



Screening of Horsegram Genotypes for Resistance against Yellow Mosaic Disease

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/jabb/2025/v28i11889>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/129130>

Original Research Article

Received: 29/10/2024

Accepted: 31/12/2024

Published: 14/01/2025

ABSTRACT

Aims: The present study aimed to evaluate the screening of horsegram genotypes for resistance to yellow mosaic disease. The disease causes decrease in number of seeds per pods, number of pods per plant. The disease may occur at any phase of plant development.

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Cite as: Pinjar, Sonam R, Prema G U, Gurupad Balol, Spurthi N Nayak, Revanappa Biradar, Subhash Kandakoor, and Bangaramma Wadeyar. 2025. "Screening of Horsegram Genotypes for Resistance Against Yellow Mosaic Disease". *Journal of Advances in Biology & Biotechnology* 28 (1):354-63. <https://doi.org/10.9734/jabb/2025/v28i11889>.

Background: Horsegram crop suffers from yellow mosaic, powdery mildew, anthracnose, dry root rot, leaf spot, rust and cottony stem rot. Yellow Mosaic Disease (YMD) is recognized as the most detrimental viral affliction among the array of diseases induced by the Yellow Mosaic Virus. The occurrence of YMD in pulse crops has resulted in significant yield reductions, which can vary between 50 to 100 per cent. The best method to overcome YMD is the development of disease resistant varieties. Henceforth, an effort has been made to evaluate horsegram genotypes to obtain sources of resistance against YMD.

Place and Duration of Study: Field experiment for screening was conducted at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka, India, during summer 2023-24.

Methodology: For screening, 148 genotypes were screened under natural epiphytotic conditions. Each genotype was sown in a 2 m row to test the resistance or susceptible reactions against YMD. A susceptible check (BGM-1) was planted after every 10 lines of test genotypes and all along the four sides of the field (infector row technique).

Results: Out of 148 genotypes evaluated, none of them were immune or resistant, 12 were moderately resistant, 47 were moderately susceptible, 46 were susceptible and remaining 43 genotypes showed highly susceptible reaction.

Conclusion: Identified moderately resistant genotypes can be utilized in YMD resistance breeding programme to develop YMD resistant varieties.

Keywords: Horsegram; screening; yellow mosaic disease; yellow mosaic virus.

1. INTRODUCTION

Horsegram (*Macrotyloma uniflorum* (Lam.) Verde.) popularly known as poor man's pulse crop, is a hardy legume valued for its quickly digested high-quality protein. It belongs to family *Leguminosae* and sub-family *Papilionaceae*. It is also known as kulthi bean, gahat, hurali, ulavalu, muthira or madras gram which is a legume native to tropical southern Asia. It is an indigenous plant cultivated in India, Africa and other Asian countries.

It is mainly cultivated in the states of Karnataka, Andhra Pradesh, Orissa, Tamil Nadu, Madhya Pradesh, Chhattisgarh, Bihar, West Bengal, Jharkhand and in foot hills of Uttaranchal and Himachal Pradesh in India. It is a popular pulse crop of Karnataka, grown in districts like Mysuru, Tumakuru, Ballari, Raichur, Bagalkot, Mandya, Hassan, Chamarajanagar, Vijayapura, Chitradurga, Kolar and Koppal districts. In India, it is cultivated in 0.507 m ha area with total production of 0.262 m t and productivity of 516 kg/ha. Karnataka ranks first in production in India with 0.096 m t and covers an area of 0.147 m ha with the productivity of 655 kg/ha, followed by Tamil Nadu with a production of 0.056 m t and an area of 0.075 m h with the productivity of 745 kg/ha (Anonymous, 2022).

Horsegram crop suffers from yellow mosaic, powdery mildew, anthracnose, dry root rot, leaf spot, rust and cottony stem rot. Among various diseases, yellow mosaic, a viral disease poses a considerable challenge to its cultivation in

peninsular India, with its initial detection occurring in the southern districts of Karnataka (Shaji et al., 2023; Kumar et al., 2021; Das et al., 2024; Parimala et al., 2011). Yellow mosaic disease (YMD) transmitted by whitefly species *Bemisia tabaci* (Gennadius), is the most serious disease of horsegram as it unfavourably affects the seed and fodder yield. The first report of the YMD of horsegram was by Williams et al., (1968).

In horsegram, the symptoms of YMD shows up as yellow colour mosaic patches on leaves which might be incompletely or totally yellow (Prema, 2013; Prema et al., 2013; Prema & Rangaswamy, 2017; Prema & Rangaswamy, 2018; Prema & Rangaswamy, 2020). Infected plants scarcely bear flowers and pods with some immature and deformed seeds. The disease causes decrease in number of seeds per pods, number of pods per plant. The disease may occur at any phase of plant development. If the incidence occurs at initial stage, plant may not blossom and the yield reduction might be as high as 90 per cent. Current study was carried out with an intention to screen horsegram genotypes for identification of sources of resistance to combat YMD which poses constraints in horsegram production.

2. MATERIALS AND METHODS

Screening of 148 horsegram genotypes was conducted to assess the resistance of various horsegram genotypes against YMD under field conditions at MARS, UAS, Dharwad, during the

summer 2023-24. Each genotype was sown in rows of 2 meters in length, with a spacing of 45 cm X 10 cm. A susceptible check (BGM-1) was planted after every 10 lines and along all four sides of the field to act as a disease source (Infector row technique). Both per cent disease incidence and per cent disease index was recorded at 15 days interval, starting from 30 DAS up to physiological maturity.

The disease incidence for individual genotype was recorded based on the formula given by Wheeler (Wheeler, 1969). Later the genotypes were classified into various categories based on disease incidence using a 0-5 arbitrary scale ranging from immune to highly susceptible, as mentioned in Table 1 (Bashir, 2005).

$$\text{Per cent disease incidence} = \frac{\text{Total number of infected plants}}{\text{Total number of plants observed}} \times 100$$

Table 1. Disease scoring scale for YMD on horsegram

Scale	Description	Category
0	No symptoms on the plants	Immune
1	1-10% plants exhibiting the symptoms	Resistant (R)
2	11-20% plants exhibiting the symptoms	Moderately Resistant (MR)
3	21-30% plants exhibiting the symptoms	Moderately Susceptible (MS)
4	31-50% plants exhibiting the symptoms	Susceptible (S)
5	>50% plants exhibiting the symptoms	Highly Susceptible (HS)

The per cent disease index was calculated by the formula given by Wheeler, (1969) and modified scale of AICRP on MULLaRP presented in Table 2 was used for disease rating (Alice & Nadarajan, 2007).

$$\text{Per cent disease index (PDI)} = \frac{\text{Sum of all the disease ratings}}{\text{No. of leaves examined} \times \text{Maximum disease rating}} \times 100$$

Table 2. Modified scale of AICRP on MULLaRP used for disease rating (0-9)

Scale	Description
0	No visible symptoms on leaves
1	Very minute yellow specks on leaves
2	Small yellow specks with restricted spread covering 0.1-5% leaf area of plant
3	Yellow mottling of leaves covering 5.1-10% leaf area of plant
4	Yellow mottling of leaves covering 10.1-15% leaf area of plant
5	Yellow mottling and discoloration of 15.1-30% leaf area of plant
6	Yellow discoloration of 30.1-50% leaf area of plant
7	Pronounced yellow mottling and discoloration of leaves and pods, reduction in leaf size and stunting of plants covering 50.1-75% foliage of plant
8	Severe yellow discoloration of leaves covering 75.1-90% of foliage, stunting of plants and reduction in pod size
9	Severe yellow discoloration of leaves covering above 90.1% of foliage of plants, stunting of plants and no pod formation

3. RESULTS AND DISCUSSION

The horsegram genotypes showed varied disease reaction against YMD. Among 148 genotypes screened, none of them showed immune or resistant reaction. However, majority of entries showed moderately susceptible, susceptible and highly susceptible reaction, few showed moderately resistant reaction (Plate 1, Tables 3 and 4).

Twelve genotypes showed moderately resistant reaction namely 14-61-41, CRHG-9, GPM-15, GPM-17, VLG-8, GPM-36a, PHG-2a, PHG-9, TCR-1517b, TCR-1734b, TRR-1799 and TCR-1816. Forty-seven genotypes namely 11-SS, AK-42, Bailhongal local, BSP-17-1, BSP-17-3, CRHG-7, CRHG-8, VLG-19, GPM-4, GPM-8, GPM-12b, GPM-18, GPM-22, GPM-24, GPM-26, GPM-28, GPM-30, GPM-32, GPM-32b, GPM-36, GPM-44-2, GPM-50, GPM-52, GPM-57, GPM-66, GPM-73, GPM-93, IC-

100938, KBHG-1, 49-08, Lone-1, PHG-2b, PHG-62, SHG-317, TCR-1517a, TCR-1675a, TCR-140, TCR-1423a, TCR-1423b, TCR-1554, TCR-1690a, TCR-1734a, TCR-1771, TRC-1801, TRC-1813, TRC-18025 and TRC-1493 showed moderately susceptible reaction.

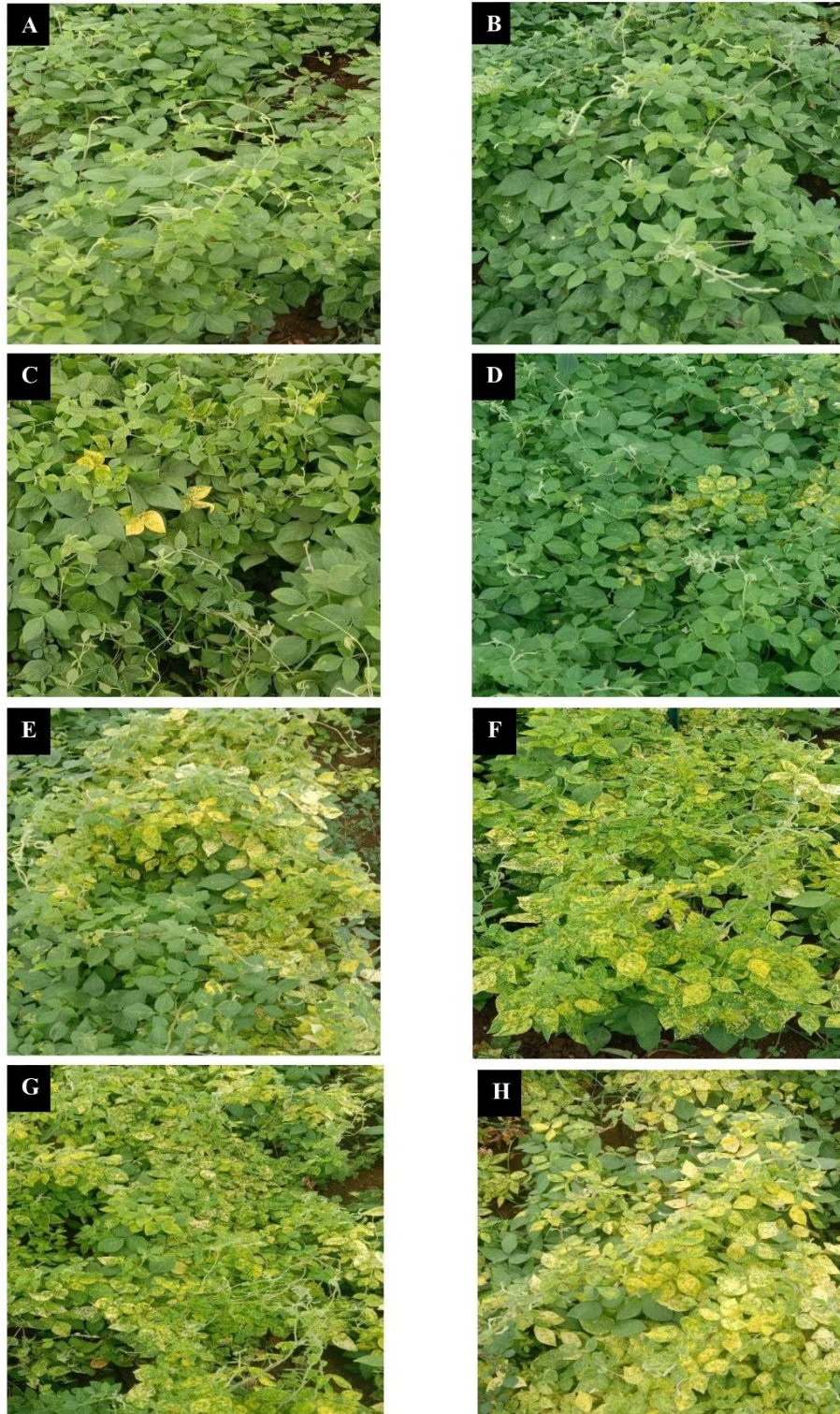


Plate 1. Reaction of different horsegram genotypes against YMD. A) PHG-9 (MR); B) CRHG-9 (MR); C) Bailhongal local (MS); D) AK-42 (MS) E) Indira Kulthi-1 (S); F) GPM-11 (S); G) BGM-1 (HS); H) CG-Kulthi-2 (HS)

Table 3. Per cent disease severity and per cent disease incidence of different germplasm lines of horsegram against YMD

Sl. No.	Genotypes	At physiological maturity		Disease scale (0-5)	Reaction
		DS (%)	DI (%)		
1	11-SS	25.92	25.00	3	MS
2	14-61-41	23.45	16.66	2	MR
3	AC-18-11	20.21	37.50	4	S
4	AK-12-7	24.07	33.33	4	S
5	AK-42	30.45	25.00	3	MS
6	ATPHG-11	26.98	40.00	4	S
7	Bailhongal local	25.46	23.52	3	MS
8	BHG-13-11	25.92	42.85	4	S
9	BSP-17-1	16.66	25.00	3	MS
10	BSP-17-2	24.46	33.33	4	S
11	BSP-17-3	26.50	28.57	3	MS
12	CG-Kulthi-2	100.00	75.00	5	HS
13	CG-Kulthi-3	100.00	60.00	5	HS
14	CRHG-5	58.35	50.00	4	S
15	CRHG-7	25.92	25.00	3	MS
16	CRHG-8	23.45	22.22	3	MS
17	CRHG-9	20.21	14.50	2	MR
18	CRHG-17	35.80	33.33	4	S
19	CRHG-19	28.57	50.00	4	S
20	CRHG-22	23.45	50.00	4	S
21	DHG-4	100.00	100.00	5	HS
22	VLG-19	25.92	28.57	3	MS
23	GPM-4	16.66	25.00	3	MS
24	GPM-5	100.00	38.48	4	S
25	GPM-8	35.80	25.00	3	MS
26	GPM-11	32.56	37.50	3	S
27	GPM-12b	28.57	23.52	3	MS
28	GPM-15	17.94	18.75	2	MR
29	GPM-17	17.94	20.00	2	MR
30	GPM-18	20.28	21.42	3	MS
31	GPM-19	17.94	33.33	4	S
32	GPM-22	17.94	22.22	3	MS
33	GPM-23	22.34	33.33	4	S
34	GPM-24	32.56	28.57	3	MS
35	GPM-26	22.46	22.22	3	MS
36	GPM-28	17.94	22.22	3	MS
37	VLG-8	26.55	15.38	2	MR
38	GPM-30	27.77	25.00	3	MS
39	GPM-32	22.78	25.00	3	MS
40	GPM-32b	27.77	22.22	3	MS
41	GPM-36a	17.94	14.28	2	MR
42	GPM-36	31.48	23.07	3	MS
43	GPM-44-2	24.36	23.07	3	MS
44	GPM-45	32.56	37.50	4	S
45	GPM-48	68.78	38.95	4	S
46	GPM-52	16.78	21.42	3	MS
47	GPM-50	25.92	27.27	3	MS
48	GPM-57	26.66	28.56	3	MS
49	GPM-58	22.22	40.00	4	S
50	GPM-59	41.97	40.00	4	S
51	GPM-61	74.65	50.00	4	S
52	GPM-62	32.78	62.50	5	HS

Sl. No.	Genotypes	At physiological maturity		Disease scale (0-5)	Reaction
		DS (%)	DI (%)		
53	GPM-64	27.77	38.46	4	S
54	GPM-66	29.78	22.22	3	MS
55	GPM-73	56.78	30.76	4	S
56	GPM-93	25.92	28.57	3	MS
57	HL-1	26.66	37.50	4	S
58	IC-100938	25.92	25.00	3	MS
59	Indira Kulthi-1	29.62	37.50	4	S
60	KBHG-1	22.45	27.27	3	MS
61	KGP-14-9	31.48	37.50	4	S
62	49-08	24.57	23.07	3	MS
63	Lone-1	25.92	28.57	3	MS
64	Lone-2	26.66	33.33	4	S
65	PHG-2a	24.56	14.28	2	MR
66	PHG-2b	29.78	22.22	3	MS
67	PHG-9	26.66	18.25	2	MR
68	PHG-62	25.92	22.22	3	MS
69	SHG-317	25.92	23.07	3	MS
70	TCR-1488	25.62	37.50	4	S
71	TCR-1517a	25.92	23.07	3	MS
72	TCR-1635	23.56	66.66	5	HS
73	TCR-1675a	23.56	22.22	3	MS
74	TCR-1690a	26.75	33.33	4	S
75	TCR-1700	67.68	37.50	4	S
76	TCR-1743	24.57	37.50	4	S
77	TCR-140	25.55	25.00	3	MS
78	TCR-1801	100.00	50.00	4	S
79	TRC-1488	29.87	66.66	5	HS
80	TRC-1503	37.03	42.85	4	S
81	TCR-1520	100.00	100.00	5	HS
82	TCR-1423a	32.45	25.00	3	MS
83	TCR-1593	67.68	45.45	4	S
84	TCR-1493	72.54	100.00	4	HS
85	TCR-1423b	30.04	22.22	3	MS
86	TCR-1517b	25.92	20.00	2	MR
87	TCR-1598	24.22	33.33	4	S
88	TCR-1554	24.44	25.00	3	MS
89	TCR-1675b	26.66	37.50	4	S
90	TCR-1690a	25.55	22.22	3	MS
91	TCR-1734a	24.57	25.00	3	MS
92	TCR-1734b	25.92	14.28	2	MR
93	TCR-1758	78.65	58.33	5	HS
94	TCR-1762	25.92	33.33	4	S
95	TCR-1771	22.45	26.66	3	MS
96	TRR-1799	16.05	15.38	2	MR
97	TRC-1801	22.45	25.00	3	MS
98	TRC-1813	28.88	25.00	3	MS
99	TRC-1816	20.67	14.28	2	MR
100	TRC-18025	30.04	25.00	3	MS
101	TRC-1493	25.96	25.00	3	MS
102	TCR-1734	23.56	37.50	4	S
103	GPM-49	24.65	38.46	4	S
104	IK-1	78.45	74.35	5	HS
105	Bilas Kulthi	85.43	68.97	5	HS
106	AK-53	70.83	46.67	4	S
107	AK-21	72.54	73.33	5	HS

Sl. No.	Genotypes	At physiological maturity		Disease scale (0-5)	Reaction
		DS (%)	DI (%)		
108	GDH-1	78.45	69.23	5	HS
109	CRHG-4	74.65	82.45	5	HS
110	CRIDA-1-18R	23.54	38.46	4	S
111	TCR-1489	23.56	100.00	5	HS
112	TCR-1552	85.43	69.23	5	HS
113	TCR-1590	72.34	73.33	5	HS
114	TCR-1675	78.65	55.56	5	HS
115	TCR-1740	22.45	50.78	4	S
116	TCR-1746	80.32	100.00	5	HS
117	TCR-1755	74.65	100.00	5	HS
118	GPM-6	72.34	100.00	5	HS
119	VLG-10	72.54	100.00	5	HS
120	VLG-15	42.33	50.00	4	S
121	PHG-02	24.56	38.46	4	S
122	TCR-1799	80.32	100.00	5	HS
123	TCR-1805	74.35	100.00	5	HS
124	TCR-1813	27.56	53.85	5	HS
125	TCR-1825	38.56	57.89	5	HS
126	TCR-1816	71.23	100.00	5	HS
127	TCR-1829	74.35	75.00	5	HS
128	GPM-44-12	22.56	100.00	5	HS
129	GPM-44-22	27.56	100.00	5	HS
130	GPM-33	20.21	40.00	4	S
131	GPM-17-1	22.34	80.95	5	HS
132	GPM-18B-1	20.21	72.73	5	HS
133	GPM-18B	20.21	85.00	5	HS
134	GPM-03	26.55	74.82	5	HS
135	GPM-02	23.45	65.00	5	HS
136	GPM-65	20.21	75.00	5	HS
137	GPM-118	22.56	77.78	5	HS
138	GPM-422	20.87	54.55	5	HS
139	TCR-1418	21.34	50.00	4	S
140	CRHG-02	65.67	85.71	5	HS
141	CRHG-26	71.23	86.36	5	HS
142	VLG-44	21.56	77.27	5	HS
143	VLG-45	20.21	100.00	5	HS
144	AK-22	28.67	32.00	4	S
145	VHG-935	20.28	36.36	4	S
146	VHG-15	40.46	34.78	4	S
147	BSP-15-1	68.90	47.37	4	S
Susceptible check					
148	BGM-1	78.45	100.00	5	HS

Note: DAS: Days after sowing, DS: Disease severity (%), DI: Disease incidence (%),

MR: Moderately resistant, MS: Moderately susceptible, S: Susceptible and HS: Highly susceptible

Forty-six genotypes namely AC-18-11, AK-12-7, ATPHG-11, BHG-13-11, BSP-17-2, CRHG-5, CRHG-17, CRHG-19, CRHG-22, GPM-5, GPM-11, GPM-19, GPM-23, GPM-45, GPM-48, GPM-58, GPM-59, GPM-61, GPM-64, HL-1, Indira Kulthi-1, KGP-14-9, Lone-2, TCR-1488, TCR-1690a, TCR-1700, TCR-1743, TCR-1801, TRC-1503, TCR-1593, TCR-1598, TCR-1675b, TCR-1762, TCR-1734, GPM-49, CRIDA-1-18R, AK-53, TCR-1740, VLG-15, PHG-02, GPM-33, TCR-

1418, AK-22, VHG-935, VHG-15 and BSP-15-1 showed susceptible reaction. The remaining forty-three genotypes namely CG-Kulthi-2, CG-Kulthi-3, DHG-4, GPM-62, TCR-1635, TRC-1488, TCR-1520, TCR-1493, TCR-1758, IK-1, Bilas Kulthi, AK-21, GDH-1, CRHG-4, TCR-1489, TCR-1552, TCR-1590, TCR-1675, TCR-1746, TCR-1755, GPM-6, VLG-10, BGM-1, TCR-1799, TCR-1805, TCR-1813, TCR-1825, TCR-1816, TCR-1829, GPM-44-12, GPM-44-22, GPM-17-1,

GPM-18B, GPM-18B-1, GPM-03, GPM-02, GPM-65, GPM-118, GPM-422, CRHG-02, CRHG-26, VLG-44, VLG-45 showed highly susceptible reaction against YMD.

Among the screened lines, the highest per cent disease incidence was observed in DHG-4, TCR-1520, TCR-1489, TCR-1493, TCR-1746, TCR-1755, GPM-6, VLG-10, TCR-1799, TCR-1805, TCR-1816, GPM-44-12, GPM-44-22, VLG-45, BGM-1 (100 %) and the lowest per cent disease incidence was observed in CRHG-9 (12.50 %). The highest per cent disease index was observed in DHG-4, TCR-1520, CG-Kulthi-2, CG-Kulthi-3, GPM-5, TRC-1801 (100 %) and the lowest per cent disease index was observed in TRR-1799 (16.05 %). Among 148 genotypes screened against YMD of horsegram, 8.11 per cent of genotypes showed moderately resistant reaction, 31.76 per cent of genotypes showed moderately susceptible reaction, 31.08 per cent of genotypes showed susceptible reaction and 29.05 per cent of genotypes showed highly susceptible reaction.

One hundred horsegram genotypes were screened against yellow mosaic virus under field conditions during 2011. Among the different

genotypes screened, 38 genotypes showed resistant reaction, 6 were moderately resistant, 3 were moderately susceptible, 23 were susceptible and remaining 30 genotypes showed highly susceptible reaction to HgYMV (Prema, 2013). Out of 110 horsegram germplasm lines evaluated under natural conditions during 2012, five genotypes viz., AK-38, HG-GP, DPI-2278, Paiyur-1 and Paiyur-2 recorded highly resistant reaction. Only three genotypes were resistant and two genotypes showed moderately resistant reaction and the remaining genotypes were moderately susceptible, susceptible and highly susceptible (Prema & Rangaswamy, 2017).

Similar results were obtained by Sushma et al., (2023) who screened thirty-seven genotypes of horsegram in a Randomized Complete Block Design (RCBD) with three replications under natural disease epiphytotic conditions at S.V. Agricultural College, ANGRAU, Tirupati, during Rabi, 2022. A total of eighteen horsegram genotypes exhibited resistant reaction with low per cent disease incidence. Among them, AVTH-12 had shown highly resistant reaction and susceptible reaction was observed in HG-17-1, BSP21-7, BSP21-4, BSP21-3, Indira Kulthi-1, BSP21-5, Bilasa and BSP21-11.

Table 4. Grouping of horsegram germplasm lines based on their reaction against YMD

Reaction	Scale	Description (% of plants exhibiting the disease symptoms)	No. of genotypes (% share of genotypes)	Genotypes
Immune	0	0	0	Nil
Resistant	1	1-10	0	Nil
Moderately Resistant	2	11-20	12 (8.11 %)	14-61-41, CRHG-9, GPM-15, GPM-17, VLG-8, GPM-36a, PHG-2a, PHG-9, TCR-1517b, TCR-1734b, TRR-1799, TCR-1816.
Moderately Susceptible	3	21-30	47 (31.76 %)	11-SS, AK-42, Bailhongal local, BSP-17-1, BSP-17-3, CRHG-7, CRHG-8, VLG-19, GPM-4, GPM-8, GPM-12b, GPM-18, GPM-22, GPM-24, GPM-26, GPM-28, GPM-30, GPM-32, GPM-32b, GPM-36, GPM-44-2, GPM-50, GPM-52, GPM-57, GPM-66, GPM-73, GPM-93, IC-100938, KBHG-1, 49-08, Lone-1, PHG-2b, PHG-62, SHG-317, TCR-1517a, TCR-1675a, TCR-140, TCR-1423a, TCR-1423b, TCR-1554, TCR-1690a, TCR-1734a, TCR-1771, TRC-1801, TRC-1813, TRC-18025, TRC-1493.
Susceptible	4	31-50	46 (31.08 %)	AC-18-11, AK-12-7, ATPHG-11, BHG-13-11, BSP-17-2, CRHG-5, CRHG-17,

Reaction	Scale	Description (% of plants exhibiting the disease symptoms)	No. of genotypes (% share of genotypes)	Genotypes
				CRHG-19, CRHG-22, GPM-5, GPM-11, GPM-19, GPM-23, GPM-45, GPM-48, GPM-58, GPM-59, GPM-61, GPM-64, HL-1, Indira Kulthi-1, KGP-14-9, Lone-2, TCR-1488, TCR-1690a, TCR-1700, TCR-1743, TCR-1801, TRC-1503, TCR-1593, TCR-1598, TCR-1675b, TCR-1762, TCR-1734, GPM-49, CRIDA-1-18R, AK-53, TCR-1740, VLG-15, PHG-02, GPM-33, TCR-1418, AK-22, VH-935, VH-15, BSP-15-1.
Highly Susceptible	5	>50	43 (29.05 %)	CG-Kulthi-2, CG-Kulthi-3, DHG-4, GPM-62, TCR-1635, TRC-1488, TCR-1520, TCR-1493, TCR-1758, IK-1, Bilas Kulthi, AK-21, GDH-1, CRHG-4, TCR-1489, TCR-1552, TCR-1590, TCR-1675, TCR-1746, TCR-1755, GPM-6, VLG-10, BGM-1, TCR-1799, TCR-1805, TCR-1813, TCR-1825, TCR-1816, TCR-1829, GPM-44-12, GPM-44-22, GPM-17-1, GPM-18B, GPM-18B-1, GPM-03, GPM-02, GPM-65, GPM-118, GPM-422, CRHG-02, CRHG-26, VLG-44, VLG-45.

4. CONCLUSION

Among 148 genotypes screened, twelve lines exhibited a moderately resistant reaction (14-61-41, CRHG-9, GPM-15, GPM-17, VLG-8, GPM-36a, PHG-2a, PHG-9, TCR-1517b, TCR-1734b, TRR-1799 and TCR-1816), forty-seven lines were moderately susceptible, forty-six lines were susceptible and forty-three lines showed highly susceptible reaction. Identified moderately resistant genotypes can be utilized in YMD resistance breeding programme to develop YMD resistant varieties.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Alice, D., & Nadarajan, N. (2007). *Pulses: Screening techniques and assessment for disease resistance*. All India Coordinated Research Project on MULLaRP-Tamil Nadu Agricultural University. Kasturi Graphics and Printers.
- Anonymous. (2022). Area, production and productivity of horsegram. Available at: www.indiastat.com.
- Bashir, M. (2005). Studies on viral disease of major pulse crops and identification of resistant sources. Technical Annual Report (April 2004 to June 2005) of ALP Project. Crop Sciences Institute, National Agricultural Research Center, Islamabad.
- Das, A., Aghora, T. S., Reddy, M. K., Nandeesha, P., & Venugopalan, R. (2024). Identification of source of resistance to Horse Gram Yellow Mosaic Disease (HgYMD) in French Bean (*Phaseolus vulgaris* L.). *Legume Research*, 47(5), 860-865.
- Kumar, P., Rani, N., & Prasad, S. M. (2021). Management of Mungbean Yellow Mosaic Virus (MYMV) disease using chemical insecticides and bio-pesticides.

- International Journal of Environment and Climate Change*, 11(12), 558-564. <https://doi.org/10.9734/ijec/2021/v11i1230634>.
- Parimala, K., Meenakumari, K. V., Sudhakar, R., & Durga, K. K. (2011). Screening of horsegram genotypes against yellow mosaic virus and powdery mildew diseases. *Indian Journal of Plant Protection*, 39(2), 160-161.
- Prema, G. U. (2013). Molecular characterization of horsegram yellow mosaic virus and its management (Ph.D. thesis, University of Agricultural Sciences, Bangalore, Karnataka, India).
- Prema, G. U., & Rangaswamy, K. T. (2017). Field evaluation of horse gram germplasm/genotypes against horsegram yellow mosaic virus (HgYMV) disease and biological transmission of horsegram yellow mosaic virus to different leguminous hosts through whiteflies. *International Journal of Agricultural Sciences*, 9(54), 4934-4939.
- Prema, G. U., & Rangaswamy, K. T. (2018). Molecular detection and characterization of coat protein gene of soybean yellow mosaic virus from Karnataka. *Annals of Agricultural Research New Series*, 39(1), 72-79.
- Prema, G. U., & Rangaswamy, K. T. (2020). Molecular characterization of DNA-A component of horse gram yellow mosaic virus (HgYMV) from southern India. *International Journal of Current Microbiology and Applied Sciences*, 9(1), 1360-1380.
- Prema, G. U., Rudraswamy, P., & Rangaswamy, K. T. (2013). Field screening of horsegram (*Macrotyloma uniflorum*) genotypes against horsegram yellow mosaic virus (HgYMV) disease. *Bioinfolet*, 10(2b), 599-601.
- Shaji, H., Kannan, R., Harish, S., Anita, B., & Sudha, M. (2023). Molecular detection of yellow mosaic virus infecting black gram and green gram in Coimbatore district. *International Journal of Plant & Soil Science*, 35(19), 1682-1689. <https://doi.org/10.9734/ijpss/2023/v35i193715>.
- Sushma, B., Manyam, P., Valli, P., Reddy, M. K., & Reddy, E. R. (2023). Identification of resistant sources against horsegram yellow mosaic disease in horsegram. *Andhra Pradesh Journal of Agricultural Sciences*, 9(3), 172-177.
- Wheeler, B. E. J. (1969). *An introduction to plant diseases*. John Wiley.
- Williams, F. J., Grewal, J. S., & Amin, K. S. (1968). Serious and new diseases of pulse crops in India in 1966. *Plant Disease Reporter*, 52(4), 300-304.

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