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Report on Pigeonpea Sterility Mosaic Virus (PSMV) Disease Incidence in CO (Rg) 8 in Tamil Nadu

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A B S T R A C T

Pigeonpea sterility mosaic virus (PPSMV), a species of the genus Emaravirus, is the causal agent of sterility mosaic disease (SMD) of pigeonpea (*Cajanuscajan* (L.) Millsp]. The aetiology of SMD, which remained a mystery for over 70 years, was resolved with the discovery of PPSMV in 2000 and its complete genome sequence in 2014. SMD is characterized by stunted and bushy plants, leaves of reduced size with chlorotic rings or mosaic symptoms, and partial or complete cessation of flower production (i.e. sterility). The causal agent of the disease is PPSMV, a virus with a segmented, negative-sense, single-stranded RNA genome, transmitted in a semi-persistent manner by an eriophyid mite *Aceriacajani* Channabassavanna (Acari: Arthropoda). Both the virus and vector are highly specific to pigeonpea and a few of its wild relatives, such as *C. scarabaeoides* and *C. cajanifolius*. A high yielding redgram culture CRG 10-01 was a cross derivative of APK 1x LRG 41 and matures in 170 to 180 days was released from TNAU. The culture reported an average grain yield of 1600 kg/ha under rainfed condition and 1800 kg/ha under irrigated condition with a yield increase of 19 percent over CO 6 and 22 percent over VBN 2.Now this variety is observed with incidence of sterility mosaic virus. While conducting the experiment on seed driller for facilitating two-way power operated weeder at Tamil Nadu Agricultural University, Coimbatore in Redgram Co (Rg) 8; the incidence of sterility mosaic was first noticed during 2017 -18 (Fig 1). Then in a Front-Line demonstration on the moisture conservation practices in Redgram Co (Rg) 8, conducted during Aug'2020 at Farmers' field of Kutladampatti, Vadipatti, Madurai also expressed with a pigeonpea sterility mosaic virus disease on 39 DAS and hence reported for the susceptibility of Co (Rg) 8 to the PSMV. This information is documented for the benefit of researchers and farmers in managing this disease.

Introduction

Pigeonpea sterility mosaic virus (PPSMV), a species of the genus Emaravirus, is the causal agent of sterility mosaic disease (SMD) of pigeonpea [*Cajanus cajan* (L.) Millsp]. The aetiology of SMD, which remained a mystery for over 70 years, was resolved with the discovery of PPSMV in 2000 and its complete genome sequence in 2014. SMD is characterized by stunted and bushy plants, leaves of reduced size with chlorotic rings or mosaic symptoms, and partial or complete cessation of flower production (i.e. sterility).

The causal agent of the disease is PPSMV, a virus with a segmented, negative-sense, single-stranded RNA genome, transmitted in a semi-persistent manner by an eriophyid mite *Aceria cajani* Channabassavanna (Acari: Arthropoda). Both the virus and vector are highly specific to pigeonpea and a few of its wild relatives, such as *C. scarabaeoides* and *C. cajanifolius*.

Under experimental conditions, PPSMV was transmitted to *Nicotiana benthamiana* by sap inoculation using fresh extract of SMD-infected leaves (but not to pigeonpea); however, purified nucleoprotein preparations are not infectious.

The virus was also transmitted to French bean (*Phaseolus vulgaris* L.) using viruliferous eriophyid mites. PPSMV is not seed transmitted in pigeonpea or other hosts known to be infected by this virus. However, pigeonpea alone and a few wild species of Cajanus were found to support the vector *A. cajani*. SMD is endemic in most of the pigeonpea-growing regions of India, but the incidence varies widely between regions and years.

In nature, *A. cajani* populations were almost exclusively observed on SMD-infected pigeonpea, but not on healthy plants, indicating a strong communalistic relationship between the virus-infected plants and the vector.

The epidemiology of SMD involves the virus, mite vector, cultivar and environmental conditions. Infected perennial and volunteer plants serve as a source for both the virus and its vector mites, and play an important role in the disease cycle. Genome organization, gene function and taxonomy: The PPSMV genome contains five segments of single-stranded RNA that are predicted to encode proteins in negative sense.

The ribonucleoprotein complex is encased in quasi-spherical, membrane-bound virus particles of 100-150 nm. The largest segment, RNA-1, is 7022 nucleotides in length and codes for RNA-dependent RNA polymerase (2295 amino acids); RNA-2, with a sequence length of 2223 nucleotides, codes for glycoproteins (649 amino acids); RNA-3, with a sequence length of 1442 nucleotides, codes for nucleocapsid protein (309 amino acids); RNA-4, with a sequence length of 1563 nucleotides, codes for a putative movement protein p4 (362 amino acids); and RNA-5, with a sequence length of 1689 nucleotides, codes for p5 (474 amino acids), a protein with unknown function.

PPSMV was recently classified as a species in the genus Emaravirus, a genus whose members show features resembling those of members of the genera Tospovirus (Family: Bunyaviridae) and Tenuivirus, both of which comprise single-stranded RNA viruses that encode proteins by an ambisense strategy.

The disease is mainly controlled using SMD-resistant cultivars. However, the occurrence of distinct strains/isolates of PPSMV in different locations makes it difficult to incorporate broad-spectrum resistance. Studies on the inheritance of SMD resistance in different cultivars against different isolates of PPSMV indicate that the resistance is mostly governed by recessive genes, although there are contrasting interpretations of the data.

Genetic engineering through RNA-interference (RNAi) and resistant gene-based strategies are some of the potential approaches for the transgenic control of SMD. Seed treatment or soil and foliar application of a number of organophosphorus-based insecticides or acaricides, which are recommended for the management of the vector mites, are seldom practised because of

prohibitive costs and also their risks to human health and the environment (Patil *et al.*, 2017).

Deep sequencing analysis of samples from three locations revealed the presence of Pigeonpea sterility mosaic virus-I and II (PPSMV-I and II) from Chevella and only PPSMV-II from Bengaluru and Coimbatore. PPSMV-I genome consisted of four while PPSMV-II encompassed six RNAs. The two viruses have modest sequence homology between their corresponding RNA 1–4 encoding RdRp, glycoprotein precursor, nucleocapsid and movement proteins and the corresponding orthologs of other emaraviruses.

However, PPSMV-II is more related to Fig mosaic virus (FMV) than to PPSMV-I. ELISA based detection methodology was standardized to identify these two viruses, uniquely.

Mite inoculation of sub-isolate Chevella sometimes resulted in few- to- many pigeonpea plants containing PPSMV-I alone. The study shows that (i) the N-terminal region of RdRp (SRD-1) of both the viruses contain "cap-snatching" endonuclease domain and a 13 AA cap binding site at the C-terminal, essential for viral cap-dependent transcription similar to the members of Bunyaviridae family and (ii) P4 is the movement protein and may belong to '30K superfamily' of MPs (Surendrakumar *et al.*, 2017).

A high yielding redgram culture CRG 10-01 was a cross derivative of APK 1x LRG 41 and matures in 170 to 180 days. The culture recorded an average grain yield of 1600 kg/ha under rainfed condition and 1800 kg/ha under irrigated condition with a yield increase of 19 percent over CO 6 and 22 percent over VBN 2. Drought tolerant CO 8 variety shown resistance to Sterility Mosaic Disease, root rot and moderately resistant to pod borer complex. This culture CRG 10-01 is released as CO 8 redgram for general cultivation in Tamil Nadu during 2017.

The variety notification proposal has been submitted to the PPV & FRA with DNA finger printing profile for approval (Bapu *et al.*, 2017). This variety is observed with PSMV infection in a field experiment during 2017 at AC&RI, Coimbatore and during 2020 in a FrontLine Demonstration on moisture conservation practices in Redgram conducted in a farmers' field, Kutaldampatti, Madurai.

Materials and Methods

A high yielding redgram culture CRG 10-01 was a cross derivative of APK 1x LRG 41 and matures in 170 to 180 days. The culture recorded an average grain yield of 1600 kg/ha under rainfed condition and 1800 kg/ha under irrigated condition with a yield increase of 19 percent over CO 6 and 22 percent over VBN 2. Drought tolerant CO 8 variety shown resistance to Sterility Mosaic Disease, root rot and moderately resistant to pod borer complex.

This culture CRG 10-01 is released as CO 8 redgram for general cultivation in Tamil Nadu during 2017.

This variety Co (Rg) 8 is being used for conducting a field trail on Seed driller for facilitating two-way power operated weeder at Agricultural College and Research Institute, Pulse Research Block, Coimbatore and was observed with PSMV disease initially during 2017. A cross confirmation results are also obtained from a Front Line Demonstration conducted during 2020 at Kutaldampatti, Madurai in a Farmers' field.

Results and Discussion

While conducting the experiment on seed driller for facilitating two way power operated

weeder at Tamil Nadu Agricultural University, Coimbatore in Redgram Co (Rg) 8during 2017 -18; the incidence of sterility mosaic was first noticed (Fig. 1). Later, the incidence of sterility mosaic was also observed initially on 39 DAS (Fig. 2) in a Front-Line demonstration conducted on moisture conservation practices in redgram using the variety Redgram Co (Rg) 8 during Aug' 2020 at Farmers' field of Kutladampatti, Vadipatti, Madurai.

Fig.1 Incidence of Sterility Yellow Mosaic Virus in Co (Rg)8 during 2017 at AC&RI, Coimbatore

Fig.2

References

Bapu, J.R. Hemavathy, A. Nadarajan, Nishaliney, Muthiah Arunachalam, Packiaraj, D. Malarvizhi, D., Kulandaivelu, Ganesamurthy, Rajeswari, E. and Dheivasigamani, Rajabaskar. (2017). CO 8: A high yielding long duration new red gram variety suitable for Tamil Nadu. Electronic Journal of Plant Breeding. 8: 1053-1056. 10.5958/0975-928X.2017.00156.9.

Patil, Basavaprabhu and Kumar, Lava. (2015). Pigeonpea sterility mosaic virus: A legume-infecting Emaravirus from South Asia. Molecular Plant Pathology. 16. 10.1111/mpp.12238.

Surender Kumar, BL Subbarao and Vipin Hallan, 2017. Molecular characterization of emaraviruses associated with Pigeonpea sterility mosaic disease. Scientific Reports 7: 11831. DOI:10.1038/s41598-017-11958-8.

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