Plant Archives Vol. 25, No. 2, 2025 pp. 1175-1181 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.168

ASSESSMENT OF MUNGBEAN GENOTYPES FOR RESISTANCE AGAINST YELLOW MOSAIC DISEASE UNDER NATURAL CONDITIONS

Pawan Kumar Kasniya[1,3*], Tarun Verma[2,3], Pawan Kumar[3], Mallikarjun Kenganal[4] and Aditya Pratap[5]

[1]Department of Plant Pathology, CCS Haryana Agricultural University, Hisar – 125004 Haryana, India
[2]Department of Entomology, CCS Haryana Agricultural University, Hisar – 125004 Haryana, India
[3]Pulses Section, Department of Genetic & Plant Breeding, CCS Haryana Agricultural University, Hisar – 125004 Haryana, India
[4]Zonal Agricultural Research Station, Kalaburagi – 585101 Karnataka, India
[5]ICAR-Indian Institute of Pulses Research, Kanpur – 208024 UP, India
*Corresponding author: pawankasniya@gmail.com
(Date of Receiving-03-06-2025; Date of Acceptance-22-08-2025)

ABSTRACT

Field evaluation of mungbean genotypes was carried out against yellow mosaic disease (YMD) during summer and *kharif* season of year 2024. In seasonal comparison studies, significant increase in the disease severity was observed in many genotypes during *kharif* season as compared to summer, highlighting the impact of seasonal variations, environmental factors and vector (whitefly) activities. Weather conditions played a significant role in increasing disease incidence during the *kharif* season, as the warm and humid environment favoured the survival and proliferation of vector populations. In contrast, the hot and dry conditions of the summer season were less conducive to disease spread, resulting in lower incidence. The results indicated the variation in disease resistance across genotypes and seasons. Such genotypes, MH 1921, PMD-11, Pusa M 23-31, Pusa M 23-32, PUSA M 23-41, Pusa M 2431, SVM 66, TCA DM-1 and MH 421 show low disease severity (d" 4.00%) and infection rate (<10%), exhibited strong resistance in both summer and *kharif* season, making them potential candidates for breeding programs. However, highly susceptible genotypes *viz.* BM 4, Kopergeon and SML 1082 should be avoided in YMD-prone regions. Further research is needed to confirm the genetic basis of resistance and seasonal disease dynamics.

***Key words*:** Infection rate, Genotype, Severity, Yellow mosaic disease, Weather conditions.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is an important pulses crop of Haryana. This crop is grown in both summer as well as *kharif* seasons and considered as a potential source of digestible proteins for human diet. Several biotic and abiotic stresses are mainly responsible for low productivity of this crop. Among the biotic stress, the yellow mosaic disease (YMD) is a major economic significance in reduction of the mungbean yield. In India, YMD was first reported in 1955 at IARI, New Delhi (Nairani 1960). The causal agent of this disease is mungbean yellow mosaic virus (MYMV), which has a wide host range and is transmitted by whitefly (*Bemisia tabaci* Genn) (Nene 1972). The early symptoms of the disease become evident with the development of yellow specks along the veins which progressively spreads and turns the entire leaf yellow. In the severe cases, the entire leaf may become chlorotic which later turns in to necrotic regions (Qazi *et al*., 2007). The disease incidence reduces yield by 5 to 100 percent depending upon disease severity, host resistance level and prevailing environmental conditions (Rathi 2002). The yield loss from the YMD depend on the stage of infection, late infection causes a 32–78 percent reduction in mungbean grain yield and infection at early growth stages may even lead up to 100 percent yield loss (Khattak *et al*., 2000).

The mungbean yellow mosaic virus belongs to genus *Begomovirus* of the family Geminiviridae (Bos 1999). It has been confirmed that at least two virus *i.e.* MYMV and MYMIV species causing yellow mosaic disease are prevalent in Indian subcontinent. Viral particles associated with YMD are found to be isometric and geminate having 18-30 nm in size with two single stranded DNA molecules (DNA A & DNA B) of 2726 and 2775 nucleotides, respectively (Morinaga *et al.*, 1990, Morinaga *et al.*, 1993, Bos 1999, Hull 2004). Mungbean yellow mosaic India virus (MYMIV) is considered to be more predominant in northern, central and eastern India, while MYMV in peninsular region of India (Karthikeyan *et al.* 2004, Malathi and John 2008, Gupta *et al.*, 2013, Aski *et al.*, 2015, Nair *et al.*, 2017). The management of YMD is focused mainly on vector (whitefly) control and development of resistant/tolerant genotypes for both (virus and vector) the stresses. Though pesticides can keep vector population below economic threshold, but do not give effective control of the disease. A more efficient and environmentally safe long-term solution is the development of mungbean cultivars resistant to both virus and its vector *B. tabaci*. A good deal of research efforts has been directed towards the screening of mungbean germplasm against YMD, thus identifying promising cultivars possessing resistance to mungbean yellow mosaic virus is a top priority for most pulses crops (Aski *et al.*, 2015, Nair *et al.*, 2017, Mishra *et al.*, 2020, Singh *et al.*, 2020, Pratap *et al.*, 2021, Mariyappan and Nandini, 2022). Host resistance is the most efficient and environmentally friendly approach to reducing yellow mosaic disease damage in mungbean. Keeping in view, the present studies were undertaken to evaluate the mungbean genotypes against against yellow mosaic disease under natural infection conditions.

Materials and Methods

Sixty-seven mungbean genotypes were sown during summer on 18, March and *kharif* season on 15, July of year 2024 to evaluate their response against YMD under natural infection conditions. Each genotype was sown in double row of 4 m length in two replications. Row to row and plant to plant distance was maintained 30 and 10 cm, respectively. Conventional agronomic practices were employed to keep the crop in good conditions. No pesticides were applied against the whitefly to ensure high population buildup throughout the experiment. Whitefly populations were recorded from the trifoliate leaves of ten plants per genotype at 40 days after sowing. The population per plant was then calculated. The data for YMD were recorded following the rating system (Table 1). The disease severity was calculated using a standard formula described by McKinney (1923) and infection rate (IR) was estimated from the total number of plants infected by YMD. The data of weather variables (maximum temperature, minimum temperature, relative humidity morning, rainfall and sunshine hours) were acquired from the meteorological observatory located 100 m from the experimental plot. The data were statistically analyzed for outcome of hierarchical clustering analysis grouped mungbean genotypes by GRAPES 1.0.0 (Gopinath *et al.*, 2020).

Table 1: Disease rating scale for yellow mosaic disease of mungbean.

Scale	Description	Reaction	D
0	No visible symptoms	Free	I
1	0.1-10% leaf area covered with symptoms	Resistant	R
3	10.1-20% leaf area covered with symptoms	Moderately Resistant	MR
5	20.1-30% leaf area covered with symptoms	Moderately Susceptible	MS
7	30.1-50% leaf area covered with symptoms	Susceptible	S
9	>50% leaf area covered with symptoms	Highly Susceptible	HS

D: Designation

Results and Discussion

Mungbean genotypes assessed against YMD had varied response across the seasons influenced by their genetic background and also virus vector population. Table 2 documents the response of mungbean genotypes to YMD under natural field conditions during summer and *kharif* seasons of 2024. The disease severity was evaluated using a 0-9 rating scale and additional parameters such as infection rate and population of whitefly (WF) were recorded for both seasons.

During summer season, fifty genotypes exhibited minimal YMD severity (0.15 to 0.80%), with a scale rating of 1 (highly resistant) and six genotypes (COGG 22-03, MGG 519, OBGG 103, PM 1803, SKNM 2210 and Pant Mung 2) showed moderate resistance with scale ratings of 3 and severity ranging from 13.90 to 19.80 per cent. Five genotypes (JLPM 707-27, BM 4, SML 2159, Kopergeon and SML 1082) fall in category of susceptible and highly susceptible (7 or 9) with disease severity above 40 percent. Disease severity was higher in *kharif* season as compared to summer season. However, nine genotypes (MH 1921, PMD-11, Pusa M 23-31, Pusa M 23-32, PUSA M 23-41, Pusa M 2431, SVM 66, TCA DM-1 and MH 421) retained resistance and show low disease severity (d”4.00%) and IR below 10%. These genotypes showed resistance during both the season with disease severity of 0.25 to 0.55 per cent and 1.60 to 3.55 per cent in summer and *kharif* season, respectively. Genotypes, SML 1082, BM 4 and Kopergeon showed

Table 2: Yellow mosaic disease and whitefly population on mungbean genotypes during summer & *kharif* season of year 2024.

S. No.	Genotype	Summer season				*Kharif* season			
		Scale (0-9)	Severity (%)	IR (%)	WF	Scale(0-9)	Severity(%)	IR (%)	WF
1	BCM 20-45	1	0.45h	3.95gh	0.25	3	17.20hi	87.55ab	2.20
2	BCM 20-49	1	0.45h	3.35h	0.30	5	23.50fg	100.00a	1.90
3	BCM 20-50	1	0.80h	4.60gh	0.30	5	24.70fg	100.00a	2.60
4	BCM 20-52	1	0.35h	3.80gh	0.25	5	23.50fg	100.00a	1.80
5	BCM 20-55	1	0.35h	4.70gh	0.45	5	27.25f	100.00a	2.30
6	BCM 20-60	1	0.55h	3.80gh	0.25	5	23.25fg	100.00a	2.80
7	BRM 15-1	1	0.35h	4.95gh	0.35	5	25.75f	100.00a	2.60
8	BRM-14	1	0.40h	5.80gh	0.45	5	26.15f	100.00a	2.70
9	CGG 20008	1	8.20g	13.00fg	0.30	3	17.65hi	41.10ghij	2.50
10	COGG 22-03	3	15.80ef	16.10ef	0.30	5	23.80fg	100.00a	2.70
11	COGG 7/912	5	26.00cd	51.65b	0.4	3	14.55hi	83.30abc	2.90
12	DGG 96	1	0.60h	5.30gh	0.30	3	16.10hi	88.85ab	2.40
13	IPM 1604-1	1	0.70h	3.05h	0.15	3	16.15hi	66.50bcdef	2.70
14	IPM 1707-1	1	0.50h	3.05h	0.25	3	16.20hi	60.75cdefg	2.70
15	Jawahar M5	1	0.30h	2.80h	0.30	5	27.45f	100.00a	2.70
16	Jawahar M6	1	0.40h	2.75h	0.20	5	26.05f	100.00a	2.90
17	JLPM 707-27	7	40.85b	21.85def	0.55	7	42.55cd	100.00a	3.60
18	MGG 389	1	0.30h	3.25h	0.50	3	15.90hi	57.55defghi	2.60
19	MGG 519	3	7.85g	17.90ef	0.45	5	25.05fg	100.00a	2.60
20	MH 18-100	1	0.35h	3.25h	0.35	3	16.65hi	72.10bcd	2.70
21	MH 1921	1	0.40h	3.05h	0.20	1	3.55j	7.50lm	3.10
22	MH 1923	1	0.40h	3.70gh	0.25	5	28.15f	100.00a	3.00
23	NVL 1337	1	0.45h	3.30h	0.25	3	16.05hi	31.30jkl	2.50
24	OBGG 103	3	19.80def	23.30de	0.35	3	13.85i	34.55hijk	3.20
25	OBGG 113	1	0.30h	3.75gh	0.30	5	25.60f	100.00a	3.20
26	PM 1803	3	14.60fg	29.15cd	0.45	5	25.90f	100.00a	3.00
27	PM 2015	1	0.30h	4.75gh	0.20	3	12.90i	31.45jkl	2.70
28	PM 2031	1	0.25h	3.70gh	0.20	3	14.60hi	58.35defgh	3.00
29	PMD-11	1	0.45h	3.40h	0.20	1	3.50j	6.95lm	2.50
30	PMS 13	1	0.30h	3.05h	0.15	3	16.50hi	33.20ijk	2.70
31	PMS 9	1	0.55h	4.20gh	0.20	5	27.00f	100.00a	3.30
32	PMS-10	1	0.35h	3.30h	0.20	3	16.40hi	46.50efghij	3.20
33	Pusa M 23-31	1	0.30h	2.85h	0.30	1	3.45j	3.95m	2.80
34	Pusa M 23-32	1	0.30h	5.95gh	0.25	1	2.50j	8.50lm	2.30
35	PUSA M 23-41	1	0.40h	5.76gh	0.35	1	2.10j	6.10lm	3.30
36	Pusa M 2431	1	0.30h	2.80h	0.30	1	2.70j	7.85lm	2.80
37	Pusa M 2441	1	8.10g	4.65gh	0.15	3	14.40hi	70.00bcde	2.90
38	RMG 1191	1	0.40h	4.15gh	0.25	7	42.95cd	100.00a	2.80
39	RMG 1196	1	0.25h	2.90h	0.10	7	44.50c	100.00a	3.10
40	RVSM 22-14	1	0.30	4.90gh	0.15	7	38.50de	100.00a	2.80
41	SKNM 2107	1	0.60h	4.35gh	0.25	3	16.10hi	45.05fghij	2.60
42	SKNM 2210	3	19.60def	16.10ef	0.50	5	19.85gh	100.00a	2.70
43	SML 2108	1	0.50h	2.45h	0.25	5	25.65f	100.00a	2.50
44	SML 2147	1	0.45h	2.75h	0.35	7	38.35de	100.00a	2.40
45	SML 2159	5	22.00de	36.25c	0.40	7	44.90c	100.00a	2.70
46	SVM 66	1	0.55h	3.70gh	0.25	1	4.00j	7.10lm	2.20
47	SVM 88	1	0.55h	4.00gh	0.35	3	14.50hi	35.90hijk	2.40
48	TAKM 140	5	24.25d	23.75de	0.25	3	15.40hi	34.70hijk	1.90

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49	TCA DM-1	1	0.30h	4.95gh	0.35	1	1.60j	9.20lm	2.50
50	TGM 130	1	0.25h	4.25gh	0.45	7	36.00e	100.00a	2.10
51	VGG 20-157	1	0.15h	3.10h	0.35	5	24.60fg	100.00a	2.40
52	VGG 20-234	1	0.55h	4.35gh	0.15	5	24.35fg	100.00a	2.90
53	SML 668	1	0.45h	3.60gh	0.45	3	14.35hi	70.00bcde	2.80
54	SML 1115	1	0.40h	2.50h	0.35	5	23.45fg	100.00a	2.90
55	Pant Mung 2	3	13.90fg	29.70cd	0.50	5	23.70fg	100.00a	3.20
56	HUM 16	1	0.50h	5.15gh	0.40	5	26.05f	100.00a	2.50
57	GM 6	1	0.25h	4.05gh	0.20	5	24.95fg	100.00a	2.10
58	IPM 02-3	1	0.30h	2.85h	0.35	3	16.10hi	65.10bcdefg	2.90
59	IPM 2-14	1	0.35h	4.05gh	0.35	3	17.55hi	71.35bcd	2.90
60	IPM 205-7	1	0.35h	2.90h	0.25	5	27.15f	100.00a	2.60
61	IPM 410-3	1	0.30h	4.25gh	0.35	5	26.65f	100.00a	2.80
62	IPM 512-1	5	25.25d	22.85de	0.35	5	26.60f	100.00a	2.90
63	Pusa 9531	1	0.35h	3.25h	0.30	5	27.00f	100.00a	3.00
64	BM 4	7	45.50b	58.15b	0.20	9	70.45b	100.00a	2.50
65	Kopergeon (SC)	9	64.70a	87.25a	0.35	9	70.40b	100.00a	3.20
66	SML 1082 (SC)	7	48.70b	51.20b	0.25	9	78.10a	100.00a	2.90
67	MH 421 (Ch)	1	0.25h	4.85gh	0.20	1	2.00j	6.50lm	2.20
Average		1.86	6.50	10.67	0.30	4.22	23.01	73.63	2.70
CD @ 0.05%		-	6.78	9.56	-	-	5.58	24.65	-
CV (%)		-	52.32	44.88	41.88	-	12.16	16.77	17.48

YMD : Yellow mosaic disease, WF : whitefly population per trifoliate leaf of plant, IR : Infection rate,

highly susceptible reaction across both seasons with severity (%) of 40.70 to 64.70 per cent and 70.40 to 78.10 per cent, respectively in summer and *kharif* season. The infection rate (IR) was significantly lower in summer for most of the genotypes. A sharp increase in IR per cent was observed in *kharif*, with several genotypes reaching 100 per cent infection, indicating higher disease pressure during this season. Genotypes, MH 1921, PMD-11, Pusa M 23-31, Pusa M 23-32, PUSA M 23-41, Pusa M 2431, SVM 66, TCA DM-1 and MH 421 maintained low IR across both the seasons, indicating the resistancee with IR per cent of 2.80 to 5.95 and 3.95 to 8.50 percent, respectively during summer and *kharif* season. Whereas, BM 4, Kopergeon and SML 1082 showed highly susceptible reactions across seasons with IR per cent of 51.20 to 87.25 and 100 per cent during summer and *kharif* season, respectively. Genotypes that became highly susceptible in *kharif* which was low IR% in summer while a drastic increase to 100% infection in *kharif*. The *kharif* season favours a dramatic rise in infection rates, likely due to favourable environmental conditions for disease transmission (e.g., increased whitefly activity). These results are in confirmation with the previous studies conducted by Karthikeyan *et al.*, (2014), Vijaya (2017) and Saable *et al.*, (2024) who reported that YMD incidence in mungbean germplasm lines ranged from 0 to 100 percent.

The seasonal disease progression was observed due to climatic factor and varying vector presence from one season to another season. Several genotypes that showed low disease severity in summer season, while developed higher infection levels in *kharif* season, likely due to environmental factors favouring viral transmission and vector activity (whitefly population). The mean disease

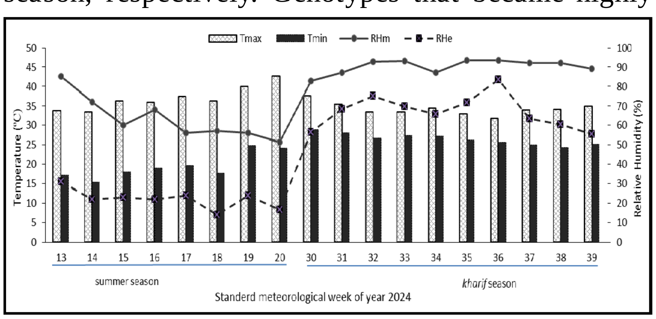

Fig. 1: Standard meteorological week wise temperature and relative humidity in summer and *kharif* season of year 2024.

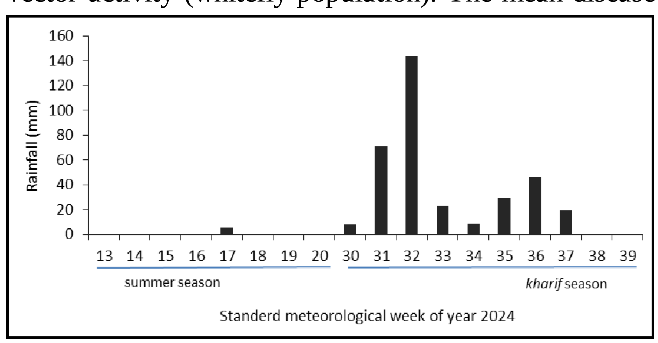

Fig. 2: Standard meteorological week wise rainfall in summer and *kharif* season of year 2024.

severity was significantly higher in *kharif* compared to summer season, indicating that *kharif* season conditions are more conducive for YMD development. The LSD (Least Significant Difference) test at 5 per cent indicates significant differences in disease severity among the genotypes across seasons. On the basis of coefficient of variation (CV) summer season showed higher variability (52.32%), suggesting a wider range of resistance and susceptibility among different genotypes. Contrary to this, *kharif* season showed less variation (12.16%), indicating that many genotypes exhibited high severity consistently in this season. LSD at 5% indicates that the variation in IR% among genotypes is statistically significant across seasons. CV suggests a wider range of resistance among genotypes in summer (44.88%) while *kharif* (16.77%) indicates that most genotypes exhibited high infection rates, reducing variability in resistance responses. The data confirms that *kharif* season is more favourable for YMD spread, leading to higher infection rates due to presence of more whitefly population as compare to summer season. The whitefly population was significantly lower in the summer season, averaging 0.30 per trifoliate leaf of plant, compared to 2.70 per trifoliate leaf of plant in *kharif* season, leading to the more infection of YMD in kharif season. The vector activities and prevailing favourable environmental conditions such as varied temperature, rainfall and dry spell experienced during the period under investigation can be cause for the more susceptibility of most of these studied genotypes in *kharif* season. It was previously reported that large variability in the incidence and severity of YMD depends on variety, location and year (Singh *et al.*, 2000, Mohan *et al.*, 2014). Parihar *et al.*, (2017) also reported the seasonal effects on outbreak of yellow mosaic disease in mungbean cultivars.

Fig. 1 and 2 summarizes weekly meteorological data for the summer and *kharif* seasons of 2024 and shows how these environmental factors relate to disease and vector parameters (such as severity, IR and WF) averaged across all genotypes. In summer, maximum temperature (T_{max}) ranged from 33.5°C to 42.6°C, minimum temperature (T_{min}) from 15.3°C to 24.8°C, while relative humidity and rainfall were generally lower. In *kharif*, T_{max} was 31.7°C to 37.6°C, T_{min} was 25.0°C to 28.8°C, higher relative humidity (above 80% in many weeks) with more rainy days. The severity, infection rate and whitefly population are noticeably higher in the *kharif* season, suggesting greater environmental stress or disease incidence. By comparing the two seasons, it can be summarised that meteorological conditions (like higher T_{max}, variations in RH and rainfall) might be contributing to differences in disease incidence and crop performance.

The hierarchical clustering analysis (Fig. 3) grouped mungbean genotypes into four distinct clusters based on

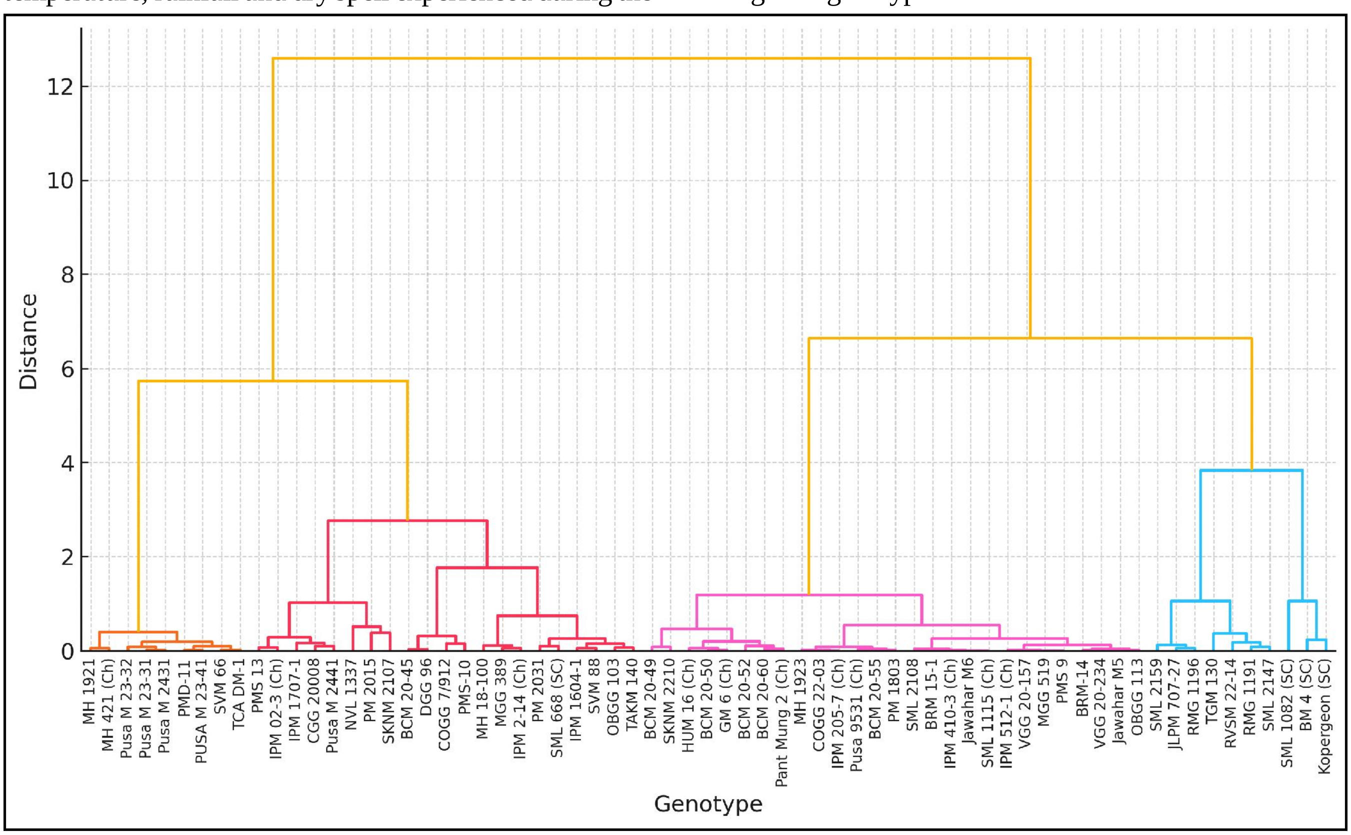

Fig. 3: Hierarchical clustering analysis of mungbean genotypes into four distinct clusters based on YMD.

Table 3: Genotype cluster assignments.

Cluster	No. of genotypes	Genotype
1	9	MH 1921, PMD-11, Pusa M 23-31, Pusa M 23-32, PUSA M 23-41, Pusa M 2431, SVM 66, TCA DM-1, MH 421
2	21	BCM 20-45, CGG 20008, COGG 7/912, DGG 96, IPM 1604-1, IPM 1707-1, MGG 389, MH 18-100, NVL 1337, OBGG 103, PM 2015, PM 2031, PMS 13, PMS-10, Pusa M 2441, SKNM 2107, SVM 88, TAKM 140, SML 668, IPM 02-3, IPM 2-14,
3	27	BCM 20-49, BCM 20-50, BCM 20-52, BCM 20-55, BCM 20-60, BRM 15-1, BRM-14, COGG 22-03, Jawahar M5, Jawahar M6, MGG 519, MH 1923, OBGG 113, PM 1803, PMS 9, SKNM 2210, SML 2108, VGG 20-157, VGG 20-234, SML 1115, Pant Mung 2, HUM 16, GM 6, IPM 205-7, IPM 410-3, IPM 512-1, Pusa 9531
4	10	JLPM 707-27, RMG 1191, RMG 1196, RVSM 22-14, SML 2147, SML 2159, TGM 130, BM 4, Kopergeon, SML 1082,

infection rate and severity of YMD. These clusters indicate varying levels of similarity among the genotypes in relation to disease resistance. The goal was to classify the genotypes into groups (clusters) that share similar characteristics regarding disease resistance. Each cluster groups genotypes that share common traits regarding disease response. The cluster 1 includes nine genotypes, MH 1921, PMD-11, Pusa M 23-31, Pusa M 23-32, PUSA M 23-41, Pusa M 2431, SVM 66, TCA DM-1 and MH 421.These genotypes share similar IR and severity levels, potentially indicating higher disease resistance compared to other clusters. Cluster 2 includes the 21 genotypes, which showing a distinct disease pattern. Cluster 3 is the largest cluster includes 27 genotypes; these genotypes shared common disease response traits. Cluster 4 represented unique genotypes (10 genotypes) with distinct IR and severity levels (Table 3), potentially indicating extreme level of susceptibility.

Statistical summary of the infection rate and severity of YMD in each cluster is presented in Table 4. The data includes the mean ± standard deviation (SD) along with the minimum and maximum values for both parameters.

Table 4: Statistical summary of genotypes of mungbean in each cluster on the basis of disease response.

Cluster	IR (%) (Mean ± SD) [Min - Max]	Severity (%) (Mean ± SD) [Min - Max]
1	6.79 ± 3.57 [2.9 - 13.2]	2.61 ± 0.83 [1.3 - 3.6]
2	55.55 ± 19.53 [15.6 - 87.5]	14.7 ± 1.56 [10.2 - 16.4]
3	100.0 ± 0.0 [100.0 - 100.0]	24.83 ± 3.03 [17.4 - 28.9]
4	100.0 ± 0.0 [100.0 - 100.0]	51.31 ± 14.89 [35.6 - 80.6]

This table helps in understanding how different clusters respond to YMD. The genotypes of cluster 1 are highly resistant to YMD with very low infection rate and disease severity. Cluster 2 contains a mix of moderately resistant and susceptible genotypes. Some genotypes show partial resistance, while others are more affected. Cluster 3 includes highly susceptible genotypes with complete infection (100%) and significant disease severity. These genotypes are unsuitable for cultivation in YMD-prone areas unless managed properly. Cluster 4 showed the extremely susceptible genotypes. Infection rate was 100 percentages and mean level of severity was 51.31% with variation of ±14.89% in range of 35.6 – 80.6% which showed the extremely high disease severity with a wide range. The genotypes in this cluster are the most susceptible, experiencing severe damage due to YMD. Their high severity makes them the worst-performing group in terms of disease resistance.

Weather conditions played a significant role in increasing disease incidence during the *kharif* season, as the warm and humid environment favoured the survival and proliferation of vector populations. In contrast, the hot and dry conditions of the summer season were less conducive to disease spread, resulting in lower incidence. This underscores the distinct climatic shift between the two seasons and highlights how the favourable conditions in *kharif* promote vector-borne disease outbreaks.

In conclusions, several genotypes maintained strong resistance across both seasons and may be promising candidates for breeding programs. *Kharif* season was more favourable for disease development, leading to increased severity in most genotypes. Breeding efforts should focus on genotypes with stable resistance across seasons. Further studies on environmental influences and vector management strategies are needed to mitigate YMD spread in *kharif* season.

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