



Current species of oomycetes associated with foot rot disease of black pepper in Vietnam

Le Dinh Thao¹ · Tran Ngoc Khanh¹ · Nguyen Van Liem¹ · Le Thu Hien¹ · Ha Minh Thanh¹ · Vu Thi Phuong Binh¹ · Thieu Thi Thu Trang¹ · Pham Thi Anh¹ · Nguyen Van Chung¹ · Pham Hong Hien¹ · Nguyen Van Long^{2,3,4} · Nguyen Quang Duy^{3,4} · Didier Lesueur^{3,4,5,6,7} · Laetitia Herrmann^{3,4} · Lambert Brau³

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Abstract

Foot rot disease caused by *Phytophthora capsici* is one of the most destructive diseases of black pepper in Vietnam and worldwide. However, other oomycete species such as *P. tropicalis* and *Pythium deliense* reported as serious threats to black pepper in India have also been recorded on this plant. The population of oomycetes occurring in black pepper plantations in Vietnam and their pathogenicity have not been investigated in the last decade. To this end, two hundred fifteen oomycete isolates were collected from the root rots and rhizospheric soil of black pepper in the Central Highlands and the Southeast region of Vietnam. Of these, 23 isolates were representatively chosen based on their origin and morphology for DNA sequence analysis of the internal transcribed spacer region, then 11 isolates were further selected for the translation elongation factor 1-alpha and the beta-tubulin gene analyses. Morphology and molecular analyses indicated that *P. capsici*, *P. cinnamomi*, *P. heveae*, *P. nicotianae*, *P. parvispora*, *P. tropicalis*, *Phytophythium vexans*, and a new species candidate *Phytophythium* sp. were identified among oomycete isolates. Of these, *P. capsici* and *P. tropicalis* could be the prevalent species in black pepper plantations in studied areas. The inoculation tests demonstrated that *P. capsici*, *P. nicotianae* and *P. tropicalis* were pathogenic on both leaves and roots of black pepper. *Phytophythium vexans* was pathogenic on root only. Meanwhile, *P. cinnamomi*, *P. heveae*, *P. parvispora* and *Phytophythium* sp. were non-pathogenic.

Keywords *Phytophthora capsici* · *Phytophythium vexans* · *Piper nigrum*

✉ Le Dinh Thao
thaoleinh.ppri@mard.gov.vn

¹ Plant Protection Research Institute (PPRI), Academy of Agricultural Sciences (VAAS), Duc Thang, Bac Tu Liem, Hanoi, Vietnam

² Research and Development Pepper Centre, The Western Highland Agriculture and Forestry Science Institute, Pleiku City, Vietnam

³ School of Life and Environmental Sciences, Faculty of Science, Engineering and Built Environment, Deakin University, Geelong, Victoria, Australia

⁴ Alliance of Bioversity International and International Center for Tropical Agriculture (CIAT), Common Microbial Biotechnology Platform (CMBP), Asia hub, Hanoi, Vietnam

⁵ Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), UMR Eco&Sols, Hanoi, Vietnam

⁶ l'Alimentation et l'Environnement (INRAE), Institut de Recherche pour le Développement (IRD), Eco&Sols, Université de Montpellier (UMR), CIRAD, Institut National de Recherche pour l'Agriculture, 34060 Montpellier, France, Montpellier SupAgro

⁷ Chinese Academy of Tropical Agricultural Sciences, Rubber Research Institute, Haikou, China

Introduction

For many years, Vietnam has been the world's largest black pepper (*Piper nigrum* L.) producing and exporting country, followed by Brazil, Indonesia, and India (Yogesh and Mokshapathy 2013; Rathore and Swathi 2020; Azahari et al. 2021). To date, black pepper is cultivated mainly in the Central Highlands and the Southeast region of Vietnam with the total area increasing from 101,600 ha in 2015 to 147,500 ha in 2018, then reducing to 131,800 ha in 2020 (General statistics office 2021). Foot rot disease or "quick wilt disease" caused by *Phytophthora capsici* is the most destructive soilborne pathogen of black pepper in many countries of the world including Vietnam (Anandaraj 2000; Truong et al. 2008; Thuy et al. 2012; Farhana 2013; Kifelew and Adugna 2018; Jibat and Alo 2021; Quy et al. 2021; Kong et al. 2022). Approximately 25–30% of the vine death of black pepper was reported in Kerala (Nambiar and Sarma 1977). Anandaraj et al. (1989) reported that up to 95% of the vines showed foot rot symptoms in individual farms of this plant in many countries. In 2016, more than 10,000 ha of black pepper in Vietnam was damaged by pathogen infections and the highest-losses occurred in most cultivated regions (Trinh et al. 2019).

Phytophthora palmivora was primarily described as a causal agent of black pepper foot rot (Muller 1937; Zentmyer et al. 1977). In recent years, *Phytophthora* species infected black pepper in India were identified into two different species, *P. capsici* and *P. tropicalis*. They are closely related species with overlapping morphological characteristics and intraspecific variations but can be distinguished based on multi-locus DNA sequence analysis (Bowers et al. 2007; Jeevalatha et al. 2021; Bhai et al. 2022). Another *Phytophthora* species, *P. nicotianae*, has also been reported to cause root and stem rot on black pepper (Drenth and Guest 2004). In the *Pythium* and *Phytophthora* genera, many species were pathogenic on black pepper such as *Phytophthora vexans* (syn. *Pythium vexans*), *Pythium butleri*, *P. deliense*, *P. helicoides*, *P. irregular*, *P. middletonii* and *P. splendens* (Liu 1977; Matsuda et al. 1998). Among these species, *Pythium deliense*, causing significant damage with yellowing and drying up symptoms, was newly reported in India (Subila and Bhai 2020).

In the previous studies, *P. capsici*, *P. cinnamomi*, *P. nicotianae* and *Pythium* sp. were isolated from diseased tissues and rhizospheric soils of black pepper in Vietnam. Of these, *P. capsici* was the main agent causing wilt symptoms, while the pathogenicity of *P. nicotianae* was unclear and *Pythium* sp. infection was not significant (Truong et al. 2008). Dung et al. (2014) revealed that the black pepper foot rot in Dak Nong province of Vietnam was caused by *P. tropicalis* instead of *P. capsici* based on the sequence

analysis of the internal transcribed spacer (ITS) region. *Phytophthora vexans* was also reported as a causal agent of black pepper root rot in Vietnam, however, the identification of this species was not confirmed (Nguyet et al. 2018). This work, therefore, aims to catalogue the species diversity and pathogenicity of current oomycete species in black pepper growing areas of Vietnam.

Materials and Methods

Sampling collection and isolation

Rhizospheric soil and root rot samples of black pepper plants showing typical symptoms of quick wilt disease were collected in the Central Highlands (Dak Lak, Dak Nong and Gia Lai provinces) and the Southeast region (Binh Phuoc and Dong Nai provinces) in 2020 and 2021. Sampling collection was conducted in two districts of each province (Fig. 1). Oomycetes from soil samples were isolated by the baiting technique (Drenth and Guest 2004) with rose petals and selective media. Thirty grams of each soil sample (60–70% humidity) were placed into a cup (12 cm high and 9 cm diameter) with 300 ml of sterilized water. After 1 hour, rose petals were dropped on the water surface and the cups were placed at room temperature (around 28° C) for 24 to 72 hours. Infected rose petals with brown symptoms were rinsed with sterilized water and pieces (3 × 3 mm) were cut from the margins of the healthy and diseased tissue and then sterilized with 70% ethanol for 30 seconds, and 5% sodium hypochlorite for 1 min, respectively. The pieces were rinsed in sterilized water and dried on sterile filter paper, then these rose pieces were placed on potato carrot agar (PCA) containing 0.01 g/L benomyl and 0.02 g/L rifampicin. The Petri dishes were incubated at 28° C for 2–3 days. Oomycete mycelia grown from rose pieces were cut from the margin of colonies and placed onto potato dextrose agar (PDA). Pure cultures of oomycetes were obtained by the hyphal tip isolation method (Tutte 1969). Oomycetes in the root rot samples were isolated according to the protocol applied for infected rose petals above.

Colony morphology and micro-morphological structures

Colony morphology of *Phytophthora* and *Phytophthora* were documented on PDA. To describe micro-morphological characteristics, oomycetes were grown on PCA Petri dishes for 3 to 5 days, and then the Petri dishes were flooded with sterile distilled water for 3 to 5 days at room temperature to induce the formation of sporangia, chlamydospores, oogonia, and antheridia. The oomycetes were mounted on glass slides

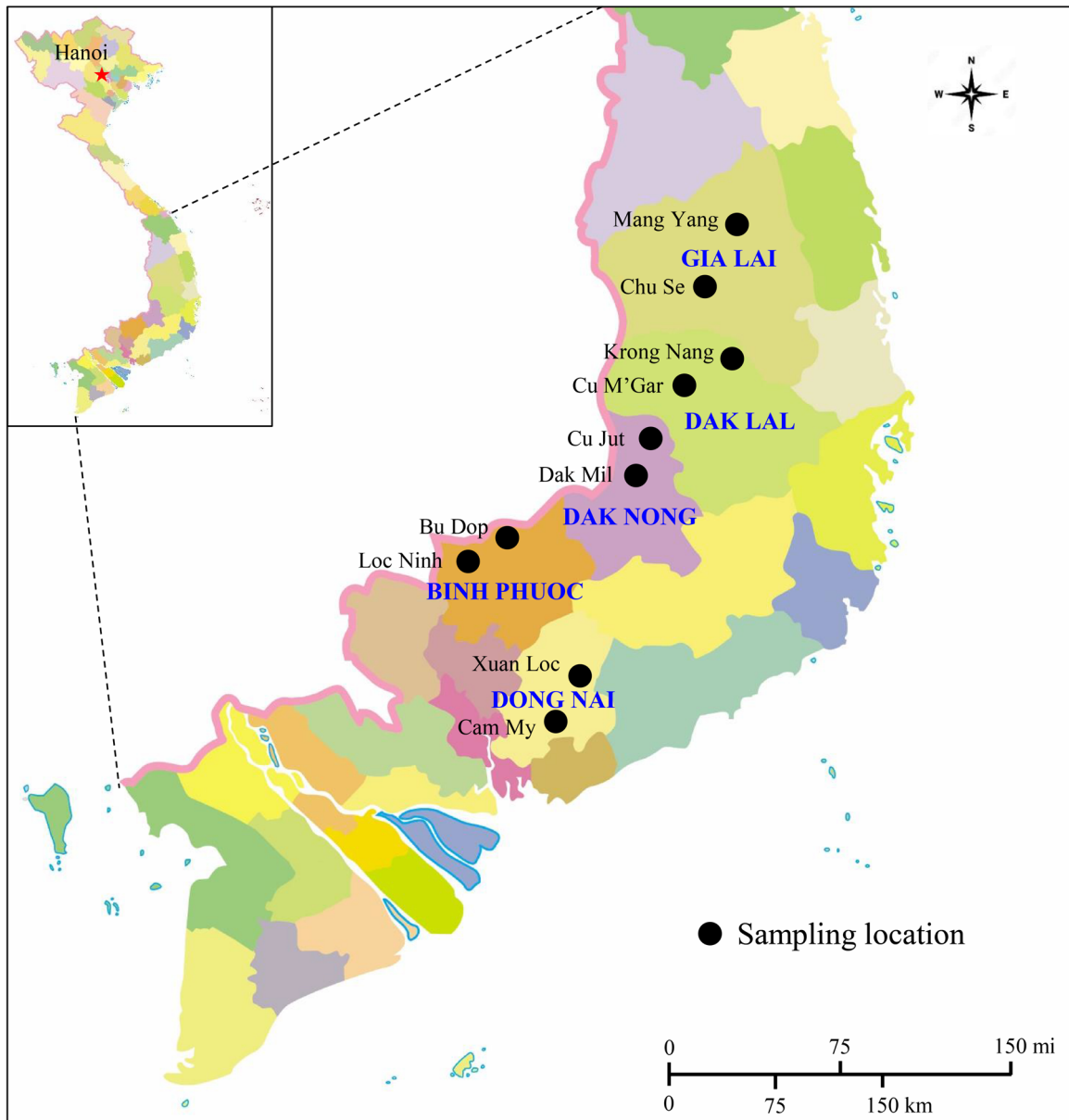


Fig. 1 Locations of original oomycete isolates collected in this study. Gia Lai (Mang Yang and Chu Se districts), Dak Lak (Krong Nang and Cu M'Gar districts), Dak Nong (Cu Jut and Dak Mil districts),

Binh Phuoc (Bu Dop and Loc Ninh districts) and Dong Nai (Xuan Loc and Cam My districts)

and the micro-morphological structures were described and measured under a light microscope. At least 30 measurements of each structure were performed with means and standard deviations (SD). The ranges were described as (min–) mean–SD – mean+SD (–max) (Thao et al. 2018).

DNA extraction, PCR amplification and sequencing

Oomycete mycelia from 3–5 days old on V8 juice were harvested, and DNA extraction was performed using the E.Z.N.A Fungal DNA Mini Kit (OMEGA BioTek, USA),

according to the manufacturer's instructions. The ITS region was amplified with the primers ITS1 (5'-TCCGTAGGTGAA CCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATAT GC-3') (White et al. 1990), following PCR conditions: initial denaturation at 95°C for 2 min; 35 cycles consisting of denaturation at 95°C for 30 s, annealing at 50°C for 50 s and extension at 72°C for 1 min; final extension at 72°C for 10 min. The translation elongation factor 1-alpha (TEF1- α) gene was amplified using the primers ELONGF1 (5'-TCACGATCGACATTGCCCTG-3') and ELONGR1 (5'-ACGGCTCGAGGATGACCATG-3') (Kroon et al. 2004),

following the amplification protocol: initial denaturation at 95°C for 3 min; 35 cycles of denaturation at 95°C for 30 s, annealing at 62°C for 30 s and extension at 72°C for 1 min; final extension at 72°C for 10 min. The beta-tubulin (TUB) gene was amplified using the primers TUBUF2 (5'-CGG TAACAACCTGGGCCAAGG-3'), TUBUR1 (5'-CCTGGT ACTGCTGGTACTCAG-3') (Kroon et al. 2004), following PCR conditions: initial denaturation at 95°C for 3 min; 35 cycles of denaturation at 95°C for 30 s, annealing at 66°C for 1 min and extension at 72°C for 1 min 30 s; final extension at 72°C for 10 min. A PCR reaction volume (25 µL) contained 2 µL template DNA (100 ng/µL), 1 µL (4.5 pMol) of each primer, 12.5 µL MyTaq HS Mix and 8.5 µL nuclease-free water. Amplifications were confirmed by gel electrophoresis. PCR products were purified by the High Pure PCR Cleanup Micro Kit (Roche Diagnostics GmbH, Germany) according to the manufacturer's instructions, and were sequenced with the amplifying primers by an ABI 3730XL automatic sequencer (Applied Biosystems, USA).

Sequence alignment and phylogenetic analysis

The raw sequences were assembled with MEGA 11 and deposited to GenBank. The alignment of each dataset, including DNA sequences in this study and reference sequences from NCBI (<http://blast.ncbi.nlm.nih.gov/>), was produced separately. The alignments were checked manually and the poorly aligned regions at the beginning and ends of sequences were excluded. The concatenated alignment of ITS, TEF1, and TUB was performed using MEGA 11.

Phylogenetic trees were generated based on the maximum likelihood (ML) method by RAxML v8.2.4 (Stamatakis 2014) with a GTR+GAMMA+I model and 1,000 maximum likelihood bootstrap replicates to test the support of the branches. Phylogenetic trees were viewed using MEGA 11, and layouts were depicted using Adobe Illustrator software.

Pathogenicity test

Representative isolates were tested for their pathogenicity on both black pepper leaves and seedlings. Black pepper seedlings were grown from healthy seeds in plastic containers (6 cm high, 6 cm top diameter and 5 cm bottom diameter) with sterilized soil, and one seedling was maintained in a cup. Ten millilitres of the zoospore suspension (1×10^4 zoospores/ml) of *Phytophthora* isolates, or sporangia, chlamydospores and oogonia suspension (1×10^3 unit/ml) of *Phytophthora* isolates were prepared and added to each container. Each species was inoculated onto 3 seedlings. Sterilized water was used in the control. The seedlings were maintained in a greenhouse at 28°C for 4 weeks. Fresh black pepper leaves were collected from the mature plants. The leaves were washed under a running tap and then surface

sterilized with 70% ethanol. One oomycete species was inoculated onto one leaf at three wound points on the upper surface. Twenty microliters of zoospore, chlamydospore, or oogonia suspensions as above were pipetted onto the wounded tissue area. The control was applied with sterilized water. The leaves were placed into an incubator at 28°C and 90% humidity in darkness for 5 days. The seedlings and leaves were monitored daily for disease symptoms. After the assessment, the seedling roots and the inoculated tissue of leaves were sampled for isolation on selective media for the detection of oomycetes. The experiment was repeated three times.

Results

Oomycete isolation

Two hundred fifteen isolates of *Phytophthora* and *Phytophthora* were isolated from rhizospheric soil and root rot samples of black pepper collected at Dak Lak, Dak Nong, Gia Lai, Binh Phuoc, and Dong Nai provinces in the years 2020 and 2021. The isolates were preserved at the Division of Plant Pathology and Phyto-immunology, Plant Protection Research Institute, Vietnam. Twenty-three representative isolates (Table 1) were selected for molecular analysis based on source, geographic origin and morphological characteristics.

Isolates obtained in this study are indicated in bold; Isolates in this study used for the multi-locus analysis (ITS, TEF1 and TUB) were indicated by ⁺; Ex-type and authentic strains are shown by ^{*}.

Phylogenetic analysis

Twenty-three representative isolates were selected for ITS sequencing. The ITS sequences were used for nucleotide BLAST searches on the NCBI for selecting the reference sequences. Eleven isolates were selected from the ITS phylogenetic tree (Fig. 2) for further DNA sequencing of TEF1- α and TUB genes. All assembled sequences generated in this study were submitted to GenBank (Table 1). The datasets of each locus consisted of 11 sequences in the present study and reference sequences. Most of the reference sequences were from ex-type and authentic strains. The concatenated alignment of ITS, TEF1- α , and TUB contained 898, 889, and 893 characters including gaps, respectively. The multi-locus phylogenetic tree (Fig. 3) showed that PPRI2188 and PPRI20911 isolates were clustered together with the ex-type strain of *P. capsici* (CPHST BL 33G) with a ML bootstrap value of 98%. Isolate PPRI20912 was grouped in a separate clade with *P. tropicalis* (CBS 434.91, ex-type strain), supported by a ML bootstrap value of 97%, and this species was considered as a sister of

Table 1 Representative isolates in this study and reference isolates used in the phylogenetic analysis

Species	Isolate	Source	Location	Collected date	GenBank accession numbers		
					ITS	TEF1	TUB
<i>Pythium canariense</i>	CBS 112353*	-	Spain	-	JX397990	-	JX397969
<i>Pythium cystogenes</i>	CBS 675.85*	-	Netherlands	-	AY707985	-	KJ595520
<i>Phytopythium helioides</i>	CBS 286.31*	-	-	-	AY598665	EF408891	EF408881
<i>Phytopythium</i> sp.	PPRI2097 ⁺	Soil of <i>Piper nigrum</i>	Bu Dop, Binh Phuoc	Sep. 2020	OQ617900	OQ630880	OQ630891
<i>Phytopythium vexans</i>	PPRI20925 ⁺	Soil of <i>Piper nigrum</i>	Mang Yang, Gia Lai	Sep. 2020	OQ617899	OQ630879	OQ630890
	PPRI2098 ⁺	Root of <i>Piper nigrum</i>	Krong Nang, Dak Lak	Sep. 2020	OQ617901	OQ630881	OQ630892
	PPRI21822	Soil of <i>Piper nigrum</i>	Mang Yang, Gia Lai	Aug. 2021	OQ617920	-	-
<i>Phytophthora agathidicida</i>	CBS 119.80*	Soil	Iran	-	GU133572	EF426555	EF426556
	CPHST BL 154*	<i>Agathis australis</i>	New Zealand	2006	MG602692	MH358951	MH493902
<i>Phytophthora capsici</i>	PPRI2188 ⁺	Root of <i>Piper nigrum</i>	Dak Mil, Dak Nong	Aug. 2021	OQ617906	OQ630886	OQ630897
	PPRI20911 ⁺	Root of <i>Piper nigrum</i>	Chu Se, Gia Lai	Sep. 2020	OQ617907	OQ630887	OQ630898
	PPRI2092	Soil of <i>Piper nigrum</i>	Mang Yang, Gia Lai	Sep. 2020	OQ617910	-	-
	PPRI2093	Root of <i>Piper nigrum</i>	Cu M'Gar, Dak Lak	Sep. 2020	OQ617911	-	-
	PPRI2094	Soil of <i>Piper nigrum</i>	Krong Nang, Dak Lak	Sep. 2020	OQ617912	-	-
	PPRI2086	Root of <i>Piper nigrum</i>	Cam My, Dong Nai	Aug. 2020	OQ617913	-	-
	PPRI2089	Soil of <i>Piper nigrum</i>	Xuan Loc, Dong Nai	Aug. 2020	OQ617914	-	-
	PPRI20910	Root of <i>Piper nigrum</i>	Bu Dop, Binh Phuoc	Sep. 2020	OQ617915	-	-
	PPRI20921	Soil of <i>Piper nigrum</i>	Cu Jut, Dak Nong	Sep. 2020	OQ617917	-	-
	CPHST BL 33G*	-	-	-	MG865467	MH358966	MH493915
<i>Phytophthora castaneae</i>	CPHST BL 47G*	<i>Castanea crenata</i>	Japan	1971	MG865470	MH358969	MH493918
<i>Phytophthora cinnamomi</i>	PPRI2087 ⁺	Soil of <i>Piper nigrum</i>	Cam My, Dong Nai	Aug. 2020	OQ617905	OQ630885	OQ630896
	CPHST BL 12*	-	-	-	MG865473	MH358972	MH493920
<i>Phytophthora cinnamomi</i> var. <i>parvispora</i>	CBS 411.96	-	Germany	-	AY302184	EU079950	LC595877
<i>Phytophthora cocois</i>	CPHST BL 157*	<i>Cocos nucifera</i>	USA	1990	MG865478	MH358977	MH493925
<i>Phytophthora heveae</i>	PPRI20913 ⁺	Soil of <i>Piper nigrum</i>	Cu M'Gar, Dak Lak	Sep. 2020	OQ617903	OQ630883	OQ630894
	CBS 296.29*	<i>Hevea brasiliensis</i>	Malaysia	1929	AF266770	AY564123	AY564067
<i>Phytophthora nicotianae</i>	PPRI20915 ⁺	Soil of <i>Piper nigrum</i>	Dak Mil, Dak Nong	Sep. 2020	OQ617904	OQ630884	OQ630895
	CPHST BL 162*	<i>Gramatophyllum</i> sp.	Indonesia	-	OP020179	MH359042	MH493986
<i>Phytophthora parvispora</i>	PPRI20920 ⁺	Soil of <i>Piper nigrum</i>	Loc Ninh, Binh Phuoc	Sep. 2020	OQ617908	OQ630888	OQ630899
	PPRI21812 ⁺	Soil of <i>Piper nigrum</i>	Bu Dop, Binh Phuoc	Aug. 2021	OQ617909	OQ630889	OQ630900
	CBS 132772*	<i>Arbutus unedo</i>	Italy	2011	KC478667	MH359051	KC609402
CPHST BL 1330G9	-	-	-	-	MG865563	MH359053	MH493996
	-	-	-	-	EU748548	KX251820	KX251819

Table 1 (continued)

Species	Isolate	Source	Location	Collected date	GenBank accession numbers		
					ITS	TEF1	TUB
<i>Phytophthora tropicis</i>	PPRI20912 ⁺	Root of <i>Piper nigrum</i>	Chu Se, Gia Lai	Sep. 2020	OQ617902	OQ630882	OQ630893
	PPRI2095	Root of <i>Piper nigrum</i>	Krong Nang, Dak Lak	Sep. 2020	OQ617916	-	-
	PPRI21818	Soil of <i>Piper nigrum</i>	Dak Mil, Dak Nong	Aug. 2021	OQ617918	-	-
	PPRI21819	Soil of <i>Piper nigrum</i>	Krong Nang, Dak Lak	Aug. 2021	OQ617919	-	-
	PPRI20914	Soil of <i>Piper nigrum</i>	Mang Yang, Gia Lai	Sep. 2020	OQ617921	-	-
	CBS 434.91*	<i>Macadamia integ-rifolia</i>	USA	-	NR_147864	LN908263	LN908272

P. capsici. Isolate PPRI20915 was segregated into a separate group with *P. nicotianae* (CPHST BL 162, authentic strain, ex-type strain not available, Abad et al. 2023), which was supported by a ML bootstrap value of 100%. Isolate PPRI20913 fell in a group with *P. heveae* (CBS 296.29, ex-type strain) supported by a ML bootstrap value of 96%. This species was a high homology with *P. agathidicida*, *P. castaneae* and *P. cocois*. Isolate PPRI2087 clustered with the ex-type strain of *P. cinnamomi* (CPHST BL 12) with a ML bootstrap value of 100%. Isolate PPRI20920 and PPRI21812 were in a group of *P. parvispora* species (CBS 132772, ex-type strain) with a ML bootstrap value of 100%, and closely related to *P. cinnamomi* species. Isolate PPRI2098 and PPRI20925 were grouped in a monophyletic clade with the reference strain of *Phytophthium vexans* (syn. *Pythium vexans*) (CBS 119.80, authentic strain, ex-type strain not available, de Cock et al. 2015) with a ML bootstrap value of 100%. Isolate PPRI2097 placed in a single clade with a distant genetic relationship from others. The ITS, TEF1- α , and TUB sequences of PPRI2097 were the highest similarity with *Phytophthium helicoides* (CBS 286.31, authentic strain, ex-type strain not available, de Cock et al. 2015), at 85.64%, 95.78% and 95.57%, respectively. Hence, isolate PPRI2097 was considered as a new species candidate of the *Phytophthium* genus.

Colony and micro-morphology

Phytophthora capsici (PPRI20911)

Colonies on PDA were depressed with limited aerial mycelia with unclear pattern to the chrysanthemum pattern, covering a 9 cm Petri dish after 7 days. Variable shapes of sporangia were observed including subglobose, ovoid, pyriform, ellipsoid,

fusiform, or distorted shapes, often with papilla, (29.7–) 39.1 – 55.1 (–65.2) \times (17.6–) 22.5 – 31.5 (–37.1) μm . Hyphal swellings were globose or subglobose. Chlamydo spores were absent (Fig. 4).

Phytophthora cinnamomi (PPRI2087)

Colonies on PDA were white and unclear pattern, covering a 9 cm Petri dish after 7 days. Sporangia were semi-papilla or non-papilla, obpyriform, ovoid or ellipsoid, (48.3–) 51.2 – 63.8 (–71.2) \times (27.7–) 32.2 – 39.0 (–41.3) μm . Hyphal swellings were abundant, globose to subglobose, or coral-loid. Chlamydo spores were globose, terminal or intercalary, (29.4–) 31.3 – 39.1 (–43.2) μm (Fig. 5).

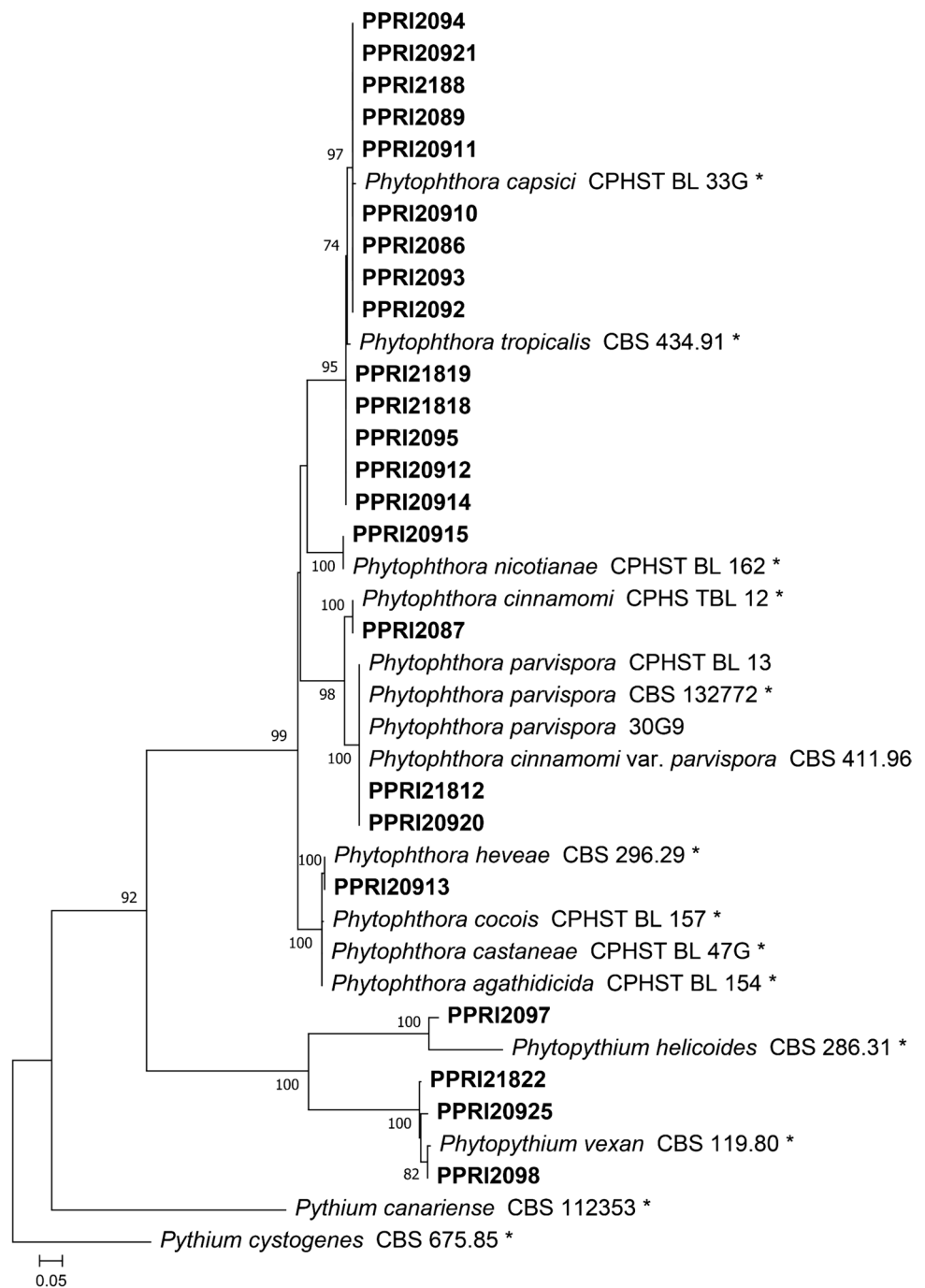
Phytophthora heveae (PPRI20913)

Colonies on PDA were white, often depressed with no distinct pattern, covering a 9 cm Petri dish after 7 days. Sporangia were globose, subglobose, ovoid, with papilla, (26.2–) 27.5 – 38.7 (–44.6) \times (19.8–) 22.0 – 29.2 (–33.2) μm . Hyphal swellings were globose to subglobose. Oogonia were spherical or subglobose, smooth, and often tapering base, (20.1–) 23.4 – 28.8 (–31.2) \times (19.8–) 22.6 – 27.2 (–29.2). Antheridia were amphigynous, spherical, or cylindrical. Chlamydo spore was absent (Fig. 6).

Phytophthora nicotianae (PPRI20915)

Colonies on PDA were white and cottony, often without a pattern or unclear pattern, covering a 9 cm Petri dish after 6 days. Sporangia were globose, subglobose, ovoid, obpyriform, and irregular shapes, often with papilla, (35.4–) 36.0 – 60.0 (–90.5) \times (27.7–) 29.9 – 36.3 (–42.3) μm .

Fig. 2 Maximum likelihood tree of the ITS region. ML bootstrap support values $\geq 70\%$ are presented at the nodes. The isolates in this study are in bold. Ex-type and authentic strains are indicated by an asterisk



Chlamydo-spores were global, terminal, or intercalary, (29.6–) 33.9 – 41.1 (–45.6) μm (Fig. 7).

***Phytophthora parvispora* (PPRI21812)**

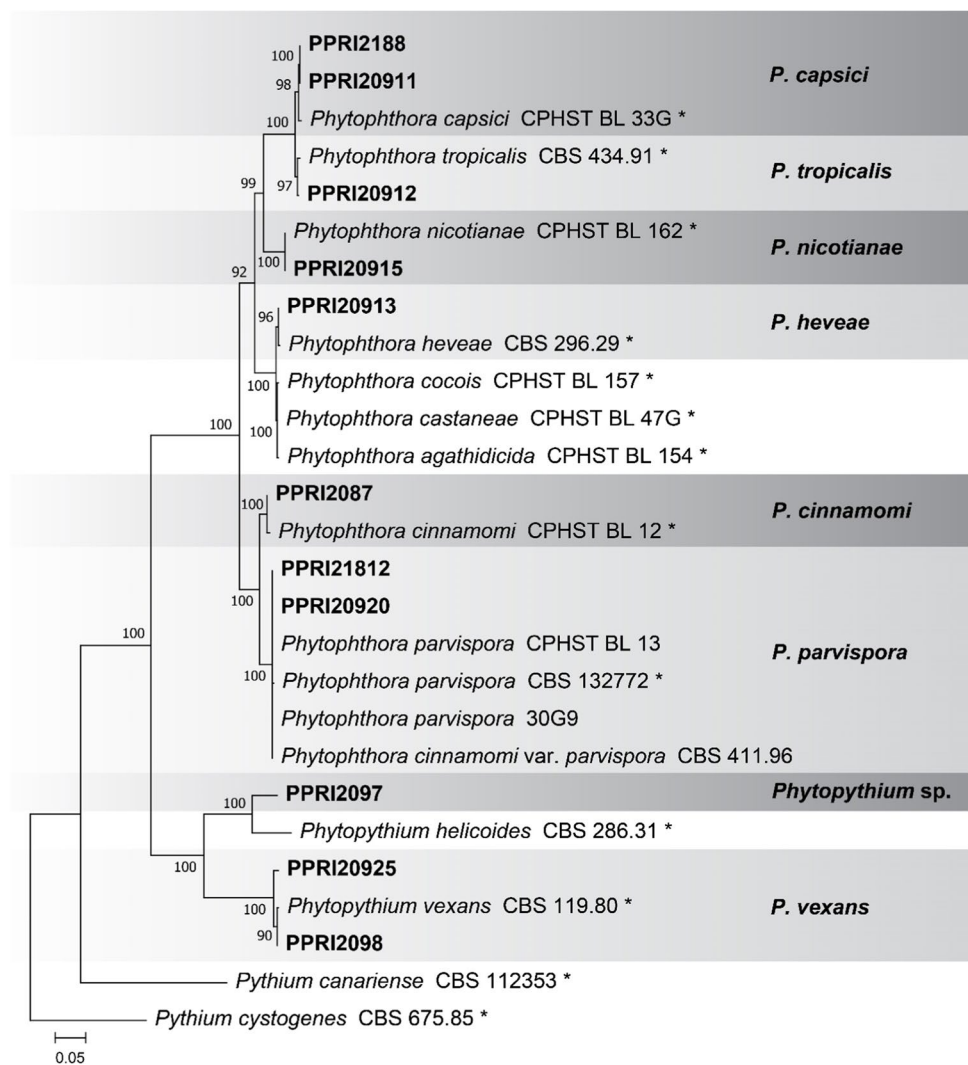
Colonies on PDA were white, cottony, and unclear pattern, covering a 9 cm Petri dish after 7 days. Sporangia were ovoid, obpyriform, or ellipsoid, semi-papilla or without papilla, (26.2–) 31.3 – 42.7 (–52.4) \times (22.5–) 24.3 – 31.9 (–37.6) μm .

Hyphal swellings were abundant, irregular, and globose to subglobose. Chlamydo-spores were globose, terminal, or intercalary, (19.4–) 21.5 – 25.3 (–26.5) μm (Fig. 8).

***Phytophthora tropicalis* (PPRI20912)**

On PDA, the colonies were unclear pattern to the chrysanthemum pattern, often depressed with limited aerial mycelia, covering a 9 cm Petri dish after 7 days. Sporangia were

Fig. 3 Maximum likelihood tree of multi-locus sequences (ITS, TEF1- α , and TUB). ML bootstrap support values $\geq 70\%$ are presented at the nodes. The isolates in this study are in bold. Ex-type and authentic strains are indicated by an asterisk



subglobose, ovoid, pyriform, ellipsoid, fusiform, or distorted shapes, often with papilla, (34.5–) 39.7 – 53.5 (–62.4) \times (25.8–) 29.0 – 35.2 (–38.5) μm . Chlamydospores were globose, terminal or intercalary, (23.5–) 27.9 – 34.7 (–37.2) μm (Fig. 9).

***Phytophthora vexans* (PPRI2098)**

Colonies on PDA were white, cottony, unclear pattern, rich in aerial mycelia and fast-growing, reaching the margin of 9 cm Petri dishes after 4 days. Sporangia were globose, subglobose, ovoid, or pyriform, with or without papilla, (16.3–) 18.5 – 24.1 (–27.8) \times (15.3–) 17.7 – 21.5 (–24.8) μm . Oogonia were spherical, smooth and terminal, (15.1–) 17.2 – 20 (–21.5) μm . Antheridia were cylindrical, often

monoclinous and broadly attached to the oogonia. Zoospores were released from sporangia via a short exit tube. (Fig. 10).

***Phytophthora* sp. (PPRI2097)**

Colonies on PDA were white, chrysanthemum pattern and fast-growing, covering a 9 cm Petri dish after 4 days. Sporangia were globose, subglobose, ovoid, with or without papilla, (19.2–) 22.5 – 28.9 (–32.5) \times (14.5–) 17.3 – 21.3 (–23.5) μm . Papilla developed at maturity to form a long discharge tube. Chlamydospores were globose, terminal or intercalary, (21.3–) 22.7 – 25.1 (–26.1) μm . (Fig. 11).

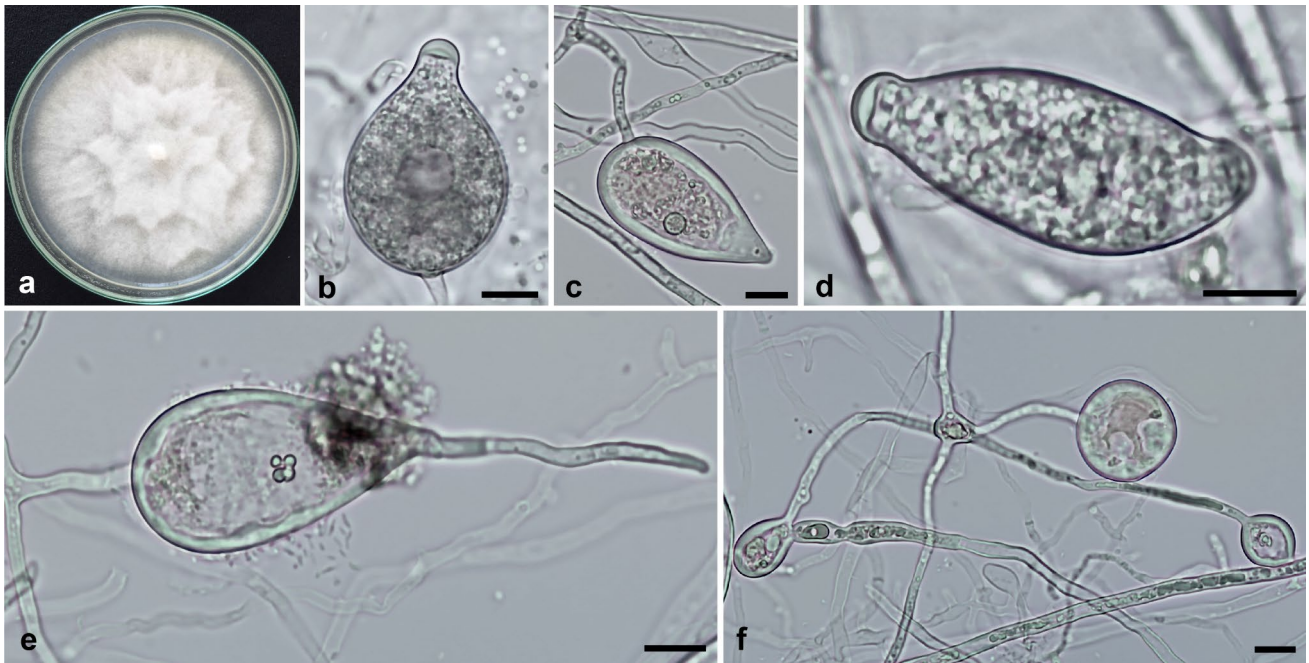


Fig. 4 *Phytophthora capsici* PPRI20911. a. Colony on PDA; b-e. Sporangia; f. Hyphal swellings; Scale bars = 10 μ m

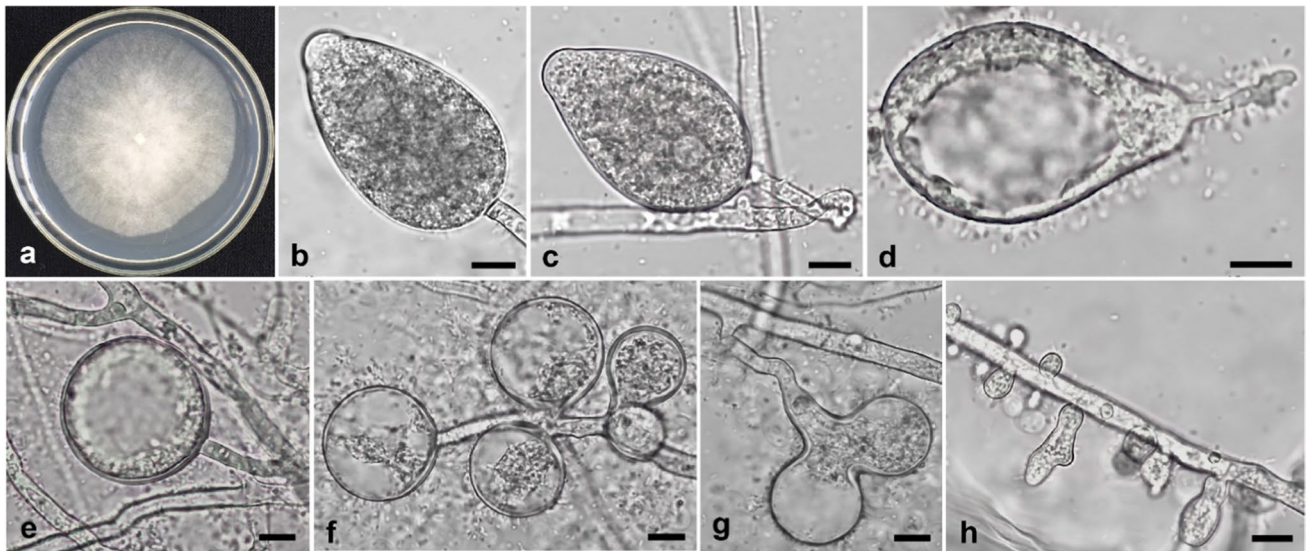


Fig. 5 *Phytophthora cinnamomi* PPRI2087. a. Colony on PDA; b-d. Sporangia; e. Chlamydospore; f-h. Hyphal swellings; Scale bars = 10 μ m

Pathogenicity

Eight representative isolates including PPRI20911 (*P. capsici*), PPRI2087 (*P. cinnamomi*), PPRI20913 (*P. heveae*), PPRI20915 (*P. nicotianae*), PPRI21812 (*P. parvispora*), PPRI20912 (*P. tropicalis*), PPRI2098 (*Phytophthium vexans*), and PPRI2097 (*Phytophthium* sp.) were used to inoculate on black pepper leaves and

seedlings. The pathogenicity tests revealed that the leaves inoculated with PPRI20911, PPRI20912 and PPRI20915 isolates showed diseased symptoms with dark brown lesions after 3 days. The seedlings inoculated with PPRI20911, PPRI20912, PPRI20915 and PPRI2098 isolates showed wilt and root rot symptoms at 10 days to 30 days post-inoculation. While, the other isolates of *P. cinnamomi*, *P. heveae*, *P. parvispora* and *Phytophthium* sp. did not produce any diseased symptoms (Figs. 12 and 13).

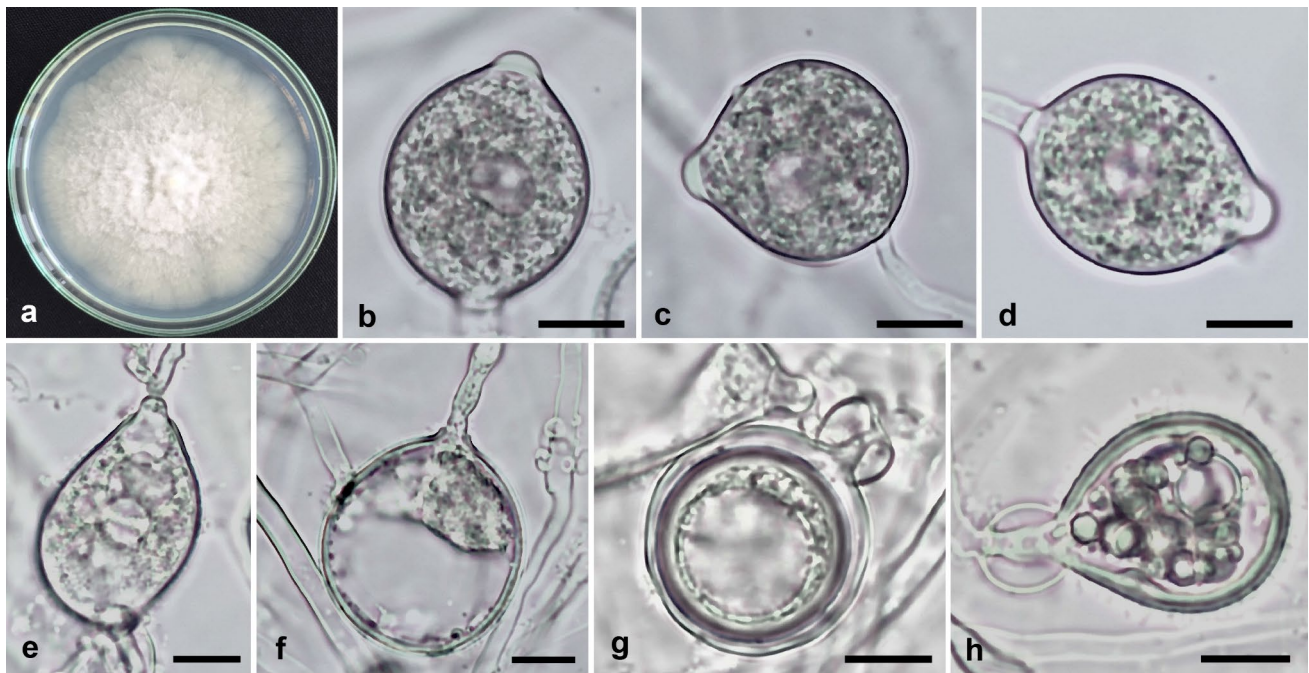


Fig. 6 *Phytophthora heveae* PPR120913. a. Colony on PDA; b-f. Sporangia; g-h. Oogonia with antheridia; Scale bars = 10 μ m



Fig. 7 *Phytophthora nicotianae* PPR120915. Colony on PDA; b-f. Sporangia; g-h. Chlamydo-spore; Scale bars = 10 μ m

The causal agents of diseased tissues of leaves and roots were re-isolated and the same original oomycetes were obtained. Non-symptom leaves and roots of healthy seedlings in the controls were re-isolated and no oomycetes

were obtained. The result indicated that *P. capsici*, *P. nicotianae* and *P. tropicalis* were infected with both leaves and roots of black pepper. While *Phytophthora vexans* infected roots only.

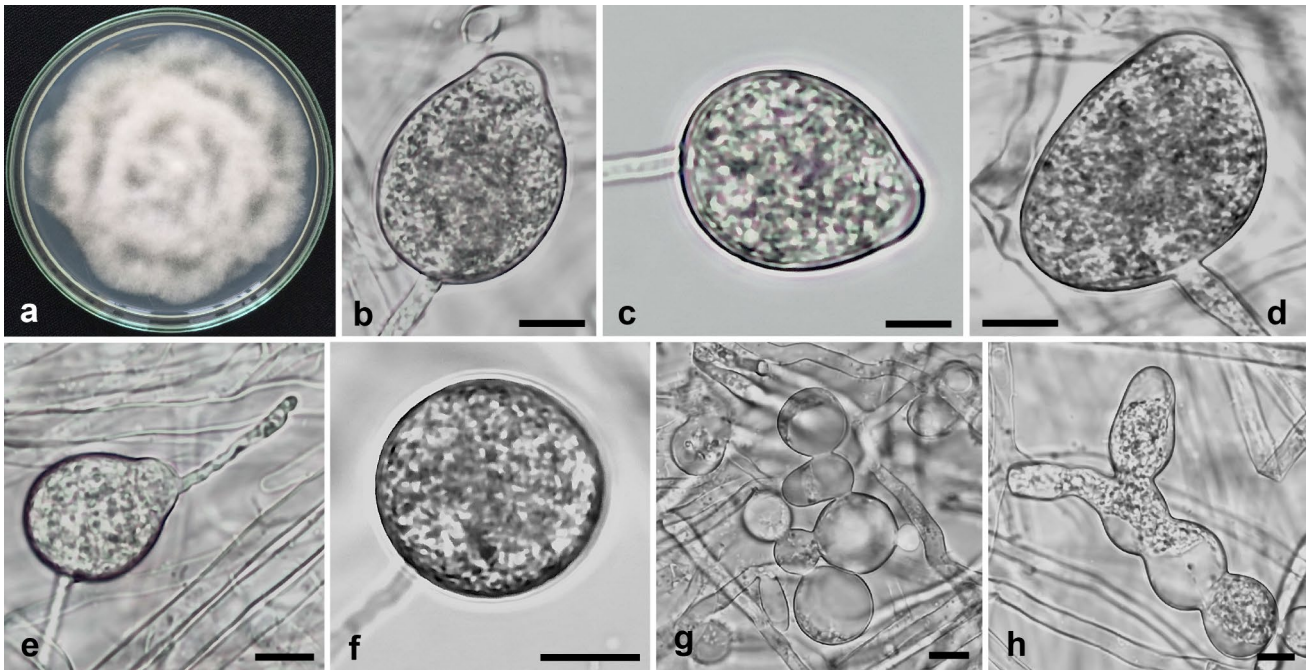


Fig. 8 *Phytophthora parvispora* PPRI21812. a. Colony on PDA; b-e. Sporangia; f. Chlamydospore; g-h. Hyphal swellings; Scale bars = 10 μ m

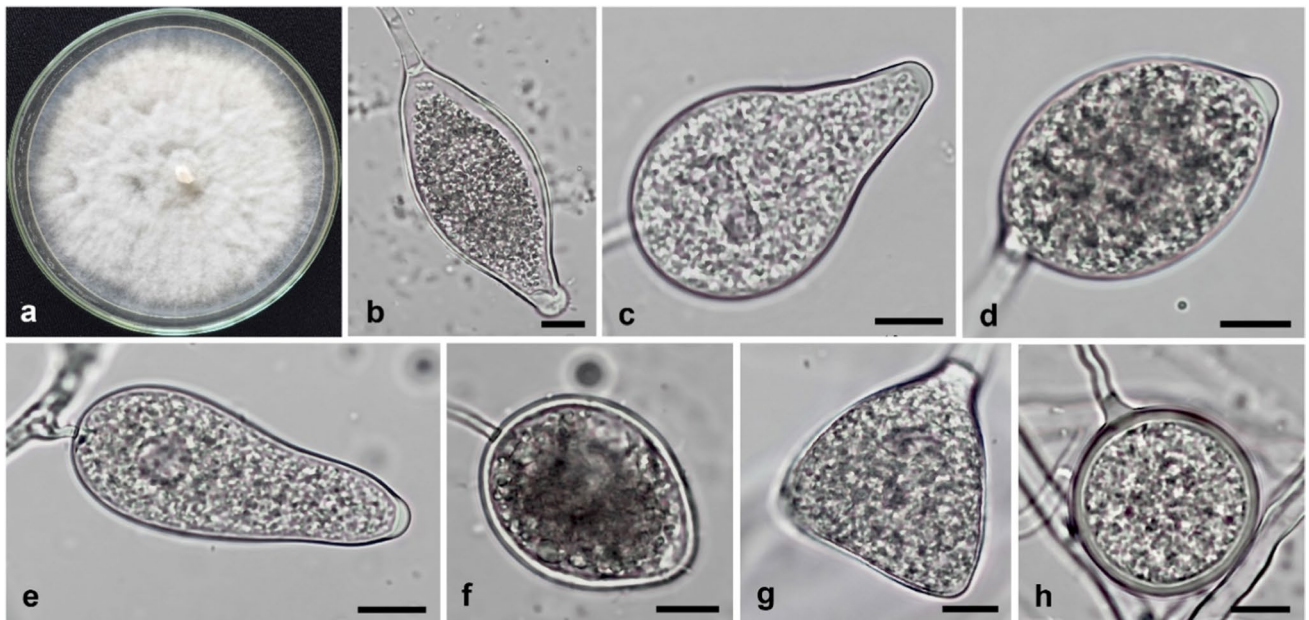


Fig. 9 *Phytophthora tropicalis* PPRI20912. a. Colony on PDA; b-g. Sporangia; h. Chlamydospore; Scale bars = 10 μ m

Discussion

Among oomycete isolates obtained from black pepper plantations in five provinces of Vietnam, six *Phytophthora* species (*P. capsici*, *P. cinnamomi*, *P. heveae*,

P. nicotianae, *P. parvispora* and *P. tropicalis*) and two *Phytophthium* species (*Phytophthium vexans* and *Phytophthium* sp.) were identified based on molecular analyses with the supporting data of morphology. *Phytophthora capsici* has been known as the most important agent of



Fig. 10 *Phytophthium vexans* (PPRI2098). a. Colony on PDA; b-f. Sporangia; f. Release of zoospores; g-h. Oogonia with antheridia; Scale bars = 10 μ m

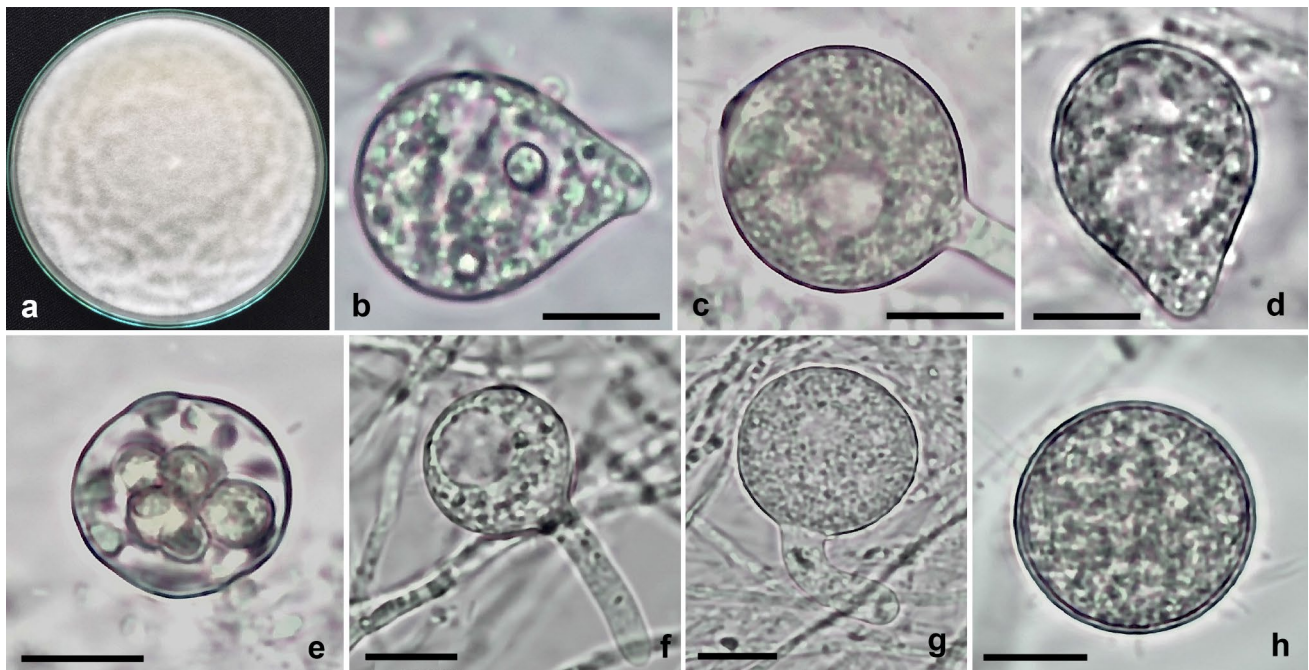


Fig. 11 *Phytophthium* sp. PPRI2097. a. Colony on PDA; b-g. Sporangia; f-g. Formation of long discharge tubes; h. Chlamydospore; Scale bars = 10 μ m

quick wilt disease in Vietnam (Truong et al. 2008; 2010; 2012; Nguyen 2015; Quy et al. 2021). However, the results of this study revealed that not only *P. capsici*, but the other

species including *P. tropicalis*, *P. nicotianae* and *Phytophthium vexans* also infected black pepper in locations sampled. According to the results of analysed samples,

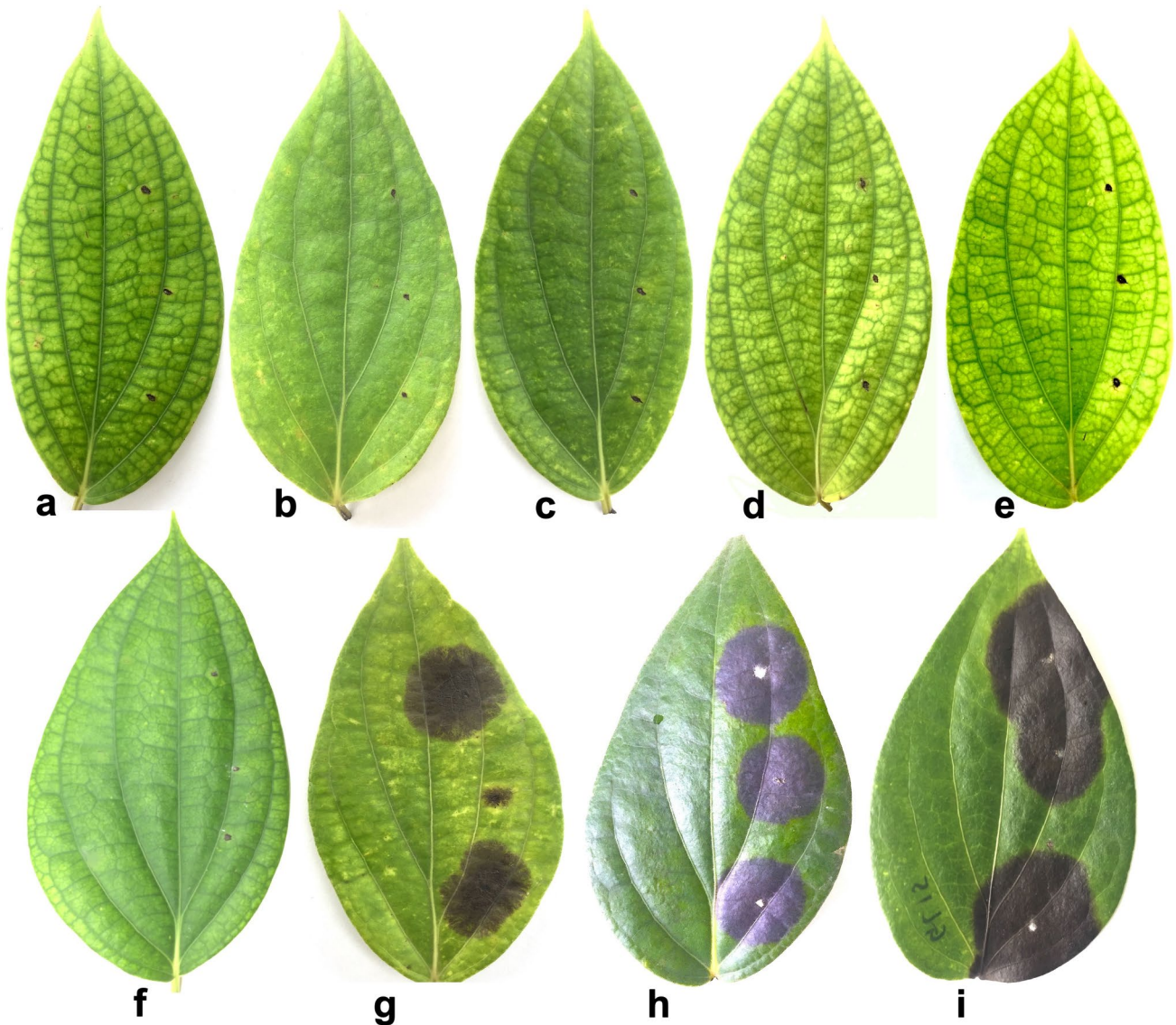


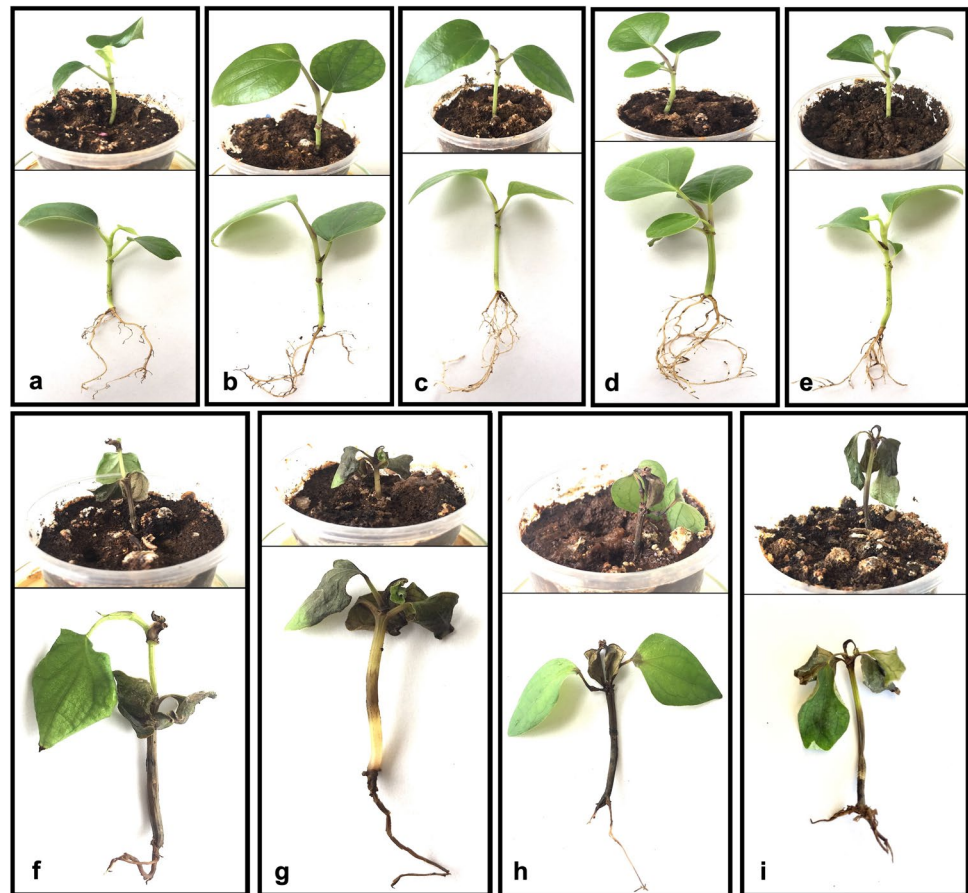
Fig. 12 Pathogenicity test of oomycetes on black pepper leaves. a-f. No disease symptoms, a. Control, b. PPRI20913 (*P. heveae*), c. PPRI2087 (*P. cinnamomi*), d. PPRI21812 (*P. parvispora*), e.

PPRI2097 (*Phytophthium* sp.) and f. PPRI2098 (*Phytophthium vexans*); g-i. Disease symptoms, g. PPRI20915 (*P. nicotianae*), h. PPRI20912 (*P. tropicalis*), and i. PPRI20911 (*P. capsici*)

Phytophthora capsici (9 isolates) was the most prevalent pathogenic species, followed by *P. tropicalis* (6 isolates), *Phytophthium vexans* (3 isolates) and *P. nicotianae* (1 isolate). *Phytophthora capsici* was present in all five provinces, in the soil and root of black pepper. Meanwhile, *P. tropicalis* was found only in the Central Highlands (Dak Lak, Dak Nong and Gia Lai provinces), in the soil and root. *Phytophthium vexans* was isolated from the soil and root in Dak Lak and Gia Lai provinces. The other pathogenic species, *P. nicotianae*, was obtained from the soil in Dak Nong province. To investigate the presence and distribution of the identified species more samples need to be collected and analysed.

Phytophthora capsici was first described by Leonian (1922) on chili pepper in New Mexico. The species was a devastating pathogen, infecting the root, crown, stem, leaf and fruit of host plants such as papaya, cacao, rubber, macadamia, black pepper, and numerous species of solanaceous and cucurbitaceous (Erwin et al. 1996; Ristaino and Johnston 1999; Hausbeck and Lamour 2004; Parada-Rojas et al. 2021). While *P. tropicalis*, named by Aragaki and Uchida (2001), was often recorded from woody perennial hosts such as cacao, breadfruit and citrus, and not usually reported on the common host plant of *P. capsici* such as pepper, tomato and cucurbits (Donahoo and Lamour 2008; Farr et al 2023). The different host ranges of these

Fig. 13 Pathogenicity test of oomycetes on black pepper seedlings. a-e. No disease symptoms, a. Control, b. PPRI20913 (*P. heveae*), c. PPRI2087 (*P. cinnamomi*), d. PPRI21812 (*P. parvispora*) and e. PPRI2097 (*Phytophthium* sp.); f-i. Disease symptoms, f. PPRI2098 (*Phytophthium vexans*), g. PPRI20915 (*P. nicotianae*), h. PPRI20912 (*P. tropicalis*), and i. PPRI20911 (*P. capsici*)



species may lead to a difference in the epidemiology of the pathogens. Current and previous studies indicate that *P. capsici* and *P. tropicalis* showed significant variation in their morphology, and chlamyospores were present in *P. tropicalis* isolates, while they were absent in *P. capsici* isolates (Bhai et al. 2022). However, hyphal swellings observed in *P. capsici* in this study were highly similar to chlamyospores. Therefore, the morphological characteristics could not be used to separate these two species and they were accurately identified based on multi-locus analysis of ITS, TEF1, and TUB.

Phytophthium vexans and *P. nicotianae* were serious pathogen species and were frequently present in avocado orchards in many countries (Machado et al. 2013; Rodriguez-Padron et al. 2018; Hernández-Pérez et al. 2019). These species also attacked citrus (Benfradj et al. 2017; Wu et al. 2020) and rubber (Zheng and Ward 1998; Zeng et al. 2005). *Phytophthium vexans* was recently reported as a causal agent of durian root rot in the Central Highlands (Thao et al. 2020) and *P. nicotianae* frequently infected citrus plants in Southern Vietnam (Patrizio et al. 2013). The host plants mentioned herein are often cultivated close to, or intercropped with black pepper, and the areas of avocado, durian and citrus are dramatically increasing. This will

become a favorable condition for the infection of *P. nicotianae* and *Phytophthium vexans*.

The results of this study suggest that *P. capsici* and *P. tropicalis* could be the prevalent species in black pepper growing areas of Vietnam. *Phytophthora nicotianae* and *Phytophthium vexans* could become widely spread pathogens to black pepper and other host plants in the future. These findings are meaningful information for developing strategies to control the disease. On the other hand, multiple infections of different oomycete species and the presence of non-pathogenic species to black pepper (*P. cinnamomi*, *P. heveae*, *P. parvispora* and *Phytophthium* sp.) in their community are still unclear.

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Data availability The sequence data obtained in this study were deposited in GenBank with accession numbers listed in Table 1.

Declarations

Conflicts of interest The authors declare that there is no conflict of interest.

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