

Original Research Article

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Incidence of Pigeon Pea Yellow Mosaic Disease and Vector Population from Chhattisgarh, India

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ABSTRACT

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Pigeon pea is an important drought tolerant pulse crop. Yellow mosaic disease (PYMD) was appeared in the farmers' field of Chhattisgarh. Present study aimed to record incidence & identify causal agent associated with PYMD and reason for low disease incidence. Survey and symptomatology was recorded in the farmers' field of Chhattisgarh. PYMD incidence and vector population was recorded in the experimental field of ICAR-NIBSM, Raipur during summer 2017. Causal agent associated with PYMD was identified by PCR. Symptoms of PYMD was characterized as yellow mosaic, mottling, shortening of leaves and stunting, the disease incidence recorded in Chhattisgarh state was between 1.5 and 6.1 per cent and whitefly vector population was recorded as 1.8 to 3.2 per plant, causal agent associated with PYMD identified as begomovirus. Low incidence of PYMD in field, high vector population and positive PCR amplification by primers specific to begomovirus infecting tomato suggest that the begomovirus infecting tomato may be adapting to pigeon pea, a non-host species. This is the first report of the occurrence yellow mosaic disease in pigeon pea in the central India particularly in Chhattisgarh.

Introduction

Pigeon pea (*Cajanus cajan* L. Millsp) is an important drought resistant leguminous food crop, used both for *dhal* and also vegetable purpose. At global level pigeonpea occupied 6.22 M ha in 22 countries and mostly in Asia and Africa. But India alone covers more than 70% area (4.65 M ha) among all pigeonpea growing countries (FAOSTAT, 2013). The crop is known to be affected by more than 50

diseases (Nene *et al.*, 1981). Among which yellow mosaic disease of pigeonpea is reported to be emerging in several agro-climatic zones of India (Biswas *et al.*, 2008). Occurrence of yellow mosaic disease of pigeon pea (PYMD) was first described by Williams *et al.*, (1968). Later Nene *et al.*, (1971) reported that the yellow mosaic of pigeon pea was caused by mungbean yellow mosaic virus (MYMV) on the basis of white fly (*Bemisia tabaci*) transmission and

symptomatology. It is reported from northern and southern parts of Delhi, Uttar Pradesh, Andhra Pradesh and Karnataka (Muniyappa and Veeresh, 1984; Manjunatha *et al.*, 2015). The virus was detected in the naturally infected pigeon pea plants and the geminate particles were measuring 15-18 X 30nm (Muniyappa *et al.*, 1987).

The infection of *Mungbean yellow mosaic India virus* (MYMIV) in the pigeon pea cultivars through whitefly transmission was achieved from mungbean infected with MYMIV as source plant (Biswas *et al.*, 2008). On the basis of coat protein sequence of begomovirus causing yellow mosaic disease in pigeon pea in Karnataka was found closely related to *Horse gram yellow mosaic virus* and *Mung bean yellow mosaic virus* (Manjunatha *et al.*, 2015). However, the begomovirus causing yellow mosaic disease in horsegram could not be transmitted by whitefly to pigeon pea and also to green gram and blackgram (Prema and Rangasamy, 2017). The virus was transmitted to healthy pigeon pea seedlings from the symptomatic plants by whitefly (Raj *et al.*, 2005). Coat protein gene sequence from these plants was found closely related to various strains of *Tomato leaf curl New Delhi virus* (ToLCNDV). The incidence of PYMD and in relation to population dynamics to whitefly vector was not known, this is paramount important in the management of PYMD. Here we report the periodical PYMD incidence and whitefly population, and detection of begomovirus in the infected samples.

Materials and Methods

Survey, symptomatology, disease incidence and whitefly populations

The surveys were carried out to monitor the incidence of yellow mosaic disease in pigeon pea in the farmers' fields of Chhattisgarh. The

symptomatology was recorded as appeared in the field. The yellow mosaic disease incidence in pigeon pea cv AL15 was recorded during summer 2017 in the experimental farm of ICAR-National Institute of Biotic Stress Management, Raipur. The disease incidence was recorded in 20 spots by counting number of plants showing yellow mosaic symptoms out of 50 plants per spot. Similarly whitefly population was also counted in the randomly selected 20 spots and in each spot the whitefly was counted per plant. In each plant three leaves were selected for counting whiteflies, one each at top, middle and bottom.

Total DNA extraction and PCR detection

The total DNA was extracted from symptomatic and asymptomatic leaves of pigeon pea cv AL15 by CTAB method as described by Doyle and Doyle (1990) with minor modifications. The total DNA extracted from 100 mg leaf tissue by liquid nitrogen and mixed with CTAB buffer along with RNase followed by incubation at 65°C for 1 hr. The supernatant was transferred to another tube and added equal amount of chloroform: isoamyl alcohol (24:1) mixed for 20 minutes and centrifuged. The DNA precipitated and stored in 1X TE buffer at -20°C. Polymerase chain reaction was done in 25µl containing 100ng of total DNA, 2mM dNTP, 10 pmoles of each primers specific to begomovirus infecting tomato (Forward- ToLCPF-AAGATATGGATGGATGAGAAC; Reverse- ToLCPR-ACATAATTATTAACCCTAACAA), 1x *Taq* DNA Buffer, 1.0 unit of *Taq* DNA polymerase, 25 mM MgCl₂. The PCR was done as initial denaturation of 94°C for 5 minutes followed by 30 cycles of denaturation 94°C for 1 minute, annealing 55°C for 1 minutes and extension 72°C for 2 minutes and final extension of 72°C for 10 minutes. The PCR products was loaded on to 1 % agarose

gel, electrophoresed and viewed under UV transilluminator and recorded.

Results and Discussion

Among the 22 districts surveyed, the incidence of yellow mosaic disease of pigeon pea was observed and recorded in Rajnandgaon, Kanker and Jagadapur districts of Chhattisgarh was 3.1, 1.5 and 5.0 per cent, respectively. The incidence of PYMD was recorded low in the field conditions of Chhattisgarh, Andhra Pradesh, Karnataka and Delhi. The disease incidence based on roving survey of different pigeon pea fields in the Kolar district of Karnataka during *khari* 2014-15 recorded from 1-5 percent (Manjunatha *et al.*, 2015). The incidence observed based on phenotypic appearance of the symptoms. However, in the most of the cases the no phenotypic symptom expression observed in pigeon pea under field condition, but the presence of begomovirus in the asymptomatic plants have been reported (Biswas *et al.*, 2008). This might be due to the age of the plants, host mechanism operating against these viruses. In this study the PYMD incidence in the experimental farm of ICAR-NIBSM was between 1.5 to 6.1 per cent. The symptoms of the disease recorded as yellow

mosaic, mottling, shortening of leaves with stunting and produce only few pods (Figure 1a). These symptoms were closely related to the symptoms of other yellow mosaic legume viruses. The symptoms depend on the host and susceptibility (Nene, 1972; Muniyappa *et al.*, 1976; Singh *et al.*, 2002; Javaria *et al.*, 2007). The virus causing PYMD was successfully transmitted from infected plants to pigeon pea seedlings that produce typical disease symptoms, but not by mechanical inoculations (Raj *et al.*, 2005).

The average of whitefly vector population per plant was observed in this study during March to June 2018 that ranged between 1.8 and 3.2. It indicates that the sufficient whitefly population was present for transmission of virus during the period of disease observation. The possibility of symptomless plants in the field could not be ruled out as they were not tested by the presence of begomovirus. Some of the symptomatic pigeon pea plants showed yellow mosaic were recovered and showed no symptoms of yellow mosaic. This could be one of reasons for lower incidence recorded during April and June (Table 1) though the enough whitefly populations available during this period.

Table.1 Average percent disease incidence and whitefly population in the field

Date of observation	Percent PYMD incidence*± SE	Average whitefly per plant [#] ± SE
21st March 2018	6.1±1.00	2.05±0.39
30th March 2018	5.1±1.13	3.2±0.49
11th April 2018	1.5±0.35	2.1±0.40
06th June 2018	2.6±0.63	1.8±0.34

SE- Standard Error

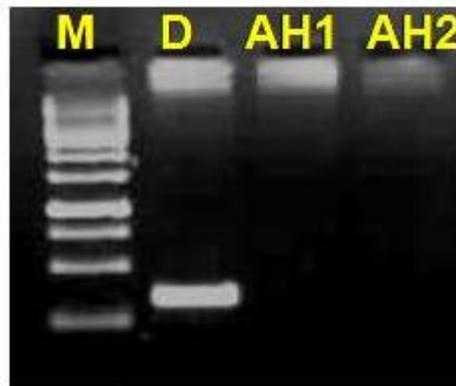
* average of randomly selected 20 spots observed and each spot contains randomly selected 50 plants.

[#] average number of whiteflies present on the randomly selected 20 plants; SE- Standard error

Fig.1 (A) Pigeon pea yellow mosaic symptomatic plant (left) apparently healthy plants (right), (B) Detection of begomovirus by PCR amplification of coat protein region. Lane M-1Kb DNA ladder; Lane D- DNA extracted from PYMD leaf sample; Lane AH1-AH2- DNA extracted from apparently healthy plant leaves



A



B

The DNA from yellow mosaic leaves was showed the positive amplification with the coat protein gene primers specific to begomoviruses infecting tomato (Figure 1b). However, no PCR amplifications was observed from DNA isolated from apparently healthy plant leaf samples. Raj *et al.*, (2005) found that the sequence of PCR amplified product from PYMD samples was closely related to ToLCNDV and the DNA of infected samples hybridized with the probe of ToLCNDV. Comparison of results obtained here with the earlier studies, the possible causal agent of PYMD in Chhattisgarh could be begomovirus infecting tomato. This is the first report of the occurrence yellow mosaic disease in pigeon pea in the central India particularly in Chhattisgarh.

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