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Potential resistant donors for yellow mosaic disease identified from endemic wild *Vigna* species

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ABSTRACT

Yellow mosaic disease (YMD), caused by at least 3 different Begomoviruses including *Mungbean yellow mosaic India virus* (MYMIV), is one of the most destructive diseases of food legumes, especially the *Vigna* spp. including mungbean and urdbean. Some wild species of *Vigna* are valuable genetic resources offering number of desirable traits including resistance to yellow mosaic disease. Therefore, the present study aimed at screening wild relatives of *Vigna* to identify potential resistant sources against MYMIV. A panel of 102 endemic wild *Vigna* accessions along with 2 susceptible checks was screened during 2017-20 against MYMIV under natural field conditions. The identity of the virus involved in causing YMD was ascertained as MYMIV in PCR by using specific primers. Thirty-five accessions were found resistant to MYMIV with no visible symptoms of the disease on plants. These included 12 accessions of *V. umbellata*, 10 of *V. trilobata*, 7 of *V. aconitifolia*, 2 each of *V. vexillata* and *V. stipulaceae* and 1 accession each of *V. silvestris* and *V. hainiana*. Simultaneously, 47 accessions were categorized as moderately resistant. The resistant accessions could be valuable genetic resources in introgression breeding programmes while few of them, especially of *V. umbellata*, *V. aconitifolia* and *V. stipulaceae* can be directly used as a cultivar after their agronomic evaluation in target environments.

***Key words:** Asiatic Vigna,* Genetic resources, Resistance, White fly, Wild *Vigna,* YMD

INTRODUCTION

Numbers of biotic and abiotic stresses have been reported to adversely affect the pulse crops leading to significant losses in their seed yield as well as grain and nutritional quality. More than a dozen viruses including different species of yellow mosaic disease-causing Begomoviruses, *Alfalfa mosaic virus* (AMV), *Bean golden yellow mosaic virus* (BGYMV*), Cowpea yellow mosaic virus* (CPMV), and *Dolichos yellow mosaic virus* (DoYMV) inflict the pulse crops at different growth stages. Among these, YMD caused by Begomoviruses (Family *Geminiviridae*, genus *Begomovirus*) is one of the most prevalent and devastating diseases, especially in the *Vigna* group of crops (Singh *et al.* 2020; Nair *et al.* 2019). Molecular analysis of YMD-causing viruses revealed the association of four bipartite begomovirus species viz., *Mungbean yellow mosaic India virus* (MYMIV), *Mungbean yellow mosaic virus* (MYMV), *Horsegram yellow mosaic virus* (HgYMV) and *Dolichos yellow mosaic virus* (DoYMV) with pulse crops (Akram *et al.,* 2015; Naimuddin et al. 2016). Among them, MYMIV, MYMV, and HgYMV are known to cause YMD in mungbean and other *Vigna* species (Malathi and John, 2008; Naimuddin *et al.,* 2016), whereas DoYMV is reported from *Dolichos* bean and cowpea (Naimuddin and Akram, 2010). High incidence and severity of YMD has been reported in South East Asia causing about 75-100% yield loss when occurring in severe form (Sudha *et al.* 2013; Kitsanachandee *et al.* 2013). The polyphagous insect-vector white fly (*Bemisia tabaci*), transmits YMD-causing viruses in a persistent manner (Singh *et al.* 2020) and therefore, the disease incidence also depends upon the retention period of white fly on the host plant (Karthikeyan *et al.,* 2012).

With >200 species, *Vigna* is an important genus of flowering plants of the legumes family with a pantropical distribution (Pratap *et al.* 2014a). Among these, 10 species having significant agronomic potential are domesticated and these contribute significantly towards food and nutritional security, especially of the vegetarian population. Besides yield contributing traits, wild accessions of several of these *Vigna* species are expected to harbour many survival-related traits (Pratap *et al.* 2014a) while many of these are considered as a reservoir of valuable genetic resources for biotic and abiotic stress tolerance and seed quality traits (Pratap *et al.* 2020, 2021; Nair *et al.* 2019). A plethora of genes conferring resistance/ tolerance to these stresses have already been transferred cultivated germplasm (Pratap *et al.* 2018). Several accessions including those of *V. umbellata*, *V. trilobata,* and *V. mungo* (Nagaraj *et al.* 1981; Singh *et al.* 2003; Gautam *et al.* 2014); *V. radiata* var. *sublobata* (Singh and Ahuja 1977; Gautam *et al.* 2014) and *V. mungo* var. *silvestris* (Reddy and Singh, 1993) have been reported to be highly resistant to YMD. Although, the YMD management strategy is mainly based on limiting white fly population by using insecticides but it is ineffective, temporary and has negative environmental influence. Contrary to this, deployment of robust donors in breeding programme for introgression of disease resistance genes is the most economical and eco-friendly method to overcome susceptibility to biotic stresses in crop plants (Pratap *et al.* 2009). Therefore, availability of suitable donors with YMD resistance in intense form and their deployment in introgression breeding requires a reliable screening and identification of wild and cultivated germplasm. Therefore, the present study was undertaken with an objective to screen the wild genetic resources of *Vigna* to identify resistant sources to YMD caused by MYMIV.

MATERIALS AND METHODS

The present study was conducted on a panel of 104 genetically diverse genotypes of *Vigna* spp. including 102 wild accessions belonging to 19 different species and 2 YMD susceptible checks viz., DGGV 2 (mungbean) and Barabanki Local (urdbean) (Table 1). The experimental materials including the susceptible checks are available in the gene bank of ICAR-IIPR, Kanpur and were either initially procured from ICAR-National Bureau of Plant Genetic Resources, Regional Station, Trichur or collected from diversity rich hot-spots of Western Ghats, Himalayan region, Central Plateau, and North-Eastern regions of India (Table 1). All accessions including susceptible checks were grown in cemented pots of 1 meter diameter consecutively for 4 years (2017-20) during *Kharif* (monsoon) season in the *Vigna* wide hybridization garden established at Main Research Campus, ICAR-Indian Institute of Pulses Research, Kanpur. Each cemented pot has been specially designed with its base hollow and drainage holes in the periphery to drain excess water and maintain optimum moisture condition. Each pot contained a potting mixture of FYM, sand and fertile soil in 1:1:2 ratios. In order to counter staggered/reduced germination in the wild accessions due to their hard and waxy seed coat, seed scarification was done following Pratap *et al.* (2015). In each accession, 20 seeds were sown in individual pot around the periphery maintaining an equal distance of 5-7 cm. between two plants. Care was taken to grow each accession in the same pot every year to avoid mixture due to natural pod shattering and dispersal of seeds. The recommended package of practices for growing mungbean and urdbean in the zone was followed to raise healthy plants while no insecticide was sprayed in order to maintain the natural whitefly population in the experiment. After sowing, all the pots were individually observed on weekly intervals for recording the yellow mosaic disease. The Factorial Analysis of Mixed Data (FAMD), a model suitable to measure the latent variables, was deployed (Sebastien *et al.* 2008) to determine the distribution of accessions based on the yellow mosaic disease score (1-9) used to categorize the resistance reactions.

Observation of yellow mosaic disease

The YMD score was recorded periodically using 1-9 scale as described in Table 2 (AICRP, MULLaRP, 2020). However, only final recording which was done 45-60 days after sowing has been taken in to consideration for the reaction categorization of the genotypes.

RESULTS AND DISCUSSION

A panel of 102 diverse *Vigna* accessions belonging to 19 *Vigna* species were screened against YMD caused by MYMIV consecutively for four years under field condition at Main Research Farm of IIPR, Kanpur. In the Northern part of India, especially Kanpur region, where the study was conducted, YMD is reported to be caused by MYMIV as already verified in earlier studies (Naimuddin and Akram 2010; Naimuddin *et al.,* 2011; Naimuddin *et al.,* 2014;) and during the period of study using the same protocol on many accessions every year. The observations on YMD in all these accessions recorded during *Kharif* 2017-20 are presented in Table 1.

It was observed that during all the four crop seasons, the YMD score was recorded minimum as 1 on a number of accessions. However, the maximum score varied as it was recorded 6 in 2018, 7 in 2017 and 2019 and 8 in 2020 on the same accessions. This indicated that yellow mosaic disease severity was higher in the year 2020. The highest YMD score was recorded on both the susceptible checks during all the crop growing seasons. It was further observed that the disease severity scores varied even within a sub-species and was not limited to a group or the geographical area of collection of different accessions

Table 1. Disease reaction of endemic wild *Vigna* accessions for yellow mosaic disease during 2017-20

S. No.	Identification number	Name of the species	Source/ Collected from	YMD Score				Average YMD score	Reaction Category
				2017	2018	2019	2020		
1	IC277021	*V. sylvestris*	Western ghats	1	1	1	1	1	R
2.	IC248326	*V. vexillata*	Not known	1	1	1	1	1	R
3	IC248343	*V. vexillata*	Not known	1	1	1	1	1	R
4	LRM/13-43	*V. trilobata*	Not known	1	1	1	1	1	R
5	LRM/13-34	*V. trilobata*	Not known	1	1	1	1	1	R
6	LRM/13-32	*V. trilobata*	Not known	1	1	1	1	1	R
7	IC276983	*V. trilobata*	Madhya Pradesh	1	1	1	1	1	R
8	IC331436	*V. trilobata*	South east region	1	1	1	1	1	R
9	IC331454	*V. trilobata*	Central plateau	1	1	1	1	1	R
10	IC331456	*V. trilobata*	Central plateau	1	1	1	1	1	R
11	Trichy local	*V. trilobata*	Western Ghats	1	1	1	1	1	R
12	Kumur local	*V. trilobata*	Western Ghats	1	1	1	1	1	R
13	IIPRW17-3	*V. trilobata*	Not known	1	1	1	1	1	R
14	RBL-50	*V. umbellata*	Not known	1	1	1	1	1	R
15	IC251445	*V. umbellata*	Thrissur, Kerala	1	1	1	1	1	R
16	PRR 2007-2	*V. umbellata*	Himalayan region	1	1	1	1	1	R
17	PRR 2008-2	*V. umbellata*	Himalayan region	1	1	1	1	1	R
18	RB-5-1	*V. umbellata*	North-east region	1	1	1	1	1	R
19	IC251439	*V. umbellata*	North-east region	1	1	1	1	1	R
20	IC251442	*V. umbellata*	North-east region	1	1	1	1	1	R
21	IC251446	*V. umbellata*	North-east region	1	1	1	1	1	R
22	IC251447	*V. umbellata*	Thrissur, Kerala	1	1	1	1	1	R
23	IC528878	*V. umbellata*	Not known	1	1	1	1	1	R
24	IC197812	*V. umbellata*	Not known	1	1	1	1	1	R
25	IIPRW 17-1	*V. umbellata*	Not known	1	1	1	1	1	R
26	LRM/13-11	*V. aconitifolia*	Not known	1	1	1	1	1	R
27	LRM/13-33	*V. aconitifolia*	Not known	1	1	1	1	1	R
28	TMV-1	*V. aconotifilia*	Not known	1	1	1	1	1	R
29	LRM/13-26	*V. aconitifolia*	Not known	1	1	1	1	1	R
30	LRM/13-37	*V. aconitifolia*	Not known	1	1	1	1	1	R
31	LRM/13-38	*V. aconitifolia*	Not known	1	1	1	1	1	R
32	LRM/13-36	*V. aconitifolia*	Not known	1	1	1	1	1	R
33	IC331450	*V. hainiana*	South east region	1	1	1	1	1	R
34	Trichy Local-1	*V. stipulaceae*	Western Ghats	1	1	1	1	1	R
35	Trichy Local-2	*V. stipulaceae*	Western Ghats	1	1	1	1	1	R
36	IC251385	*V. mungo* var. *mungo*	Thrissur, Kerala	1	2	3	3	2.25	MR
37	IC251393	*V. mungo* var. *mungo*	Thrissur, Kerala	2	2	3	5	3	MR
38	IC251383	*V. mungo* var. *mungo*	Thrissur, Kerala	3	3	4	6	4	MR
39	IC251386	*V. mungo* var. *mungo*	Thrissur, Kerala	3	3	4	4	3.5	MR
40	IC251390	*V. mungo* var. *mungo*	Thrissur, Kerala	2	2	3	4	2.75	MR
41	IC260725	*V. radiata*	Thrissur, Kerala	2	3	4	4	3.25	MR
42	IC571775	*V. radiata*	Not known	3	3	4	4	3.5	MR
43	IC251425	*V. radiata* var. *radiata*	Thrissur, Kerala	3	3	5	5	4	MR
44	IC251426A	*V. radiata* var. *radiata*	Thrissur, Kerala	3	2	5	5	3.75	MR
45	IC251431	*V. radiata* var. *radiata*	Thrissur, Kerala	2	2	3	2	2.25	MR
46	IC251423	*V. radiata* var. *setulosa*	Thrissur, Kerala	2	2	4	5	3.25	MR
47	IC349699	*V. radiata* var. *sublobata*	Thrissur, Kerala	2	3	4	4	3.25	MR
48	IC256158	*V. radiata* var. *sublobata*	Thrissur, Kerala	3	2	4	4	3.25	MR
49	IC253924	*V. radiata* var. *sublobata*	Thrissur, Kerala	2	2	4	5	3.25	MR
50	IC251416	*V. radiata* var. *sublobata*	Thrissur, Kerala	2	2	4	5	3.25	MR
51	IC253920	*V. radiata* var. *sublobata*	Himalayan region	2	2	4	6	3.5	MR
52	JAP/10-47	*V. trinervia* var. *bourneae*	Thrissur, Kerala	1	2	3	3	2.25	MR
53	IC247407	*V. trinervia* var. *bourneae*	Thrissur, Kerala	3	2	5	6	4	MR
54	IC210563	*V. trinervia* var. *bourneae*	Thrissur, Kerala	1	2	4	2	2.25	MR
55	IC277036	*V. sylvestris*	Thrissur, Kerala	2	3	4	4	3.25	MR
56	IC277014	*V. sylvestris*	Western ghats	3	3	6	4	4	MR
57	IC203864	*V. dalzeliana*	Thrissur, Kerala	2	2	5	4	3.25	MR
58	IC331615	*V. dalzeliana*	Himalayan region	3	3	4	4	3.5	MR
59	RBL-6	*V. umbellata*	Not known	3	3	5	4	3.75	MR
60	IC251440	*V. umbellata*	Thrissur, Kerala	3	3	4	6	4	MR
61	IC251441	*V. umbellata*	Thrissur, Kerala	2	2	2	4	2.5	MR
62	IC248343	*V. vexillata*	Not known	3	4	5	4	4	MR

63	IC251435	*V. trilobata*	Thrissur, Kerala	1	2	3	4	2.5	MR
64	IC251436	*V. trilobata*	Thrissur, Kerala	2	3	3	4	3	MR
65	IC251437	*V. trilobata*	Thrissur, Kerala	3	3	5	4	3.75	MR
66	LRM/13-24	*V. trilobata*	Not known	2	2	4	4	3	MR
67	LRM/13-30	*V. trilobata*	Not known	2	3	4	5	3.5	MR
68	JAP/10-9	*V. trilobata*	Western ghats	2	2	3	5	3	MR
69	JAP/10-7	*V. trilobata*	Western ghats	2	2	3	4	2.75	MR
70	IC349701	*V. trilobata*	Western ghats	2	2	5	5	3.5	MR
71	JAP/10-7	*V. trilobata*	Western ghats	2	2	3	2	2.25	MR
72	LRM/13-44	*V. aconitifolia*	Not known	2	3	5	6	4	MR
73	IC331448	*V. hainiana*	South east region	3	3	4	4	3.5	MR
74	IC251376	*V. hainiana*	Central plateau	2	4	4	5	3.75	MR
75	IC251381	*V. hainiana*	Central plateau	2	3	3	4	3	MR
76	IC298665	*V. unguiculata*	Thrissur, Kerala	2	2	3	3	2.5	MR
77	NS B007	*V. unguiculata*	Himalayan region	2	2	4	4	3	MR
78	TCR 279	*V. unguiculata*	Not known	2	2	3	2	2.25	MR
79	Goa Cowpea 3	*V. unguiculata*	Not known	2	2	4	4	3	MR
80	JAP/10-51	*V. trinervia*	Western Ghats	2	3	2	2	2.25	MR
81	IIPRW17-2	*V. khandalensis*	Not known	2	3	4	5	3.5	MR
82	IC251372	*V. glabrescens*	Central plateau	2	2	5	6	3.75	MR
83	IC 251432	*V. radiata*	Thrissur, Kerala	3	3	5	6	4.25	MS
84	IC251433	*V. radiata*	Thrissur, Kerala	3	3	5	6	4.25	MS
85	IC251434	*V. radiata*	Thrissur, Kerala	3	3	6	6	4.5	MS
86	IC251394	*V. mungo* var. *mungo*	Thrissur, Kerala	3	4	5	6	4.5	MS
87	IC251396	*V. mungo* var. *mungo*	Thrissur, Kerala	3	4	6	5	4.5	MS
88	IC251387	*V. mungo* var. *mungo*	North- East Region	4	3	5	7	4.75	MS
89	IC251427	*V. radiata* var. *radiata*	Thrissur, Kerala	3	4	6	4	4.25	MS
90	IC247406	*V. radiata* var. *sublobata*	Thrissur, Kerala	3	3	6	5	4.25	MS
91	IC277039	*V. sylvestris*	Thrissur, Kerala	3	4	7	6	5	MS
92	IC277031	*V. sylvestris*	Western ghats	2	3	6	7	4.5	MS
93	IC251419	*V. radiata* var. *setulosa*	Thrissur, Kerala	3	4	4	6	4.25	MS
94	IC210575	*V. pilosa*	Thrissur, Kerala	3	3	6	5	4.25	MS
95	IC210576	*V. pilosa*	Western ghats	3	3	6	7	4.75	MS
96	IC210580	*V. pilosa*	Western ghats	3	4	5	6	4.5	MS
97	IC251444	*V. umbellata*	Thrissur, Kerala	3	4	5	6	4.5	MS
98	Mung Seed-1	*V. radiata*	Not known	2	4	6	5	4.25	MS
99	IC251397	*V. mungo* var. *mungo*	Thrissur, Kerala	4	4	7	7	5.5	S
100	IC247408	*V. dalzeliana*	Thrissur, Kerala	4	4	7	7	5.5	S
101	IC251438	*V. trilobata*	Thrissur, Kerala	3	3	7	7	5	S
102	JAP/10-5	*V. trilobata*	Western ghats	3	4	7	7	5.25	S
103	DGGV 2	*V. radiata*	Susceptible check	6	6	7	8	6.75	S
104	Barabanki Local	*V. mungo*	Susceptible check	7	6	7	8	7	S

Table 2. Disease Scoring Scale for YMD

Score	Symptoms	Reaction
1	No visible disease symptoms on leaves	R
2	Small yellow specks with restricted spread covering 0.1 to 5% leaf area	
3	Yellow mottling of leaves covering 5.1 to 10% leaf area	MR
4	Yellow mottling of leaves covering 10.1 to 15% leaf area	
5	Yellow mottling of leaves covering 15.1 to 30% leaf area	MS
6	Yellow discoloration of 30.1 to 50% leaf area	S
7	Pronounced yellow mottling and discoloration of leaves and pods, reduction in leaf size and stunting of plants covering 50.1 to 75% foliage	HS
8	Severe yellow discoloration of leaves covering 75.1 to 90% of foliage, stunting of plants and reduction in pod size	
9	Severe yellow discoloration of entire leaves covering above 90.1% of foliage, stunting of plants and no pod formation	

R = Resistant, MR = Moderately Resistant, MS = Moderately Susceptible, S = Susceptible, HS= Highly Susceptible

(Table 1) since a variable range of disease severity and resistance were observed within the different sub-species. Similar observations on variable disease incidence in endemic *Vigna* sub-species have also been reported earlier (Singh *et al.* 2020; Gautam *et al.* 2014; Sudha *et al.* 2013) suggesting the need for their evaluation in multiple seasons and multiple locations. Variable disease incidence among the different accessions in the present study could be further attributed to their inherent genetic potential as well as the prevailing environmental conditions. As per earlier studies, YMD incidence and its severity greatly depends upon the white fly population during crop season as well as their retention period on foliar parts of the plants (Anokhe *et al.* 2018; Karthikeyan *et al.* 2014; Czosnek, 2008; Czosnek *et al.* 2002). Comparatively drier environment during *Kharif* 2019 and 2020 as compared to 2017 and 2018 (data not given) due to less rainfall during the peak crop growth could be another reason for increased white fly population in the initial two years of study. White fly population is also reported to be highly affected by the planting locations and season (Laosatit *et al.* 2020). Under field conditions, the higher temperature favours, while high-rainfall and high-humidity limit the white fly population (Rahman *et al.*, 2006; Islam *et al.*, 2012). Likewise, high-altitude regions with low-humidity also influence the YMD incidence and disease severity (Alam *et al.* 2014).

Among the different accessions, 35 (33.65%) accessions were categorized as resistant with no visible disease symptoms on plants. Simultaneously, 47 accessions (45.19%) were categorized as moderately resistant, 16 accessions (15.38%) as moderately susceptible and the remaining 6 accessions (5.77%) including the 2 susceptible checks were susceptible. The 35 resistant accessions included 12 accessions of *V. umbellata* (IC251445, PRR-2007-2, PRR-2008-2, RB-5-1, IC251439, IC251442, IC251446, IC251447, RBL-50, IC528878, IC197812, IIPRW 17-1; 10 of *V. trilobata* (LRM/13-43, LRM/13-34, LRM/13-32, IC276983, IC331436, IC331454, IC331456, Trichy local, Kumur local and IIPRW17-3; 7 of *V. aconitifolia* (LRM/13-11, LRM/13-33, LRM/13-26, LRM/13-37, LRM/13-38, LRM/13-36, TMV-1); 2 each of *V. stipulaceae* (Trichy Local-1, Trichy Local-2*)* and *V. vexillata* (IC248326, IC248343*)* and 1 accession each of *V. sylvestris* (IC277021) and *V. hainiana* (IC331450) (Figure 1). Further, FAMD analysis also grouped the accessions into four major groups viz, resistant, moderately resistant, moderately susceptible and susceptible as per the disease scoring data and categorization of disease reactions (Figure 2). While categorizing the resistant reactions it was also considered that none of these should have witnessed any other reaction than resistant in any of the years and these accessions have been consistently resistant to MYMIV. Keeping in view that none of the above accessions was affected by YMD

Fig 1. *Vigna* accessions identified as resistant: LRM/13-11: *V. aconitifolia* (A), PRR-2008-2: *V. umbellata* (B), LRM-13-34: *V. trilobata* (C), RBL-50: *V. umbellata* (D), moderately susceptible: LRM/13-44: *V. aconitifolia* (E), and susceptible: DGGV 2 (F)

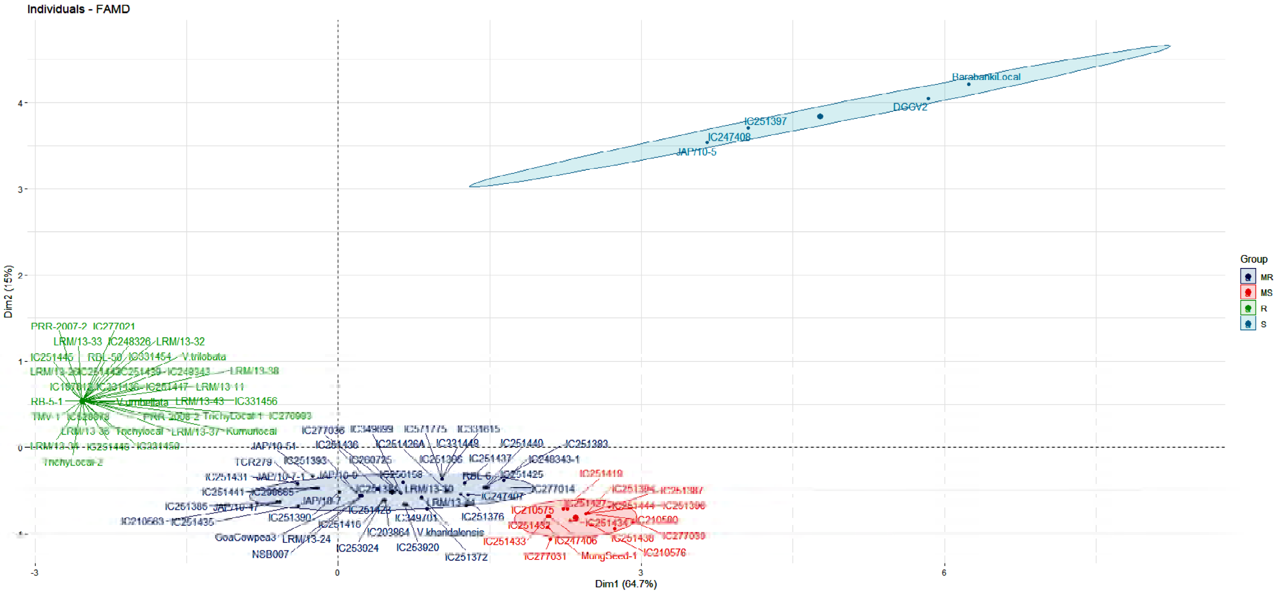

Fig 2. FAMD plot grouping accessions based on yellow mosaic disease score (1-9) disease reactions "resistance (left) and 'susceptibility' (right)

in any of the years and the plant growth and development remained normal, these could be deployed in introgression breeding for YMD resistance in *Vigna* crops, especially mungbean and urdbean. Resistance to YMD has also been reported in accessions of *V. umbellata*, *V. trilobata,* and *V. mungo* in earlier studies (Nagaraj *et al.* 1981; Singh *et al.* 2003; Gautam *et al.* 2014). Likewise, the sub-gene pool of wild types in accession PLN 5 of *V. radiata* var. *sublobata* (Singh and Ahuja 1977) and IW 3390 of *V. mungo* var. *Silvestris* (Reddy and Singh 1993) were also identified as potential sources of MYMV resistance, and TC 1966 of *V. radiata* var. *sublobata* was identified to carry bruchid tolerance gene (Tomooka *et al.* 1992). Among the above accessions identified as resistant to YMD, the accession IC 251442 of *V. umbellata* has also been reported to be photo-and thermo-period insensitive (Pratap *et al.* 2014b) as well as resistant to bruchid (*Callosobruchus maculatus* F.) (Revanasidda *et al.* 2021, communicated). Therefore, this accession can be especially a valuable genetic resource and be efficiently deployed towards introgression of YMD resistance as well as photo-thermo period insensitivity and bruchid tolerance in mungbean and urdbean. In earlier experiments, *V. radiata* × *V. umbellata* crosses were successfully generated to transfer resistance to MYMV and other desirable traits into mungbean (Verma and Brar, 1996). Pal *et al.* (2005) successfully produced inter-specific crosses between *V. mungo* and *V. umbellata*. Mung bean × rice bean crosses were also generated to incorporate MYMV resistance and other desirable traits into mungbean (Verma and Brar 1996). Singh *et al.* (2003) also produced successful hybrids between *V. radiata* and *V. umbellata* and the hybrids possessed intermediate morphology with MYMV resistance. Remaining accessions had variable levels of susceptibility with 10 accessions and the two checks being highly susceptible.

CONCLUSION

This study identified 35 *Vigna* accessions which are resistant to YMD caused by MYMIV with no visible symptoms (YMD score is 1) of the disease consecutively for four years. The identified resistant accessions could be utilized to develop mapping populations to map genomic regions conferring the resistance to MYMIV. Further, fine mapping would help in cloning of genes that would help in understanding the molecular mechanism of resistance and could be introgressed in the susceptible but otherwise agronomically superior accessions through marker-assisted selection. These accessions could also be directly used as a cultivar after their agronomic evaluation in target environments. This study also advocates identifying more such wild genetic and cultivated genetic resources which could be used in *Vigna* improvement programmes.

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