



Data in Brief

Genome sequences of six *Phytophthora* species associated with forests in New ZealandD.J. Studholme^a, R.L. McDougal^{b,*}, C. Sambles^a, E. Hansen^c, G. Hardy^d, M. Grant^a, R.J. Ganley^b, N.M. Williams^b^a Biosciences, University of Exeter, Exeter, UK^b Scion (New Zealand Forest Research Institute, Ltd.), Rotorua, New Zealand^c Department of Botany and Plant Pathology, Oregon State University, OR, USA^d Centre for Phytophthora Science and Management, School of Veterinary and Life Sciences, Murdoch University, WA, Australia

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ABSTRACT

In New Zealand there has been a long association of *Phytophthora* diseases in forests, nurseries, remnant plantings and horticultural crops. However, new *Phytophthora* diseases of trees have recently emerged. Genome sequencing has been performed for 12 *Phytophthora* isolates, from six species: *Phytophthora pluvialis*, *Phytophthora kernoviae*, *Phytophthora cinnamomi*, *Phytophthora agathidicida*, *Phytophthora multivora* and *Phytophthora* taxon Totara. These sequences will enable comparative analyses to identify potential virulence strategies and ultimately facilitate better control strategies. This Whole Genome Shotgun data have been deposited in DDBJ/ENA/GenBank under the accession numbers LGTT00000000, LGTU00000000, JPWV00000000, JPWU00000000, LGSK00000000, LGSJ00000000, LGTR00000000, LGTS00000000, LGSM00000000, LGSL00000000, LGSO00000000, and LGSN00000000.

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Specifications

Organism/cell line/tissue	Various <i>Phytophthora</i> species, see Table 1.
Sex	Not applicable
Sequencer or array type	Illumina Hi-Seq
Data format	Analyzed; i.e. raw data filtered and assembled
Experimental factors	Genomic sequence of pure microbial cultures
Experimental features	Genomic sequence of pure microbial cultures
Consent	Not applicable. Data are available without restriction.
Sample source location	Various, see Table 1.

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314435.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_000785725.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_000785735.1

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314425.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314365.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314455.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314345.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314355.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314375.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314925.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314505.1

http://www.ncbi.nlm.nih.gov/assembly/GCA_001314445.1

2. Experimental design, materials and methods

Trees in forests, woodlands and primary production are threatened by a growing number of pests and diseases. Particularly prevalent among emerging eukaryotic pathogens is the genus *Phytophthora*. Here we present genome sequences of two isolates from each of six species of *Phytophthora* chosen for their relevance and impact on New Zealand plantation and native forests [1] (Table 1). The isolates were selected to, where possible, to capture temporal, geographic or host preference differences.

Phytophthora pluvialis is a foliar pathogen of *Pinus radiata*, responsible for red needle cast disease [2]. The disease results in premature defoliation, impacting growth and production. *Phytophthora kernoviae* has also been isolated from *P. radiata* affected by red needle cast in New Zealand [2], although it is more commonly known for its severe impact on beech and ornamentals in the UK [3].

Phytophthora agathidicida [4] (formerly called *Phytophthora* taxon agathis or PTA) is a root and collar/stem canker pathogen responsible for dieback in kauri (*Agathis australis*), an iconic tree native to New

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Table 1
Phytophthora species and strains sequenced.

Species	Strain	Substrate/host	Location	Year of isolation	Reference
<i>P. pluvialis</i>	NZFS 3000	<i>Pinus radiata</i>	Gisborne, New Zealand	2008	[16]
<i>P. pluvialis</i>	LC9-1 ^a	Raintrap isolate	Oregon, USA	2009	
<i>P. kernoviae</i>	NZFS 2646	<i>Annona cherimola</i>	Northland, New Zealand	2005	[3]
<i>P. kernoviae</i>	NZFS 3630	<i>Pinus radiata</i>	Tokoroa, New Zealand	2011	
<i>P. cinnamomi</i>	NZFS 3750	<i>Pinus radiata</i>	Nelson, New Zealand	2013	[17]
<i>P. cinnamomi</i>	MP94-48	<i>Eucalyptus marginata</i>	Western Australia	1994	
<i>P. agathidicida</i>	NZFS 3772	<i>Agathis australis</i>	Auckland, New Zealand	2013	[4]
<i>P. agathidicida</i>	NZFS 3770 ^{a,b}	<i>Agathis australis</i>	Coromandel, New Zealand	2006	
<i>P. multivora</i>	NZFS 3378	<i>Idesia polycarpa</i>	Auckland, New Zealand	2010	[10]
<i>P. multivora</i>	NZFS 3448	<i>Metrosideros kermadecensis</i>	Auckland, New Zealand	2010	
<i>P. taxon totara</i>	NZFS 3727	<i>Podocarpus totara</i>	Northland, New Zealand	2011	McDougal, R. (unpublished)
<i>P. taxon totara</i>	NZFS 3642	<i>Podocarpus totara</i>	Gisborne, New Zealand	2011	

^a Type strain.^b Alternative strain name ICMP 17027, ex-holotype, [4].

Zealand. The pathogen was originally identified as *Phytophthora heveae* [5], but was more recently recognized as a distinct species [6].

Phytophthora cinnamomi is associated both with disease of *P. radiata* in forest nurseries [7] and with mortality in shelterbelts [8]. This aggressive root pathogen has decimated the Jarrah forest in Western Australia and has a worldwide distribution and very broad host range, likely infecting over 3000 species, causing root rot and stem cankers [9].

Phytophthora multivora is an aggressive pathogen associated with trees and plants in Western Australia including *Eucalyptus marginata*, *Eucalyptus gomphocephala*, *Banksia menziesii* and *Banksia grandis* [10]. In New Zealand, *P. multivora* is found in exotic forests, natural ecosystems and horticultural settings [1]. Together with *P. cinnamomi* and *Phytophthora cryptogea*, it is also one of the multiple species commonly isolated from soil around Kauri trees exhibiting dieback, caused by *P. agathidicida* [6,11].

Phytophthora taxon totara (PTT) represents an as-yet undescribed species isolated from *Podocarpus totara* foliage exhibiting needle browning and needle loss in the lower part of the crown. *P. taxon totara* was isolated from the foliage of this conifer and appears to be phylogenetically distinct among sequenced *Phytophthora* species, sharing sequence similarity with members of Clade 3 [12].

The genomic DNA from each isolate was sequenced using paired 100-nt Illumina HiSeq reads and assembled *de novo* assembly using SPAdes v 3.5.0 [13] and SSPACE Standard v. 3.0 [14]. Completeness of the genome assemblies was assessed using CEGMA (Core Eukaryotic Genes Mapping Approach) [15]. Genome assemblies and raw sequence data are available using the GenBank and Sequence Read Archive (SRA) accession numbers listed in Table 2.

Phytophthora genomic sequence data will be used, in conjunction with transcriptomic analyses, to identify putative factors involved in pathogen-host interactions. These resources will also enable comparative studies to related tree pathogens such as *Phytophthora pinifolia* and *Phytophthora ramorum*. Genomic resources will also enable the development of diagnostic tools for application to biosecurity and studies of pathogen ecology.

This Whole Genome Shotgun data have been deposited in DDBJ/ENA/GenBank under the accession numbers listed in Table 2.

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Table 2
Assembly statistics for the genome sequences reported in this study.

Species	Strain	Accession numbers: GenBank ^a and SRA	Total size (bp)	Number of scaffolds	Scaffold N ₅₀ (bp)	CEGMA coverage: % complete (% partial)
<i>P. pluvialis</i>	NZFS 3000	LGTT00000000 SRX1116285	52,734,927	5397	23,461	94.35 (97.98)
<i>P. pluvialis</i>	LC9-1	LGTT00000000 SRX1116286	53,621,061	4221	31,667	94.35 (97.58)
<i>P. kernoviae</i>	NZFS 2646	JPWV00000000 SRX1374322	37,287,305	1238	106,380	94.35 (96.77)
<i>P. kernoviae</i>	NZFS 3630	JPWU00000000 SRX1374272	37,413,357	1295	102,333	93.15 (95.97)
<i>P. cinnamomi</i>	NZFS 3750	LGSK00000000 SRX1117106	53,969,337	6270	23,905	93.55 (96.37)
<i>P. cinnamomi</i>	MP94-48	LGSJ00000000 SRX1117107	53,691,444	5777	24,869	93.55 (96.77)
<i>P. agathidicida</i>	NZFS 3772	LGTR00000000 SRX1116282	37,340,450	3701	19,799	95.56 (96.77)
<i>P. agathidicida</i>	NZFS 3770	LGTS00000000 SRX1116283	37,238,500	3689	19,537	95.97 (97.18)
<i>P. multivora</i>	NZFS 3378	LGSN00000000 SRX1117110	40,062,232	2762	47,236	94.76 (96.37)
<i>P. multivora</i>	NZFS 3448	LGSL00000000 SRX1117108	40,329,992	2768	46,546	94.76 (95.97)
<i>P. taxon totara</i>	NZFS 3727	LGSO00000000 SRX1117779	54,902,777	6026	21,950	94.76 (97.18)
<i>P. taxon totara</i>	NZFS 3642	LGSN00000000 SRX1117780	55,580,915	4314	31,387	95.16 (97.18)

^a Data have been deposited at GenBank under these accession numbers, and the versions described in this paper are versions XXXX01000000.

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