International Journal of Agriculture, Environment and Biotechnology
Citation: *IJAEB*: **15**(01): 01-09, March 2022
DOI: 10.30954/0974-1712.01.2022.1

ASSOCIATION FOR AGRICULTURE ENVIRONMENT AND BIOTECHNOLOGY

GENETICS & PLANT BREEDING

Identification of Donors of Mungbean and Urdbean against Yellow Mosaic Disease

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Paper No. 952 **Received:** 14-11-2021 **Revised:** 26-01-2022 **Accepted:** 28-02-2022

ABSTRACT

Mungbean (*Vigna radiata* L.) and urdbean (*Vigna mungo* L.) are major pulses crops predominantly cultivated during rainy season in northern and central India and during winter season in costal belt. In India, mungbean and urdbean productivity is constrained by a number of foliar and root diseases. Exploitation of host plant resistance for the development of high yielding varieties is the most economical and feasible component of integrated diseases management (IDM), hence remain a major objective of the crop improvement programmes around the world. The present investigation was undertaken to identify resistant donors against yellow mosaic disease (YMD) and therefore 200 germplasm accessions of mungbean and 100 of urdbean procured from ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi and ICAR-Indian Institute of Pulses Research (ICAR-IIPR), Kanpur were phenotyped under natural field conditions, besides molecular characterization of viral pathogen and monitoring growth parameters. None of the mungbean and urdbean lines were found resistant to YMD during two seasons of the screening. However, 16 mungbean and 41 urdbean accessions manifested moderate resistant reaction, respectively and were identified as potential donors against MYMIV for utilization in breeding programme. These accessions also performed well with respect to growth parameters and grain yield. The sequence analysis of virus revealed 99.08 to 95.95 percent similarities with *Mungbean yellow mosaic India virus* (MYMIV) infecting distinct hosts from different geographical regions.

HIGHLIGHTS

- The study could identify the donors of mungbean and urdbean against *Mungbean yellow mosaic virus*.

Keywords: Mungbean, urdbean, MYMIV, phenotyping, phylogenetic analysis, resistance breeding

Mungbean (*Vigna radiata* L.) and urdbean (*Vigna mungo* L.) are important short duration (60-75 days) food legume grain crops from Family *Fabaceae* and known for their wider adaptability. These crops fit well under various cropping systems and are important for the sustainability of agricultural production base, particularly of cereal-cereal cropping system of the Indo-Gangetic plains. In India, mungbean and urdbean are among the staple pulse crops, covering an area of about 4.3 and 4.9 million hectares (ha), respectively with an estimated production of ~2.64 and ~2.38 million tons (m t), respectively (DES, Govt. of India 3rd Advanced Estimate, 2020-2021). India is importing huge quantity of urdbean and mungbean to meet domestic demand and large gaps between demand and supply exists. To save precious foreign exchange, suitable high yielding varieties possessing multiple diseases resistance, matching phenology

How to cite this article: Sushmita, V.T., Arya, M., Jambhulkar, P.P., Manjunatha, N., Singh, A. and Chaturvedi, S.K. (2022). Identification of Donors of Mungbean and Urdbean against Yellow Mosaic Disease. *Int. J. Ag. Env. Biotech.*, **15**(01): 01-09.

Source of Support: RLBCAU, Jhansi; **Conflict of Interest:** None

and integrated crop production technologies need to be developed for various seasons and agro-ecological conditions. Although yield potential of mungbean is in the range of 2.5–3.0 t/ha, however, its average productivity is staggering low at around 0.55 t/ha due to abiotic and biotic constraints, poor crop management practices and non-availability of quality seeds (Chauhan *et al.* 2010; Pratap *et al.* 2019a) with almost similar situation with urdbean. The production trends over the last decade indicate a significant potential for yield improvement to meet the growing demand of pulses as cheapest source of protein for predominantly vegetarian population of the country. One of the major biotic factors constraining realization of higher yield at farmers' fields in both mungbean and urdbean include *Mungbean yellow mosaic virus* (MYMV) disease transmitted by white fly (*Bemisia tabaci*) with an incidence of 4-40 per cent (Bashir *et al*. 2006; Iqbal *et al*. 2011). In repeated samplings over consecutive years in India it is now confirmed that at least two viral strains i.e. MYMV and MYMIV species causing yellow mosaic disease (YMD) are prevalent in Indian subcontinent. Of which, MYMIV is considered to be more predominant in northern, central and eastern India and the other MYMV in peninsular region of India (Karthikeyan *et al*. 2004; Malathi and John 2008 b; Naimuddin and Akram, 2010; Parihar *et al.* 2017).

The reported economical yield losses in these two crops have been estimated to about 85% due to YMD in India (Karthikeyan *et al.* 2014). Though judicious use of pesticides can manage the viral diseases of mungbean and urdbean to some extent, their large-scale use is neither cost effective nor eco-friendly. Hence, development of varieties with genetic resistance to such pathogens is the most effective and sustainable approach for integrated disease management. Even though there are few resistant varieties developed against YMD of mungbean and urdbean, there are chances of breakdown of resistance due to narrow genetic base and emergence of new races of pathogens and insect biotypes. Therefore, identification of stable resistant sources is continuously required for the development of resistant varieties (Akhtar *et al*. 2011). Accordingly, resistance donors to develop YMD resistant varieties in mungbean and urdbean has been identified by different researchers over the last decade by using common acceptable scale based on severity of disease (Panduranga *et al.* 2011; Paul *et al.* 2013; Suman *et al.* 2015; Khaliq *et al.* 2017; Abrol and Sharma 2018; and Dharajiya *et al.* 2018). The study reported here was conducted in Bundelkhand region of the Indian state of Uttar Pradesh, which has a leading position in terms of area and production of pulses. There are very limited reports related to identification of resistant sources and varieties against viral diseases of mungbean and urdbean to recommend region specific resistant varieties. Therefore, phenotyping under natural field conditions was targeted to identify YMD resistant donors of mungbean and urdbean against the viral diseases so that high yielding varieties can be insulated against YMD and promoted in Bundelkhand region, which is known as Mini Pulse Bowl.

MATERIALS AND METHODS

The field experiments were conducted at the Experimental Farm of the Rani Lakshmi Bai Central Agricultural University (RLBCAU), Jhansi (Uttar Pradesh) which is located at 25.51° N latitude, 78.56° E longitude, and 227 m above MSL. Sowing of the germplasm accessions was performed manually during *kharif* season on 27th July, 2019 and 24th July, 2020. Each accession was represented by a row length of 4 m with a uniform spacing of 45 cm and 10 cm between the rows and the plants, respectively. Susceptible checks (Bundelkhand Local for both the crops) and standard check varieties (SML 668, Samrat, TMB 37, MH421 for mungbean and IPU 2-43 for urdbean) were sown for comparing disease severity of the test accessions. Standard agronomic practices were followed, except plant protection, to raise crops successfully for further studies on disease development in both the crops. The disease severity under field conditions was recorded during the period from the first appearance of the disease till maturity. Ten plants were randomly selected from each accession and tagged for recording the observations at 15 days interval by observing the disease appearance on plants and scoring was done using standard rating scales as adopted by Bashir *et al*. (2006). The entire data was pooled and per cent disease index (PDI) was calculated from the above scales using the following formula (Wheeler 1969).

Per cent Disease Index =

$$\frac{\text{Summation of all rating}}{\text{Total number of ratings} \times \text{Maximum disease grade}} \times 100$$

Isolation of DNA

Samples were collected from the plants showing YMD symptoms under field conditions, carefully placed in tagged polythene bags, and brought to the laboratory. The total genomic DNA was extracted using CTAB method (Lodhi *et al.* 1994) from the most susceptible genotypes of both mungbean (DAAV 2, PS16 and RMG991) and urdbean (BG367, IC 39227 and IC 600673) genotypes. The quantification of DNA was done at 260 nm and 280 nm wavelength using a UV-spectrophotometer to check its quantity, purity and integrity.

Primer synthesis and PCR amplification of viral DNA

The degenerated oligonucleotide primers already available from coat protein region (520 bp) were synthesized (Bangalore Genei Pvt. Ltd.). The forward (5′ TAATATTACCKGWKGVCCSC3′) and reverse primers (5′ TGGACYTTRCAWGGBCCTTCACA3′) were used for amplification of genomic DNA obtained from YMD infected samples (Maheshwari *et al*. 2013). Subsequently, the viral DNA alongwith the negative control were subjected to PCR amplification keeping the annealing temperature as 58 °C.

One per cent gel was prepared by melting 1g agarose in 100 ml of 1x TAE (Tris buffer) added with 2-3 µl ethidium bromide. Sufficient amount of 1x TAE buffer was added in the electrophoresis tank to cover gel up to 10 mm depth. Each well of the gel was loaded with 8 µl PCR products along with 4 µl loading dye (HIMEDIA) along with 50 bpDNA ladder (HIMEDIA). Electrophoresis was performed for about 35-40 minutes under 50 volts. Agarose gel with migrated DNA fragments were visualized under gel documentation (Bio-Rad Laboratories). Further, the amplified products of CP region were sequenced by Sanger method at M/s Eurofins Scientific India Pvt. Ltd., Bengaluru, India.

Phylogenetic analysis

The retrieved sequences were deposited in the GenBank, National Centre for Biotechnology Information (NCBI) database (genbankhttps://www.ncbi.nlm.nih.gov) and accession numbers were secured. Sequences picked-up from the CP region were subjected to nBLAST to find out the homology with available nucleotide sequences from the viral DNA database available at NCBI. The nucleotide sequences that were showing higher homology were saved for phylogenetic and molecular relationships. The reliable reference sequences fetched from GenBank and viral DNA sequences from present study were aligned using the ClustalW program available in MEGA × software (*https://www.megasoftware.net/*) with default parameters. The phylogenetic tree was constructed using MEGA X software following the Maximum Likelihood method adopting 1000 bootstrap replications (Kumar *et al.* 2018).

RESULTS AND DISCUSSION

During phenotyping of the germplasm accessions of mungbean and urdbean under field condition during *kharif* 2019 and *kharif* 2020 the inceptive disease symptoms of the YMD commenced on younger leaves at around 30 days after sowing. The yellow spots were scattered along the leaf lamina and more concentrated near leaf veins and midrib region. Later the spots coalesced giving irregular patches of green and yellow colour on the leaf leading to typical mosaic pattern. Finally, the symptoms covered the entire leaf area and became completely chlorotic as the disease progressed in susceptible accessions (Fig. 1 & 2).

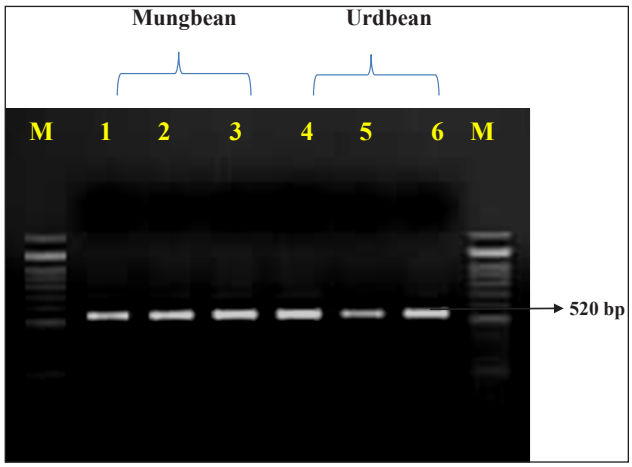
Fig. 1: Symptom of yellow mosaic disease on mungbean leaves

Fig. 2: Symptom of yellow mosaic disease on urdbean leaves

The infected plant remains stunted exhibiting delayed maturation with few flowers and small sized pods. In most susceptible ones, pods also turned yellow with deformed seeds that led to

poor seed quality and less harvest. Early infection i.e. before flowering even caused death of the plants leading to complete yield loss, whereas late infections affected the quantity and quality of the economic produce.

The viral DNA was isolated directly by extracting total genomic DNA from the infected plants (mungbean genotypes DAAV 2, PS16 and RMG991 and urdbean genotypes BG367, IC 39227 and IC 60067 genotypes.) leaves displaying typical symptoms of YMD using CTAB method and later subjected to PCR amplification of partial viral coat protein (CP) gene using degenerated *Begomovirus* specific primers. The amplification of 520 bp of CP region was obtained from the DNA of the infected samples using forward and reverse primers (Fig. 3).



Lane M: Marker; Lane 1: DAAV-2; Lane 2: PS-16; Lane 3: RMG-991; Lane 4: BG-367; Lane 5: IC 392273; Lane 6: IC 600673.

Fig. 3: PCR amplification of DNA of MYMIV using universal *Begomovirus* specific primers for CP region

No amplification was observed in the negative control indicating the association of *Mungbean yellow mosaic virus* (MYMV) with YMD in both, mungbean and urdbean crops.

The BLAST homology analysis of the sequence obtained for amplified partial CP region was carried out. The sequence obtained for coat protein region of Jhansi isolate was submitted to GenBank, NCBI and accession number MT783246 was obtained. The sequence analysis displayed 99.08-95.95 percent similarity with *Mungbean yellow mosaic* India *virus* (MYMIV), which infect distinct hosts from different geographical regions. The partial nucleotide sequence of the study isolates shared maximum identity of 99.08% with MYMIV infecting *Dolichos* (GenBank Accession No. AY547317) from Uttar Pradesh and 98.40% with the mungbean isolate (GenBank Accession No. FM208839) reported from Pakistan.

A phylogenetic analysis based on nucleotide sequences of CP region along with other sequences obtained from GenBank, NCBI revealed that the isolated pathogen in the present study is grouped with MYMIV and thus supported the morphological identification. Further, the phylogenetic tree displayed close relation between MYMIV causing YMD in mungbean and urdbean and the isolate from *Dolichos* plant (Fig. 4) of Uttar Pradesh (GenBank Accession No. AY547317).

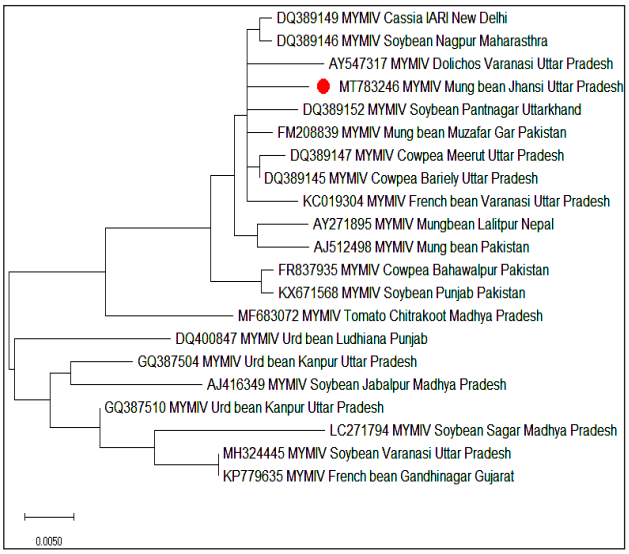


Fig. 4: Maximum likelihood phylogenetic tree generated from CP region of MYMIV isolates from mungbean and reference sequences from NCBI at bootstrap values of 1000 replicates (MEGA X)

Similar findings were reported in an earlier study where the band of approximately 520 bp consistently amplified using group specific begomoviral primers for amplification of partial coat protein gene of the MYMV (Deepa *et al.* 2017 b). The findings of Maheshwari *et al*. (2014) indicated that the CP region is efficient enough to provide a simple, rapid, and reliable method for early detection of YMV infections in pulses, thereby help to develop proper management strategies to control these viruses. MYMV was also characterized by Prema and Rangaswamy (2018) by sequencing the coat protein gene and later its phylogenetic analysis with the known *begomoviral* sequences retrieved from GenBank.

Screening of the germplasm

200 mungbean germplasm along with three varieties SML 668, Samrat and MH 421 were screened against YMD in mungbean. Scoring on the disease resistance scale (Bashir *et al*. 2006) revealed 16 accessions as moderately resistant where the disease severity ranged from 27.78 to 38.39 per cent (Table 1). Germplasm accessions such as IC 118971, IC 314674, Pusa 672, and CO-8 showed lesser disease severity (27.78%) as compared to other moderately resistant germplasm accessions. Further, the accessions viz. MASH 338, SML668, Indore Mung, Pusa 672, Brazil, Co 4, Pant Mung 8, ML2037, IC 285532, PLM 187 SML 668, SML191 and IC 616493 showed consistent moderately resistant (MR) reaction during *kharif* 2020.

Similarly, out of 100 accessions of urdbean screened, 41 germplasm accessions were found moderately resistant with an average disease severity ranging from 27.78 to 38.89 per cent. The genotypes viz., UH 8038, SPS 7, IPU 99-213, IPU 99-123, IPU 2K-99-224, IPU-99-31, STY 2115, PGRU 95018, SPS5, IPU 99-144, IC- 530658, IC 565276, IC565247, IC41718 and IC 530452 displayed better resistance than other germplasm accessions with a disease severity of 27.78 per cent (Table 1). However during *kharif* 2020, the accessions IPU-99-232, IPU-99-31, IC 565276 displayed resistant reaction and several other accessions namely, SPS5, PGRU99028, IC-530658, PLU53A, PLU103, IC 530501, IC 565272, IC 570267, IC 600255 showed moderately resistant reaction consistently for two seasons. These results are comparable with other findings while reporting SML 668as moderately resistant against MYMV (Paul *et al*. 2013; Akhtar *et al*. 2016) and PS 16 as susceptible accession at Ranchi region (Akhtar *et al*. 2016). VBN (Gg) 2 manifested susceptible reaction during screening of mungbean genotypes by Mahalingam *et al*. (2018). Further, a study reported from Gujarat

Table 1: Disease reaction of mungbean entries against yellow mosaic disease during *Kharif* 2019

Reaction	No. of entries	Range of PDI (%)	Score	Entries
MR	16	27.78-38.89	3	IC 118971, IC 314674, IC 3204, IC 19420, PUSA 672, CO-8, IC 56112, SONA YELLOW, ML 1256, PM 6, PANT MUNG 8, BRAZIL, CO-4, ML-2037, IC 285532, PLM 187
MS	80	44.44-55.56	4	IC 314347, EC 496839, IC 282141, IC 348964, IC 73401, IC 398988, IC 314851, IC 541818, IC 314697, IC 314538, IC 119106, IC 76499, IC 15567, IC 52046, IC 314419, IC 373199, IC 76389, IC 249566, IC 103821, IC 121203, SML 832, IPM 312 43K, IPM02-3, KM 2241, PUSA 9972, ML 1299, BM 64, BANGLADESH LONG POD, ML 515, IPM 99 125, PDM 178, IPM 2-2-3, PDM 54, CO-7, TJM -3, ML- 1464, OUM 11-15, NH-805, CHINA MUNG-2, TARM -1, PUSA BOLD-2, IPM 2K-14-15, IPM 2-19, ML-5, INDORE MUNG, IPM 5-2-8, VMS-6, IPM 306-6, IC 76378, IC 76322, PLM 771, IC 252012, PLM 780, PLM 656, IC 305249, PLM 510, IC 76466, PLM 652, IC 8924, IC 76464, IC 76377, IC 76418, IC 314322, IC 52083, IC 121220, IC 417873, IC 76451, BM 63, NM 1, MGG 347, SML 1455, IPO 1-539, SM-48, PUSA 0891, IC 11443-1, PLM 783
S	75	61.11-77.78	5	MASH -1008, EC 520034-1, IC 314854, IC 305291, IC 121301, IC 314649, IPM 205-7, PUSA 9531, IPM 2K 14 9, MASH 338, PM 2, MH 2-15, SONA GREEN, V-1133, IC 121237, IC 37395, IC 314512, IC 52046, IC 296169, IC 333213, IC 488524, PAIRY MUNG, IC 39400, IC 305284, IC 314841, IPM 06 5, GANGA 8, MGG295, PUSA 9072, PAU 911, AKM 96-2, OMG 1030 (PMR), DAAV-2, PS-16, RMG-991, RMG-353, KOPERGAON, TARM 2, IC 540483, IC 76338, IC 76503, IC 18915, IC 76477, PLM 1032, IC 9225, IC 314568, IC 296672, IC 148531, ML 2056, BDYR 2, DGG 5, HUM 1, MGG 351, TARM -15, PRATEEKSHA NEPAL, PAIRY MUNG, SML 191, GM-4, OMG-1045(PMR), BHUTAN LM 1, SML 1082, IC 9127-1, IC-507454, PLM 501, IC 764-76, PLM 482, IC 76474, PLM 655, IC 305291, PLM 646, PLM 653,IC 76463, IC 76453, PLM 190, PLM188
HS	29	83.33-94.44	6	PDM 11, IC 421089, SUKETI 1, AKP/NP/8/9, COGG 912, K 851, KM11-584, IPM409-4, JBT 46/23, VAMBAN 2, VBN (Gg-2), IC 76414, IC 10187, IC 763502, IC 305241, IC 8422, IC 397142, PLM 998, PLM 772, PLM 647, IC 76448, IC 76444, IC 1082, LBG 623, ADT 3, IC 76361, IC 76370, PLM 24, PDM 11

Table 2: Average mean and range of plant growth characters of moderately resistant mungbean (16) and urdbean genotypes (41)

Plant characters	Mungbean		Urdbean	
	Mean + S.D	Range	Mean + S.D	Range
Plant height (cm)	67.25±13.68	27.5 to 91.5	65.74±26.03	31.5 to 108.5
Pod length (cm)	5.25±1.16	3.0 to 6.75	3.70±0.44	2.75 to 4.5
Number of cluster per plant	5.46±2.55	2.5 to13.0	7.56±2.72	3 to 13.5
Number of pods per cluster	2.60±0.42	2.0 to 3.0	2.90±0.75	1 to 4
Number of seeds per pod	6.48±0.79	5.5 to 8.5	5.90±0.85	4.5 to 7

revealed that HUM 1 unveiled susceptible reaction out of 35 mungbean genotypes during *Kharif* 2019 (Dharajiya *et al.* 2018), akin to the results of the present study. However, the germplasm accessions CoGG 912, SML 1082 and Kopergaon local expressed moderately susceptible reaction in their studies, although CoGG 912 sighted highly susceptible and SML 1082 and Kopergaon local susceptible reaction in the present trial. Chandra *et al*. (2019) also supported the findings regarding HUM 1 while screening mungbean genotypes against MYMV at Ayodhya (India). The moderately susceptible reaction was observed in Pusa Bold 2 and SML 191 however SM 48, ML 515, ML 5 and IPM 306-6 displayed susceptible reaction (Singh and Singh 2019). The susceptible reaction was also observed in Kopergaon and moderately resistant reaction in MH 421 against MYMV in mungbean (Abhay *et al*. 2020) that were affirmative to the results reported in the present study. Similarly, K 851 and COGG 912 scored in the highly susceptible category in our experiment similar to the observations recorded earlier at Varanasi and Raichur (Bhanu *et al.* 2017; Deepa *et al*. 2017 a). The possible reason for this variation in the susceptibility of genotypes to the virus may be due to host plant interactions with pest, pathogen and environment.

Similar work on screening of the urdbean germplasm was carried out by Singh *et al*. (2008) at Jammu and the genotype IPU99-23 showed susceptible reaction whereas in the study under report IPU99-23 showed moderately susceptible reaction. Kumar and Bal (2012) reported PGRU 95018 as resistant at Gurdaspur, though it exhibited moderately resistant reaction in the present study at Jhansi. Gopi *et al*. (2016) evaluated 49 germplasm lines against MYMV in urdbean at Guntur, in which PU 30 showed moderately resistant reaction similar to findings of the our study. However, SPS 7 displayed resistant reaction towards MYMV (Shamim and Pandey 2014) in Uttar Pradesh, although it was moderately resistant in the current findings. The absence of resistant sources within the test germplasm accessions highlights the need for evaluation of larger number of accessions for exploiting new sources of germplasm to overcome the limited genetic diversity in cultivated mungbean and urdbean (Nair *et al*. 2019) for disease resistance breeding.

Study on plant growth parameters of mungbean and urdbean

The details of the *per se* performance and range among 200 germplasm accessions of mungbean and 100 of urdbean with respect to five agronomic traits has been presented in Table 2. In mungbean, the maximum variation was recorded for plant height followed by number of cluster per plant and pod length, whereas minimum variation was apparent in the number of pods per cluster. The general mean for plant height varied from 27.5 cm (PLM 187) to 91.5 cm (ML 1256). The mean pod length was 5.25 cm with a range of 3.0-6.75 cm. The genotype DGG 5 exhibited maximum pod length followed by Co 4 and IC 314322, whereas the smallest pods were observed in PLM 187. A wide range of variation was recorded among the 200 mungbean accessions for number of clusters per plant with a general mean of 5.46 {2.5 (IC 285532, PLM 187, Pant Mung 8, IC 118971)} to 13 (Pusa 672). The average number of pods per cluster (2.60) was observed with the minimum number as 2 pods in IC 285532, PLM 187, Pant Mung 8, Sona Yellow, IC 56112, IC 19420 and maximum 3 pods in IC 314322, IC 73401, IC 76499, ML-2037, NM 1, IC 3204, Pusa 672, CO 8, ML 1256, CO 4 and ML-2037. The general mean for number

of seeds per pod (6.48 seeds) ranged from 5.5 to 8.5. The maximum number of seeds per pod (7) was observed in Pusa 672, DGG 5 and IC 3204.

In urdbean genotypes, the mean plant height was 65.74 cm in with large variations from 31.5 cm (IC 570267) to 108.5 cm (IPU2K-99-224). The mean pod length exhibited a general mean of 3.70 cm and varied from 2.75 cm (IC 565272) to 4.5 cm (IC 565276). The cluster per plant (3-13.5) and pods per plant (1-4) also displayed wide variations. PLU 81 had maximum number of clusters per plant (13.5) followed by PGRU 95018 (12.5), IPU 99-123 (12) and PDU 8 (11), whereas IC 565276 flashed minimum clusters. The genotypes PDU-8 (4) and PLU 81 (3.5) displayed maximum number of pods per cluster, while genotypes IC 566025, PLU 103 and IC 565291 relatively exhibited lesser number of pods per cluster. The number of seeds per pod ranged from 4.5 to 7 (with Mean 5.50) indicating that most of the genotypes were of medium size. Bag *et al*. (2014) reported that T-9 have on an average 5.4 seeds per pod close to our findings.

In the present study, PLU 81, PGRU 95018, IPU 99-123 and PDU 8 displayed most promising yield contributing attributes *viz*. clusters per plant, pods per cluster and seeds per pod. PLU 81 had the maximum clusters per plant (13.5) followed by PGRU 95018 (12.5), IPU 99-123 (12) and PDU 8 (11). PDU 8 also had maximum number of pods per cluster (4) followed PGRU 95018, IPU 99-123, PLU 81 (mean 3.5 clusters per plant). Further, PDU 8, PGRU 95018 and IPU 99-123 had more number (6.5) of seeds per pod.

Sarkar *et al.* (2014) also reported that mungbean PM 2 genotype had 76.16 cm of plant height with pod length of 7.88 cmsimilar to the observations recorded in our study (mean plant height 75.0 cm; mean pod length 5.5). Further, according to Annual Report (2013-14) of the ICAR-IIPR genotypes viz., Pusa 672, PDM 11, Samrat was having the height of >40 cm and Narendra Moong 1 which supported the result obtained in the current investigation where the height of Pusa 672, PDM 11, Samrat and Narendra Moong 1 (NM1) is 74.5 cm, 82 cm, 71 cm and 68 cm, respectively.

In the present investigation, based on the study on the disease scoring and plant growth parameters, the mungbean accessions viz., Pusa 672, ML 1256, Pant Mung 8, ML-2037, IC 285532, PLM 187, IC 118971, IC 314674, Brazil and IC 3204; and urdbean genotypes viz., PGRU 95018, IPU 99-123, IPU-99-232, IPU-99-31, IC 565276 and PDU 8 were identified as potential donors against MYMIV and can be utilized for breeding YMD resistant varieties.

CONCLUSION

Resistance breeding remain a focused objective of most of the crop improvement programs as it is the most effective, economical, and sustainable approach to manage biotic stress to combat the outbreak of diseases. Even though few resistant varieties have been developed against YMD ases of mungbean and urdbean, there is possibility of breakdown of resistance/tolerance due to narrow genetic base and emergence of new races of pathogens and insect biotypes (vector). Therefore, identification of resistant sources needs to be explored immediately for the development of resistant varieties. In the set of screened germplasm of mungbean and urdbean, no resistant lines to *Mungbean yellow mosaic India virus* (MYMIV) were found. However, some geno types of mungbean (16) and urdbean (41) displayed moderately resistant reaction to MYMIV.

The phylogenetic analysis of the coat protein sequence of viral DNA and its cluster based comparison revealed that the viral strain prevailing at Jhansi is MYMIV and can be grouped with the clusters of MYMIV. The nucleotide sequence of the isolate shared 99.08% identity with MYMIV infecting *dolichos* from Uttar Pradesh. Since the pathogen strains vary from region to region, the results may be helpful in identifying the pathogen strain prevalent in Bundelkhand region.

Based on the study on the plant growth parameters, the mungbean genotypes Pusa 672, ML 1256, Brazil; and IC 3204; and urdbean genotypes PGRU 95018, IPU 99-123 and PDU 8 were identified as potential donors for resistance breeding for moderate tolerance against MYMIV.

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