Data in Brief

Genome sequences of six 
Phytophthora 
species associated with forests in 
New Zealand

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A B S T R A C T

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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Keywords:
Phytophthora
P. pluvialis
P. agathidicida
Genome
Forest pathogen

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/assembly/GCA_00134445.1
http://www.ncbi.nlm.nih.gov/assembly/GCA_00134455.1
http://www.ncbi.nlm.nih.gov/assembly/GCA_00134345.1
http://www.ncbi.nlm.nih.gov/assembly/GCA_00134375.1
http://www.ncbi.nlm.nih.gov/assembly/GCA_00134925.1
http://www.ncbi.nlm.nih.gov/assembly/GCA_00134505.1
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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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 multispora is an aggressive pathogen associated with trees and plants in Western Australia including *Eucalyptus marginata*, *Eucalyptus gomphocephala*, *Bankia menziesii* and *Bankia grandis* [10]. In New Zealand, *P. multivora* is found in exotic forests, natural ecosystems and horticultural settings [11]. 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 Grade 3 [12].

The genomic DNA from each isolate was sequenced using paired 100-bp Illumina HiSeq reads and assembled de novo assembling using SPAdes v 3.5.0 [13] and SPACeS 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 1

| Species          | Strain           | Substrate/host | Location         | Year of isolation | Reference |
|------------------|------------------|----------------|------------------|-------------------|-----------|
| *P. pluvialis*   | NZFS 3000        | *Pinus radiata*| Gisborne, New Zealand | 2008             | [16]      |
| *P. pluvialis*   | LC9-1*           | Raintrap isolate | Oregon, USA      | 2009             |           |
| *P. kernoviae*   | NZFS 2646        | *Annona cherimola* | Northland, New Zealand | 2005           | [3]       |
| *P. kernoviae*   | NZFS 3630        | *Pinus radiata* | Tokoroa, New Zealand | 2011           |           |
| *P. cinnamomi*   | NZFS 3750        | *Pinus radiata* | Nelson, New Zealand | 2013           | [17]      |
| *P. cinnamomi*   | MP95-48          | *Eucalyptus marginata* | Western Australia | 1994           |           |
| *P. agathidicida*| NZFS 3772        | *Agathis australis* | Auckland, New Zealand | 2013           | [4]       |
| *P. agathidicida*| NZFS 3770a,b     | *Agathis australis* | Coromandel, New Zealand | 2006           |           |
| *P. multivora*   | NZFS 3378        | *Idemia polycarpa* | Auckland, New Zealand | 2010           | [10]      |
| *P. multivora*   | NZFS 3448        | *Metrosideros kermadecensis* | Auckland, New Zealand | 2010           |           |
| *P. taxon totara*| NZFS 3727        | *Podocarpus totara* | Northland, New Zealand | 2011           | McDougal, R. (unpublished) |
| *P. taxon totara*| NZFS 3642        | *Podocarpus totara* | Gisborne, New Zealand | 2011           |           |

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* Type strain.

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* Alternative strain name ICMP 17027, ex-holotype, [4].

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### Table 2

| Species | Strain | Accession numbers: GenBank* and SRA | Total size (bp) | Number of scaffolds | Scaffold N50 (bp) | CEGMA coverage: % complete (% partial) |
|---------|--------|----------------------------------|-----------------|---------------------|-------------------|---------------------------------------|
| *P. pluvialis* | NZFS 3000 | LGTT000000000 SRX1116285 | 52,734,927 | 5397 | 23,461 | 94.35 (97.98) |
| *P. pluvialis* | LC9-1 | LGTU000000000 SRX1116286 | 53,621,061 | 4221 | 31,667 | 94.35 (97.98) |
| *P. kernoviae* | NZFS 2646 | JPPW000000000 SRX1174322 | 37,287,305 | 1238 | 106,380 | 94.35 (96.77) |
| *P. kernoviae* | NZFS 3630 | JPPW000000000 SRX1174272 | 37,413,357 | 1295 | 102,333 | 93.15 (95.97) |
| *P. cinnamomi* | NZFS 3750 | LGSK000000000 SRX1117106 | 53,969,337 | 6270 | 23,905 | 93.55 (96.37) |
| *P. cinnamomi* | MP95-48 | LGJ000000000 SRX1117107 | 53,691,444 | 5777 | 24,869 | 95.56 (96.77) |
| *P. agathidicida* | NZFS 3777 | LGTR000000000 SRX1116282 | 37,340,450 | 3701 | 19,799 | 95.56 (96.77) |
| *P. agathidicida* | NZFS 3770 | LGTS000000000 SRX1116283 | 37,238,500 | 3689 | 19,537 | 95.97 (97.18) |
| *P. multivora* | NZFS 3378 | LGSO000000000 SRX1117110 | 40,062,232 | 2762 | 47,236 | 94.76 (96.37) |
| *P. multivora* | NZFS 3448 | LGSO000000000 SRX1117108 | 40,329,992 | 2768 | 46,346 | 94.76 (95.97) |
| *P. taxon totara* | NZFS 3727 | LGSN000000000 SRX1117779 | 54,902,777 | 6026 | 21,950 | 94.76 (97.18) |
| *P. taxon totara* | NZFS 3642 | LGSN000000000 SRX1117780 | 55,580,915 | 4314 | 31,387 | 95.16 (97.18) |

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* Data have been deposited at GenBank under these accession numbers, and the versions described in this paper are versions XXXX010000000.
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