



Characterization and Pathogenic Variability of *Macrophomina phaseolina* (Tassi) Goid. Causing Dry Root Rot of Black Gram in Tamil Nadu

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ABSTRACT

Background: Dry root rot incited by *Macrophomina phaseolina* is a major soil-borne disease limiting black gram productivity, particularly under moisture conditions in tropical regions. Despite its economic importance, information on pathogen variability across different agro climatic zones of Tamil Nadu remains limited. The present investigation was undertaken to assess disease incidence, isolate and characterize the pathogen and evaluate variability among different isolates.

Methods: A systematic roving survey was conducted during September-November 2025 in major black gram-growing districts of Tamil Nadu. Diseased samples were collected and the pathogen was isolated using the tissue segment method. The isolates were characterized based on cultural and morphological traits and further confirmed through molecular analysis using ITS region amplification. Pathogenicity of the isolates was evaluated under pot culture conditions using a completely randomized design.

Result: The survey revealed that dry root rot incidence ranged from 13.33% to 28.00% across different locations. A total of five isolates of *M. phaseolina* were obtained, exhibiting considerable variation in growth and virulence. Among them, the Villupuram isolate showed maximum radial growth and recorded the highest disease incidence (53.33%), indicating greater virulence. Molecular characterization confirmed the identity of the pathogen and sequence analysis was deposited in GenBank (Accession No: PZ054021.1). The observed variability among isolates highlights the need for location-specific management strategies.

Key words: Black gram, Disease incidence, Dry root rot, ITS characterization, *Macrophomina phaseolina*, Pathogenic variability.

INTRODUCTION

Black gram (*Vigna mungo* L.) is an important pulse crop cultivated widely in India for its high protein content and role in improving soil fertility through biological nitrogen fixation (Anonymous, 2022). It serves as a major source of dietary protein for a large section of the population and contributes significantly to sustainable cropping systems, particularly in rainfed and semi-arid regions. Despite its agronomic and nutritional importance, the productivity of black gram remains low due to several biotic and abiotic constraints, among which soil-borne diseases pose a serious threat to crop establishment and yield stability.

Dry root rot, caused by the necrotrophic fungus *Macrophomina phaseolina* (Tassi) Goid. is one of the most devastating soil-borne diseases affecting black gram and other pulse crops (Elmerich *et al.*, 2022). The pathogen infects about 500 plant species and is commonly found in tropical and subtropical locations around the world. *Macrophomina phaseolina* survives in soil and crop residues primarily in the form of microsclerotia, which can persist for extended periods in the absence of a host. These survival structures enable the pathogen to withstand adverse environmental conditions and contribute to the recurrence of the disease in successive cropping seasons (Pamala *et al.*, 2023). The survival and persistence of *M. phaseolina* in soil through microsclerotia have been documented by earlier studies (Dhingra and Sinclair, 1978; Songa and Hillocks, 1998; Su *et al.*, 2001).

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Infected plants often exhibit bark shredding, wilting, yellowing of the leaves and subsequent drying of the entire plant. The root system becomes dry, brittle and discoloured, with cortical shredding, resulting in premature plant mortality. High temperatures, moisture stress and poor soil conditions, all of which are common in many pulse-growing areas of India (Yamunarani *et al.*, 2023) often make the disease worse.

Field surveys play a crucial role in determining the distribution, incidence and severity of plant diseases and provide essential baseline information for designing effective disease management strategies. Several studies have reported variable incidence of dry root rot of black gram across different agro-climatic regions, influenced by factors such as soil type, cropping system, cultivar susceptibility, and environmental conditions (Patel *et al.*, 2023). Surveys conducted in black gram-growing regions have also reported variation in dry root rot incidence caused by *M. phaseolina* (Israel and Prakash, 2013). Region-specific data on the occurrence and pathogenic behaviour of *M. phaseolina* in black gram-growing areas of Tamil Nadu remain limited. The management of dry root rot is particularly challenging due to the soil-borne nature of the pathogen, its broad host range and the limited availability of resistant cultivars. The broad host range and complex epidemiology of *M. phaseolina* require integrated disease management strategies for effective control (Sinclair, 1982; Gupta *et al.*, 2012). Chemical control options are often ineffective under field conditions, emphasizing the need for accurate identification of the pathogen and an understanding of its pathogenic variability. Host resistance evaluation and eco-friendly management approaches using bio-agents and organic amendments have been studied for reducing *M. phaseolina* infection in pulse crops (Kumar *et al.*, 2024).

Isolation and characterization of the causal pathogen are essential for confirming disease etiology and understanding variability among pathogen populations. Morphological and cultural characterization, including colony growth pattern, pigmentation and microsclerotia formation, have traditionally been used for the identification of *M. phaseolina* (Patel *et al.*, 2023). Morphological and cultural variability among *M. phaseolina* isolates has been reported from different geographical regions (Raut and Nimbalkar, 2017). In addition, pathogenicity testing is critical for establishing the virulence of isolates and fulfilling Koch's postulates. Sorghum seed-based inoculum is commonly employed for pathogenicity assays under controlled conditions, as it provides uniform and reliable infection. Molecular characterization using DNA-based techniques has further strengthened the accurate identification of *M. phaseolina* and has revealed genetic diversity among isolates from different hosts and geographical regions. PCR-based detection methods and ITS-based molecular approaches have been successfully used for accurate identification and characterization of fungal pathogens (Babu *et al.*, 2007). Such variability in pathogenicity and genetic makeup has significant implications for disease management, resistance breeding and epidemiological studies (Manjunatha and Saifulla, 2023). Variations in morphological, genetic and pathogenic characteristics among *M. phaseolina* isolates have been reported from different hosts (Islam and Ali, 2011; Kaur *et al.*, 2010; Kaur and Chauhan, 2012).

In this context, the present investigation was undertaken to assess the incidence and distribution of dry root rot of black gram in selected districts of Tamil Nadu, isolation and characterization of *M. phaseolina* associated with the disease and evaluation of pathogenicity of different isolates under controlled conditions. Particular emphasis was placed on identifying virulent isolates to support the molecular characterization.

MATERIALS AND METHODS

Survey and assessment of dry root rot incidence in black gram

The present investigation was carried out at SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai, Chengalpattu District, Tamil Nadu, India. A roving survey was conducted from September to November 2025 to assess the incidence of dry root rot of black gram in four major black gram-growing districts of Tamil Nadu following the survey method described by Kamala and Kennedy (2021). In each district, representative fields were selected at random. Disease incidence was recorded by examining plants along a zig-zag (W-shaped) transect in each field. A minimum of 100 plants per field was observed for typical dry root rot symptoms such as sudden wilting, yellowing of foliage, drying of plants without leaf drop and dry, brittle roots with shredding of the cortical tissues.

Disease incidence was calculated using the following formula:

$$\text{Disease incidence (\%)} = \frac{\text{Number of infected plants}}{\text{Total number of plants observed}} \times 100$$

The incidence data were summarized district-wise to understand the distribution and prevalence of dry root rot in the surveyed regions.

Collection of diseased samples

Black gram plants showing typical symptoms of dry root rot were carefully uprooted from the surveyed fields. The root systems were gently cleaned to remove adhering soil particles and then packed in sterile paper bags. Each sample was properly labelled with details such as location, district and date of collection. The samples were transported to the laboratory and processed for pathogen isolation within 24 hours of collection.

Isolation and purification of *Macrophomina phaseolina*

Isolation of the pathogen was done by using the tissue segment method followed by Meena *et al.* (2020). Diseased root portions were washed thoroughly under running tap water and chopped into small pieces (approximately five mm in length) from the junction of healthy and diseased tissues. The root segments were surface sterilized with 70% ethanol for one minute and then rinses three times in

sterile distilled water. The sterilized tissues were blotted dry with sterile filter paper and aseptically placed on potato dextrose agar (PDA) plates.

The inoculated plates were incubated at $25\pm 2^{\circ}\text{C}$ under dark conditions and monitored daily for fungal growth. Hyphal tips originating from the tissue segments were transferred to fresh PDA plates to obtain pure cultures. A total of five fungal isolates were obtained from various locations and maintained on PDA slants at 4°C for future research.

Morphological and cultural characterization

The purified isolates were initially identified based on cultural and morphological characteristics following the description by Sarr *et al.* (2014). Each isolate was inoculated at the centre of PDA plates using a five mm mycelial disc and incubated at $25\pm 2^{\circ}\text{C}$. Colony characteristics such as colour, texture, growth pattern and rate of radial growth was recorded at regular intervals. Microscopic observations were made by mounting small portions of mycelium in lactophenol cotton blue and examining under a compound microscope to observe hyphal characteristics and microsclerotia formation.

Molecular characterization of *M. phaseolina*

The CTAB method was used to extract genomic DNA from the representative isolate (VPM) of actively growing mycelium. The internal transcribed spacer (ITS) region of ribosomal DNA was amplified by universal primers ITS1 and ITS4 (Schoch *et al.*, 2012). PCR amplification was performed in a thermal cycler under standard conditions. The amplified PCR products were visualized and purified by agarose gel electrophoresis and the sequencing was carried out at PAR Laboratory, Tiruchirappalli, Tamil Nadu, India. The acquired ITS sequence was compared with sequences available in the NCBI database using BLAST analysis. The sequence of the isolate was deposited in the GenBank database with accession number PZ054021.1.

Pathogenicity test of *M. phaseolina*

Preparation of sorghum seed inoculum

Sorghum seeds were soaked overnight in water then drained and transferred into 250 mL conical flasks at the rate of 100 g per flask and sterilized at 121°C for 20 minutes on two consecutive days. After cooling, each flask was inoculated with actively growing mycelial discs of *M. phaseolina*

and incubated at $25\pm 2^{\circ}\text{C}$ for 10-12 days, with recurrent shaking to ensure uniform colonization of the seeds (Kapadiya *et al.*, 2024).

Pot culture experiment

The pathogenicity of five isolates of *M. phaseolina* was tested under pot culture conditions using a Completely Randomized Design (CRD) with five replications per isolate including control. Earthen pots were filled with sterilized potting mixture (soil: sand: FYM in the ratio of 2:1:1). In each pot 20 healthy blackgram seeds were sown in sterilized soil without the addition of pathogen inoculum. The pots were maintained under natural environment conditions and irrigated as required (Kumar *et al.*, 2024). Sorghum seed inoculum of *M. phaseolina* was mixed thoroughly with the potting mixture at 5% (w/w) at 20th day after sowing.

Disease assessment and re-isolation

Plants were observed daily for the development of disease symptoms and disease incidence was recorded from 10 to 20 days after inoculation of pathogen. Disease incidence was calculated as the percentage of plants showing typical dry root rot symptoms in each pot.

The pathogen was re-isolated from infected plants of all isolates and its identity was confirmed based on cultural and morphological characteristics, thereby fulfilling Koch's postulates (Patel *et al.*, 2023).

RESULTS AND DISCUSSION

Incidence of black gram dry root rot in surveyed districts

The roving survey conducted during September to November 2025 revealed the widespread occurrence of dry root rot of black gram in all the surveyed locations across four districts of Tamil Nadu. The disease was recorded in five locations of the districts viz., Villupuram, Cuddalore, Kallakurichi and Chengalpattu district (two locations). Typical symptoms of root rot were observed in the field included sudden wilting, yellowing of foliage, drying of plants and dry, brittle roots with shredding of cortical tissues.

Disease incidence varied among the surveyed locations. In Chengalpattu district, disease incidence ranged from 13.33% to 21.33% across two locations. An incidence of 14.00% was recorded in Kallakurichi district, whereas Cuddalore district recorded the highest disease incidence (28.00%) among all surveyed locations. In Villupuram district, dry root rot incidence was recorded as

Table 1: Incidence of black gram dry root rot in different districts of Tamil Nadu.

Districts	Location	Latitude	Longitude	Disease incidence (%)
Chengalpattu	Kilpattu	12.368313°N	79.755156°E	13.33
Chengalpattu	Porpanankaranai	12.399261°N	79.737106°E	21.33
Kallakurichi	Kallakurichi	11.779332°N	79.367475°E	14.00
Cuddalore	Kattumayilur	11.576153°N	79.118433°E	28.00
Villupuram	Senjikuppam	11.765734°N	79.376091°E	20.00

20.00%. The variation in disease incidence indicated the differences in local environmental conditions and crop management practices. The presence of dry root rot in all surveyed districts confirmed the widespread distribution of the disease in black gram-growing areas of Tamil Nadu. The disease incidence recorded from different surveyed locations is presented in Table 1 and the field symptoms observed during the survey are illustrated in Fig 1 and 2.

Isolation and identification of *M. phaseolina*

Isolation of the pathogen from diseased root samples resulted in the recovery of five fungal isolates. All isolates produced fast-growing colonies on potato dextrose agar (PDA), which were initially grey to whitish and later turned dark grey to black. The cultures produced abundant microsclerotia, a characteristic feature of *M. phaseolina*. Based on cultural and morphological characteristics, all five isolates were tentatively identified as *M. phaseolina*.

Cultural and radial growth characteristics of *M. phaseolina* isolates

The five isolates of *M. phaseolina* showed variation in colony growth rate on PDA medium. Radial growth was recorded from 24 hours after inoculation (Day 2) continuously. All isolates exhibited rapid mycelial growth however, differences in growth rate based on days to cover the plate were observed among the isolates.

The isolate of Villupuram district (VPM) exhibited fast radial growth and covered the entire Petri plate (90 mm) on fifth day of inoculation followed by the isolates of Kallakurichi (KK), Chengalpattu (CGP1) and Cuddalore (CDE) and Chengalpattu (CGP2) isolates covered the plates on sixth day of inoculation.

Culture of all the isolates initially produced thin, hyaline to light grey mycelium with a cottony to slightly fluffy texture. With increased incubation time, the colonies became dense and greyish to dark grey, followed by profuse microsclerotia formation. The radial growth pattern of different isolates of *M. phaseolina* on PDA medium is presented in Table 2, while the cultural characteristics of the isolates are shown in Fig 3.

Pathogenic variability among *M. phaseolina* isolates

All five isolates of *M. phaseolina* were found to be pathogenic to black gram under pot culture conditions, producing typical dry root rot symptoms, such as poor seedling emergence, yellowing, wilting and dry, brittle root symptoms. No disease symptoms were observed in the uninoculated control plants.

Disease progression of dry root rot

Disease incidence was recorded at regular intervals from 10 to 20 days after inoculation (DAI) and the results are presented in Table 3. The disease symptoms were first

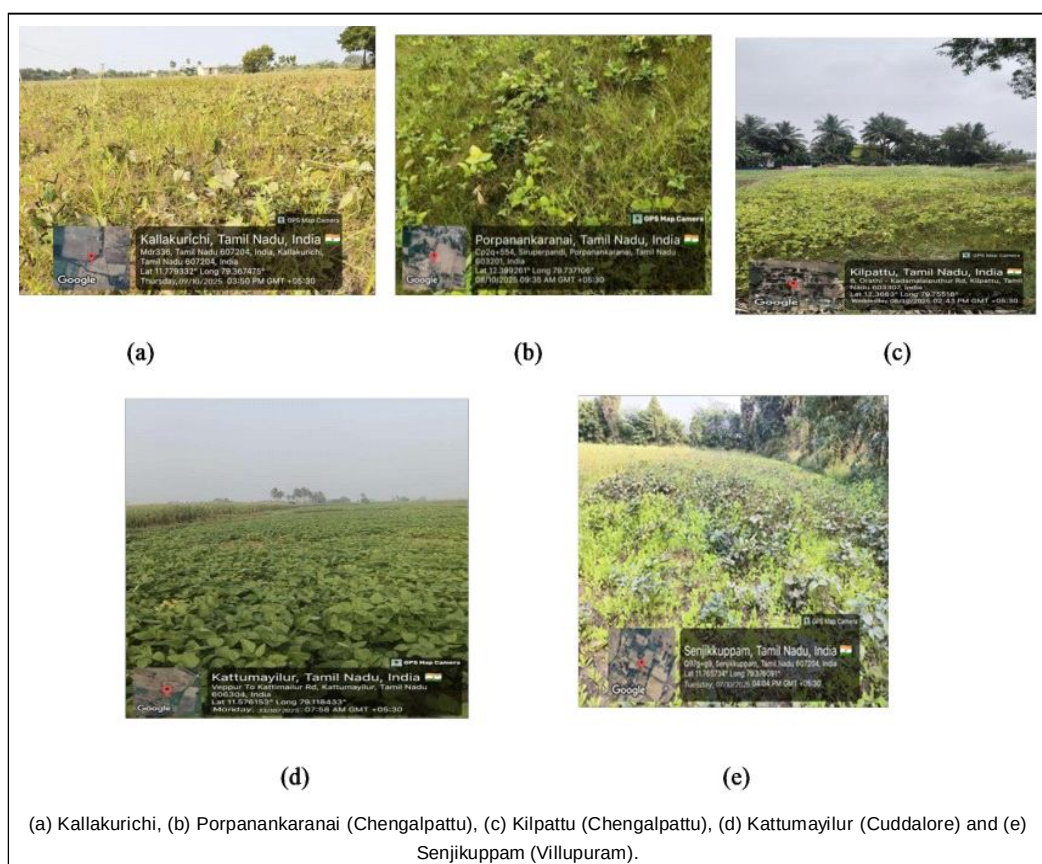


Fig 1: Field view of black gram crops surveyed for dry root rot incidence in different districts of Tamil Nadu.

observed at 10 DAI and increased progressively with time in all isolates. The pathogenic variability and symptom development caused by different isolates under pot culture conditions are illustrated in Fig 4.

Among the isolates, VPM showed rapid disease development and recorded the highest disease incidence (55.00%) at 20 DAI, indicating its high virulence. The isolates CDE (32.00%) and KK (26.00%) showed moderate disease incidence, whereas CGP-2 (23.00%) exhibited intermediate pathogenicity. The lowest disease incidence was observed in CGP-1 (19.00%).

To further validate the observed variation among isolates, the final disease incidence recorded at 20 days after inoculation (DAI) was subjected to statistical analysis. The data were analyzed using analysis of variance (ANOVA) under a completely randomized design (CRD) and the significance of differences among the isolates was determined using the critical difference (CD) at 5% level.

The pathogen was successfully re-isolated from the infected root tissues of inoculated plants showing typical dry root rot symptoms. The re-isolated cultures exhibited morphological and cultural characteristics similar to the original isolates of *M. phaseolina*. No pathogen was isolated from the uninoculated control plants. This confirmed the pathogenicity of the isolates and fulfilled Koch's postulates.

Following the pathogenicity test, the isolate VPM was identified as the most virulent based on the severity of symptoms produced in the host plants. Hence, the isolate was selected for further morphological and molecular characterization. The observed pathogenic variability among isolates highlighted the existence of diverse pathogen populations in different agro-climatic regions.

Similar differences in virulence and disease development among *M. phaseolina* isolates have been reported in several crops (Khan, 2007; Sharma *et al.*, 2010; Mengistu *et al.*, 2011). Such variability has important implications for disease management.

Microscopic observation of the cultures revealed typical morphological characteristics of the *M. phaseolina*. The fungus produced hyaline, septate hyphae and numerous dark microsclerotia. The microsclerotia were spherical to irregular in shape and were distributed



Fig 2: Typical dry root rot symptom of black gram caused by *M. phaseolina*, showing dry, brittle roots with shredding of cortical tissues.

Table 2: Radial mycelial growth of *M. phaseolina* isolates on PDA.

Isolate code	District/Location	Radial mycelial growth (mm)				
		Day 2	Day 3	Day 4	Day 5	Day 6
CGP 1	Chengalpattu/Kilpattu	15.00	45.00	77.00	90.00	90.00
CGP 2	Chengalpattu/Porpanankaranai	08.00	29.00	57.00	73.00	90.00
KK	Kallakurichi/Kallakurichi	18.00	43.00	75.00	90.00	90.00
VPM	Villupuram/Senjikuppam	20.00	49.00	81.00	90.00	90.00
CDE	Cuddalore/Katamayilur	14.00	38.00	73.00	85.00	90.00

Table 3: Disease progression of *M. phaseolina* isolates on blackgram under pot culture conditions.

Isolate code	District/Location	Disease incidence (%)* (Days after inoculation)					
		10	12	14	16	18	20
VPM	Villupuram/Senjikuppam	15.00 ^a	25.00 ^a	35.00 ^a	50.00 ^a	50.25 ^a	55.00 ^{ab}
CGP 1	Chengalpattu/Kilpattu	8.00 ^{bc}	10.00 ^c	13.00 ^c	13.00 ^c	19.00 ^b	19.00 ^c
CGP 2	Chengalpattu/Porpanankaranai	5.00 ^{cd}	9.00 ^c	9.00 ^c	16.00 ^c	22.00 ^b	23.00 ^{bc}
KK	Kallakurichi/Kallakurichi	2.00 ^d	10.00 ^c	11.00 ^c	17.00 ^c	24.00 ^b	26.00 ^{bc}
CDE	Cuddalore/Katamayilur	11.00 ^b	17.00 ^b	23.00 ^b	27.00 ^b	26.00 ^b	32.00 ^b

*Mean of five replications.

**The different alphabets showed the significant variation among the isolates.

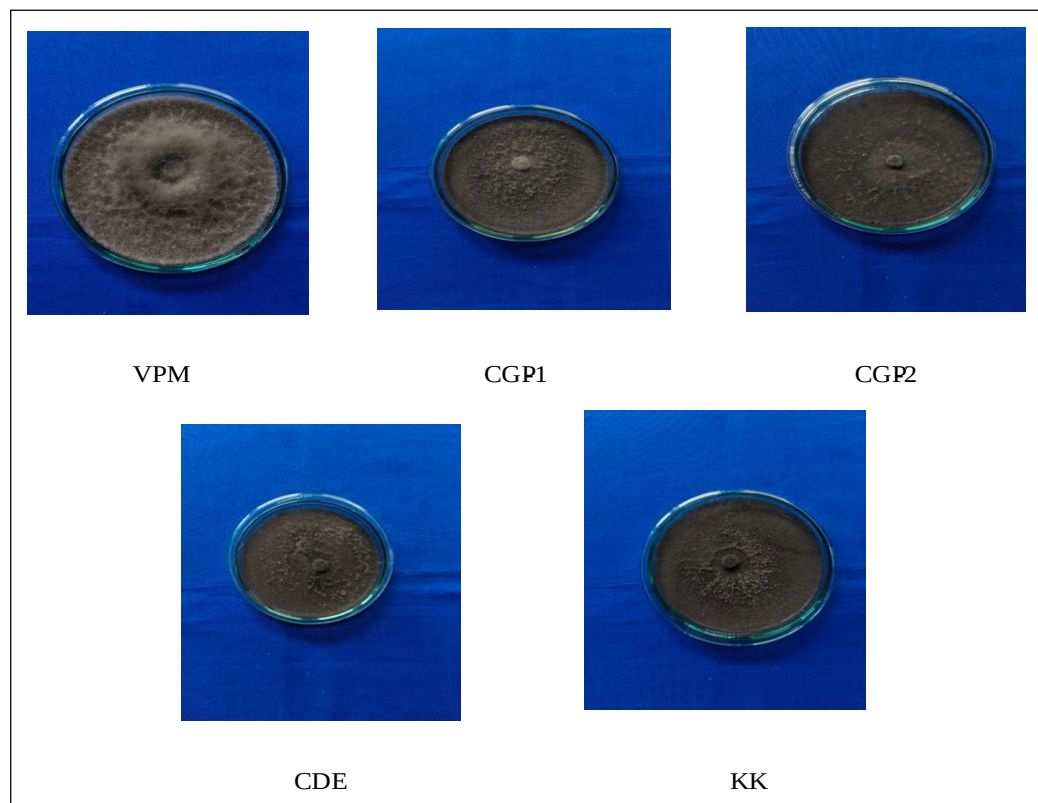
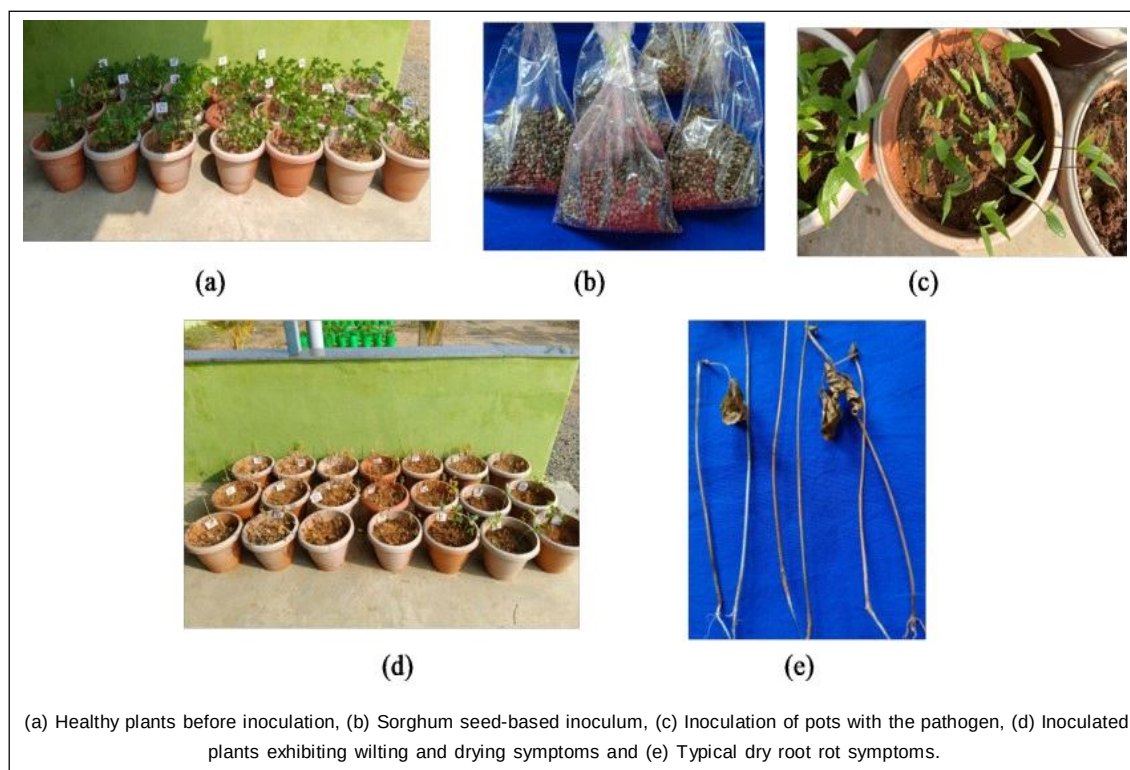


Fig 3: Cultural characteristics of five isolates of *M. phaseolina* isolated from dry root rot-infected black gram plants.



(a) Healthy plants before inoculation, (b) Sorghum seed-based inoculum, (c) Inoculation of pots with the pathogen, (d) Inoculated plants exhibiting wilting and drying symptoms and (e) Typical dry root rot symptoms.

Fig 4: Pathogenicity test of *M. phaseolina* isolates on black gram under pot culture conditions.

throughout the mycelial network. These structures serve as survival propagules of the pathogen. The microscopic characteristics of *M. phaseolina* including microsclerotia, hyphae and pycnidiospores are presented in Fig 5.

Molecular identification of *M. phaseolina*

The ITS rDNA region of the representative isolate VPM was successfully amplified using ITS1 and ITS4 primers. The PCR amplification produced a fragment of approximately

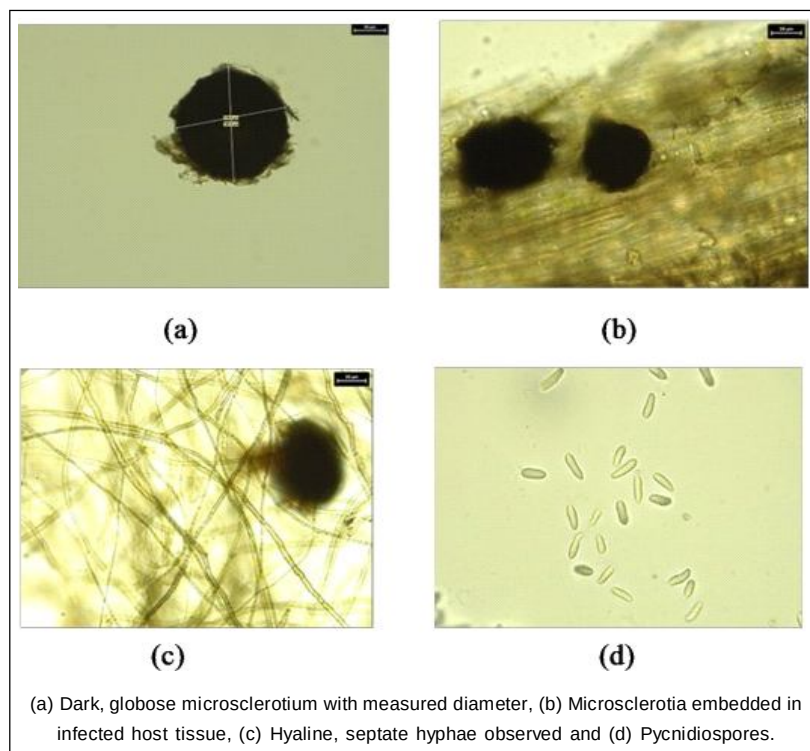


Fig 5: Microscopic morphological characteristics of *Macrophomina phaseolina* isolated from black gram.

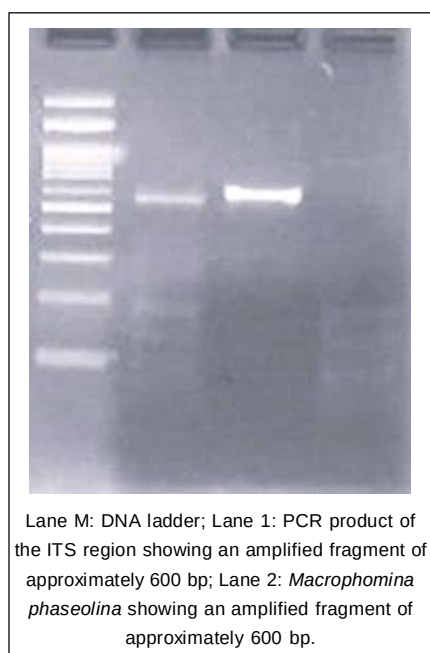


Fig 6: PCR amplification of ITS rDNA region of *M. phaseolina* isolate VPM.

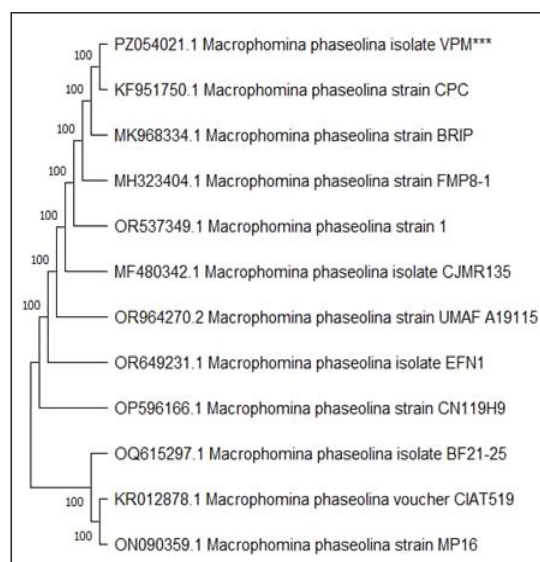


Fig 7: Phylogenetic tree based on ITS rDNA sequences showing the relationship between *M. phaseolina* isolate VPM (GenBank accession number PZ054021.1) and other reference strains retrieved from the NCBI database.

600 bp, confirming successful amplification of the ITS region. The amplified product was sequenced using Sanger sequencing at PAR Laboratory, Tiruchirappalli.

BLAST analysis of the obtained sequence revealed a high similarity with *M. phaseolina* sequences available in the NCBI GenBank database. The sequence of the present isolate was deposited in the GenBank database with the accession number PZ054021.1.

Phylogenetic analysis based on ITS sequences demonstrated that the isolate VPM clustered closely with other reference strains of *M. phaseolina*, confirming its molecular identity. PCR amplification of the ITS region and phylogenetic relationship of the isolate VPM with reference strains are presented in Fig 6 and 7 respectively.

CONCLUSION

The present investigation clearly demonstrated the widespread occurrence of dry root rot of black gram in major growing regions of Tamil Nadu, with disease incidence varying significantly across locations. The successful isolation and identification of *M. phaseolina* from infected samples confirmed its role as the causal agent of the disease. Morphological, cultural and molecular characterization validated the identity of the pathogen and revealed noticeable variability among the isolates. Among the isolates studied, the Villupuram isolate (VPM) exhibited higher radial growth and maximum disease incidence under pot culture conditions, indicating its highly virulent nature.

Overall, the findings emphasize the need for region specific and integrated disease management strategies to effectively control dry root rot in black gram. Further studies focusing on host resistance and eco-friendly management approaches are essential for sustainable crop protection and improved productivity.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

Not applicable.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

REFERENCES

- Anonymous. (2022). Directorate of Pulse Development. *Annual Report on Pulses Production in India*. Government of India, Ministry of Agriculture and Farmers Welfare, New Delhi.
- Babu, B.K., Saxena, A.K., Srivastava, A.K. and Arora, D.K. (2007). Identification and detection of *Macrophomina phaseolina* by species-specific oligonucleotide primers and probe. *Mycologia*. **99**(6): 797-803.
- Dhingra, O.D. and Sinclair, J.B. (1978). *Biology and pathology of Macrophomina phaseolina*. Viçosa: Universidade Federal de Viçosa, Brazil.
- Elmerich, C.N., Kumar, V., Dikshit, H.K., Singh, N.P. et al. (2022). Blackgram-*Macrophomina phaseolina* interactions and identification of novel sources of resistance. *Plant Disease*. **106**: 1542-1550.
- Gupta, G.K., Sharma, S.K. and Ramteke, R. (2012). Biology, epidemiology and management of charcoal rot of soybean. *Journal of Plant Pathology*. **94**: 255-266.
- Islam, M.T. and Ali, M.S. (2011). Pathogenic variability of *Macrophomina phaseolina*. *Journal of Agricultural Science*. **3**: 23-30.
- Israel, S. and Prakash, M. (2013). Survey and incidence of dry root rot of black gram caused by *Macrophomina phaseolina*. *African Journal of Agricultural Research*. **8**(9): 870-874.
- Kamala, K. and Kennedy, J.S. (2021). Survey and assessment of dry root rot incidence in pulse crops caused by *Macrophomina phaseolina*. *International Journal of Plant Protection*. **14**(2): 112-116.
- Kapadiya, R.K., Rakholiya, K.B. and Patel, J.V. (2024). Pathogenicity of *Macrophomina phaseolina* (Tassi) Goid. causing stem canker of pigeonpea. *Biological Forum-An International Journal*. **16**(9): 43-45.
- Kaur, S., Dhillon, G.S. and Brar, S.K. (2010). Genetic diversity among isolates of *Macrophomina phaseolina*. *Journal of Plant Pathology*. **92**: 419-425.
- Kaur, S., Dhillon, G.S. and Chauhan, V.B. (2012). Morphological and pathogenic variability in *Macrophomina phaseolina*. *Plant Disease Research*. **27**: 15-20.
- Khan, S.N. (2007). *Macrophomina phaseolina* as causal agent for charcoal rot of sunflower. *Mycopathologia*. **164**: 231-236.
- Kumar, M., Kumhar, D.R., Garg, S. and Partap, M. (2024). Evaluation for the resistance of green gram (*Vigna radiata* L.) germplasm against *Macrophomina phaseolina*. *Legume Research*. **47**(3): 505-507. doi: 10.18805/LR-4501.
- Manjunatha, S.V. and Saifulla, M. (2023). Morphological and molecular characterization of Indian *Macrophomina phaseolina* isolates causing dry root rot. *Journal of Biological Sciences*. **15**: 67-75.
- Meena, M., Gupta, S.K. and Sharma, R. (2020). Isolation and identification of *Macrophomina phaseolina* associated with dry root rot disease in pulses. *Indian Phytopathology*. **73**(4): 655-660.
- Mengistu, A., Wrather, J.A. and Rupe, J.C. (2011). Charcoal rot of soybean. *Plant Health Progress* **12**: 1-7.
- Pamala, D., Rajeswari, B., Naik, M.K. et al. (2023). Prevalence of dry root rot caused by *Macrophomina phaseolina* and pathogenic variability in Southern India. *Frontiers in Fungal Biology*. **4**: 1189043.

- Patel, R., Singh, A., Kumar, P. et al. (2023). Molecular characterization of *Macrophomina phaseolina* associated with black gram and analysis of pathogenic variability. *Journal of Experimental Agriculture and Food Science*. **5**: 45-53.
- Raut, J.G. and Nimbalkar, S.A. (2017). Morphological and cultural variability in *Macrophomina phaseolina*. *International Journal of Current Microbiology and Applied Sciences*. **6**: 2146-2154.
- Sarr, M.P., Ndiaye, M., Groenewald, J.Z. and Crous, P.W. (2014). Genetic diversity in *Macrophomina phaseolina*. *Persoonia*. **32**: 199-211.
- Schoch, C.L., Seifert, K.A., Huhndorf, S., Robert, V., Spouge, J.L., Levesque, C.A. and Chen, W. (2012). Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for fungi. *Proceedings of the National Academy of Sciences*. **109(16)**: 6241-6246.
- Sharma, M., Mangala, U.N., Krishnamurthy, M. and Vadez, V. (2010). Drought and dry root rot of chickpea caused by *Macrophomina phaseolina*. *Field Crops Research*. **118**: 354-359.
- Sinclair, J.B. (1982). Compendium of soybean diseases. American Phytopathological Society, St. Paul, Minnesota.
- Songa, W. and Hillocks, R.J. (1998). Survival of *Macrophomina phaseolina* in soil. *Plant Pathology*. **47**: 223-229.
- Su, G., Suh, S.O., Schneider, R.W. and Russin, J.S. (2001). Host specialization in the charcoal rot fungus *Macrophomina phaseolina*. *Phytopathology*. **91**: 120-126.
- Yamunarani, K., Venkatesan, T., Sivakumar, M. et al. (2023). Eco-friendly management of dry root rot in black gram caused by *Macrophomina phaseolina*. *International Journal of Environment and Climate Change*. **13(10)**: 1234-1242.