Short Communication

Screening and identification of resistant pigeonpea (*Cajanus cajan*) genotypes against sterility mosaic disease under field and artificial inoculation conditions

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ABSTRACT

Sterility mosaic disease (SMD), caused by the pigeonpea sterility mosaic virus (PPSMV) and transmitted by the eriophyid mite *Aceria cajani*, is a major biotic constraint severely limiting pigeonpea (*Cajanus cajan*) productivity across India. Identifying stable host-plant resistance is essential for sustainable disease management. In the present study, a total of 81 All India Coordinated Research Project on Pigeonpea (AICRP) entries and 48 germplasm accessions were evaluated for SMD resistance under field conditions using the infector-row technique and artificial leaf-stapling inoculation at the National Pulses Research Centre (NPRC), Vamban, Tamil Nadu, during Kharif 2016. Disease incidence across tested entries ranged from 0.0 to 36.25 per cent. Among the screened AICRP entries, 13 short-duration genotypes (AL 1922, AL 2028, VRG 06-003, PADT-16, PUSA 2016-2, CRG 2013-12, AL 2000, AL 1931, AKTE 12-02, PT-723-3-1-1, BDN 711, WRGE 93 and WRGE 102) and 18 long-duration genotypes (GJP 1502, BRG 16-1, BRG 16-2, PT-002, BDN 2013-14, WRGE 65, ICPL 15084, ICPL 15036, PUSA 161, PUSA 162, MAL 46, MAL 47, MAL 6, MAL 13, PUSA 163, PUSA 151, CRG 2013 and CRG 2012-25) were identified as resistant, while the susceptible national check ICP 8863 recorded 36.25 per cent disease incidence. Furthermore, 14 redgram germplasm accessions (ICP 11174, ICP 6648, ICP 49111, ICP 11206, ICP 13988, P 11227, RG 50, IIRG-101, PL 59176, ICP 7624, VRG 959-1, VRG 59-1, VRG 05-011 and SKPIP 206) displayed robust field resistance. These identified resistant genotypes serve as valuable donor parents for resistance breeding programmes aiming to develop high-yielding, SMD-resistant pigeonpea cultivars.

Keywords: Pigeonpea; Sterility mosaic disease; Resistant genotypes; Artificial inoculation; Field evaluation

INTRODUCTION

Pigeonpea {*Cajanus cajan* (L) Millsp} is an essential legume crop; however, its productivity is severely constrained by its susceptibility to numerous biotic stresses under field conditions (Saxena et al 2004).

In India, the most widespread and economically significant diseases affecting pigeonpea production are sterility mosaic disease (SMD), *Fusarium* wilt, *Phytophthora* blight and *Alternaria* blight (Reddy et al 1998). Among these, SMD poses one of the most substantial threats to yield stability across the Indian subcontinent (Mitra 1931).

SMD is often termed the 'green plague' due to its potential to spread rapidly in epidemic proportions while causing excessive vegetative growth without flower or pod production (Singh et al 1999, Jones et al 2004, Patil and Kumar 2015). Affected plants are characteristically stunted and bushy, featuring chlorotic rings or mosaic patterns on reduced leaves, along with a partial or complete cessation of flowering (Patil and Kumar 2015). The magnitude of overall yield loss is heavily dependent on the developmental stage of the

crop at the time of infection, with early-stage infections often leading to near-total crop loss (Singh et al 1999).

The causal agent of SMD is pigeonpea sterility mosaic virus (PPSMV), a species belonging to the genus *Emaravirus*, which possesses a segmented, negative-sense, single-stranded RNA genome.

PPSMV is naturally transmitted in a semi-persistent manner by the eriophyid mite, *Aceria cajani* Channabassavanna. Both the viral pathogen and its mite vector exhibit high host specificity, primarily targeting cultivated pigeonpea (*C cajan*) and a limited number of wild relatives, such as *C scarabaeoides* and *C cajanifolius* (Kalaichelvi 2020).

Furthermore, differential host reactions reported across varying geographical regions strongly suggest the prevalence and regional distribution of distinct PPSMV strains.

Given the high variability of the pathogen and the economic severity of the disease, identifying reliable sources of genetic resistance is critical for sustainable disease management. Therefore, the main objective of the present study was to screen pigeonpea (redgram) genotypes to identify host plant resistance against sterility mosaic disease under both natural field conditions and artificial inoculation techniques.

MATERIAL and METHODS

The pigeonpea genotypes were evaluated for their reaction to SMD under field conditions at the National Pulses Research Centre (NPRC), Vamban, Tamil Nadu, during the Kharif season of 2016. Each test entry was sown in two 5-meter rows. To ensure uniform natural inoculum pressure, a infector-row technique was employed, wherein one row of a highly susceptible check variety was planted after every two rows of test entries.

Standard agronomic and cultural practices were strictly followed to ensure optimal crop growth; however, chemical insecticide applications were completely withheld to promote the proliferation of the eriophyid mite vector (*A cajani*) and facilitate natural disease spread. Additionally, to guarantee high disease pressure and avoid field escapes, the leaf-stapling technique was carried out to artificially inoculate the test entries with SMD.

RESULTS and DISCUSSION

The disease incidence ranged from 0.0 to 36.25 per cent. The resistant entries against SMD are given in Table 1.

Evaluation of pigeonpea germplasm against sterility mosaic disease

A total of 48 pigeonpea germplasm lines were evaluated under field conditions to determine their reaction to SMD. Disease incidence across the evaluated accessions varied widely, ranging from 0.0 to 25.0 per cent. Among the 48 germplasm lines screened, 14 entries exhibited strong field resistance, namely ICP 11174, ICP 6648, ICP 49111, ICP 11206, ICP 13988, P 11227, RG 50, IIRG-101, PL 59176, ICP 7624, VRG 959-1, VRG 59-1, VRG 05-011, and SKPIP 206.

A total of 81 AICRP entries were screened for resistance to SMD under field conditions as well as artificially through stapling. A total of 13 short duration entries, namely AL 1922, AL 2028, VRG 06-003, PADT-16, PUSA 2016-2, CRG 2013-12, AL 2000, AL 1931, AKTE 12-02, PT-723-3-1-1, BDN 711, WRGE 93 and WRGE 102 and 18 long duration entries, namely GJP 1502, BRG 16-1, BRG 16-2, PT-002, BDN 2013-14, WRGE 65, ICPL 15084, ICPL 15036, PUSA 161, PUSA 162, MAL 46, MAL 47, MAL 6, MAL 13, PUSA 163, PUSA 151, CRG 2013 and CRG 2012-25, were identified as resistant to SMD.

The susceptible check ICP 8863 recorded 36.25 per cent SMD incidence. Fourteen redgram germplasms were evaluated, namely ICP 11174, ICP 6648, ICP 49111, ICP 11206, ICP 13988, P 11227, RG 50, IIRG-101, PL 59176 and ICP 7624.

Out of 25 genotypes screened under field conditions by the infector row technique, three entries, namely BDN 2, IPA 8F and MA6, showed a resistant reaction to SMD consistently for three years, with mean disease incidences of 8.3, 6.9 and 8.7 per cent respectively.

Seven genotypes, namely BRG1, BRG3, BSMR 736, ICP 7035, ICP 2376, IPA 15F and KPL 44, were categorized as moderately resistant genotypes, with disease incidence ranging from 14.8 to 19.2 per cent (Rajeswari et al 2024).

Table 1. Reaction of pigeonpea entries under initial varietal trial (IVT) and advanced varietal trial (AVT) displaying resistance against SMD

Trial category/maturity group	Resistant genotypes/entries
IVT Extra Early entries	AL 1922, AL 2028, VRG 06-003, PADT-16, PUSA 2016-2
IVT Early entries	CRG 2013-12, AL 2000, AL 1931
IVT Medium entries	GJP 1502, BRG 16-1, BRG 16-2, PT-002, BDN 2013-14, WRGE 65, ICPL 15084, ICPL 15036
IVT Mid early entries	AKTE 12-02, PT-723-3-1-1, BDN 711, WRGE 93, WRGE 102
AVT Medium entries	PUSA 151, CRG 2013, CRG 2012-25
AVT Late entries	PUSA 161, PUSA 162 MAL 46, MAL 47, MAL 6, MAL 13, PUSA 163

Tharageshwari et al (2019) reported that out of ninety four genotypes studied, only four genotypes (DPP 2-89, DPP 3-182, IC 22557 and ICP 3666) showed a highly resistant reaction to SMD infection, whereas, fifty-four genotypes showed a highly sensitive reaction.

Prabhavathi and Ramappa (2018) reported that all twenty two IVT medium duration entries were susceptible to SMD except Bahar; however, only one IVT early duration entry, RKPV405-10, showed a resistant reaction, while the others showed a susceptible reaction.

Dhanushasree (2022) found that seventy four pigeonpea genotypes were evaluated along with the susceptible national check ICP 8863 and resistant check CO(Rg)7 for SMD screening using the leaf stapling method. Genotypes were monitored for disease incidence and scored at every 15-day interval. Based on the per cent disease incidence (PDI), the genotypes were classified into susceptible, moderately resistant and resistant. It was reported that only two genotypes, namely BWR 153 and CRG 16-07, showed a resistant reaction with disease incidence ranging from 0.1 to 10 per cent, while genotypes namely ICP 7919, IC 339057, IC 74016, IPAE15-05, AL 2250, CRG 16-01, PusaArhar 21-14, PusaArhar 21-27, BWR 253, ICP 9808 and ICP 7234 were moderately resistant with disease incidence ranging from 10.1 to 25 per cent.

CONCLUSION

The screening of 81 AICRP entries and 48 germplasm accessions under both natural field pressure and artificial leaf-stapling conditions successfully identified key sources of resistance against sterility mosaic disease (SMD) in pigeonpea.

A total of 31 AICRP entries (13 short-duration and 18 long-duration) and 14 germplasm accessions consistently demonstrated strong resistant reactions, exhibiting significantly lower disease incidence compared to the susceptible check ICP 8863.

To capitalize on these findings, future efforts should focus on validating the phenotypic resistance of these identified lines through molecular markers and genomic tools. Validated donor entries can then be strategically integrated into conventional and marker-assisted backcross breeding programmes to develop high-yielding, durable SMD-resistant pigeonpea cultivars.

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