flowering (46) and days to maturity (75) and lowest mean values for the number of pods per plant (16), seed yield per plant (6.18 g), biological yield per plant (35.00 g), 100 seed weight (3.09 g). Along with these, genotypes in this cluster were least affected by MYMV (2.3).

Genotypes in cluster IV exhibited the highest mean for number of pods per plant (25) and the second-highest number of clusters per plant (11.7). Cluster V genotypes were maximum affected by MYMV (7.40) and had the minimum number of seeds per pod (6.5) but exhibited the second-highest harvest index (4.13). Cluster VI genotypes had second highest mean for harvest index (21.93) after genotypes of cluster VIII (22.70). Genotypes of cluster VII showed the minimum mean for number of branches per plant (1.40), plant height (48) and several number of clusters per plant (6.40). Cluster VIII (19 genotypes) genotypes were showed the earliest flowering (37) and maturity period (64) with minimum plant height and have a maximum harvest index (22.70). Cluster IX genotypes exhibited the maximum mean for the plant height (85). Cluster X comprises of single genotype that is ML 1628, showed the maximum number of pods per plant (25.70), seed yield per plant (12.37), biological yield per plant (70.27) and 100-seed weight (4.22) along with minimum days to 50% flowering (37).

**Table 2: Direct (diagonal) and indirect (off-diagonal) path coefficient based on genotypic correlation on seed yield in mungbean.**

Traits	DF	DM	NB	PH	NC	NP	NS	BY	HI	HSW	MYMV	SY
<b>DF</b>	<b>0.053</b>	-0.047	0.001	-0.007	-0.016	0.005	-0.009	-0.223	-0.437	-0.005	-0.001	<b>-0.683**</b>
<b>DM</b>	0.042	<b>-0.060</b>	0.002	-0.010	-0.012	0.004	-0.007	0.193	-0.683	-0.005	-0.001	<b>-0.538**</b>
<b>NB</b>	0.009	-0.017	<b>0.007</b>	-0.005	0.001	0.001	-0.003	-0.022	-0.121	-0.002	0.001	<b>-0.150*</b>
<b>PH</b>	0.019	-0.030	0.002	<b>-0.020</b>	0.002	-0.002	-0.002	0.209	-0.326	-0.003	-0.001	<b>-0.152*</b>
<b>NC</b>	-0.016	0.014	0.000	-0.001	<b>0.054</b>	-0.009	0.007	0.586	0.092	0.001	0.000	<b>0.727**</b>
<b>NP</b>	-0.027	0.022	0.000	-0.004	0.042	<b>-0.011</b>	0.009	0.621	0.166	0.002	0.000	<b>0.819**</b>
<b>NS</b>	-0.022	0.020	-0.001	0.002	0.017	-0.005	<b>0.021</b>	0.314	0.214	0.004	-0.001	<b>0.563**</b>
<b>BY</b>	-0.012	-0.012	0.000	-0.004	0.033	-0.007	0.007	<b>0.967</b>	-0.294	0.002	-0.001	<b>0.676**</b>
<b>HI</b>	-0.032	0.056	-0.001	0.009	0.007	-0.003	0.006	-0.386	<b>0.737</b>	0.005	0.001	<b>0.398**</b>
<b>HSW</b>	-0.021	0.028	-0.001	0.005	0.004	-0.002	0.007	0.161	0.282	<b>0.012</b>	0.000	<b>0.475**</b>
<b>MYMV</b>	0.004	-0.004	-0.001	-0.001	0.001	0.000	0.001	0.159	-0.099	0.001	<b>-0.008</b>	<b>0.052</b>

**Residual effect = 0.00596**

**DF:** Days to 50% flowering, **DM:** Days to maturity, **NB:** Number of branches per plant, **PH:** Plant height (cm), **NC:** Number of clusters per plant, **NP:** Number of pods per plant, **NS:** Number of seeds per pod, **BY:** Biological yield per plant (g), **HI:** Harvest index (%), **HSW:** 100 seed weight (g), **MYMV:** Mungbean Yellow Mosaic Virus, **SY:** Seed yield per plant (g)

**Table 3: Cluster membership and number of genotypes present in each cluster of mungbean.**

Cluster No.	Names of genotypes	No. of Genotypes
1	2KM 101, 2KM 111, 2KM 112, 2KM 115, 2KM 117, 2KM 138, 2KM 216, AKM 9904, COGG 13-19, EC 470096, EC 581523B, GANGA 8, HUM 16, HUM 7, IC 103196, IC 39574, IPM 02-14, IPM 02-17, IPM 03-2, IPM 302-2, KM 2211, KM 2328, M 395, M 605, MH 539, MH 709, MH 729, MH 921, MH 98-1, ML 1451, ML 1907, ML 2037, ML 759, NBPGR 150, NDMZ 13-11, NDMZ 13-12, NDMZ 15-2, NDMZ 215-1, OUM 11-5, PANT M-5, PDM 96-262, PLM 24, PLM 62, PM 11-51, PM 99-3, Pusa 0672, Pusa 1142, Pusa 1501, Pusa 1502, Pusa 1542, Pusa 1601, Pusa 9531, Pusa Ratna, RMG 991, Samrat, SML 1115, SML 1781, TRCM 155-1, VGG-1	59
2	ADGG 13034, Asha, ML 735, ML 776, Pusa 0871, Pusa 1141, VGG-2	7
3	CH 210-3, EC 251552, EC 30400, EC 393407, EC 393410, EC 399233, EC 470090	7
4	COGG 1102, COGG 13-14, PLM 76	3
5	COGG-8, GM- 9926 YMV, SML 1082, SML 668, TMB 196	5
6	EC 581523, TMB 163	2
7	HUM 27	1
8	IC 15276, IPM 02-19, IPM 06-5, IPM 2-03, IPM 205-7, IPM 312-19, IPM 312-394, IPM 409-4, IPM 410-3, KM 2241, MH 521, MH 560, MH 565, Pusa 1642, SHIM 12-1, SML 1018, SML 1023, SML 1194, TMB 131	19
9	ML 1108, Pusa Vishal	2
10	ML 1628	1
<b>Total</b>		<b>106</b>

**Table 4: Inter (off-diagonal) and Intra (diagonal) cluster distances in mungbean.**

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	30.22	40.20	58.61	44.90	41.49	43.20	56.30	45.10	45.69	46.10
II		23.01	61.25	35.84	55.11	60.96	74.23	67.77	38.40	48.80
III			25.19	57.80	56.43	40.29	42.48	69.07	65.77	82.66
IV				16.08	40.89	63.45	69.06	70.24	41.91	63.36
V					19.23	44.54	52.48	50.59	54.69	61.51
VI						7.56	36.62	38.35	51.13	65.41
VII							0.00	48.02	71.79	84.01
VIII								29.25	57.00	61.55
IX									16.22	16.22
X										0.00

**Table 5: Cluster mean for different traits in mungbean.**

Cluster	DF	DM	NB	PH (cm)	NC	NP	NS	BY (g)	HI (%)	HSW (g)	MYMV	SY (g)
I	40	70	3.5	65	11.1	23	10.0	53.06	18.39	3.40	3.3	9.70
II	41	75	4.0	79	9.7	23	10.6	55.67	16.69	3.10	4.0	9.27
III	46	75	3.9	65	7.0	16	10.2	35.00	17.70	3.09	2.3	6.18
IV	43	74	3.6	79	11.7	25	6.8	47.32	16.15	3.13	5.3	7.58
V	39	67	3.5	64	9.8	22	6.5	45.96	15.89	4.13	7.4	7.15
VI	37	71	3.9	60	7.9	19	10.6	38.50	21.93	3.64	3.0	8.42
VII	45	70	1.4	48	6.4	17	10.5	40.28	17.75	3.80	5.0	7.15
VIII	37	64	3.1	52	10.4	23	10.7	45.65	22.70	3.67	3.1	10.25
IX	40	68	3.6	85	9.3	22	10.4	46.83	20.72	3.71	3.0	9.69
X	37	71	3.3	67	12.8	25	11.2	70.27	17.70	4.22	3.0	12.37

**Screening of mungbean genotypes against MYMV disease.** One hundred six mungbean genotypes were evaluated in field condition for MYMV using infector row technique by growing infector row after every five test rows and all around the experimental plot borders and MYMV was observed at three intervals (35, 45 and 55 days after sowing) (Fig. 5). The results obtained have been furnished in Table 6. The percentage of incidence of YMD (average) ranged from 0.33 to 53.65 in different genotypes.

This strict evaluation revealed that none of the genotype was found immune, 23 genotypes viz., 2KM 112, AKM

9904, EC 251552, EC 30400, EC 399233, EC 470090, EC 581523, EC 581523B, HUM 7, MH 521, MH 560, MH 565, MH 98-1, ML 2037, ML 735, Pusa 1501, 2KM 111, 2KM 216, CH 210-3, EC 470096, MH 709, MH 729, SML 1023 were found resistant, 42 genotypes viz., 2KM 101, 2KM 115, 2KM 117, 2KM 138, IC 103196, IC 15276, IC 39574, IPM 02-17, IPM 02-19, IPM 03-2, IPM 06-5, IPM 2-03, IPM 205-7, IPM 312-19, IPM 312-394, IPM 409-4, M 395, M 605, MH 539, MH 921, ML 1108, ML 1451, ML 1628, ML 1907, ML 759, ML 776, NDMZ 13-12, NDMZ 15-2, PDM 96-262, PLM 24, PM 11-51, Pusa 1141, Pusa

1142, Pusa 1502, Pusa 1601, Pusa 9531, Pusa Vishal, SML 1018, SML 1115, SML 1194, SML 1781, TRCM 155-1, were found moderately resistant, 33 genotypes viz., Asha, COGG 13-14, COGG 13-19, EC 393407, EC 393410, Ganga 8, HUM 27, IPM 02-14, IPM 410-3, KM 2211, KM 2241, KM 2328, NDMZ 13-11, NDMZ 215-1, PANT M-5, PLM 76, PM 99-3, Pusa 0672, Pusa 0871, Pusa 1542, Pusa Ratna, RMG 991, Samrat, SHIM 12-1, TMB 131, TMB 163, TMB 196, VGG-1, HUM 16, IPM 302-2, PLM 62, Pusa 1642, VGG-2, were

found moderately susceptible, six genotypes (ADGG 13034, COGG-8, SML 668, COGG 1102, NBPGR 150, OUM 11-5,) were found susceptible and two genotypes (GM- 9926 YMV, SML 1082) were found highly susceptible. Nainu and Murugan (2020); Deepa *et al.* (2017); Suman *et al.* (2018); Mahanta *et al.* (2019) also concluded that most of the genotypes were falling under resistant to moderately resistant category in their research results.

**Table 6: Grouping of mungbean genotypes screened against yellow mosaic disease.**

Sr. No.	Scale	Disease Reaction	Name of Genotypes	Total Genotypes
1.	1	Resistant	2KM 112, AKM 9904, EC 251552, EC 30400, EC 399233, EC470090, EC 581523, EC 581523B, HUM 7, MH 521, MH 560, MH 565, MH 98-1, ML 2037, ML 735, Pusa 1501, 2KM 111, 2KM 216, CH 210-3, EC 470096, MH 709, MH 729, SML 1023	23
2.	3	Moderately Resistant	2KM 101, 2KM 115, 2KM 117, 2KM 138, IC 103196, IC 15276, IC 39574, IPM 02-17, IPM 02-19, IPM 03-2, IPM 06-5, IPM 2-03, IPM 205-7, IPM 312-19, IPM 312-394, IPM 409-4, M 395, M 605, MH 539, MH 921, ML 1108, ML 1451, ML 1628, ML 1907, ML 759, ML 776, NDMZ 13-12, NDMZ 15-2, PDM 96-262, PLM 24, PM 11-51, Pusa 1141, Pusa 1142, Pusa 1502, Pusa 1601, Pusa 9531, Pusa Vishal, SML 1018, SML 1115, SML 1194, SML 1781, TRCM 155-1	42
3.	5	Moderately susceptible	Asha, COGG 13-14, COGG 13-19, EC 393407, EC 393410, GANGA 8, HUM 27, IPM 02-14, IPM 410-3, KM 2211, KM 2241, KM 2328, NDMZ 13-11, NDMZ 215-1, PANT M-5, PLM 76, PM 99-3, Pusa 0672, Pusa 0871, Pusa 1542, Pusa Ratna, RMG 991, Samrat, SHIM 12-1, TMB 131, TMB 163, TMB 196, VGG-1, HUM 16, IPM 302-2, PLM 62, Pusa 1642, VGG-2	33
4.	7	Susceptible	ADGG 13034, COGG-8, SML 668, COGG 1102, NBPGR 150, OUM 11-5	6
5.	9	Highly susceptible	GM- 9926 YMV, SML 1082	2
<b>Total</b>				<b>106</b>



**Fig. 5.** Yellow Mosaic Disease Infected lines in the field of pulses section, Deptt. of G&PB.

## CONCLUSIONS

From the findings of the present investigation, it could be concluded that the one hundred and six mungbean genotypes differed significantly for all yield and its attributing traits. Based on yield and its attributing traits along with MYMV screening, the genotypes viz., ML 1628, ML 2037, SML 1023, MH 521, MH 560, MH 565, IPM 312-394, IPM 410-3 and EC 581523 showed sufficient genetic diversity, contrasting traits and maximum resistance against MYMV among all the genotypes and these can be used in mungbean breeding programs for further improvement and resistance donor.

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