

An expanded phylogeny for the genus *Phytophthora*

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Abstract: A comprehensive phylogeny representing 142 described and 43 provisionally named *Phytophthora* species is reported here for this rapidly expanding genus. This phylogeny features signature sequences of 114 ex-types and numerous authentic isolates that were designated as representative isolates by the originators of the respective species. Multiple new subclades were assigned in clades 2, 6, 7, and 9. A single species *P. lillii* was placed basal to clades 1 to 5, and 7. *Phytophthora stricta* was placed basal to other clade 8 species, *P. asparagi* to clade 6 and *P. intercalaris* to clade 10. On the basis of this phylogeny and ancestral state reconstructions, new hypotheses were proposed for the evolutionary history of sporangial papillation of *Phytophthora* species. Non-papillate ancestral *Phytophthora* species were inferred to evolve through separate evolutionary paths to either papillate or semi-papillate species.

Key words:
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INTRODUCTION

The genus *Phytophthora* has had profound impacts on human history by causing agriculturally and ecologically important plant diseases (Erwin & Ribeiro 1996). Among the most notorious *Phytophthora* species is *P. infestans*, cause of the late blight disease, which was the primary cause of the Irish potato famine from 1845 to 1852 in which approximately one million people died and 1.5 million emigrated from Ireland (Turner 2005). Another example is the sudden oak death pathogen, *P. ramorum*, that has killed millions of coast live oak, tanoak and Japanese larch trees, and has permanently altered the forest ecosystems in California and Oregon, USA (Goheen *et al.* 2002, Rizzo *et al.* 2002, Rizzo *et al.* 2005). Other species, such as *P. cinnamomi*, *P. nicotianae*, and *P. sojae*, can also cause highly destructive plant diseases (Erwin & Ribeiro 1996). The impact caused by *Phytophthora* species has continued to increase with the emergence of new pathogens and diseases. The number of species known in the genus has doubled during the past decade due to extensive surveys in previously unexplored ecosystems such as natural forests (Jung *et al.* 2011, 2017, Rea *et al.* 2010, Reeser *et al.* 2013, Vettraino *et al.* 2011), streams (Bezuidenhout *et al.* 2010, Brazee *et al.* 2017, Reeser *et al.* 2007, Yang *et al.* 2016), riparian ecosystems (Brasier *et al.* 2003a, 2004, Hansen *et al.* 2012), and irrigation systems (Hong *et al.* 2010, 2012, Yang *et al.* 2014a, b). The total number of formally named species in the genus was about 58 in 1996 (Erwin & Ribeiro 1996), but now is more than 150. In addition, some provisionally or informally named species are also expected to be formally described in the near future.

A sound taxonomic system is foundational for correctly identifying *Phytophthora* species and safeguarding agriculture, forestry, and natural ecosystems. Traditionally, taxonomy of the genus was based on morphological characters. A fundamental morphology-based classification of *Phytophthora* species was established by Waterhouse (1963) who classified the species into six groups based on the morphology of sporangia, homothallism, and configuration of antheridia. However, plasticity in morphological characters amongst isolates of individual species is significant, so is homology or homoplasy among different species. For example, isolates of *P. constricta* (Rea *et al.* 2011), *P. gibbosa* (Jung *et al.* 2011), *P. lateralis* (Kroon *et al.* 2012), *P. mississippiiae* (Yang *et al.* 2013), and *P. multivesiculata* (Ilieva *et al.* 1998) all produce a mixture of semi-papillate and non-papillate sporangia. Many non-papillate species recovered from irrigation water such as *Phytophthora hydropathica* (Hong *et al.* 2010) and *P. irrigata* (Hong *et al.* 2008) were morphologically inseparable from *P. drechsleri*, while sequence analyses demonstrated that they are distinct species. Also, production of many morphological structures and physiological features needs specific environmental conditions, while observation of these features requires substantial training and expertise. Difficulty in obtaining important morphological data can impair accurate species identification.

With the advent of DNA sequencing, the taxonomic concept for the genus has evolved from morphology to molecular phylogeny-based (Blair *et al.* 2008, Cooke *et al.* 2000, Kroon *et al.* 2004, Lara & Belbahri 2011, Martin *et al.* 2014, Martin & Tooley 2003, Robideau *et al.* 2011, Villa *et al.* 2006). In particular, the availability of whole genome

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sequences from *P. sojae*, *P. ramorum* (Tyler *et al.* 2006) and *P. infestans* (Haas *et al.* 2009) enabled the identification of genetic markers useful for multi-locus phylogenies (Blair *et al.* 2008).

Cooke *et al.* (2000) developed the first molecular phylogeny for the genus by analyzing sequences of the internal transcribed spacer region (ITS) of 51 species. Kroon *et al.* (2004) constructed a phylogeny based on sequences of four nuclear and mitochondrial genes of 48 species, and Blair *et al.* (2008) produced a sophisticated phylogeny based on sequences of seven nuclear genetic markers. That multi-locus phylogeny divided 82 *Phytophthora* species into 10 phylogenetically well-supported clades. Martin *et al.* (2014) analyzed sequences of seven nuclear and four mitochondrial genes of 90 formally named and 17 provisional species and provided phylogenies including 10 clades, almost identical to that of Blair *et al.* (2008), except that *P. quercina* and *P. sp. ohioensis* were excluded from clade 4 and grouped into a potentially new clade.

A comprehensive molecular phylogeny is required to understanding the evolution of *Phytophthora* species. Although discordance has been found between the molecular phylogeny and the morphology-based taxonomy (Cooke *et al.* 2000, Ersek & Ribeiro 2010), correlations have been observed between molecular phylogenies and individual morphological and physiological traits. Recent studies indicated that species in individual clades or subclades are mostly identical in sporangial papillation, and optimum and maximum growth temperatures (Cooke *et al.* 2000, Kroon *et al.* 2012, Martin *et al.* 2012, Yang 2014). However, there was limited to no correlation between phylogeny and the morphology of sexual organs, such as antheridial configuration (Cooke *et al.* 2000, Kroon *et al.* 2012, Martin *et al.* 2012, Yang 2014). These studies have implied that divergence in sporangial morphology and variation in environmental specialization may be the keys in the evolutionary history of *Phytophthora* species. Nevertheless, these hypotheses need to be further tested and the exact evolutionary history of the genus *Phytophthora* warranted more investigation.

In this study, an expanded phylogeny, including more than 180 *Phytophthora* taxa, many not included in any previous phylogeny, was constructed. Sequences of seven nuclear genetic markers were used for construction of the phylogeny. In light of this phylogeny, ancestral state reconstructions were conducted on the sporangial papillation of *Phytophthora* species. Important evolutionary divergence events and associated changes in the sporangial morphology of *Phytophthora* species are discussed.

MATERIALS AND METHODS

Isolate selection

A total of 376 *Phytophthora* isolates representing 142 described and 43 provisionally named species, plus one isolate of each *Elongisporangium undulatum* (basionym: *Pythium undulatum*), *Halophytophthora fluviatilis*, and *Phytopyrium vexans* (basionym: *Pythium vexans*) as outgroup taxa were included (Table 1). These included 114 ex-types (Table 2). Also included were 164 authentic isolates

that were designated as representative isolates by the originators of the respective species names (Table 1). The majority of these isolates were provided by the originators of the respective species, while the rest were purchased from the Westerdijk Fungal Biodiversity Institute (CBS), Utrecht, The Netherlands.

DNA extraction

To extract genomic DNA (gDNA), an approximately 5 × 5 mm culture plug of each isolate was taken from the actively growing area of a fresh culture. This was then grown in 20 % clarified V8 broth (lima bean broth for growing a *P. infestans* isolate 27A8) at room temperature (ca. 23 °C) for 7–14 d to produce a mycelial mass. The mass was then blot-dried using sterile tissue paper and then lysed in liquid nitrogen or using a FastPrep®-24 system (MP Biomedicals, Santa Ana, CA). gDNA was extracted using the DNeasy® Plant Mini kit (Qiagen, Valencia, CA) or the Maxwell® Plant DNA kit in combination with a Maxwell® Rapid Sample Concentrator (Promega, Madison, WI).

DNA amplification and sequencing

A set of primers for seven genetic markers were used for DNA amplification including 60S Ribosomal protein L10 (60S), beta-tubulin (Btub), elongation factor 1 alpha (EF1α), enolase (Enl), heat shock protein 90 (HSP90), 28S ribosomal DNA (28S), and tigA gene fusion protein (TigA) as indicated in Blair *et al.* (2008). PCR reaction mixtures were prepared with the Takara *Taq* DNA polymerase (Takara Shuzo, Shiga, Japan) according to the manufacturer's instructions. The PCR cycling protocol was the same as indicated by Blair *et al.* (2008), except that the Eppendorf® Mastercycler® Pro thermal cycler (Eppendorf, Hamburg) was used in this study. All PCR products were evaluated for successful amplification using agarose gel electrophoresis. Unsuccessful PCR amplifications were repeated using a modified protocol to attempt successful amplifications by optimizing annealing temperature using gradient PCR (typically with lower annealing temperatures) or using the GoTaq® Flexi DNA Polymerase (Promega, Madison, WI) PCR mixture system.

Prior to sequencing, excess primer and dNTPs were removed from successful PCR products with shrimp alkaline phosphatase and exonuclease I (USB Catalog # 70092Y and 70073Z). One unit of each enzyme was added to 15 µL PCR product, incubated at 37 °C for 30 min, followed by heat inactivation at 65 °C for 15 min. Sequencing was performed with both amplifying primers as well as internal primers, if any, for individual genetic markers at the University of Kentucky Advanced Genetic Technologies Center (Lexington, KY). Derived sequencing files were visualized with FinchTV version 1.4.0 (Geospiza, Seattle, WA). Sequences of each isolate with all primers for individual genetic markers were aligned with Clustal W (Larkin *et al.* 2007) and edited manually to correct obvious sequencing errors and code ambiguous sites according to the International Union of Pure and Applied Chemistry (IUPAC) nucleotide ambiguity codes to produce a consensus sequence. All sequences produced in this study have been deposited in GenBank (Supplementary Table 1).

Among 379 isolates (including three isolates of the outgroup taxa) in the following phylogenetic analyses,

Table 1. Information regarding isolates used in this study. GenBank accession numbers are listed in Table S1.

(Sub)clade ^a	Species ^b	Papilla ^c	Isolate identification ^d					Isolate origins				Year	Reference	
			CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location			
1a	<i>P. cactorum</i>	P	22E6				P10194	p25		Rhododendron sp.	Ohio, USA	n.a. ^f	(Schroter 1886)	
			22E7		16693	21168	P0715	p6		n.a.	UK	n.a.		
			22E8		16694, MYA-3653	50470	P10193	p7		<i>Malus</i> sp.	Zimbabwe	n.a.		
	<i>P. hedraiaandra</i>	P	33F3		MYA-4165			p225		<i>Rhododendron</i> sp.	Minnesota, USA	2002	(de Cock & Lévesque 2004)	
			38C2							Irrigation water	Virginia, USA	2006		
	<i>P. idaei</i>	P	62A5	111725			P19523		T	<i>Viburnum</i> sp.	The Netherlands	2001		
			34D4	971.95	MYA-4065	313728	P6767	p220	T	<i>Rubus idaeus</i>	Scotland, UK	1987	(Kennedy & Duncan 1995)	
	<i>P. pseudotsugae</i>	P	62A1	968.95	52938	331662	P10339		A	<i>Rubus idaeus</i>	Scotland, UK	1985		
									T	<i>Pseudotsuga menziesii</i>	Oregon, USA	n.a.	(Hamm & Hansen 1983)	
	1b	<i>P. aff. hedraiaandra</i>	P	33F4				p226		<i>Rhododendron</i> sp.	Minnesota, USA	2003	n.a.	
<i>P. aff. pseudotsugae</i>		P	29B3				p185	A	<i>Pseudotsuga menziesii</i>	Oregon, USA	1975	n.a.		
<i>P. clandestina</i>		P	32G1	347.86	58713, 60438	278933	P3943	p200	T	<i>Trifolium subterraneum</i>	Australia	1985	(Taylor et al. 1985)	
<i>P. iranica</i>		P	33D8		MYA-4064	287317		p215	A	<i>Trifolium subterraneum</i>	Australia	1985		
			38D4					p304		n.a.	Australia	n.a.		
<i>P. tentaculata</i>		P	61J4	374.72	60237	158964	P3882	p218	T	<i>Solanum melongena</i>	Iran	1969	(Ershad 1971)	
			29F2	552.96			P8497			A	<i>Chrysanthemum leucanthemum</i>	Germany	n.a.	(Kröber & Marwitz 1993)
1c		<i>P. andina</i>	SP	30D5							<i>Bacopa</i> sp.	The Netherlands	2004	
				30G8		MYA-3655						<i>Argyranthemum frutescens</i>	Germany	2004
		<i>P. infestans</i>	SP	60A2					p460	A	<i>Solanum betaceum</i>	Ecuador	n.a.	(Oliva et al. 2010)
	60A3							p461	A	<i>Solanum betaceum</i>	Ecuador	n.a.		
	<i>P. ipomoeae</i>	SP	27A8				P13365		T	<i>Solanum brevifolium</i>	Ecuador	2001		
			31B4					P10650		A	<i>Solanum tuberosum</i>	Mexico	1992	(De Bary 1876)
	<i>P. mirabilis</i>	SP	31B5	109229			P10226		A	<i>Ipomoea longipedunculata</i>	Mexico	n.a.	(Flier et al. 2002)	
			31B6					P10225	T	<i>Ipomoea longipedunculata</i>	Mexico	1999		
	<i>P. phaseoli</i>	SP	30C1		64069, MYA-4062		P3006	p145	A	<i>Mirabilis jalapa</i>	Mexico	n.a.	(Galindo-A & Hohl 1985)	
			30C2		64070, MYA-4063		P3007	p153	A	<i>Mirabilis jalapa</i>	Mexico	n.a.		
<i>P. phaseoli</i>	SP	23B4					p106		<i>Phaseolus lunatus</i>	Delaware, USA	2000	(Thaxter 1889)		
		35B6				P10145			<i>Phaseolus lunatus</i>	Delaware, USA	2000			
						P10150			<i>Phaseolus lunatus</i>	Delaware, USA	n.a.			

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^a										Isolate origins				
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference			
1	<i>P. nicotianae</i>	P	22F9		15410, MYA-4037						p23		<i>Nicotiana tabacum</i>	North Carolina, USA	n.a.	(Breda de Haan 1896)
			22G1		15409, MYA-4036						p22		<i>Nicotiana tabacum</i>	North Carolina, USA	n.a.	
2a	<i>P. botryosa</i>	P	22H8 46C2 62C6	MYA-4059 26481 581.69							p44 p384		<i>Metrosideros excelsa</i> <i>Citrus</i> sp. <i>Hevea</i> sp. <i>Hevea brasiliensis</i> <i>Hevea brasiliensis</i> <i>Hevea brasiliensis</i>	California, USA California, USA Thailand Thailand Malaysia Malaysia	2002 n.a. n.a. n.a. 1966 1986	(Chee 1969)
	<i>P. citrophthora</i>	P	03E5		130422	P6945					p132		Irrigation water	Virginia, USA	2000	(Smith & Smith 1906)
			26H3 22F8 35D3								p31 p47 p276		n.a. <i>Colocasia esculenta</i> <i>Colocasia esculenta</i>	n.a. n.a. Hawaii, USA	n.a. 1992 2005	(Raciborski 1900)
	<i>P. himalsilva</i>	P	61G2	128767								T	<i>Quercus leucotricophora</i>	Nepal	2005	(Vettrai et al. 2011)
			61G3	128753								A	<i>Quercus leucotricophora</i>	Nepal	2005	
	<i>P. meadii</i>	P	22G5 61J9	MYA-4043 219.88							p75		<i>Citrus</i> sp.	India	1992	(McRae 1918)
	<i>P. occultans</i>	SP	65B9	101557	129185							T	<i>Hevea brasiliensis</i>	India	1987	(Man In't Veld et al. 2015)
	<i>P. terminalis</i>	SP	65B8	133865								T	<i>Buxus sempervirens</i>	The Netherlands	1998	(Man In't Veld et al. 2015)
	<i>P. aff. citrophthora</i>	P	26H4								p32		n.a.	The Netherlands	2010	(Man In't Veld et al. 2015)
	<i>P. aff. himalsilva</i>	P	61G4	128754	342898	P10341						A	<i>Syringa</i> sp.	n.a.	n.a.	
	<i>P. sp. 46C3</i>	n.a.	46C3									A	<i>Castanopsis</i> sp.	England, UK	1990	
	<i>P. sp. P6262</i>	n.a.		66767		P6713					p385		<i>Hevea brasiliensis</i>	Nepal	2005	n.a.
	<i>P. sp. P6310</i>	n.a.				P6262						A	<i>Hevea brasiliensis</i>	Malaysia	n.a.	n.a.
	<i>P. capsici</i>	P	22F4	15399, MYA-4034		P6310					p8		<i>Theobroma cacao</i> <i>Capsicum annum</i>	Indonesia New Mexico, USA	n.a. 1948	(Leonian 1922)
2b			31E5 62B4 42B2 42B3 45G4	46012 121656 121969 MYA-4554 MYA-4555 46731									<i>Theobroma cacao</i> <i>Cucumis sativus</i> <i>Nicotiana tabacum</i> <i>Nicotiana tabacum</i> <i>Persea americana</i> <i>Persea americana</i> <i>Solanum lycopersicum</i>	Mexico Michigan, USA Brazil Brazil California, USA California, USA Argentina	1964 1997 n.a. 1995 n.a. n.a. n.a.	(Abad et al. 2011) (Hong et al. 2009) (Hotson & Hartge 1923)

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^a										Isolate origins			Reference
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year			
	<i>P. siskiyouensis</i>	SP	41B7	122779	MYA-4187		P15122	T	Stream water	Oregon, USA	2003		(Reeser et al. 2007)		
	<i>P. tropicalis</i>	P	41B8 22H5			p27	A	Soil <i>Vanilla</i> sp.	Oregon, USA Tahiti	2003 n.a.			(Aragaki & Uchida 2001)		
	<i>P. aff. capsici</i>	P	35C8 22F5	434.91	76651, MYA-4218 15427, MYA-4035	p272 p9	T	<i>Macadamia integrifolia</i> <i>Nicotiana tabacum</i>	Hawaii, USA North Carolina, USA	n.a. n.a.			n.a.		
	<i>P. sp. brasiliensis</i>	n.a.			46705	P0630	A	<i>Theobroma cacao</i>	Brazil	1969			(Oudemans & Coffey 1991)		
2c	<i>P. acerina</i>	SP	61H1	133931			T	<i>Acer pseudoplatanus</i>	Italy	2010			(Ginetti et al. 2014)		
	<i>P. capensis</i>	SP	61H2 62C1	128319		P1819	A T	Soil <i>Curtisia dentata</i>	Italy South Africa	2010 n.a.			(Bezuidenhout et al. 2010)		
	<i>P. citricola</i>	SP	62C2 62C3	128320 128321		P1822 P1823	A A	Stream water <i>Olea campensis</i>	South Africa South Africa	n.a. 1986			(Sawada 1927)		
	<i>P. multivora</i>	SP	33H8 33J2 55C5	221.88 295.29 124094	60440	p396 p375	T A T	<i>Citrus sinensis</i> <i>Citrus</i> sp. Soil	Taiwan Japan Western Australia, Australia	1987 1929 2007			(Scott et al. 2009)		
	<i>P. pachypleura</i>	SP	61H6				A	Soil	UK	2006			(Henricot et al. 2014)		
	<i>P. pini</i>	SP	61H7 61H8 22F1		502404		T A A	<i>Acuba japonica</i> Soil <i>Rhododendron</i> sp.	UK UK West Virginia, USA	2008 2009 1987			(Hong et al. 2011)		
	<i>P. plurivora</i>	SP	45F1 22E9		64532 MYA-3657	p343 p101	T	<i>Pinus resinosa</i> <i>Kalmia latifolia</i>	Minnesota, USA Western Australia, Australia	1925 1998			(Jung & Burgess 2009)		
	<i>P. sp. 22F3</i>	SP	22F2			p52	A	<i>Rhododendron</i> sp. cv. "Olga Mezitt"	New York, USA	n.a.					
	<i>P. sp. 28D1</i>	SP	33H9 22F3	379.61		p33	A	<i>Rhododendron</i> sp. n.a.	Germany Ohio, USA	1958 n.a.			n.a.		
	<i>P. sp. citricola VIII</i>	SP	28D1 28D3			p119 p121	A A	<i>Fagus sylvatica</i> <i>Fagus sylvatica</i>	New York, USA New York, USA	n.a. n.a.			n.a.		
	<i>P. sp. pini-like</i>	SP	27D9 56G1				A A	Unidentified leaf <i>Taxus</i> sp.	Hainan, China Pennsylvania, USA	n.a. 2011			n.a.		
	<i>P. taxon emzansi</i>	SP	61F2				A	<i>Agathosma betulina</i>	South Africa	2005			(Bezuidenhout et al. 2010)		

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^a										Isolate origins			Reference
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year			
2d	<i>P. bisheria</i>	SP	61F3 29D2						A	Agathosma betulina Rubus idaeus cv. Canby	South Africa Wisconsin, USA	2005 1989		(Abad et al. 2008)	
			31E6	122081			P10117		T	<i>Fragaria xananassa</i> <i>Rhododendron</i> sp.	North Carolina, USA North Carolina, USA	1999 n.a.			
2e	<i>P. elongata</i>	SP	33J3 33J4 55C4						A A T	n.a. n.a. Soil	Australia Australia Western Australia, Australia	1995 1995 2004		(Rea et al. 2010)	
		P	47G6				P1620		A	<i>Eucalyptus smithi</i>	South Africa	n.a.		(Maseko et al. 2007)	
		SP to NP	47G7 47G8	545.96			P10410		A T T	<i>Eucalyptus smithi</i> <i>Eucalyptus smithi</i> <i>Cymbidium</i> sp.	South Africa South Africa The Netherlands	n.a. 2001 n.a.		(Ilieva et al. 1998)	
3	<i>P. taxon aquatilis</i> <i>P. ilicis</i>	SP	38J5		MYA-4577			A	Stream water	Virginia, USA	2006		(Hong et al. 2012)		
		SP	23A7		56615, MYA-3897		P3939	p113	A	<i>Ilex</i> sp.	Canada	n.a.		(Buddenhagen & Young 1957)	
4	<i>P. nemorosa</i>		34D6 62A7	114348				T	<i>Quercus</i> sp. <i>Ilex aquifolium</i>	Germany The Netherlands	1999 n.a.				
		SP	28J3		MYA-4061		p141		T	<i>Umbellularia californica</i>	California, USA	n.a.		(Hansen et al. 2003)	
		SP	41C4 60B3		MYA-2948 MYA-4930		p320		T T	<i>Lithocarpus densiflorus</i> Rainwater	California, USA Oregon, USA	n.a. 2008		(Reeser et al. 2013)	
		SP	30A8 30B1	111772	MYA-4222		p284		T	<i>Quercus robur</i>	Germany	1997		(Jung et al. 2003)	
4	<i>P. psychrophila</i>	SP	29J5 29J6	803.95		p285		A T	<i>Quercus robur</i> <i>Quercus robur</i>	Germany Germany	1997 1995		(Jung et al. 2002)		
		P	47G5	121939	MYA-4083		p288		A	<i>Quercus ilex</i>	France	1996			
4	<i>P. arenaria</i>	P	55C2	127950		P16948		A	<i>Eucalyptus dunni</i>	South Africa	n.a.			(Maseko et al. 2007)	
		P	62B7	125800				T	Soil	Western Australia, Australia	2009		(Rea et al. 2011)		
	<i>P. megakarya</i>	P	22H7		MYA-4040		p42		<i>Theobroma cacao</i>	Western Australia, Australia Africa	2009 n.a.		(Brasier & Griffin 1979)		

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^a										Isolate origins		
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference	
5	<i>P. palmivora</i>		61J5	238.83	42100	202077		T	<i>Theobroma cacao</i>	Cameroon	n.a.			
			61J6	239.83	42099	106327		A	<i>Theobroma cacao</i>	Nigeria	n.a.			
		P	22G8		MYA-4039		P10213	p65		Florida, USA	n.a.	(Butler 1910)		
			22G9		MYA-4038			p26		Costa Rica	n.a.			
	<i>P. quercetorum</i>	P	15C7						Soil	South Carolina, USA	1997	(Baici et al. 2008)		
			15C8						Soil	South Carolina, USA	1997			
	<i>P. quercina</i>	P	30A4	783.95				A	<i>Quercus robur</i>	Germany	1995	(Jung et al. 1999)		
			30A5	784.95	MYA-4084			T	<i>Quercus robur</i>	Germany	1995			
	6a	<i>P. sp. ohioensis</i>	n.a.	30A7						Serbia	2003			
				67D5				P16050		Soil	Ohio, USA	2006	n.a.	
<i>P. agathidicida</i>		P	22H6		MYA-4060			T	<i>Agathis australis</i>	New Zealand	2006	(Weir et al. 2015)		
		P	30E7						<i>Castanea</i> sp.	Japan	n.a.	(Katsura 1976)		
<i>P. castaneae</i>			61J7	587.85	36818	325914		T	Soil	Hainan, China	n.a.			
		P	67D6					T	Soil	Taiwan	n.a.			
<i>P. cocois</i>		P	22J1			180616		T	<i>Cocos nucifera</i>	Hawaii, USA	1990	(Weir et al. 2015)		
		P	22J2		16701, MYA-3895			T	<i>Heaveae</i> sp.	Malaysia	n.a.	(Thompson 1929)		
<i>P. gemini</i>		NP	46H1	123382				A	soil	Tennessee, USA	1964			
			46H2	123383				A	<i>Zostera marina</i>	The Netherlands	1999	(Man in't Veld et al. 2011)		
<i>P. humicola</i>	NP	32F8	200.81	52179, MYA-4080			T	Soil	The Netherlands	1999				
		32F9				P3826	p198		Taiwan	1976	(Ko & Ann 1985)			
<i>P. inundata</i>	NP	30J3			390121		T	<i>Phaseolus vulgaris</i>	Taiwan	n.a.				
		30J4					T	<i>Olea</i> sp.	Spain	1996	(Brasier et al. 2003b)			
<i>P. rosacearum</i>	NP	22J9		MYA-3662			A	<i>Salix matsudana</i>	UK	1972				
		41C1					A	<i>Pistacia vera</i>	Iran	n.a.				
<i>P. sp. 48H2</i>	NP	48H2		MYA-4456			T	<i>Prunus</i> sp.	California, USA	1987	(Hansen et al. 2009)			
	NP	62C9					A	<i>Malus domestica</i>	California, USA	n.a.				
<i>P. sp. personii</i>	n.a.						A	Stream water	Virginia, USA	2008	n.a.			
		40A7				P11555	A	Stream water	Taiwan	2013	n.a.			
<i>P. taxon walnut</i>	NP	40A7					A	<i>Nicotiana tabacum</i>	North Carolina, USA	n.a.				
		43G1					A	Irrigation water	Virginia, USA	2006	(Brasier et al. 2003a)			
<i>P. amnicola</i>	NP	61G6	131652				T	Irrigation water	Virginia, USA	2007				
							T	Stream water	Western Australia, Australia	2009	(Crous et al. 2012)			

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins			
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference		
<i>P. bilorbang</i>		NP	62C5	133867									The Netherlands	n.a.	
		NP	61G8	131653									Western Australia, Australia	2010	(Aghighi et al. 2012)
<i>P. borealis</i>		NP	60B2	132023	MYA-4881								Alaska, USA	2008	(Hansen et al. 2012)
<i>P. crassamura</i>		NP	66C9										Italy	2012	(Scanu et al. 2015)
<i>P. fluvialis</i>		NP	66D1	140357									Italy	2011	
		NP	55B6	129424									Western Australia, Australia	2009	(Crous et al. 2011)
<i>P. gibbosa</i>		NP to SP	55B7										Western Australia, Australia	2009	(Jung et al. 2011)
<i>P. gonapodyides</i>		NP	62B8	127951									Western Australia, Australia	2009	
		NP	21J5		46726			p117					England, UK	n.a.	(Buisman 1927, Petersen 1910)
<i>P. gregata</i>		NP	34A8	554.67	60351								n.a.	1967	
		NP	55B8						P6872				Reservoir water	2009	(Jung et al. 2011)
<i>P. lacustris</i>		NP	62B9	127952									Soil	2009	
		NP	61D6										Germany	2003	(Nechwatal et al. 2013)
<i>P. litoralis</i>		NP	61D8										Germany	2003	
		NP	61E1										Germany	2006	
<i>P. megasperma</i>		NP	55B9	127953									England, UK	1972	
		NP	62C7	402.72	58817				389725	P10337			Western Australia, Australia	2008	(Jung et al. 2011)
<i>P. mississippiae</i>		NP	62C7	402.72	58817				32035	P3599			Washington DC, USA	1931	(Drechler 1931)
<i>P. mississippiae</i>		NP to SP	57J1										Mississippi, USA	2012	(Yang et al. 2013)
			57J2										Mississippi, USA	2012	
<i>P. ornamentata</i>			57J3										Mississippi, USA	2012	
		NP	66D2	140647									Mississippi, USA	2012	(Scanu et al. 2015)

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins			Reference
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year			
	<i>P. pinifolia</i>	NP	66D3 47H1	122924				A T	Soil <i>Pinus radiata</i>	Italy Chile	2012 2007		(Duran et al. 2008)		
	<i>P. riparia</i>	NP	47H2 60B1	122922 132024	MYA-4882			A T	<i>Pinus radiata</i> Stream water	Chile Oregon, USA	2007 2006		(Hansen et al. 2012)		
	<i>P. thermophila</i>	NP	55C1	127954				T	Soil	Western Australia, Australia	2004		(Jung et al. 2011)		
	<i>P. x-stagnum</i>	NP	36H8					A	Irrigation water	Virginia, USA	2006		(Yang et al. 2014c)		
			36J7 43F3 44F9		MYA-4926			A T A	Irrigation water Irrigation water Irrigation water	Virginia, USA Virginia, USA Virginia, USA	2006 2007 2007				
	<u><i>P. sp.</i> 26E1</u>	NP	26E1			p116		A	<i>Malus domestica</i>	New York, USA	n.a.		n.a.		
	<i>P. sp. canalensis</i>	n.a.						A	Canal water	California, USA	2002		n.a.		
	<u><i>P. sp. delaware</i></u>	NP	63H4 63H7			P10456		A A	Pond water Pond water	Delaware, USA Delaware, USA	2014 2014		n.a.		
	<u><i>P. sp. gregata-like</i></u>	NP	22J5		16698			A	n.a.	n.a.	n.a.		n.a.		
	<u><i>P. sp. megasperma-like</i></u>	NP	23A1					A	<i>Prunus</i> sp.	California, USA	n.a.		n.a.		
			23A3		MYA-3660	p79		A	<i>Actinidia chinensis</i>	California, USA	1987		n.a.		
6	<i>P. asparagi</i>	NP	33D7			384046		A	<i>Asparagus officinalis</i>	New Zealand	1980		(Crous et al. 2012)		
			62C4	132095	MYA-4826			T	<i>Asparagus officinalis</i>	Michigan, USA	2006		n.a.		
7a	<i>P. sp. sulawesiensis</i>	n.a.						A	<i>Syzygium aromaticum</i>	Indonesia	1989		n.a.		
	<i>P. attenuata</i>	NP	67C5			P6306		T	Soil	Taiwan	2013		(Jung et al. 2017)		
	<i>P. europaea</i>	NP	30A3 34C2						<i>Quercus</i> sp. <i>Quercus</i> sp.	France Germany	1998 1999		(Jung et al. 2002)		
			62A2	109049				T	Soil	France	1998				
	<i>P. flexuosa</i>	NP	67C3					T	Soil	Taiwan	2013		(Jung et al. 2017)		
	<i>P. formosa</i>	NP	67C4					T	Soil	Taiwan	2013		(Jung et al. 2017)		
	<i>P. fragariae</i>	NP	22G6 30C5		11374				<i>Fragaria xananassa</i> <i>Fragaria xananassa</i>	Maryland, USA Virginia, USA	n.a. n.a.		(Hickman 1940)		
			61J3	209.46				T	<i>Fragaria xananassa</i>	England, UK	n.a.		(Jung et al. 2017)		
	<i>P. intricata</i>	NP	67B9		181417	P6231		T	Soil	Taiwan	2013		(Jung et al. 2017)		
	<i>P. rubi</i>	NP	30D7					A	<i>Rubus</i> sp.	Australia	n.a.		(Man in 't Veld 2007)		
			41D5 46C7		90442			T	<i>Rubus</i> sp. <i>Rubus idaeus</i> cv. "Glen Clova"	Norway Scotland, UK	2005 n.a.				
	<i>P. uliginosa</i>	NP	62A3	109054		P10413		T	Soil	Poland	1998		(Jung et al. 2002)		

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins			
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference		
7b	<i>P. xalni</i>	NP	62A4	109055		P10328	p205	A	Soil	Germany	1998				
			32J6	392317	MYA-4081				A	<i>Alnus glutinosa</i>	France	1996	(Brasier et al. 2004, Husson et al. 2015)		
	<i>P. xcambivora</i>		32J7	392318			p206	A	<i>Alnus</i> sp.	Austria	1996				
			47A7			392314		T	<i>Alnus</i> sp.	UK	1994				
			47A8					A	<i>Alnus</i> sp.	The Netherlands	n.a.				
		NP	22F6		46719, MYA-4076		p64		<i>Abies</i> sp.	Oregon, USA	n.a.	(Buisman 1927, Jung et al. 2017)			
	<i>P. xheterohybrida</i>	NP	26F8		MYA-4075		p38	T	n.a.	New York, USA	n.a.				
		NP	67C1						Stream water	Taiwan	2013	(Jung et al. 2017)			
	<i>P. xincrassata</i>	NP	67C2					T	Stream water	Taiwan	2013	(Jung et al. 2017)			
		NP	33F7				p229	A	Soil	West Virginia, USA	2005	n.a.			
7c	<i>P. asiatica</i>	NP	45G1		90455		A	<i>Robinia pseudoacacia</i>	Jiangsu, China	n.a.		(Rahman et al. 2014a)			
			46C6		56194		p388	A	<i>Robinia pseudoacacia</i>	Jiangsu, China	n.a.				
	<i>P. cajani</i>	NP	61H3	133347			p214	T	<i>Pueraria lobata</i>	Japan	2005				
			33D9				p348	A	<i>Cajanus cajani</i>	India	n.a.	(Amin et al. 1978)			
			45F6		44389		p349	T	<i>Cajanus cajani</i>	India	n.a.				
			45F7		44388		P3105	A	<i>Cajanus cajani</i>	India	n.a.				
	<i>P. melonis</i>	NP	32F6		MYA-4079		p196	A	<i>Cucumis sativus</i>	China	n.a.		(Katsura 1976)		
			41B4				p318	A	<i>Cucumis sativus</i>	Iran	n.a.				
	<i>P. niederhauserii</i>	NP	45F3	582.69	52854		p312	T	<i>Cucumis sativus</i>	Japan	n.a.				
			01D5				p57	A	Irrigation water	Virginia, USA	2000	(Abad et al. 2014)			
		23J6		MYA-4163		P10617	A	Unknown ornamental	Israel	n.a.					
		31E7				p169	A	<i>Thuja occidentalis</i>	North Carolina, USA	2001					
<i>P. pisi</i>	NP	60A4					T	Pea	Sweden	2009	(Heyman et al. 2013)				
		60A5					A	Pea	Sweden	2009					
<i>P. pistaciae</i>	NP	33D6		MYA-4082		p216	T	<i>Pistacia vera</i>	Iran	1986	(Mirabolfathy et al. 2001)				
		41A9				p314	A	<i>Pistacia vera</i>	Iran	n.a.					
<i>P. sojiae</i>	NP	22D8	312.62	16705, MYA-3899	131375	p19		<i>Glycine max</i>	Ontario, Canada	1959	(Kaufmann & Gerdemann 1958)				
		28F9				p236		<i>Glycine max</i>	Mississippi, USA	1970					
<i>P. vignae</i>	NP	45G6		46735		p357	A	<i>Glycine max</i>	n.a.	n.a.	(Purss 1957)				
		45G9		64832		p379		<i>Vigna unguiculata</i>	Sri Lanka	n.a.					
		46C1	112.76	64129	316196	P3420	p380		n.a.	n.a.					
	NP	23B1		15400, MYA-4057		p10		<i>Camellia japonica</i>	South Carolina, USA	n.a.	(Rands 1922)				

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins		
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference	
7d	<i>P. parvispora</i>	23B2	15401, MYA-4058			p11		T	<i>Persea americana</i>	Puerto Rico	1960			
		61J1	144.22	22938	P2110				<i>Cinnamomum burmannii</i>	Indonesia	1922			
	<i>P. sp. ax</i>	30G9		MYA-4078			p178	A	<i>Beaucarnea</i> sp.	Germany	1991	(Scanu et al. 2014)		
		46F6						A	<i>Beaucarnea</i> sp.	Germany	1992			
	<i>P. fragariaefolia</i>	66C7	132771					A	<i>Arbutus unedo</i>	Italy	2008			
		66C8	132772					T	<i>Arbutus unedo</i>	Italy	2011			
	8a	<i>P. drechsleri</i>	46H5					A	<i>Ilex glabra</i> cv. "Shamrock"	Virginia, USA	2008	n.a.		
			61H4	135747				T	<i>Fragaria xananassa</i>	Japan	2005	(Rahman et al. 2014b)		
	8a	<i>P. nagaii</i>	61H5	133248				T	<i>Rosa</i> sp.	Japan	1968	(Rahman et al. 2014b)		
			61H9	113.19	180615	P1738			<i>Solanum lycopersicum</i>	Ireland	n.a.	(Pethybridge & Lafferty 1919)		
8a	<i>P. erythroseptica</i>	15E5					T	Soil	South Carolina, USA	1997	(Tucker 1931)			
		15E6						Soil	South Carolina, USA	1998				
	<i>P. medicaginis</i>	23J5	292.35	46724		P1087	p41	T	<i>Beta vulgaris</i> var. <i>altissima</i>	California, USA	n.a.			
		61J2	129.23			P10331		T	<i>Gerbera jamesonii</i>	New Hampshire, USA	2003			
	<i>P. pseudocryptogea</i>	23A4		MYA-3900			p37	T	<i>Solanum tuberosum</i>	Ireland	n.a.	(Pethybridge 1913)		
		28F1		44390		P1057	p124	T	<i>Medicago sativa</i>	Ohio, USA	n.a.	(Hansen & Maxwell 1991)		
	<i>P. richardiae</i>	31E8		60353, 46734		P10355	p170	T	<i>Zantedeschia</i> sp.	California, USA	1975			
		45F5	240.30	325930		P3103	p347	T	<i>Solanum marginatum</i>	Ecuador	n.a.	(Safaifarhani et al. 2015)		
	<i>P. sansomeana</i>	47H3		MYA-4455			P10811	T	<i>Zantedeschia aethiopica</i>	Japan	1989	(Buisman 1927)		
		47H4						T	<i>Zantedeschia aethiopica</i>	Japan	1989			
<i>P. trifolii</i>	47H5						A	<i>Glycine</i> sp.	Indiana, USA	n.a.				
	29B2		MYA-3901			p142	A	<i>Trifolium vesiculosum</i>	Indiana, USA	n.a.				
<i>P. aff. cryptogea</i>	62A9	117687					T	<i>Trifolium</i> sp.	Mississippi, USA	n.a.	(Hansen & Maxwell 1991)			
	22G2	308.62	15402, MYA-4161	325907		p12	T	<i>Aster</i> sp.	Mississippi, USA	n.a.				

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins		
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference	
8b	<i>P. aff. erythroseptica</i>	NP	22J4		MYA-4041		p50	n.a.	n.a.	Ohio, USA	n.a.	n.a.		
			33A1				p207	<i>Solanum tuberosum</i>	Maine, USA	2004				
	<i>P. sp. kelmania</i>	NP	24A7		MYA-4162		p102	A	<i>Abies concolor</i>	West Virginia, USA	1998	n.a.		
			31E4				p166	A	<i>Abies fraseri</i>	North Carolina, USA	2002			
	<i>P. brassicae</i>	SP	29D8	686.95		P10613		A	<i>Brassica oleracea</i>	The Netherlands	1995	(Man in't Veld et al. 2002)		
			61J8	179.87		P7517, P19521		T	<i>Brassica oleracea</i>	The Netherlands	1986			
	<i>P. cichorii</i>	SP	62A8	115029				T	<i>Cichorium intybus</i> var. <i>foliosum</i>	The Netherlands	2004	(Berrier et al. 2013)		
	<i>P. dauci</i>	SP	61E5	127102				T	<i>Daucus carota</i>	France	2009	(Berrier et al. 2013)		
			32E5						<i>Daucus carota</i>	France	2004			
			32E6						<i>Daucus carota</i>	France	2004			
8c	<i>P. lactucae</i>	SP	61F4				p194	T	<i>Lactuca sativa</i>	Greece	2001	(Berrier et al. 2013)		
			61F7					A	<i>Lactuca sativa</i>	Greece	2002			
			61F8					A	<i>Lactuca sativa</i>	Greece	2003			
	<i>P. primulae</i>	SP	29E9	620.97		P10728			<i>Primula acaulis</i>	Germany	1997	(Tomlinson 1952)		
			29F1						<i>Primula</i> sp.	The Netherlands	1998			
	<i>P. aff. brassicae-2</i>	n.a.		112968				A	<i>Allium cepa</i>	Switzerland	n.a.	n.a.		
	<i>P. aff. cichorii</i>	SP	61E3	133815				A	<i>Cichorium intybus</i> var. <i>foliosum</i>	UK	1999	n.a.		
			29E7					A	<i>Allium porrum</i>	The Netherlands	n.a.	n.a.		
	<i>P. taxon castitis</i>	SP	61E7	131246				A	<i>Fragaria xananassa</i>	Sweden	1995	(Berrier et al. 2013)		
	<i>P. taxon parsley</i>	SP	61G1					A	<i>Petroselinum crispum</i>	Greece	2006	(Berrier et al. 2013)		
		49J8	121655	MYA-3638		P10974	T	<i>Rhododendron</i> sp.	Tennessee, USA	2004	(Donahoo et al. 2006)			
<i>P. hibernalis</i>	SP	22H1	270.31	60352	36906	P6871	p115		Portugal	1931	(Carne 1925)			
		32F7	114104	56353, MYA-3896	134760	P3822	p197		Western Australia, Australia	1958				
<i>P. lateralis</i>	NP to SP	22H9		MYA-3898			p51	A	<i>Chamaecyparis lawsoniana</i>	Oregon, USA	n.a.	(Tucker & Milbrath 1942)		
		29A9		201856			p128		<i>Chamaecyparis lawsoniana</i>	California, USA	1997			
<i>P. ramorum</i>	SP	32G2							<i>Camellia japonica</i>	South Carolina, USA	n.a.	(Weirres et al. 2001)		

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Papilla ^c	Isolate identification ^d					Isolate origins					Reference
			CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	
8d	<i>P. austrocedrae</i>	SP	33F2 41B5		MYA-4073					Quercus agrifolia Austrocedrus chilensis	California, USA Argentina	n.a. n.a.	(Greslebin et al. 2007)
		<i>P. obscura</i>	SP	41B6 60E9	122911 129273	MYA-4074				Austrocedrus chilensis Soil	Argentina Germany	2005 1994	(Grünwald et al. 2012)
8	<i>P. syringae</i>		SP	60F1						Pieris sp.	Oregon, USA	2009	
		60F2							Kalmia latifolia	Oregon, USA	n.a.		
		21H9			34002			p187		Citrus sp.	California, USA	n.a.	(Klebahn 1905)
		23A6			MYA-3659			p35		n.a.	New York, USA	n.a.	
9a (cluster 9a1)	<i>P. stricta</i>	NP	58A1		MYA-4944				Irrigation water	Mississippi, USA	2012	(Yang et al. 2014a)	
			58A2						Irrigation water	Mississippi, USA	2012		
			58A3						Irrigation water	Mississippi, USA	2012		
			58A4						Irrigation water	Mississippi, USA	2012		
			40A6		MYA-4578					Irrigation water	Virginia, USA	2006	(Hong et al. 2012)
			40E3							Irrigation water	Virginia, USA	2006	
	<i>P. chrysanthemi</i>	NP	44G9						Irrigation water	Virginia, USA	2007		
			61E9						Chrysanthemum sp.	Japan	1998	(Naher et al. 2011)	
			61F1	123163					Chrysanthemum xmorifolium	Japan	2000		
	<i>P. hydrogena</i>	NP	44G8						Irrigation water	Virginia, USA	2007	(Yang et al. 2014b)	
			46A3		MYA-4919					Irrigation water	Virginia, USA	2007	
	<i>P. hydropathica</i>	NP	46A4						Irrigation water	Virginia, USA	2007		
			05D1		MYA-4460			p366		Irrigation water	Virginia, USA	2000	(Hong et al. 2010)
			5C11		MYA-4459			p365		Irrigation water	Virginia, USA	2000	
			04E4		MYA-4458			p335		Irrigation water	Virginia, USA	2000	(Hong et al. 2008)
	<i>P. macilentosa</i>	NP	23J7		MYA-4457				Irrigation water	Virginia, USA	2000		
			44E4					p108		Stream water	Virginia, USA	2007	
			58A5							Irrigation water	Mississippi, USA	2012	(Yang et al. 2014a)
	<i>P. parsiana</i>	NP	58A6						Irrigation water	Mississippi, USA	2012		
			58A7		MYA-4945					Irrigation water	Mississippi, USA	2012	
			58A8							Irrigation water	Mississippi, USA	2012	
			47C3			395329				Ficus carica	Iran	1991	(Mostowfizadeh-Ghalamfarsa et al. 2008)

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins					
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference				
9a (cluster 9a2)	<i>P. virginiana</i>	NP	40A9									A	Irrigation water	Virginia, USA	2006	(Yang & Hong 2013)	
			44G6									A	Irrigation water	Virginia, USA	2007		
			46A2		MYA-4927							T	Irrigation water	Virginia, USA	2007		
		<i>P. aff. parsiana G1</i>	NP	47C7								A	<i>Pistacia vera</i>	Iran	n.a.	n.a.	
				47C8								A	<i>Pistacia vera</i>	Iran	n.a.	n.a.	
		<i>P. aff. parsiana G2</i>	NP	47C5		395328	P8618					A	<i>Pistacia vera</i>	Iran	1992		
				47C6		395330						A	<i>Pistacia vera</i>	Iran	1992	n.a.	
		<i>P. aff. parsiana G3</i>	NP	47D5		395331						A	<i>Pistacia vera</i>	Iran	1992		
				47D8								A	<i>Pistacia vera</i>	Iran	n.a.	n.a.	
				47E1								A	<i>Pistacia vera</i>	Iran	n.a.	n.a.	
9a (cluster 9a3)	<i>P. sp. 35G4</i>	NP	35G4								A	Irrigation water	Virginia, USA	2005	n.a.		
	<i>P. sp. 38D9</i>	NP	38D9								A	<i>Dianthus caryophyllus</i>	Taiwan	n.a.	n.a.		
	<i>P. sp. 40J5</i>	NP	40J5								A	Unknown leaf in seawater	Hainan, China	n.a.	n.a.		
		<i>P. sp. cuyabensis</i>	n.a.									A	n.a.	Ecuador	1993	n.a.	
		<i>P. sp. lagoariana</i>	NP	60B4								A	n.a.	Ecuador	n.a.	n.a.	
				60B5								T	n.a.	Ecuador	n.a.	n.a.	
				33E1								A	n.a.	Ecuador	1993		
		<i>P. macrochlamydospora-G1</i>	SP	33E1										New South Wales, Australia	n.a.	(Irwin 1991)	
				31E9										New South Wales, Australia	1994		
		<i>P. macrochlamydospora-G2</i>	SP	31E9										Queensland, Australia	n.a.	(Irwin 1991)	
9b			33D5										<i>Zantedeschia aethiopica</i>	The Netherlands	1927		
		<i>P. quininea</i>	NP	45F2								A	<i>Cinchona officinalis</i>	Peru	n.a.	(Crandall 1947)	
				46C4								T	<i>Cinchona officinalis</i>	Peru	n.a.		
		<i>P. insolita</i>	NP	327E1										Waterfall water	Hainan, China	n.a.	(Ann & Ko 1980)
				38E1								T	Soil	Taiwan	1980		
	<i>P. polonica</i>	NP	40G9								A	Irrigation water	Virginia, USA	2006	(Belbahri et al. 2006)		
			43F9										Irrigation water	Virginia, USA	2007		
			49J9										Soil	Poland	2006		
			46H6								A	<i>Eucalyptus saligna</i>	New Zealand	1999	(Dick et al. 2006)		
			46H7								T	<i>Eucalyptus saligna</i>	New Zealand	1992			
			46H8								A	<i>Eucalyptus saligna</i>	New Zealand	2000			

Table 1. (Continued).

(Sub)clade ^a	Species ^b	Isolate identification ^d										Isolate origins		
		Papilla ^c	CH	CBS	ATCC	IMI	WPC	MG	Type ^e	Host or Substrate	Location	Year	Reference	
	<i>P. constricta</i>	NP to SP	55C3	125801		P10721		A	<i>Eucalyptus saligna</i>	New Zealand	1998			
								T	Soil	Western Australia, Australia	2006	(Rea et al. 2011)		
	<i>P. fallax</i>	NP	46J2			P10722		T	<i>Eucalyptus delegatensis</i>	New Zealand	1997	(Dick et al. 2006)		
			46J3					A	<i>Eucalyptus nitens</i>	New Zealand	2000			
			46J5					A	<i>Eucalyptus nitens</i>	New Zealand	2000			
10	<i>P. boehmeriae</i>	P	45F9	291.29		P10725		A	<i>Eucalyptus fastigata</i>	New Zealand	2004			
	<i>P. gallica</i>	NP	50A1	111474	180614	P6950		T	<i>Boehmeria nivea</i>	Taiwan	1927	(Sawada 1927)		
			61D5	111475		P16826		T	<i>Quercus robur</i>	France	1998	(Jung & Nechwatal 2008)		
	<i>P. gondwanensis</i>	P	22G7		MYA-3893	P16827		A	<i>Phragmites australis</i>	Germany	2004			
			45B7	140632	TSD-7			T	Stream water	Ohio, USA	n.a.	(Crous et al. 2015)		
	<i>P. intercalaris</i>	NP	48A1					A	Stream water	Virginia, USA	2007	(Yang et al. 2016)		
			49A7	140631				A	Stream water	Virginia, USA	2008			
	<i>P. kernoviae</i>	P	46C8			P10956	p390		<i>Rhododendron ponticum</i>	England, UK	2004	(Brasier et al. 2005)		
			46J6			P10681			<i>Annona cherimola</i>	New Zealand	2002			
			46J8			P10671			Soil	New Zealand	2003			
	<i>P. morindae</i>	P	62B5	121982				T	<i>Morinda citrifolia</i> var. <i>citrifolia</i>	Hawaii, USA	2005	(Neison & Abad 2010)		
n.a.	<i>P. sp. boehmeriae-like</i>	P	45F8	357.52	60173	P1378	p350	A	<i>Citrus sinensis</i>	Argentina	1939	n.a.		
	<i>P. filiii</i>	NP		135746				T	<i>Lilium</i> sp.	Japan	1987	(Rahman et al. 2015)		
outgroup	<i>Elongisporangium undulatum</i>	P		101728	337230	P10342		T	<i>Larix</i> sp.	Scotland, UK	1989	(Uzuhashi et al. 2010)		
	<i>Phytophthora vexans</i>	P		340.49	12194	P3980		T	n.a.	n.a.	n.a.	(de Cock et al. 2015)		
	<i>Halophytophthora fluviatilis</i>	P	57A9		MYA-4961			T	Stream water	Virginia, USA	2011	(Yang & Hong 2014)		

^a Molecular (sub)clade as designated in Fig. 1^b Names of taxa informally designated for the first time in this study are underlined.^c Sporangial papillation: NP = non-papillate, P = papillate, and SP = semi-papillate.^d Isolate identification abbreviations: CH, Chuanxue Hong laboratory at Virginia Polytechnic Institute and State University, Virginia Beach, VA, USA; CBS, Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; ATCC, American Type Culture Collection, Manassas, VA, USA; IMI, CABI Biosciences, UK; WPC, the World Phytophthora Genetic Resource Collection at University of California, Riverside, USA; MG, Mannon E. Gallegly laboratory at West Virginia University, USA. Local identifications of respective isolates are provided in Table S1.^e Ex-types (T) or authentic (A) isolates (designated as representative isolates by the originators of the respective species).^f n.a. = not available.

Table 2. Numbers of species and ex-types included in phylogenies for the genus *Phytophthora* in previous studies and this study.

Phylogeny in	Number of species		Number of ex-types
	Formal	Provisional	
Cooke <i>et al.</i> (2000)	49	2	9
Kroon <i>et al.</i> (2004)	46	2	18
Blair <i>et al.</i> (2008)	72	10	16
Martin <i>et al.</i> (2014)	90	17	31
This study	142	43	114

all seven phylogenetic markers from 321 isolates were sequenced in this study. Sequences of all markers from 49 isolates by Blair *et al.* (2008) were also included in the analyses. Additionally, for seven isolates, sequences of one or two genes were newly produced in this study while the remaining gene sequences were from Blair *et al.* (2008). Sequences from *P. lillii* (CBS 135746) and *P. sp. ohioensis* (ST18-37) were obtained from Rahman *et al.* (2015) and from the Phytophthora Database (Park *et al.* 2013), respectively.

Phylogenetic analyses

Concatenated sequences of all isolates were aligned using Clustal X version 2.1 (Larkin *et al.* 2007). The alignment was edited in BioEdit version 7.2.5 (Hall 1999) to trim aligned concatenated sequences to an equal size and set missing data to question marks. The edited alignment was then analyzed in jModelTest version 2.1.7 (Posada 2008) to select the most appropriate model for the following phylogenetic analyses. Maximum likelihood (ML) analysis was performed using RAxML version 8.2.0 (Stamatakis 2014) with the selected model and 1000 bootstrap replicates. Maximum parsimony (MP) analysis was conducted using PAUP version 4.0a147 (Swofford 2002) with 1000 bootstrap replicates. Bayesian analysis (BA) was performed using MrBayes version 3.2.6 (Ronquist *et al.* 2012) for two million generations with the selected model. Phylogenetic trees were viewed and edited in FigTree version 1.4.2. Alignment and phylogenetic trees from all methods have been deposited in TreeBASE (S19303).

Ancestral character state reconstructions of sporangial papillation

Information on the sporangial papillation of individual species was compiled from the literature (Erwin & Ribeiro 1996, Gallegly & Hong 2008, Kroon *et al.* 2012, Martin *et al.* 2012) with emphasis given to their respective original descriptions (Table 1). Both likelihood and parsimony ancestral state reconstructions were performed on the ML tree from the phylogenetic analyses using Mesquite version 3.03 (Maddison & Maddison 2017).

RESULTS

Sequences, alignment, and phylogenetic model

PCR amplification and sequencing was successful for almost all isolates and seven genetic markers. Failure to obtain sequences only occurred occasionally for a few isolates,

such as the EF1 α gene of *Phytophthora bilobang* (61G8), the Enl gene of *P. macrochlamydozpora* (33E1, 31E9, and 33D5), and *P. quininea* (45F2), and TigA of *P. megasperma* (62C7) (Supplementary Table 1). These failures were set as missing data in the alignment. After trimming, each isolate was represented by an 8435-bp concatenated sequence in the alignment including gaps and missing data. This included 496 bp for 60S, 1136 bp for Btub, 965 bp for EF1 α , 1169 bp for Enl, 1758 bp for HSP90, 1270 bp for 28S, and 1641 bp for TigA (TreeBASE S19303). The general time reversible nucleotide substitution model with gamma-distributed rate variation and a proportion of invariable sites (GTR+I+G) was identified by jModelTest as the most appropriate model for the phylogenetic analyses.

An expanded phylogeny including 10 clades and basal taxa

The three phylogenetic analysis methods, including ML, MP, and BA analyses (TreeBASE S19303), resulted in similar tree topologies. The topology and branch lengths of the ML inference are shown in Fig. 1. The monophyly of each of the previously recognized 10 clades was generally well supported with a few exceptions. Specifically, all clades except for clade 4 were highly supported by > 95 % bootstrap values in ML analysis and 100 % posterior probability (PP) in BA analysis (Fig. 1). Clades 1–3, 5, 7, and 10 were also highly supported by > 95 % bootstrap values in the MP analysis (Fig. 1). However, clades 6, 8, and 9, were only moderately supported with bootstrap numbers of 68, 61, and 52 in the MP analysis, respectively (Fig. 1).

As nearly half of all taxa included in this phylogeny were recently described, all clades in this phylogeny are expanded here to various extents compared to previously published phylogenies. The general structure of clades 1, 3, 5, 8 and 10 remained as previously assigned by Blair *et al.* (2008) and Martin *et al.* (2014) with additions of new species. For example, clade 1 was divided into three well-supported subclades and *P. nicotianae* was placed basal to subclades 1b and 1c (Fig. 1). Clade 8 was divided into four generally well-supported subclades, except *P. stricta*, which was placed basal to all clade 8 species (Fig. 1). New subclades were assigned to clade 2 (Fig. 2), clade 6 (Fig. 3), clade 7 (Fig. 4) and clade 9 (Fig. 5).

Several species were placed basal to other species in their respective clades. First, the cluster of *P. quercina* and *P. sp. ohioensis* was placed basal to other species of clade 4 in all three analyses. The bootstrap supports of the ML and MP analyses, and PP (percentage) for the separation of this cluster from that of *P. alticola*, *P. arenaria*, *P. megakarya*, *P. palmivora*, and *P. quercetorum* in clade 4 were only 48, 78, and 84, respectively (Fig. 1). Second, *P. lillii* was excluded from all known clades; it was placed basal to clades 1–5 and 7 (Fig. 1). Third, in clade 6, bootstrap support for the ML and MP analyses, and PP for all species except *P. asparagi* and *P. sp. sulawesiensis* were 100/100/100 (Fig. 3). This set of support numbers decreased to 99/92/100 when *P. sp. sulawesiensis* was included, and to 100/68/100 when further including *P. asparagi* (Fig. 3). Fourth, the support numbers for clade 8 species excluding *P. stricta* was 100/100/100, but 96/61/100 when *P. stricta* was included (Fig. 1). Fifth,

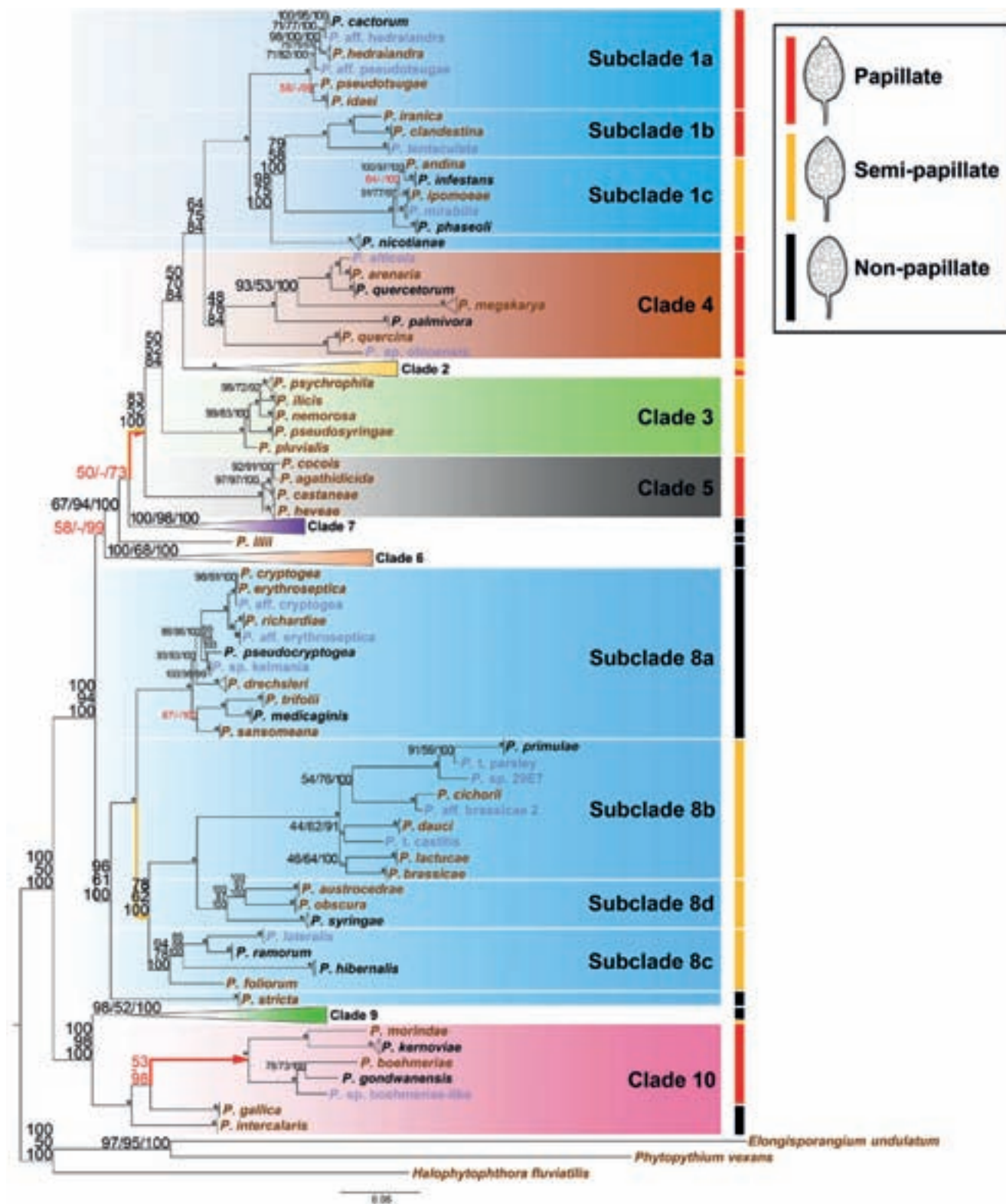


Fig. 1. A phylogeny for the genus *Phytophthora* based on concatenated sequences of seven nuclear genetic markers. Topology and branch lengths of maximum likelihood analysis are shown. Bootstrap values for maximum likelihood and maximum parsimony, and Bayesian posterior probabilities (percentages) are indicated on individual nodes and separated by a forward slash. An asterisk is used in place of nodes with unambiguous (100%) support in all three analyses. A dash is used in place of a topology from an analysis ambiguous to the other two analyses and these sets of numbers with ambiguity in one analysis are also highlighted in red. Detailed structures of clades 2, 6, 7, and 9 are shown in Figs 2–5, respectively. Species represented by ex-types and authentic isolates are written in brown and blue, respectively. Branches indicating three hypothesized evolutionary paths with all species producing papillate or semi-papillate sporangia are drawn in red or orange, respectively. Scale bar indicates number of substitutions per site.

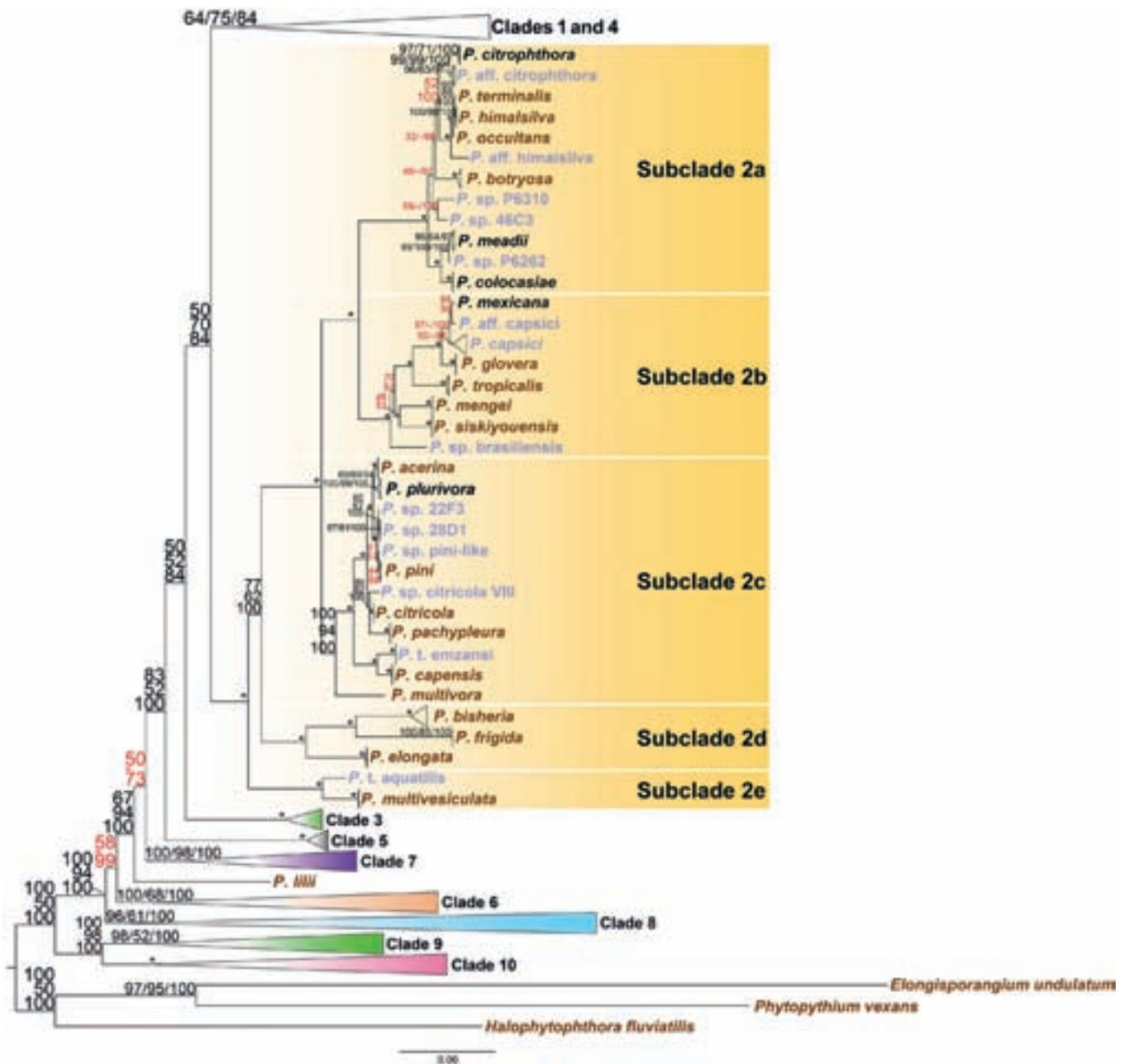


Fig. 2. Structure of *Phytophthora* clade 2 in a genus-wide phylogeny for the genus *Phytophthora* based on concatenated sequences of seven nuclear genetic markers. Topology and branch lengths of maximum likelihood analysis are shown. Bootstrap values for maximum likelihood and maximum parsimony, and Bayesian posterior probabilities (percentages) are indicated on individual nodes and separated by a forward slash. An asterisk is used in place of nodes with unambiguous (100%) support in all three analyses. A dash is used in place of a topology from an analysis ambiguous to the other two analyses and these sets of numbers with ambiguity in one analysis are also highlighted in red. Species represented by ex-types and authentic isolates are written in brown and blue, respectively. Scale bar indicates number of substitutions per site.

all papillate species in clade 10 (Table 1) formed a well-supported main cluster, while two more recently described non-papillate species, *P. gallica* and *P. intercalaris*, were placed basal to the main cluster (Fig. 1).

New subclades in clades 2, 6, 7, and 9

(a) Clade 2

In addition to the previously recognized subclades 2a and 2b, many species, such as *P. acerina*, *P. capensis*, *P. citricola*, *P. multivora*, *P. pachypleura*, *P. plurivora*, and *P. pini* in the commonly referred to "*Phytophthora citricola*-complex"

defined a new subclade 2c (Fig. 2). Furthermore, *P. bisheria*, *P. frigida*, and *P. elongata* formed new subclade 2d and the cluster of *P. multivesiculata* and *P. taxon aquatilis* formed new subclade 2e, with maximum support values in each case (Fig. 2).

(b) Clade 6

Subclade 6a included *P. gemini*, *P. humicola*, *P. inundata*, *P. rosacearum*, *P. sp. personii*, *P. sp. 48H2*, *P. sp. 62C9* and *P. taxon walnut*. The cluster of *P. rosacearum* and *P. taxon walnut* could not be separated from that represented by *P. gemini* with only moderate support values for separation

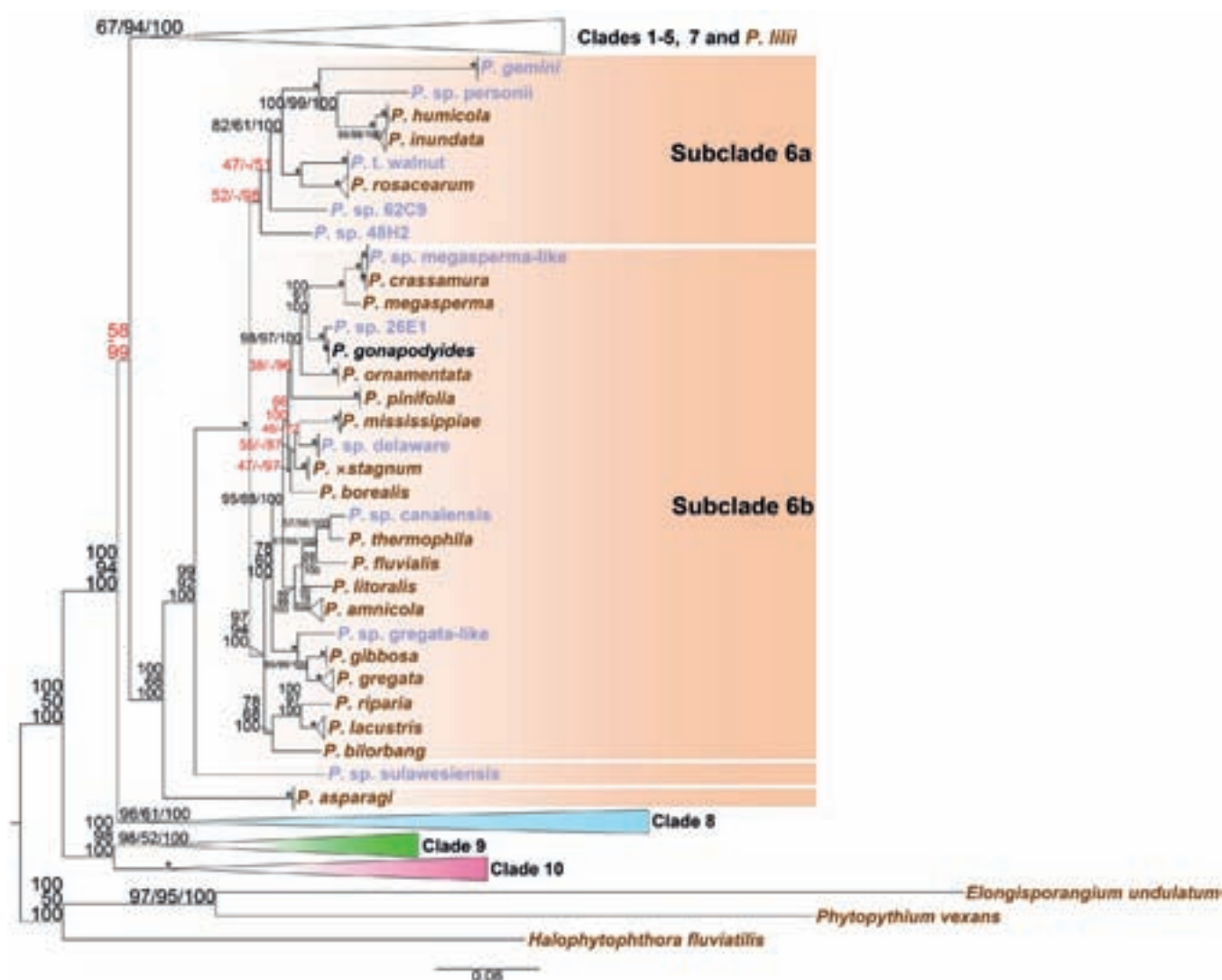


Fig. 3. Structure of *Phytophthora* clade 6 in a genus-wide phylogeny for the genus *Phytophthora* based on concatenated sequences of seven nuclear genetic markers. Topology and branch lengths of maximum likelihood analysis are shown. Bootstrap values for maximum likelihood and maximum parsimony, and Bayesian posterior probabilities (percentages) are indicated on individual nodes and separated by a forward slash. An asterisk is used in place of nodes with unambiguous (100 %) support in all three analyses. A dash is used in place of a topology from an analysis ambiguous to the other two analyses and these sets of numbers with ambiguity in one analysis are also highlighted in red. Species represented by ex-types and authentic isolates are written in brown and blue, respectively. Scale bar indicates number of substitutions per site.

(82/61/100) (Fig. 3). Isolates 62C9 and 48H2, belonging to two new species, had ambiguous placements within subclade 6a among the three analyses (Fig. 3). With approximately 20 species newly included in the present phylogeny, the previously recognized “*P. megasperma*-*P. gonapodyides* complex” (Brasier *et al.* 2003a), subclade II of clade 6 (Jung *et al.* 2011), or subclade 6b (Kroon *et al.* 2012) expanded and its separation from subclade 6a was well-supported by 100/100/100 values (Fig. 3). Within subclade 6b, separation of the cluster of *P. bilorbang*, *P. lacustris*, and *P. riparia* from the other subclade 6b species was highly supported by 97/94/100 (Fig. 3), indicating that these three species may define a new subclade, although this is not done in this study. *Phytophthora* sp. *sulawesiensis* was placed basal to other clade 6 species except for *P. asparagi*, while *P. asparagi* was basal to all other species in clade 6 (Fig. 3). *Phytophthora asparagi* was previously assigned as subclade 6c (Kroon *et al.* 2012) and subclade III of clade 6 (Jung *et al.* 2011);

considering that the support value of MP analysis was only moderate (68 %) when this single taxon was included (Fig. 3), this previous assignment as a subclade was not adopted here. In addition, in order to be consistent with subclade names in other clades, subclades 6a and 6b were used here instead of subclades I and II by Jung *et al.* (2011).

(c) Clade 7

Four subclades were distinguished in clade 7. Separation of the previously assigned subclades 7a and 7b was only moderately supported by values 71/56/100 (Fig. 4). The general structure of subclade 7a remained the same even with the addition of seven new taxa. Six of these new species, including *P. attenuata*, *P. flexuosa*, *P. formosa*, *P. intricata*, *P. xheterohybrida*, and *P. xincrassata* were recently recovered from forest soils and streamwater in Taiwan (Jung *et al.* 2017). On the other hand, *P. cinnamomi* and *P. parvispora* were separated from subclade 7b. They,

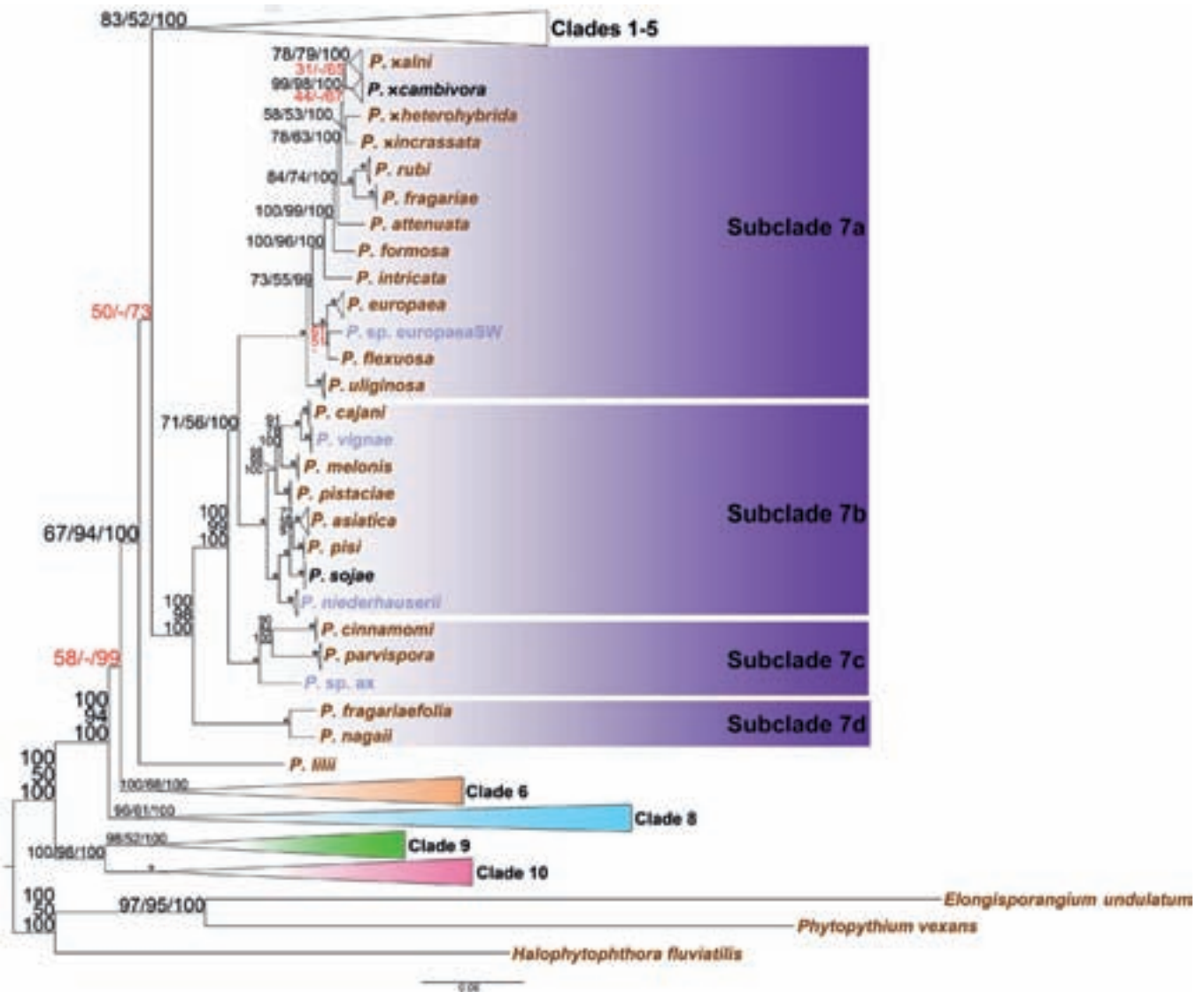


Fig. 4. Structure of *Phytophthora* clade 7 in a genus-wide phylogeny for the genus *Phytophthora* based on concatenated sequences of seven nuclear genetic markers. Topology and branch lengths of maximum likelihood analysis are shown. Bootstrap values for maximum likelihood and maximum parsimony, and Bayesian posterior probabilities (percentages) are indicated on individual nodes and separated by a forward slash. An asterisk is used in place of nodes with unambiguous (100 %) support in all three analyses. A dash is used in place of a topology from an analysis ambiguous to the other two analyses and these sets of numbers with ambiguity in one analysis are also highlighted in red. Species represented by ex-types and authentic isolates are written in brown and blue, respectively. Scale bar indicates number of substitutions per site.

along with a provisional species, *P. sp. ax* from Virginia, USA (Table 1), formed a distinct new subclade 7c (Fig. 4). The new subclade 7d, including two recently described species from Japan (Rahman *et al.* 2014b), *P. fragariaefolia* and *P. nagaii*, was placed basal to other subclades in clade 7 (Fig. 4).

(d) Clade 9

The split of clade 9 into two subclades 9a and 9b was highly supported in ML (98 %) and BA (100 %) analyses and moderately supported in the MP (52 %) analysis (Fig. 5). However, monophyly was highly supported for subclade 9b (100/100/100) but not for subclade 9a (44/-/95) (Fig. 5). Within subclade 9a, three monophyletic clusters were formed: 9a1, 9a2, and 9a3. However, support for the separation of these three clusters was moderate or ambiguous. In particular, the MP results did not produce any consistent separation of the three clusters (Fig. 5). Cluster 9a1 included many

recently described high-temperature tolerant species, such as *P. aquimorbida*, *P. chrysanthemi*, *P. hydropathica*, *P. macilentosa*, *P. parsiana*, and *P. virginiana*). The cluster of *P. macrochlamydospora* (two lineages with two isolates in each lineage, Table 1) and *P. quininea* constituted 9a2 (Fig. 5). The cluster of two other high-temperature tolerant species *P. insolita* and *P. polonica* constituted 9a3 (Fig. 5). The well-supported cluster of *P. captiosa*, *P. constricta*, and *P. fallax* was assigned as subclade 9b (Fig. 5).

Evolutionary history of sporangial papillation inferred from ancestral character state reconstructions

Sporangial papillation of individual species is indicated in Table 1 and Fig. 6. Due to the size of the cladograms, clusters including species with the same sporangial papillation within each (sub)clade were compressed in Mesquite. Both

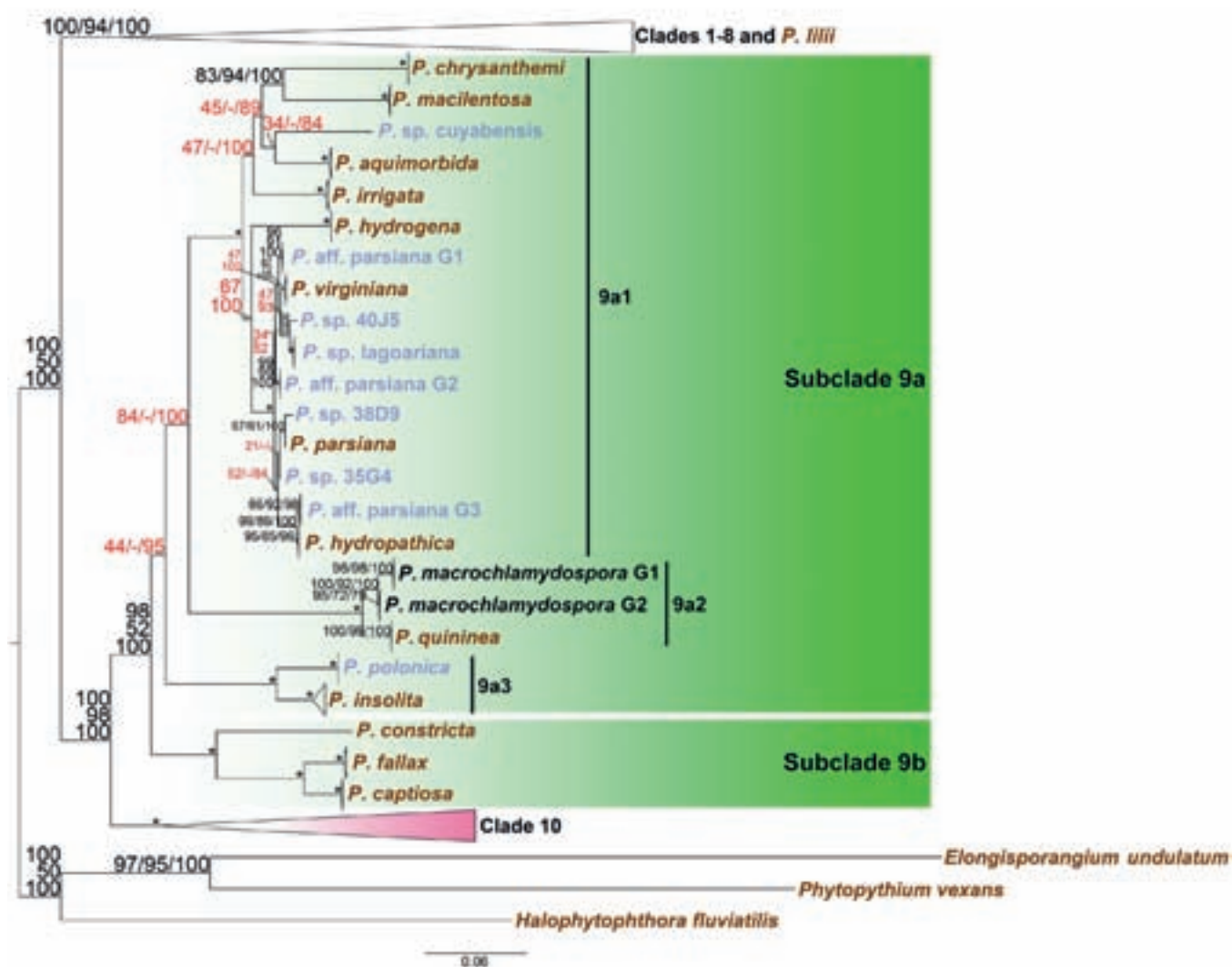


Fig. 5. Structure of *Phytophthora* clade 9 in a genus-wide phylogeny for the genus *Phytophthora* based on concatenated sequences of seven nuclear genetic markers. Topology and branch lengths of maximum likelihood analysis are shown. Bootstrap values for maximum likelihood and maximum parsimony, and Bayesian posterior probabilities (percentages) are indicated on individual nodes and separated by a forward slash. An asterisk is used in place of nodes with unambiguous (100 %) support in all three analyses. A dash is used in place of a topology from an analysis ambiguous to the other two analyses and these sets of numbers with ambiguity in one analysis are also highlighted in red. Species represented by ex-types and authentic isolates are written in brown and blue, respectively. Scale bar indicates number of substitutions per site.

likelihood and parsimony methods suggested that non-papillate is the progenitor state of *Phytophthora* species, and that semi-papillate and papillate types were derived from the non-papillate. The analyses indicated three major clusters of semi-papillate and (or) papillate species diverged from the non-papillate ancestors. First, species in clades 1 to 5 (semi-papillate or papillate) diverged from non-papillate species in clade 7 and *P. liliifolia* (Fig. 6). Second, species in subclades 8b to 8d (semi-papillate) diverged from non-papillate subclade 8a species (Fig. 6). Third, papillate clade 10 species including *P. boehmeriae*, *P. gondwanensis*, *P. kernoviae*, and *P. morindae* diverged from the non-papillate *P. gallica* and *P. intercalaris* (Fig. 6). Several species such as *P. macrochlamydospora*, *P. mississippiiae*, *P. gibbosa*, and *P. constricta* also evolved to produce partially semi-papillate sporangia (Fig. 6).

DISCUSSION

Here we presented an expanded phylogeny for the genus *Phytophthora*, encompassing 142 formally named and 43 provisionally recognized species (Table 2). In addition to this comprehensive coverage, this expanded phylogeny features over 1500 signature sequences generated from 278 ex-type and authentic isolates of 162 *Phytophthora* taxa (Supplementary Table 1). Furthermore, this study provided new insights into the evolutionary history of sporangial papillation in *Phytophthora*.

The expanded phylogeny provides a sound taxonomic framework for this agriculturally and ecologically important genus. One hundred and fourteen ex-types were included, representing 80 % of the 142 formally named species in this phylogeny. The majority of the 29 species not represented by ex-types, such as *P. gonapodyides*, *P. infestans*, *P. meadii*, *P. mexicana*, and *P. nicotianae*, were described long ago without

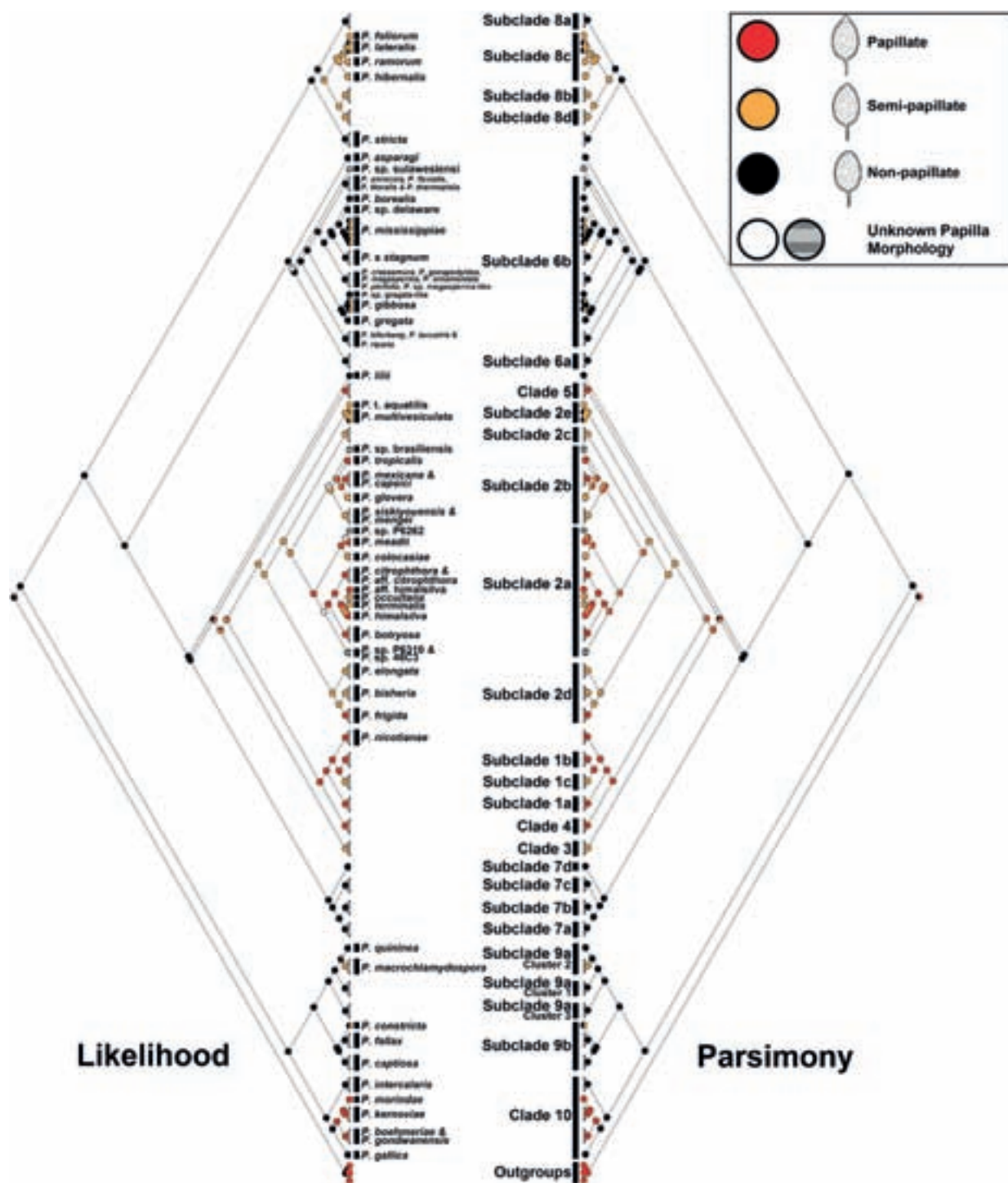


Fig. 6. Ancestral state reconstructions of sporangial papillation for the genus *Phytophthora* based on likelihood (left cladogram) and parsimony (right cladogram). Trace character history analyses were performed on the maximum likelihood phylogeny in Mesquite. Clusters including species of uniform sporangial papillation within individual (sub)clades were compressed in Mesquite.

designation of an ex-type culture. Likewise, almost all the 43 provisional species in this phylogeny were represented by authentic isolates from the originators of the respective species (Table 1 and Supplementary Table 1). This new framework will facilitate identification of new taxa in the future. As the genus continues to rapidly expand, some recently described species were not included in this study: *P. mekongensis* in subclade 2a (Puglisi et al. 2017), *P. amaranthi* in subclade 2b (Ann et al. 2016), *P. boodjera* in clade 4 (Simamora et al. 2015), *P. chlamydospora* in subclade 6b (Hansen et al.

2015), *P. uniformis* (basonym: *P. alni* subsp. *uniformis*) and *P. xmultiformis* (basonym: *P. alni* subsp. *multiformis*) in subclade 7a (Brasier et al. 2004, Husson et al. 2015), *P. pseudolactucaea* in subclade 8b (Rahman et al. 2015), and *P. prodigiosa* (Puglisi et al. 2017) and *P. pseudopolonica* (Li et al. 2017) in subclade 9a. Likewise, some informally designated species also were not included: such as *P. taxon humicola*-like, *P. taxon kwongan*, and *P. taxon rosacearum*-like in subclade 6a (Jung et al. 2011). These and other emerging species are yet to be incorporated in the overall phylogeny of the genus.

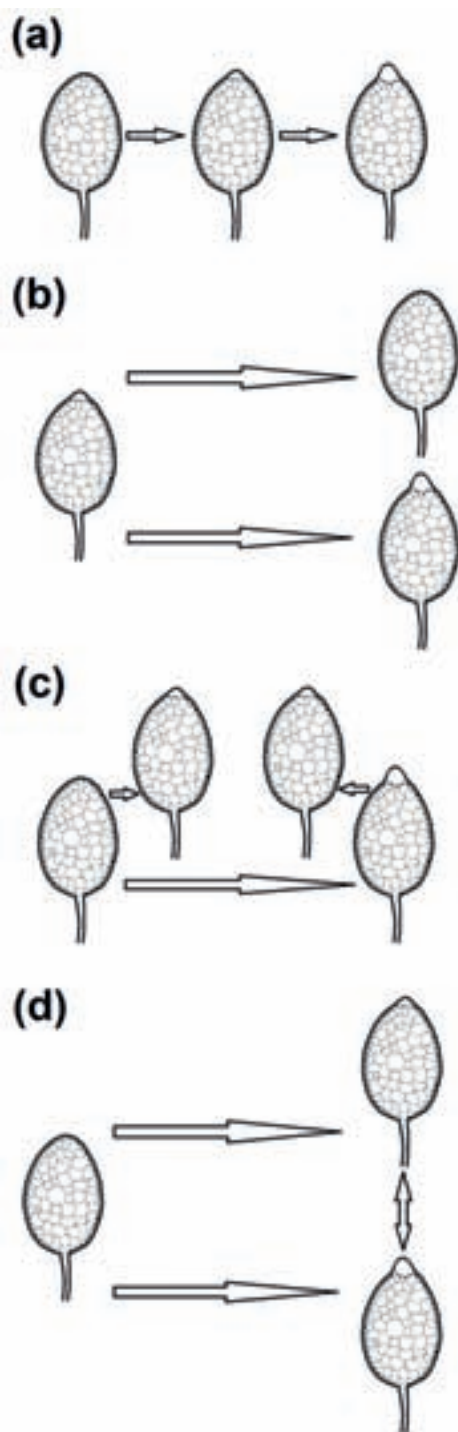


Fig. 7. Illustration of hypotheses on evolution of *Phytophthora* and associated changes in sporangial papillation: (a) species producing papillate sporangia evolved from non-papillate ancestors. Semi-papillation is considered as intermediate between non-papillation and papillation (Blackwell 1949, Cooke *et al.* 2000, Erwin & Ribeiro 1996); (b) some semi-papillate species, exemplified by *P. primulae* in the group III of Waterhouse (1963), are primitive and evolved to be non-papillate and papillate through two evolutionary paths, by Brasier (1983); (c) papillate species evolved from non-papillate ancestors. Semi-papillate species have been considered as morphological variants of papillate or non-papillate species, by Cooke *et al.* (2000); (d) a new hypothesis developed in this study that non-papillate ancestors evolved directly to either papillate or semi-papillate species. Some semi-papillate species further evolved to be papillate, or vice versa.

The generation of over 1500 signature sequences from ex-types and authentic isolates in this study will aid researchers and first responders in correctly identifying *Phytophthora* cultures to the species level. DNA sequencing of selected genetic markers has become common practice in the identification of *Phytophthora* cultures (Kang *et al.* 2010). However, it is recognized that the accuracy of culture identity determined by this approach depends on the quality of the reference sequences used – and currently many sequence deposits are erroneously identified in public repositories, including GenBank (Kang *et al.* 2010). These errors originated in sequence deposits of cultures that were identified by morphological characters alone, and compounded by those identified through sequence matches to erroneous reference sequences or by single DNA markers (Kang *et al.* 2010). In this study, 29 isolates were found associated with an erroneous or modified identity (Supplementary Table 2). For instance, isolate 29B3 in clade 1 was identified as *P. pseudotsugae* and used as a key isolate for this species by Gallegly & Hong (2008). However, its sequences were distinct from those of the *P. pseudotsugae* ex-type (ATCC 52938). In the phylogenetic tree, it was basal to the cluster of *P. cactorum* and *P. hedraiaandra*, thus its species identity was changed to *P. aff. pseudotsugae* (Fig. 1). In clade 2, isolate 26H4 was identified as *P. citrophthora* (Gallegly & Hong 2008) but sequences and phylogeny showed that it was close to but distinct from *P. citrophthora* isolates 03E5 and 26H3. It formed a cluster with isolate IMI 342898 (P10341), which was coded as *P. sp. aff. colocasiae-1* by Martin *et al.* (2014). The identity of both isolates was then changed to *P. aff. citrophthora* (Fig. 2). Similarly, in clade 8, isolate 22G2 had been identified as *P. cryptogea*, although it was distinct from the *P. cryptogea* ex-type 61H9 (CBS 113.19). In the phylogenetic tree, it was basal to the cluster of *P. cryptogea* and *P. erythroseptica*, and the species identity was consequently changed to *P. aff. cryptogea* (Fig. 1). Changes in the identifications of these isolates, including the new and original names used, are indicated in Supplementary Table 2. The changes in the naming of these isolates highlights the importance of using signature sequences from ex-type or authentic isolates as references in future culture identification. In order to facilitate this practice, the signature sequences generated from ex-types or authentic isolates in the present study are marked as '(ex-type)' or '(authentic)', respectively, under the 'isolate' section in the 'feature' table of GenBank deposits. The research, diagnostic and regulatory communities are encouraged to use these sequences as references in future culture identification.

This study provided new insights into the evolutionary history of sporangial morphology in the genus *Phytophthora*, a subject that has fascinated generations of mycologists and plant pathologists. There have been three major hypotheses regarding the development of papillation, as illustrated in Fig. 7a, b, and c, respectively. First, papillate species were considered as descendants of *Pythium*-like, non-papillate ancestors and semi-papillation has been considered as intermediate between non-papillation and papillation (Blackwell 1949, Cooke *et al.* 2000, Erwin & Ribeiro 1996). Second, some semi-papillate species, exemplified by *P. primulae* in the group III of Waterhouse (1963) are

primitive; they were suggested to have evolved to papillate and non-papillate species through two distinct evolutionary lines (Brasier 1983). Third, semi-papillate sporangia are morphological variants of papillate and non-papillate types (Cooke *et al.* 2000). Here we suggest that the non-papillate type is ancestral, and that non-papillate species could have evolved directly into either semi-papillate or papillate species (Fig. 7d). The evolution to semi-papillate species is exemplified by those in subclades 8b–d (Fig. 1), while evolution to papillate species is illustrated by *P. boehmeriae* and other papillate species in clade 10 (Fig. 1). The relationship between semi-papillate and papillate species appears to be more complicated (Fig. 7d). We also hypothesize that some semi-papillate species, such as those in subclade 1c, may have diverged from papillate ancestors, while some papillate species such as *P. frigida* may have evolved from semi-papillate ancestors of subclade 2d (Fig. 6).

These new hypotheses are supported by the results from phylogeny and ancestral state reconstructions that suggest three major evolutionary paths in sporangial papillation of *Phytophthora* species (Fig. 1). First, the ancestor of modern species in clades 1–5 evolved to be papillate or semi-papillate (Figs 1, 6) while diverging from the common non-papillate ancestor of clade 7 species (Figs 1, 6). Second, the common ancestor of species in subclades 8b–d diverged from that of subclade 8a species while acquiring semi-papillation (Figs 1, 6). Third, the common ancestor of five clade 10 species in the main cluster including *P. boehmeriae*, *P. gondwanensis*, *P. kernoviae*, *P. morindae*, and *P. sp. boehmeriae*-like, acquired papillate sporangia while diverging from two non-papillate clade 10 species, *P. gallica* and *P. intercalaris* (Figs 1, 6). Besides these three major groups of papillate or semi-papillate species, a few species may have evolved to acquire semi-papillation independently, such as *P. macrochlamydospora* in clade 9 (Fig. 6). This evolutionary process may be underway for some other species including *P. constricta*, *P. gibbosa*, and *P. mississippiiae*, which all produce both semi-papillate and non-papillate sporangia (Fig. 6). Furthermore, evolutionary reversion to partial production of non-papillate sporangia may have occurred in *P. multivesiculata* and *P. lateralis* in two semi-papillate subclades 2e and 8c, respectively (Fig. 6). However, that conclusion is uncertain due to limited and ambiguous data from species in these two subclades. Specifically, *P. lateralis* was ambiguously reported as non-papillate (Erwin & Ribeiro 1996, Gallegly & Hong 2008, Martin *et al.* 2012, Tucker & Milbrath 1942) or non- to semi-papillate (Kroon *et al.* 2012) in different studies. In subclade 2e, the only sister taxon of *P. multivesiculata*, *P. taxon aquatilis*, was provisionally described as semi-papillate, but only based on a single isolate (Hong *et al.* 2012). Evolutionary reversion in the sporangial papillation of these two species requires validation in the future. Also, more studies are warranted to analyze additional characters based on phylogenies with better clade-to-clade resolutions and provide a more comprehensive picture on the evolutionary history of *Phytophthora* species.

That a number of species were placed basal to other species in their respective clades in this expanded phylogeny presents a significant challenge to the monophyly of their

respective clades and the current 10-clade system. First, *P. stricta* was initially placed close to other species in subclade 8a based on sequences of the cytochrome *c* oxidase 1 (*cox1*) gene, but was not grouped in any ITS clade (Yang *et al.* 2014a). This species was grouped in clade 8 in our expanded phylogeny by ML and BA analyses (Fig. 1); the monophyly of this clade was only moderately supported (61 %) in the MP analysis (Fig. 1). Second, the monophyly of clade 6 including *P. asparagi* was only moderately supported (68 %) in the MP analysis (Fig. 3). Third, although the inclusion of *P. intercalaris* in clade 10 was supported with maximum values, the exact positions of this species and *P. gallica* were still unresolved since the next node was only moderately supported (53 %) in the ML analysis and ambiguous in the MP analysis (Fig. 1). Fourth, similar to the finding of Blair *et al.* (2008), support for the monophyly of clade 4 including *P. quercina* and *P. sp. ohioensis* was only moderate (48/78/84). Also, similar ambiguity in the placement of the '*P. quercina* – *P. sp. ohioensis*' cluster was observed among different phylogenetic approaches, and using different datasets including nuclear, mitochondrial, and combined nuclear and mitochondrial sequences (Martin *et al.* 2014). Fifth, this phylogeny confirmed the finding by Rahman *et al.* (2015) that *P. lillii* was not grouped in any clade of the current 10-clade system (Fig. 1). This species was not assigned as a distinct clade in our study, due to the relatively low clade-to-clade resolutions (Fig. 1). Further analyses are warranted to determine whether this unique species should be assigned as a new clade.

Although many branches in the expanded phylogeny have consistent maximum support in all three methods, some have only moderate to low or inconsistent support. These results highlight the challenges of correctly inferring the evolutionary separation of many closely related *Phytophthora* species, even when concatenated sequences from seven phylogenetic markers were used. It can be expected that as the cost of gene sequencing drops further, it will become possible to increase phylogenetic resolution among *Phytophthora* species by using concatenations of much larger numbers of genes. For example, Ye *et al.* (2016) used 293 concatenated housekeeping proteins to infer a robust phylogeny of seven fully sequenced *Phytophthora* species and confirmed that downy mildews (represented by three genome sequences) are nested within the genus *Phytophthora*, close to *Phytophthora* clade 4 (Ye *et al.* 2016). However, even with full genome sequences, ambiguity may not be completely resolved in cases where speciation has involved large populations of sexually reproducing individuals, for example, as a result of geographic separation. In these cases, there may be many sequence polymorphisms shared among separated species and these may confound the inference of a reliable phylogeny. Resolution of this level of ambiguity may require sequencing the whole genome of many isolates from the species of interest as well as using improved phylogenetic and coalescent methods.

With the number of described *Phytophthora* species increasing, recent studies have raised an important concern in the accurate detection of species boundaries using phylogenetic data (Jung & Burgess 2009, Pánek *et al.* 2016,

Safaiefarahani *et al.* 2015). One example is the status of *P. hedraiaandra* as a distinct species in subclade 1a (Pánek *et al.* 2016). As evidenced by the amplified fragment length polymorphism (AFLP) and phylogenetic analysis based on sequences of ITS, phenolic acid decarboxylase, and *cox1* genes, a recent study concluded that *P. hedraiaandra* was just one lineage of *P. cactorum*, while morphological data provided only limited information to delimitate these two species (Pánek *et al.* 2016). Also, phylogenetic analyses in this study indicated that *P. cactorum* and *P. hedraiaandra* cluster with strong support (98/100/100), and *P. aff. hedraiaandra* isolate 33F4 (previously identified as *P. hedraiaandra* Supplementary Table 2), was clustered with *P. cactorum* (Fig. 1). Phylogenies based on nuclear sequences prior to this study also supported *P. hedraiaandra* as closely related to *P. cactorum* (Blair *et al.* 2008, Martin *et al.* 2014). However, in the phylogenies based on concatenated sequences of four mitochondrial loci, and combined seven nuclear and four mitochondrial loci, *P. hedraiaandra* was basal to the cluster of *P. cactorum* and *P. pseudotsugae*, and clustered with *P. idaei*, respectively (Martin *et al.* 2014). *Phytophthora cactorum* and *P. hedraiaandra* also have very distinctive single-strand-conformation polymorphism patterns (Gallegly & Hong 2008). Apparently, more investigations are warranted to resolve the *P. cactorum* complex. Likewise, indistinct boundaries are present among species in other subclades, such as the '*P. citricola* complex' or subclade 2c (Brazee *et al.* 2017, Jung & Burgess 2009), the '*P. cryptogea* complex' in subclade 8a (Safaiefarahani *et al.* 2015, 2016) and cluster 9a1 in subclade 9a including *P. hydropathica* (Hong *et al.* 2010), *P. parsiana* (Mostowfizadeh-Ghalamfarsa *et al.* 2008), *P. virginiana* (Yang & Hong 2013) and other provisionally designated species. Accurately delimiting these closely related species within the genus remains an important task.

This expanded phylogeny has highlighted the importance and difficulty of accurately interpreting the position of hybrid *Phytophthora* species. As exemplified by *P. xalni* (Brasier *et al.* 2004, Husson *et al.* 2015), many hybrid species have been identified among emerging plant pathogens (Jung *et al.* 2017, Man in't Veld *et al.* 2012, Nirenberg *et al.* 2009). Due to the presence of multiple alleles originated from parent species in their nuclear genes, phylogenetic analysis of these hybrids based on nuclear sequences alone may not produce a robust placement. As illustrated in this phylogeny, the placement of hybrid species may be ambiguous. Specifically, in subclade 6b, support values for the placement of *P. xstagnum* and its closely related species, *P. mississippiiae*, *P. borealis*, and *P. sp. delaware* were moderate in the ML and BA analyses and ambiguous in the MP analysis (Fig. 3). Similarly, in subclade 7a, the placement of *P. xalni*, *P. xcambivora*, *P. xheterohybrida*, and *P. xincrassata* cluster was not well resolved due to ambiguous placement in the MP analysis and moderate support values in the other two analyses (Fig. 4). Adding mitochondrial sequences into the phylogenetic analyses may be a solution to this problem. However, due to the uniparental inheritance of mitochondria, the hybrids and their maternal parents are inseparable by mitochondrial sequences and their placements could conflict with nuclear analyses (Martin *et al.* 2014).

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Supplementary Table 1

Supplementary Table 1. Information of all isolates included in the phylogenetic analyses including local, international and alternative isolate numbers, species identities, hosts and substrates, origins, year, sporangial papillation and GenBank accession numbers.

(Sub)clade	Species	Isolate identification										GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β-TUB	EF1a	Enolase	HSP90	28S	TiGa			
1a	<i>P. cactorum</i>	22E6				P10194	p25	S814 (Schmittthener)	KX250369	KX250370	KX250371	KX250372	KX250373	KX250374	KX250375			
1a	<i>P. cactorum</i>	22E7	16693	021168	P0715	p6	IFO 31151, N93, NCTC 2082	EU080284	EU080285	EU080286	EU080287	EU080288	EU080289	EU080290				
1a	<i>P. cactorum</i>	22E8	16694, MYA-3653	050470	P10193	p7	N94	KX250376	KX250377	KX250378	KX250379	KX250380	KX250381	KX250382				
1a	<i>P. hedraiaandra</i>	33F3	MYA-4165			p225	MNT8 (Blanchette)	KX250383	KX250384	KX250385	KX250386	KX250387	KX250388	KX250389				
1a	<i>P. hedraiaandra</i>	38C2						KX250390	KX250391	KX250392	KX250393	KX250394	KX250395	KX250396				
1a	<i>P. hedraiaandra</i>	62A5	111725			P19523		KX250397	KX250398	KX250399	KX250400	KX250401	KX250402	KX250403				
1a	<i>P. idaei</i>	34D4	971,95	MYA-4065	313728	P6767	p220	SCRI R77, PD 94/959	EU080129	EU080130	EU080131	EU080132	EU080133	EU080134	EU080135			
1a	<i>P. idaei</i>	62A1	968,95					KX250404	KX250405	KX250406	KX250407	KX250408	KX250409	KX250410				
1a	<i>P. pseudotsugae</i>		52938	331662	P10339			EU080426	EU080427	EU080428	EU080429	EU080430	EU080431	EU080432				
1a	<i>P. aff. hedraiaandra</i>	33F4				p226	268 (Hansen)	KX250411	KX250412	KX250413	KX250414	KX250415	KX250416	KX250417				
1a	<i>P. aff. pseudotsugae</i>	29B3				p185	333 (Hansen)	KX250418	KX250419	KX250420	KX250421	KX250422	KX250423	KX250424				
1b	<i>P. clandestina</i>	32G1	347,86	58713, 60438	278933	P3943	p200	EU079866	EU079867	EU079868	EU079869	EU079870	EU079871	EU079872				
1b	<i>P. clandestina</i>	33D8	MYA-4064	287317		p215	SCR P197 CLA2	KX250425	KX250426	KX250427	KX250428	KX250429	KX250430	KX250431				
1b	<i>P. clandestina</i>	38D4				p304	HLNat 148	KX250432	KX250433	KX250434	KX250435	KX250436	KX250437	KX250438				
1b	<i>P. iranica</i>	61J4	374,72	60237	158964	P3882	p218	KX250439	KX250440	KX250441	KX250442	KX250443	KX250444	KX250445				
1b	<i>P. tentaculata</i>	29F2	552,96			P8497		EU079955	EU079956	EU079957	EU079958	EU079959	EU079960	EU079961				
1b	<i>P. tentaculata</i>	30D5						KX250446	KX250447	KX250448	KX250449	KX250450	KX250451	KX250452				
1b	<i>P. tentaculata</i>	30G8	MYA-3655					KX250453	KX250454	KX250455	KX250456	KX250457	KX250458	KX250459				
1c	<i>P. andina</i>	60A2				p460	EC3394	KX250460	KX250461	KX250462	KX250463	KX250464	KX250465	KX250466				
1c	<i>P. andina</i>	60A3				p461	EC3425	KX250467	KX250468	KX250469	KX250470	KX250471	KX250472	KX250473				
1c	<i>P. andina</i>					P13365		EU080182	EU080183	EU080184	EU080185	EU080186	EU080187	EU080188				
1c	<i>P. infestans</i>	27A8						KX250474	KX250475	KX250476	KX250477	KX250478	KX250479	KX250480				
1c	<i>P. infestans</i>					P10650		EU079625	EU079626	EU079627	EU079628	EU079629	EU079630	EU079631				
1c	<i>P. ipomoeae</i>	31B4				P10226		EU080837	EU080838	EU080839	EU080840	EU080841	EU080842	EU080843				
1c	<i>P. ipomoeae</i>	31B5	109229			P10225		PIC99169, MUCL 30219	EU080830	EU080831	EU080832	EU080833	EU080834	EU080835	EU080836			
1c	<i>P. ipomoeae</i>	31B6				P10227		EU080844	EU080845	EU080846	EU080847	EU080848	EU080849	EU080850				
1c	<i>P. mirabilis</i>	30C1	64069, MYA-4062			P3006	p145	KX250481	KX250482	KX250483	KX250484	KX250485	KX250486	KX250487				
1c	<i>P. mirabilis</i>	30C2	64070, MYA-4063			P3007	p153	KX250488	KX250489	KX250490	KX250491	KX250492	KX250493	KX250494				
1c	<i>P. phaseoli</i>	23B4				p106		KX250495	KX250496	KX250497	KX250498	KX250499	KX250500	KX250501				
1c	<i>P. phaseoli</i>	35B6						KX250502	KX250503	KX250504	KX250505	KX250506	KX250507	KX250508				
1c	<i>P. phaseoli</i>					P10145		EU080748	EU080749	EU080750	EU080751	EU080752	EU080753	EU080754				
1c	<i>P. phaseoli</i>					P10150		EU080761	EU080762	EU080763	EU080764	EU080765	EU080766	EU080767				
1	<i>P. nicotianae</i>	22F9	15410, MYA-4037			p23	N25	KX250509	KX250510	KX250511	KX250512	KX250513	KX250514	KX250515				
1	<i>P. nicotianae</i>	22G1	15409, MYA-4036			p22	N15	KX250516	KX250517	KX250518	KX250519	KX250520	KX250521	KX250522				
1	<i>P. nicotianae</i>					P10116		EU079962	EU079963	EU079964	EU079965	EU079966	EU079967	EU079968				

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β-TUB	EF1a	Enolase	HSP90	28S	TigA			
1	<i>P. nicotianae</i>				P1452			W-8	EU080503	EU080504	EU080505	EU080506	EU080507	EU080508	EU080509			
2a	<i>P. botryosa</i>	22H8		MYA-4059		p44		Tsao 62-2	KX250523	KX250524	KX250525	KX250526	KX250527	KX250528	KX250529			
2a	<i>P. botryosa</i>	46C2		26481		p384		Chee 1117	KX250530	KX250531	KX250532	KX250533	KX250534	KX250535	KX250536			
2a	<i>P. botryosa</i>	62C6	581,69		136915	P3425		Chee 1075	KX250537	KX250538	KX250539	KX250540	KX250541	KX250542	KX250543			
2a	<i>P. botryosa</i>				130422	P6945		Tan 1462	EU079934	EU079935	EU079936	EU079937	EU079938	EU079939	EU079940			
2a	<i>P. citrophthora</i>	03E5				p132		Tsao 590	KX250544	KX250545	KX250546	KX250547	KX250548	KX250549	KX250550			
2a	<i>P. citrophthora</i>	26H3				p31			KX250551	KX250552	KX250553	KX250554	KX250555	KX250556	KX250557			
2a	<i>P. colcasiae</i>	22F8		MYA-4159		p47			KX250558	KX250559	KX250560	KX250561	KX250562	KX250563	KX250564			
2a	<i>P. colcasiae</i>	35D3				p276		Uchida H1676	KX250565	KX250566	KX250567	KX250568	KX250569	KX250570	KX250571			
2a	<i>P. himalsilva</i>	61G2	128767					NP44	KX250572	KX250573	KX250574	KX250575	KX250576	KX250577	KX250578			
2a	<i>P. himalsilva</i>	61G3	128753					NP61	KX250579	KX250580	KX250581	KX250582	KX250583	KX250584	KX250585			
2a	<i>P. meadii</i>	22G5		MYA-4043		p75			KX250586	KX250587	KX250588	KX250589	KX250590	KX250591	KX250592			
2a	<i>P. meadii</i>	61J9	219,88		129185				KX250593	KX250594	KX250595	KX250596	KX250597	KX250598	KX250599			
2a	<i>P. occultans</i>	65B9	101557					PD981818110	KX250600	KX250601	KX250602	KX250603	KX250604	KX250605	KX250606			
2a	<i>P. terminalis</i>	65B8	133865					PD010104885512-1	KX250607	KX250608	KX250609	KX250610	KX250611	KX250612	KX250613			
2a	<i>P. aff. citrophthora</i>	26H4				p32		678 (Tsao)	KX250614	KX250615	KX250616	KX250617	KX250618	KX250619	KX250620			
2a	<i>P. aff. citrophthora</i>				342898	P10341			EU080384	EU080385	EU080386	EU080387	EU080388	EU080389	EU080390			
2a	<i>P. aff. himalsilva</i>	61G4	128754					NP86	KX250621	KX250622	KX250623	KX250624	KX250625	KX250626	KX250627			
2a	<i>P. sp. 46C3</i>	46C3		66767		p385		Moy 1413	KX250628	KX250629	KX250630	KX250631	KX250632	KX250633	KX250634			
2a	<i>P. sp. P6262</i>					P6262		Rajalakashmy #46	EU079887	EU079888	EU079889	EU079890	EU079891	EU079892	n.a.			
2a	<i>P. sp. P6310</i>					P6310		#066	EU080537	EU080538	EU080539	EU080540	EU080541	EU080542	EU080543			
2b	<i>P. capsici</i>	22F4		15399, MYA-4034		p8		N58	KX250635	KX250636	KX250637	KX250638	KX250639	KX250640	KX250641			
2b	<i>P. capsici</i>			46012		P0253		Romero4018	EU080851	EU080852	EU080853	EU080854	EU080855	EU080856	EU080857			
2b	<i>P. capsici</i>		121656			P10386		OP97, Lamour 51	EU079543	EU079544	EU079545	EU079546	EU079547	EU079548	EU079549			
2b	<i>P. glovera</i>	31E5				p167		Abad 11091.1	KX250642	KX250643	KX250644	KX250645	KX250646	KX250647	KX250648			
2b	<i>P. glovera</i>	62B4	121969			P11685		Abad 11099 No. 23. BPI 878720	KX250649	KX250650	KX250651	KX250652	KX250653	KX250654	KX250655			
2b	<i>P. mingei</i>	42B2		MYA-4554		p340		M218.z.1	KX250656	KX250657	KX250658	KX250659	KX250660	KX250661	KX250662			
2b	<i>P. mingei</i>	42B3		MYA-4555		p341		M220.z.1	KX250663	KX250664	KX250665	KX250666	KX250667	KX250668	KX250669			
2b	<i>P. mexicana</i>	45G4	554,88	46731	092550	P0646	p355	N317	KX250670	KX250671	KX250672	KX250673	KX250674	KX250675	KX250676			
2b	<i>P. siskiyuensis</i>	41B7	122779	MYA-4187		P15122		Hansen WA5-030403	KX250677	KX250678	KX250679	KX250680	KX250681	KX250682	KX250683			
2b	<i>P. siskiyuensis</i>	41B8						Hansen 33-2-7-0603	KX250684	KX250685	KX250686	KX250687	KX250688	KX250689	KX250690			
2b	<i>P. tropicalis</i>	22H5				p27		Tsao FP59	KX250691	KX250692	KX250693	KX250694	KX250695	KX250696	KX250697			
2b	<i>P. tropicalis</i>	35C8	434,91	76651, MYA-4218		p272		Uchida H245	KX250698	KX250699	KX250700	KX250701	KX250702	KX250703	KX250704			
2b	<i>P. aff. capsici</i>	22F5		15427, MYA-4035		p9		N14	KX250705	KX250706	KX250707	KX250708	KX250709	KX250710	KX250711			

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M. Gallegly	Other	60S	β-TUB	EF1a	Enolase	HSP90	28S	TigA			
2b	<i>P. sp. brasiliensis</i>			46705		P0630					GM11	EU080419	EU080420	EU080421	EU080422	EU080423	EU080424	EU080425
2c	<i>P. acerina</i>	61H1	133931								B057	KX250712	KX250713	KX250714	KX250715	KX250716	KX250717	KX250718
2c	<i>P. acerina</i>	61H2									B080	KX250719	KX250720	KX250721	KX250722	KX250723	KX250724	KX250725
2c	<i>P. capensis</i>	62C1	128319			P1819						KX250726	KX250727	KX250728	KX250729	KX250730	KX250731	KX250732
2c	<i>P. capensis</i>	62C2	128320			P1822						KX250733	KX250734	KX250735	KX250736	KX250737	KX250738	KX250739
2c	<i>P. capensis</i>	62C3	128321			P1823					von Broembesen 8555K2B	KX250740	KX250741	KX250742	KX250743	KX250744	KX250745	KX250746
2c	<i>P. citricola</i>	33H8	221,88	60440	21173	P0716	p396				N107	KX250747	KX250748	KX250749	KX250750	KX250751	KX250752	KX250753
2c	<i>P. citricola</i>	33J2	295,29				p375					KX250754	KX250755	KX250756	KX250757	KX250758	KX250759	KX250760
2c	<i>P. multivora</i>	55C5	124094								WAC13201	KX250775	KX250776	KX250777	KX250778	KX250779	KX250780	KX250781
2c	<i>P. pachypleura</i>	61H6									5955-2006	KX250782	KX250783	KX250784	KX250785	KX250786	KX250787	KX250788
2c	<i>P. pachypleura</i>	61H7			502404						53593-2008	KX250789	KX250790	KX250791	KX250792	KX250793	KX250794	KX250795
2c	<i>P. pachypleura</i>	61H8									105415/09	KX250796	KX250797	KX250798	KX250799	KX250800	KX250801	KX250802
2c	<i>P. pini</i>	22F1		MYA-3656			p53					KX250803	KX250804	KX250805	KX250806	KX250807	KX250808	KX250809
2c	<i>P. pini</i>	45F1		64532			p343					KX250810	KX250811	KX250812	KX250813	KX250814	KX250815	KX250816
2c	<i>P. plurivora</i>	22E9		MYA-3657			p101					KX250817	KX250818	KX250819	KX250820	KX250821	KX250822	KX250823
2c	<i>P. plurivora</i>	22F2					p52					KX250824	KX250825	KX250826	KX250827	KX250828	KX250829	KX250830
2c	<i>P. plurivora</i>	33H9	379,61									KX250831	KX250832	KX250833	KX250834	KX250835	KX250836	KX250837
2c	<i>P. sp. 22F3</i>	22F3					p33				S813	KX250845	KX250846	KX250847	KX250848	KX250849	KX250850	KX250851
2c	<i>P. sp. 28D1</i>	28D1					p119					KX250761	KX250762	KX250763	KX250764	KX250765	KX250766	KX250767
2c	<i>P. sp. 28D1</i>	28D3					p121					KX250768	KX250769	KX250770	KX250771	KX250772	KX250773	KX250774
2c	<i>P. sp. citricola VIII</i>	27D9									HHFL	KX250838	KX250839	KX250840	KX250841	KX250842	KX250843	KX250844
2c	<i>P. sp. pini-like</i>	56G1									Moorman 11-1958a	KX250852	KX250853	KX250854	KX250855	KX250856	KX250857	KX250858
2c	<i>P. taxon emzansi</i>	61F2									STE-U 6272	KX250859	KX250860	KX250861	KX250862	KX250863	KX250864	KX250865
2c	<i>P. taxon emzansi</i>	61F3									STE-U 6269	KX250866	KX250867	KX250868	KX250869	KX250870	KX250871	KX250872
2d	<i>P. bisheria</i>	29D2									Jeffers W.116	KX250873	KX250874	KX250875	KX250876	KX250877	KX250878	KX250879
2d	<i>P. bisheria</i>	31E6	122081			P10117					Cg 2.3.3	EU080741	EU080742	EU080743	EU080744	EU080745	EU080746	EU080747
2d	<i>P. bisheria</i>					P1620					Benson 411	EU080612	EU080613	EU080614	EU080615	EU080616	EU080617	EU080618
2d	<i>P. elongata</i>	33J3									SG1-1 952	KX250880	KX250881	KX250882	KX250883	KX250884	KX250885	KX250886
2d	<i>P. elongata</i>	33J4									SG1-1 2952	KX250887	KX250888	KX250889	KX250890	KX250891	KX250892	KX250893
2d	<i>P. elongata</i>	55C4	125799								VHS 13482	KX250894	KX250895	KX250896	KX250897	KX250898	KX250899	KX250900
2d	<i>P. frigida</i>	47G6									CMW19433	KX250901	KX250902	KX250903	KX250904	KX250905	KX250906	KX250907
2d	<i>P. frigida</i>	47G7									CMW19434	KX250908	KX250909	KX250910	KX250911	KX250912	KX250913	KX250914
2d	<i>P. frigida</i>	47G8									CMW20311	KX250915	KX250916	KX250917	KX250918	KX250919	KX250920	KX250921
2e	<i>P. multivesiculata</i>	29E3	545,96								PD 95/8679	EU080065	EU080066	EU080067	EU080068	EU080069	EU080070	EU080071
2e	<i>P. multivesiculata</i>	30D4									PD 95/4744	KX250922	KX250923	KX250924	KX250925	KX250926	KX250927	KX250928

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β-TUB	EF1a	Enolase	HSP90	28S	TigA			
6a	<i>P. humicola</i>	32F8	200.81	52179, MYA-4080		P3826	p198		KX251139	KX251140	KX251141	KX251142	KX251143	KX251144	KX251145			
6a	<i>P. humicola</i>	32F9				P6702	p199		KX251146	KX251147	KX251148	KX251149	KX251150	KX251151	KX251152			
6a	<i>P. inundata</i>	30J3			390121		p291	Brasier P894	KX251153	KX251154	KX251155	KX251156	KX251157	KX251158	KX251159			
6a	<i>P. inundata</i>	30J4			389751		p298	Brasier P246B	KX251160	KX251161	KX251162	KX251163	KX251164	KX251165	KX251166			
6a	<i>P. inundata</i>					P8619		PH-15-21-93	EU080202	EU080203	EU080204	EU080205	EU080206	EU080207	EU080208			
6a	<i>P. rosacearum</i>	22J9		MYA-3662			p82	Hansen 62	KX251431	KX251432	KX251433	KX251434	KX251435	KX251436	KX251437			
6a	<i>P. rosacearum</i>	41C1					p321	Hansen 63	KX251438	KX251439	KX251440	KX251441	KX251442	KX251443	KX251444			
6a	<i>P. rosacearum</i>	47J1		MYA-4456				Hansen 52, Mircetich 20-3-9	KX251445	KX251446	KX251447	KX251448	KX251449	KX251450	KX251451			
6a	<i>P. sp. 48H2</i>	48H2							KX251480	KX251481	KX251482	KX251483	KX251484	KX251485	KX251486			
6a	<i>P. sp. 62C9</i>	62C9						Jung TW65	KX251487	KX251488	KX251489	KX251490	KX251491	KX251492	KX251493			
6a	<i>P. sp. personii</i>					P11555		Abad P51.8 P38X-S	EU080312	EU080313	EU080314	EU080315	EU080316	EU080317	EU080318			
6a	<i>P. taxon walnut</i>	40A7							KX251452	KX251453	KX251454	KX251455	KX251456	KX251457	KX251458			
6a	<i>P. taxon walnut</i>	43G1							KX251459	KX251460	KX251461	KX251462	KX251463	KX251464	KX251465			
6b	<i>P. amnicola</i>	61G6			131652			DH228	KX251167	KX251168	KX251169	KX251170	KX251171	KX251172	KX251173			
6b	<i>P. amnicola</i>	62C5			133867			PD 01205336971	KX251174	KX251175	KX251176	KX251177	KX251178	KX251179	KX251180			
6b	<i>P. biloribang</i>	61G8			131653			SA262	KX251181	KX251182	n.a.	KX251183	KX251184	KX251185	KX251186			
6b	<i>P. borealis</i>	60B2		132023	MYA-4881			AKWA58.1-0708	KX251187	KX251188	KX251189	KX251190	KX251191	KX251192	KX251193			
6b	<i>P. crassamura</i>	66C9						PH094	KX251194	KX251195	KX251196	KX251197	KX251198	KX251199	KX251200			
6b	<i>P. crassamura</i>	66D1			140357			PH138	KX251201	KX251202	KX251203	KX251204	KX251205	KX251206	KX251207			
6b	<i>P. fluvialis</i>	55B6			129424				KX251208	KX251209	KX251210	KX251211	KX251212	KX251213	KX251214			
6b	<i>P. gibbosa</i>	55B7						VHS22007	KX251215	KX251216	KX251217	KX251218	KX251219	KX251220	KX251221			
6b	<i>P. gibbosa</i>	62B8			127951			VHS21998	KX251222	KX251223	KX251224	KX251225	KX251226	KX251227	KX251228			
6b	<i>P. gonapodyides</i>	21J5					p117		KX251229	KX251230	KX251231	KX251232	KX251233	KX251234	KX251235			
6b	<i>P. gonapodyides</i>	34A8			554.67	60351	P6872		KX251236	KX251237	KX251238	KX251239	KX251240	KX251241	KX251242			
6b	<i>P. gregata</i>	55B8						VHS21992	KX251243	KX251244	KX251245	KX251246	KX251247	KX251248	KX251249			
6b	<i>P. gregata</i>	62B9			127952			VHS21962	KX251250	KX251251	KX251252	KX251253	KX251254	KX251255	KX251256			
6b	<i>P. lacustris</i>	61D6						UKN-Ph1	KX251257	KX251258	KX251259	KX251260	KX251261	KX251262	KX251263			
6b	<i>P. lacustris</i>	61D8						UKN-Ph15	KX251264	KX251265	KX251266	KX251267	KX251268	KX251269	KX251270			
6b	<i>P. lacustris</i>	61E1						UKN-Ph33	KX251271	KX251272	KX251273	KX251274	KX251275	KX251276	KX251277			
6b	<i>P. lacustris</i>				389725	P10337		PIPHAS-P566	EU080530	EU080531	EU080532	EU080533	EU080534	EU080535	EU080536			
6b	<i>P. littoralis</i>	55B9			127953			VHS 20763	KX251278	KX251279	KX251280	KX251281	KX251282	KX251283	KX251284			
6b	<i>P. megasperma</i>	62C7			402.72	58817	P3599		KX251285	KX251286	KX251287	KX251288	KX251289	KX251290	n.a.			
6b	<i>P. mississippiiae</i>	57J1							KX251291	KX251292	KX251293	KX251294	KX251295	KX251296	KX251297			
6b	<i>P. mississippiiae</i>	57J2							KX251298	KX251299	KX251300	KX251301	KX251302	KX251303	KX251304			
6b	<i>P. mississippiiae</i>	57J3				MYA-4946			KX251305	KX251306	KX251307	KX251308	KX251309	KX251310	KX251311			

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers				
		Local (CH)	CBS	ATCC	IMI	WPC	M. Gallegly	Other	60S	β -TUB	EF1a	Enlase	HSP90	28S	TigA	
7a	<i>P. uliginosa</i>	62A4	109055			P10328		Jung IFB-ULI 2	EU079692	EU079693	EU079694	EU079695	EU079696	EU079697	EU079698	
7a	<i>P. xalni</i>	32J6	392317	MYA-4081		p205		P834	KX251574	KX251575	KX251576	KX251577	KX251578	KX251579	KX251580	
7a	<i>P. xalni</i>	32J7	392318			p206		P883	KX251581	KX251582	KX251583	KX251584	KX251585	KX251586	KX251587	
7a	<i>P. xalni</i>	47A7			392314			P772	KX251588	KX251589	KX251590	KX251591	KX251592	KX251593	KX251594	
7a	<i>P. xalni</i>	47A8						WMV20010932	KX251595	KX251596	KX251597	KX251598	KX251599	KX251600	KX251601	
7a	<i>P. xcambivora</i>	22F6		46719, MYA-4076		p64		Tsao P592	KX251494	KX251495	KX251496	KX251497	KX251498	KX251499	KX251500	
7a	<i>P. xcambivora</i>	26F8		MYA-4075		p38		NY216	KX251501	KX251502	KX251503	KX251504	KX251505	KX251506	KX251507	
7a	<i>P. xheterohybrida</i>	67C1						Jung TW30	KX251637	KX251638	KX251639	KX251640	KX251641	KX251642	KX251643	
7a	<i>P. xincrassata</i>	67C2						Jung TW43m5	KX251644	KX251645	KX251646	KX251647	KX251648	KX251649	KX251650	
7a	<i>P. sp. europaeaSW</i>	33F7				p229		BM4/6 (Balci)	KX251602	KX251603	KX251604	KX251605	KX251606	KX251607	KX251608	
7b	<i>P. asiatica</i>	45G1		90455		p352		Ho Lu625	KX251651	KX251652	KX251653	KX251654	KX251655	KX251656	KX251657	
7b	<i>P. asiatica</i>	46C6		56194		p388		Ho 523 (P31)	KX251658	KX251659	KX251660	KX251661	KX251662	KX251663	KX251664	
7b	<i>P. asiatica</i>	61H3						NBRC109140, Tokui-1	KX251665	KX251666	KX251667	KX251668	KX251669	KX251670	KX251671	
7b	<i>P. cajani</i>	33D9				p214		DCSCR231	KX251672	KX251673	KX251674	KX251675	KX251676	KX251677	KX251678	
7b	<i>P. cajani</i>	45F6		44389		p348		Erwin P4	KX251679	KX251680	KX251681	KX251682	KX251683	KX251684	KX251685	
7b	<i>P. cajani</i>	45F7		44388		p349		Erwin P2	KX251686	KX251687	KX251688	KX251689	KX251690	KX251691	KX251692	
7b	<i>P. melonis</i>	32F6		MYA-4079		p196			KX251693	KX251694	KX251695	KX251696	KX251697	KX251698	KX251699	
7b	<i>P. melonis</i>	41B4				p318		Banhashemi PH.6.42.92	KX251700	KX251701	KX251702	KX251703	KX251704	KX251705	KX251706	
7b	<i>P. melonis</i>	45F3		582,69				Ho H513	KX251707	KX251708	KX251709	KX251710	KX251711	KX251712	KX251713	
7b	<i>P. niederhauserii</i>	01D5				p312			KX251714	KX251715	KX251716	KX251717	KX251718	KX251719	KX251720	
7b	<i>P. niederhauserii</i>	23J6		MYA-4163		p57		Ribeiro Israel 2	KX251721	KX251722	KX251723	KX251724	KX251725	KX251726	KX251727	
7b	<i>P. niederhauserii</i>	31E7				p169		Abad 5212	KX251728	KX251729	KX251730	KX251731	KX251732	KX251733	KX251734	
7b	<i>P. pisi</i>	60A4						Heyman 97603	KX251735	KX251736	KX251737	KX251738	KX251739	KX251740	KX251741	
7b	<i>P. pisi</i>	60A5						Heyman 2150	KX251742	KX251743	KX251744	KX251745	KX251746	KX251747	n.a.	
7b	<i>P. pistaciae</i>	33D6		MYA-4082		p216		DCSCR533, S16	KX251748	KX251749	KX251750	KX251751	KX251752	KX251753	KX251754	
7b	<i>P. pistaciae</i>	41A9				p314		Banhashemi PH.6.44.93	KX251755	KX251756	KX251757	KX251758	KX251759	KX251760	KX251761	
7b	<i>P. sojiae</i>	22D8		312,62		p19		N9	KX251762	KX251763	KX251764	KX251765	KX251766	KX251767	KX251768	
7b	<i>P. sojiae</i>	28F9				p236		Tyler P6497	KX251769	KX251770	KX251771	KX251772	KX251773	KX251774	KX251775	
7b	<i>P. vignae</i>	45G6		46735		p357		Purs 901, Zentmeyer P.606,	KX251776	KX251777	KX251778	KX251779	KX251780	KX251781	KX251782	
7b	<i>P. vignae</i>	45G9		64832		p379			KX251783	KX251784	KX251785	KX251786	KX251787	KX251788	KX251789	
7b	<i>P. vignae</i>	46C1		112,76		p380			KX251790	KX251791	KX251792	KX251793	KX251794	KX251795	KX251796	
7c	<i>P. cinnamomi</i>	23B1		15400, MYA-4057		p10		N311	KX251797	KX251798	KX251799	KX251800	KX251801	KX251802	KX251803	
7c	<i>P. cinnamomi</i>	23B2		15401, MYA-4058		p11		N33	KX251804	KX251805	KX251806	KX251807	KX251808	KX251809	KX251810	

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification					GenBank accession numbers								
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β -TUB	EF1a	Enolase	HSP90	28S	TigA
7c	<i>P. cinnamomi</i>	61J1	144,22	46671	22938	P2110			KX251811	KX251812	KX251813	KX251814	KX251815	KX251816	KX251817
7c	<i>P. parvispora</i>	30G9		MYA-4078		p178	Verres BBA65507		KX251818	KX251819	KX251820	KX251821	KX251822	KX251823	KX251824
7c	<i>P. parvispora</i>	46F6					Verres BBA65508		KX251825	KX251826	KX251827	KX251828	KX251829	KX251830	KX251831
7c	<i>P. parvispora</i>	66C7	132771				Scanu PH028		KX251832	KX251833	KX251834	KX251835	KX251836	KX251837	KX251838
7c	<i>P. parvispora</i>	66C8	132772				Scanu PH072		KX251839	KX251840	KX251841	KX251842	KX251843	KX251844	KX251845
7c	<i>P. sp. ax</i>	46H5							KX251846	KX251847	KX251848	KX251849	KX251850	KX251851	KX251852
7d	<i>P. fragariaefolia</i>	61H4	135747				NBRC109709, CH05NSU11, MAFF244058		KX251853	KX251854	KX251855	KX251856	KX251857	KX251858	KX251859
7d	<i>P. nagaii</i>	61H5	133248				NBRC109131, CH04PHR12, MAFF244047		KX251860	KX251861	KX251862	KX251863	KX251864	KX251865	KX251866
8a	<i>P. cryptogea</i>	61H9	113,19		180615	P1738	BPIC 1189		KX251867	KX251868	KX251869	KX251870	KX251871	KX251872	KX251873
8a	<i>P. drechsleri</i>	15E5					Jeffers AF.021		KX251874	KX251875	KX251876	KX251877	KX251878	KX251879	KX251880
8a	<i>P. drechsleri</i>	15E6					Jeffers D.200		KX251881	KX251882	KX251883	KX251884	KX251885	KX251886	KX251887
8a	<i>P. drechsleri</i>	23J5	292,35	46724		P1087			KX251888	KX251889	KX251890	KX251891	KX251892	KX251893	KX251894
8a	<i>P. drechsleri</i>	61J2	129,23		34684	P1693	VKM F-1807		EU079506	EU079507	EU079508	EU079509	EU079510	EU079511	EU079512
8a	<i>P. erythrosetica</i>	23A4							KX251895	KX251896	KX251897	KX251898	KX251899	KX251900	KX251901
8a	<i>P. medicaginis</i>	28F1							KX251902	KX251903	KX251904	KX251905	KX251906	KX251907	KX251908
8a	<i>P. medicaginis</i>	31E8							KX251909	KX251910	KX251911	KX251912	KX251913	KX251914	KX251915
8a	<i>P. pseudocryptogea</i>	45F5	240,30	60353, 46734	325930	P10811	63689		EU080626	EU080627	EU080628	EU080629	EU080630	EU080631	n.a.
8a	<i>P. richardiae</i>	47H3					CH 89-1, Suguro 3-3		KX251916	KX251917	KX251918	KX251919	KX251920	KX251921	KX251922
8a	<i>P. richardiae</i>	47H4					Zentmeyer P642		KX251923	KX251924	KX251925	KX251926	KX251927	KX251928	KX251929
8a	<i>P. richardiae</i>	47H5					CH89-19, Kamazaki1		EU080496	EU080497	EU080498	EU080499	EU080500	EU080501	EU080502
8a	<i>P. sansomeana</i>	29B2					Hansen 1819B		KX251930	KX251931	KX251932	KX251933	KX251934	KX251935	KX251936
8a	<i>P. sansomeana</i>	62A9	117687				Hansen 2323		KX251937	KX251938	KX251939	KX251940	KX251941	KX251942	KX251943
8a	<i>P. sansomeana</i>	22G2	308,62	15402, MYA-4161	325907		Hansen 92-84		KX251944	KX251945	KX251946	KX251947	KX251948	KX251949	KX251950
8a	<i>P. trifolii</i>	22J4					Hansen 33		KX251951	KX251952	KX251953	KX251954	KX251955	KX251956	KX251957
8a	<i>P. aff. erythrosetica</i>	33A1					Hansen 32		KX251958	KX251959	KX251960	KX251961	KX251962	KX251963	KX251964
8a	<i>P. aff. erythrosetica</i>	24A7					N57		KX251965	KX251966	KX251967	KX251968	KX251969	KX251970	KX251971
8a	<i>P. sp. kelmania</i>	31E4					S720		KX251972	KX251973	KX251974	KX251975	KX251976	KX251977	KX251978
8a	<i>P. sp. kelmania</i>	29D8	686,95				Lambert 2004S-1		KX251979	KX251980	KX251981	KX251982	KX251983	KX251984	KX251985
8a	<i>P. sp. kelmania</i>	29D8	686,95				Abad 02-119A, Ph4-1		KX251986	KX251987	KX251988	KX251989	KX251990	KX251991	KX251992
8b	<i>P. brassicae</i>	29D8	686,95				Man in 't Veld PD 95/691KX251993		EU079605	EU079606	EU079607	EU079608	EU079609	EU079610	EU079611
8b	<i>P. brassicae</i>	29D8	686,95						KX251994	KX251995	KX251996	KX251997	KX251998	KX251999	KX251999

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β-TUB	EF1a	Enlase	HSP90	28S	TigA			
8b	<i>P. brassicae</i>	61J8	179,87			P7517, P19521			KX252000	KX252001	KX252002	KX252003	KX252004	KX252005	KX252006			
8b	<i>P. cichorii</i>	62A8	115029					KX252007	KX252008	KX252009	KX252010	KX252011	KX252012	KX252013				
8b	<i>P. dauci</i>	61E5	127102			BorfSP370		KX252014	KX252015	KX252016	KX252017	KX252018	KX252019	KX252020				
8b	<i>P. dauci</i>	32E5				Breton 134-1		KX252021	KX252022	KX252023	KX252024	KX252025	KX252026	KX252027				
8b	<i>P. dauci</i>	32E6				Breton 143-1		KX252028	KX252029	KX252030	KX252031	KX252032	KX252033	KX252034				
8b	<i>P. dauci</i>	32E7				Breton 148-1	p194	KX252035	KX252036	KX252037	KX252038	KX252039	KX252040	KX252041				
8b	<i>P. lactucae</i>	61F4				BPIC 1985		KX252042	KX252043	KX252044	KX252045	KX252046	KX252047	KX252048				
8b	<i>P. lactucae</i>	61F7				BPIC 1988		KX252049	KX252050	KX252051	KX252052	KX252053	KX252054	KX252055				
8b	<i>P. lactucae</i>	61F8				BPIC 1991		KX252056	KX252057	KX252058	KX252059	KX252060	KX252061	KX252062				
8b	<i>P. primulae</i>	29E9	620,97			Man in 't Veld PD97/875	p286	KX252063	KX252064	KX252065	KX252066	KX252067	KX252068	KX252069				
8b	<i>P. primulae</i>	29F1				Man in 't Veld PD98/87201	p287	KX252070	KX252071	KX252072	KX252073	KX252074	KX252075	KX252076				
8b	<i>P. aff. brassicae-2</i>		112968			Bolay #84182	P6207	EU079880	EU079881	EU079882	EU079883	EU079884	EU079885	EU079886				
8b	<i>P. aff. cichorii</i>	61E3	133815			SCRACE5388		KX252077	KX252078	KX252079	KX252080	KX252081	KX252082	KX252083				
8b	<i>P. sp. 29E7</i>	29E7				Man in 't Veld PD92/214		KX252091	KX252092	KX252093	KX252094	KX252095	KX252096	KX252097				
8b	<i>P. taxon castitis</i>	61E7	131246			CH112		KX252098	KX252099	KX252100	KX252101	KX252102	KX252103	KX252104				
8b	<i>P. taxon parsley</i>	61G1				BPIC 2584		KX252105	KX252106	KX252107	KX252108	KX252109	KX252110	KX252111				
8c	<i>P. foliorum</i>	49J8	121655	MYA-3638		LT192		KX252112	KX252113	KX252114	KX252115	KX252116	KX252117	KX252118				
8c	<i>P. hibernalis</i>	22H1	270,31	60352	036906	BPIC 1137	p115	KX252119	KX252120	KX252121	KX252122	KX252123	KX252124	KX252125				
8c	<i>P. hibernalis</i>	32F7	114104	56353, MYA-3896	134760	Ho H17.1, WA648	p197	KX252126	KX252127	KX252128	KX252129	KX252130	KX252131	KX252132				
8c	<i>P. lateralis</i>	22H9		MYA-3898		CM P631	p51	KX252133	KX252134	KX252135	KX252136	KX252137	KX252138	KX252139				
8c	<i>P. lateralis</i>	29A9		201856		Hansen 366	p128	KX252140	KX252141	KX252142	KX252143	KX252144	KX252145	KX252146				
8c	<i>P. ramorum</i>	32G2				Jeffers 04-4398		KX252147	KX252148	KX252149	KX252150	KX252151	KX252152	KX252153				
8c	<i>P. ramorum</i>	33F2				Garbelotto Pr-102		KX252154	KX252155	KX252156	KX252157	KX252158	KX252159	KX252160				
8d	<i>P. austrocedrae</i>	41B5		MYA-4073		Greslebin 195		KX252161	KX252162	KX252163	KX252164	KX252165	KX252166	KX252167				
8d	<i>P. austrocedrae</i>	41B6	122911	MYA-4074		Greslebin 203		KX252168	KX252169	KX252170	KX252171	KX252172	KX252173	KX252174				
8d	<i>P. obscura</i>	60E9	129273			BBA 2/94-11B		KX252175	KX252176	KX252177	KX252178	KX252179	KX252180	KX252181				
8d	<i>P. obscura</i>	60F1				JP-09-059 HH-B		KX252182	KX252183	KX252184	KX252185	KX252186	KX252187	KX252188				
8d	<i>P. obscura</i>	60F2				P-09-011		KX252189	KX252190	KX252191	KX252192	KX252193	KX252194	KX252195				
8d	<i>P. syringae</i>	21H9		34002		P0649	p187	KX252196	KX252197	KX252198	KX252199	KX252200	KX252201	KX252202				
8d	<i>P. syringae</i>	23A6		MYA-3659			p35	KX252203	KX252204	KX252205	KX252206	KX252207	KX252208	KX252209				
8	<i>P. stricta</i>	58A1		MYA-4944				KX252210	KX252211	KX252212	KX252213	KX252214	KX252215	KX252216				
8	<i>P. stricta</i>	58A2						KX252217	KX252218	KX252219	KX252220	KX252221	KX252222	KX252223				
8	<i>P. stricta</i>	58A3						KX252224	KX252225	KX252226	KX252227	KX252228	KX252229	KX252230				
8	<i>P. stricta</i>	58A4						KX252231	KX252232	KX252233	KX252234	KX252235	KX252236	KX252237				

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification						GenBank accession numbers						
		Local (CH)	CBS	ATCC	IMI	WPC	M. Gallegly Other	60S	β-TUB	EF1a	Enlase	HSP90	28S	TigA
9a (cluster 9a1)	<i>P. sp. 38D9</i>	38D9					Ko WK	KX252488	KX252489	KX252490	KX252491	KX252492	KX252493	KX252494
9a (cluster 9a1)	<i>P. sp. 40J5</i>	40J5				Ho Boao 3-2		KX252495	KX252496	KX252497	KX252498	KX252499	KX252500	KX252501
9a (cluster 9a1)	<i>P. sp. cuyabensis</i>				P8213	103		EU080664	EU080665	EU080666	EU080667	EU080668	EU080669	EU080331
9a (cluster 9a1)	<i>P. sp. lagoariana</i>	60B4			P8220	148		EU080358	KX252502	EU080359	EU080360	EU080361	EU080362	EU080363
9a (cluster 9a1)	<i>P. sp. lagoariana</i>	60B5			P8217	145		KX252503	KX252504	KX252505	KX252506	KX252507	KX252508	KX252509
9a (cluster 9a1)	<i>P. sp. lagoariana</i>				P8223	155		EU080364	EU080365	EU080366	EU080367	EU080368	EU080369	EU080370
9a (cluster 9a2)	<i>P. macrochlamydozona-G133E1</i>				P10264	UQ778, DAR52299		KX252510	KX252511	KX252512	n.a.	KX252513	KX252514	KX252515
9a (cluster 9a2)	<i>P. macrochlamydozona-G1</i>				P10267	UQ1163, T10446 (QDP)		EU080004	EU080005	EU080006	EU080007	EU080008	EU080009	EU080010
9a (cluster 9a2)	<i>P. macrochlamydozona-G231E9</i>				P8017	p171		EU080658	EU080659	EU080660	n.a.	EU080661	EU080662	EU080663
9a (cluster 9a2)	<i>P. macrochlamydozona-G233D5</i>	240.30	60353			351473	Cooke SCP551	KX252516	KX252517	KX252518	n.a.	KX252519	KX252520	KX252521
9a (cluster 9a2)	<i>P. quinea</i>	45F2	56964			340618		EU080107	EU080108	EU080109	n.a.	KX252522	EU080110	KX252523
9a (cluster 9a2)	<i>P. quinea</i>	46C4	46733			p386	CMW 31062, Crandall No. C-66, Ho H35.1	EU079802	EU079803	EU079804	KX252524	EU079805	EU079806	EU079807
9a (cluster 9a3)	<i>P. insolita</i>	27E1	MYA-4077			p123	CMW 31062, Crandall No. C-67	KX252525	KX252526	KX252527	KX252528	KX252529	KX252530	KX252531
9a (cluster 9a3)	<i>P. insolita</i>	38E1	38789			288805	Ho HW	EU080175	EU080176	EU080177	EU080178	EU080179	EU080180	EU080181
9a (cluster 9a3)	<i>P. insolita</i>						Ko TA5131	EU080209	EU080210	EU080211	EU080212	EU080213	EU080214	EU080215
9a (cluster 9a3)	<i>P. polonica</i>	40G9			P6703		= cv0609-129	KX252532	KX252533	KX252534	KX252535	KX252536	KX252537	KX252538
9a (cluster 9a3)	<i>P. polonica</i>	43F9					= bc0701-163	KX252539	KX252540	KX252541	KX252542	KX252543	KX252544	KX252545
9a (cluster 9a3)	<i>P. polonica</i>	49J9			P15005		GD7e	EU080256	KX252546	EU080258	EU080259	EU080260	EU080261	EU080262
9b	<i>P. captiosa</i>	46H6					NZFS 310.37	KX252547	KX252548	KX252549	KX252550	KX252551	KX252552	KX252553
9b	<i>P. captiosa</i>	46H7			P10719		NZFS 310C	EU079658	EU079659	EU079660	EU079661	EU079662	EU079663	EU079664
9b	<i>P. captiosa</i>	46H8					NZFS 430	KX252554	KX252555	KX252556	KX252557	KX252558	KX252559	KX252560
9b	<i>P. captiosa</i>				P10721		NZFS 310.35	EU079665	EU079666	EU079667	EU079668	EU079669	EU079670	EU079671
9b	<i>P. constricta</i>	55C3	125801				VHS 16130	KX252561	KX252562	KX252563	KX252564	KX252565	KX252566	KX252567
9b	<i>P. fallax</i>	46J2					NZFS 310L	KX252568	KX252569	KX252570	KX252571	KX252572	KX252573	KX252574
9b	<i>P. fallax</i>	46J3					NZFS 450	KX252575	KX252576	KX252577	KX252578	KX252579	KX252580	KX252581
9b	<i>P. fallax</i>	46J5					NZFS 448	KX252582	KX252583	KX252584	KX252585	KX252586	KX252587	KX252588
9b	<i>P. fallax</i>				P10725		NZFS 1719	EU080034	EU080035	EU080036	EU080037	EU080038	EU080039	EU080040
10	<i>P. boehmeriae</i>	45F9	291.29			P6950	GAL1, MB497405	EU080161	EU080162	EU080163	EU080164	EU080165	EU080166	EU080167
10	<i>P. gallica</i>	50A1	111474			P16826		KX252589	KX252590	KX252591	KX252592	KX252593	KX252594	KX252595
10	<i>P. gallica</i>	61D5	111475			P16827	GAL2	KX252596	KX252597	KX252598	KX252599	KX252600	KX252601	KX252602
10	<i>P. gondwanensis</i>	22G7		MYA-3893			S833	KX252603	KX252604	KX252605	KX252606	KX252607	KX252608	KX252609
10	<i>P. intercalaris</i>	45B7	140632	TSD-7				KX252610	KX252611	KX252612	KX252613	KX252614	KX252615	KX252616
10	<i>P. intercalaris</i>	48A1						KX252617	KX252618	KX252619	KX252620	KX252621	KX252622	KX252623
10	<i>P. intercalaris</i>	49A7	140631					KX252624	KX252625	KX252626	KX252627	KX252628	KX252629	KX252630

Supplementary Table 1. (Continued).

(Sub)clade	Species	Isolate identification										GenBank accession numbers					
		Local (CH)	CBS	ATCC	IMI	WPC	M.Gallegly	Other	60S	β -TUB	EF1a	Enolase	HSP90	28S	TigA		
10	<i>P. kernoviae</i>	46C8				P10956	p390	CSL 2286, PRI 712	EU080041	EU080042	EU080043	EU080044	EU080045	EU080046	KX252631		
10	<i>P. kernoviae</i>	46J6				P10681		ICMP 14761, Hill LYN701	EU079645	EU079646	EU079647	EU079648	EU079649	EU079650	EU079651		
10	<i>P. kernoviae</i>	46J8				P10671		ICMP 15082	EU080027	EU080028	EU080029	EU080030	EU080031	EU080032	KX252632		
10	<i>P. morindae</i>	62B5	121982					Nelson Ph697, P238, BPI 878721	KX252633	KX252634	KX252635	KX252636	KX252637	KX252638	KX252639		
10	<i>P. sp. boehmeriae-like</i>	45F8	357,52	60173	32199	P1378	p350		KX252640	KX252641	KX252642	KX252643	KX252644	KX252645	KX252646		
n.a.	<i>P. lillii</i>		135746					EL-8701, NBRC 32174, AB856779 MAFF 237500	AB856779	AB856782	AB856788	AB856791	AB856794	AB856797	AB856800		
outgroup	<i>Elongisporangium undulatum</i>		101728			337230	P10342		EU080440	EU080441	EU080442	n.a.	EU080443	EU080444	EU080445		
outgroup	<i>Phytophthium vexans</i>		340,49	12194		P3980		CMI 22 044	EU080483	EU080484	EU080485	n.a.	EU080486	EU080487	EU080488		
outgroup	<i>Halophytophthora fluvialilis</i>	57A9		MVA-4961					KX252668	KX252669	KX252670	KX252671	KX252672	KX252673	KX252674		

Supplementary Table 2

Supplementary Table 2. A list of the 29 isolates found associated with an erroneous or modified identity in this study and their identities as used in this study.

Isolate numbers									
Local	CBS	ATCC	IMI	Gallegly	WPC	Other	(Sub)clade	Identity in this study	Original identity
33F4				p226		MNT63 (Blanchette)	1a	<i>P. aff. hedraiaandra</i>	<i>P. hedraiaandra</i> (Gallegly & Hong 2008, Schwingle <i>et al.</i> 2006)
29B3				p185		333 (Hansen)	1a	<i>P. aff. pseudotsugae</i>	<i>P. pseudotsugae</i> (Gallegly & Hong 2008, Hamm & Hansen 1983)
26H4				p32		678 (Tsao)	2a	<i>P. aff. citrophthora</i>	<i>P. citrophthora</i> (Gallegly & Hong 2008)
61G4	128754		342898		P10341		2a	<i>P. aff. colocasiae-1</i>	(Martin <i>et al.</i> 2014)
46C3		66767		p385	P6713	NP86 Moy 1413	2a	<i>P. aff. himalsilva</i>	<i>P. himalsilva</i> (Vettraino <i>et al.</i> 2011)
22F5		15427, MYA-4035		p9	P6262	Rajalakshmy #46	2a	<i>P. sp. P6262</i>	<i>P. sp. aff. colocasiae-2</i> (Martin <i>et al.</i> 2014)
22F3				p33	P6310	#066	2a	<i>P. sp. P6310</i>	<i>P. citrophthora</i> (Martin <i>et al.</i> 2014)
22J5		16698		p16		N14	2b	<i>P. aff. capsici</i>	<i>P. capsici</i> (Gallegly & Hong 2008)
23A1				p81	P8619	S813 PH-15-21-93	2c	<i>P. sp. 22F3</i>	<i>P. pini</i> (Hong <i>et al.</i> 2011), <i>P. citricola</i> Cil I (Gallegly & Hong 2008)
23A3		MYA-3660		p79		N65	6a	<i>P. inundata</i>	<i>P. sp. drechsleri-like</i> (Blair <i>et al.</i> 2008)
33F7				p229		Hansen 61	6b	<i>P. sp. gregata-like</i>	<i>P. erythroseptica</i> (Gallegly & Hong 2008)
01D5				p312		Hansen 50	6b	<i>P. sp. megasperma-like</i>	<i>P. megasperma</i> Meg I (Gallegly & Hong 2008)
23J6		MYA-4163		p57		Balci BM4/6	6b	<i>P. sp. megasperma-like</i>	<i>P. megasperma</i> Meg I (Gallegly & Hong 2008)
22G2	308,62	15402, MYA-4161	325907	p12		Ribeiro Israel 2	7a	<i>P. sp. europaea SW</i>	<i>P. europaea</i> (Gallegly & Hong 2008)
22J4		MYA-4041		p50		N57	7b	<i>P. niederhauserii</i>	<i>P. drechsleri</i> (Gallegly & Hong 2008)
33A1				p207		S720	7b	<i>P. niederhauserii</i>	<i>P. drechsleri</i> (Gallegly & Hong 2008)
32E6				p194	P10728	Breton 143-1	8a	<i>P. aff. cryptogea</i>	<i>P. cryptogea</i> (Gallegly & Hong 2008)
32E7						Breton 148-1	8a	<i>P. aff. erythroseptica</i>	<i>P. erythroseptica</i> (Gallegly & Hong 2008)
61E3	133815					SCRACE5388	8a	<i>P. aff. erythroseptica</i>	<i>P. erythroseptica</i> (Gallegly & Hong 2008)
29E7						Man in't Veld PD92/214	8b	<i>P. dauci</i>	<i>P. sp. aff. brassicae-1</i> (Martin <i>et al.</i> 2014)
47C5			395328		P8618	Banihashemi PH-15-19-92, PH-21-4-08, SUC19	8b	<i>P. dauci</i>	<i>P. porri</i> (Gallegly & Hong 2008)
47C6			395330			SUR16, Banihashemi PH-21-6-08	9a	<i>P. aff. cichorii</i>	<i>P. cichorii</i> (Bertier <i>et al.</i> 2013)
			395331			SUR17, Banihashemi PH-21-7-08	9a	<i>P. aff. cichorii</i>	<i>P. porri</i> (Gallegly & Hong 2008)
						Man in't Veld PD92/214	9a	<i>P. aff. cichorii</i>	<i>P. parsiana</i> (Mostowfizadeh-Ghalamfarsa <i>et al.</i> 2008), <i>P. sp. zentmyei</i> (WPS)
						Banihashemi PH-15-19-92, PH-21-4-08, SUC19	9a	<i>P. aff. cichorii</i>	<i>P. parsiana</i> (Mostowfizadeh-Ghalamfarsa <i>et al.</i> 2008)
						SUR16, Banihashemi PH-21-6-08	9a	<i>P. aff. cichorii</i>	<i>P. parsiana</i> (Mostowfizadeh-Ghalamfarsa <i>et al.</i> 2008)
						SUR17, Banihashemi PH-21-7-08	9a	<i>P. aff. cichorii</i>	<i>P. parsiana</i> (Mostowfizadeh-Ghalamfarsa <i>et al.</i> 2008)

Supplementary Table 2. (Continued).

Local	CBS	ATCC	Isolate numbers				(Sub)clade	Identity in this study	Original identity
			IMI	Gallegly	WPC	Other			
22G7		MYA-3893			S833	10	<i>P. gondwanensis</i>	<i>P. boehmeriae</i> (Gallegly & Hong 2008)	
45F8	357,52	60173	32199	p350	P1378	10	<i>P. sp. boehmeriae-like</i>	<i>P. boehmeriae</i> (Gallegly & Hong 2008)	

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