Draft genomes of two Australian strains of the plant pathogen, *Phytophthora cinnamomi*[version 1; referees: 2 approved]

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Abstract

**Background:** The oomycete plant pathogen, *Phytophthora cinnamomi*, is responsible for the destruction of thousands of species of native Australian plants, as well as several crops, such as avocado and macadamia, and has one of the widest host-plant ranges of the *Phytophthora* genus. The currently available genome of *P. cinnamomi* is based on an atypical strain and has large gaps in its assembly. To further studies of the pathogenicity of this species, especially in Australia, more robust assemblies of the genomes of more typical strains are required. Here we report the genome sequencing, draft assembly, and preliminary annotation of two geographically separated Australian strains of *P. cinnamomi*.

**Findings:** Some 308 million raw reads were generated for the two strains. Independent genome assembly produced final genomes of 62.8 Mb (in 14,268 scaffolds) and 68.1 Mb (in 10,084 scaffolds), which are comparable in size and contiguity to other *Phytophthora* genomes. Gene prediction yielded > 22,000 predicted protein-encoding genes within each genome, while BUSCO assessment showed 82.5% and 81.8% of the eukaryote universal single-copy orthologs to be present in the assembled genomes, respectively.

**Conclusions:** The assembled genomes of two geographically distant isolates of *Phytophthora cinnamomi* will provide a valuable resource for further comparative analysis and evolutionary studies of this destructive pathogen, and further annotation of the presented genomes may yield possible targets for novel pathogen control methods.

This article is included in the Global Open Data for Agriculture and Nutrition gateway.
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Introduction

Phytophthora cinnamomi is a highly virulent plant pathogen that has a devastating impact on the Australian ecosystem, namely in the south-western areas of Western Australia and much of the south and east coasts of Victoria and New South Wales. In the south west Botanical Province of Western Australia, alone, over 40% of the 5710 plant species present have been shown to be susceptible to P. cinnamomi. Significant genetic and phenotypic variation can occur within a signal clonal lineage of P. cinnamomi and susceptibility of a given host plant species has been shown to vary from site to site. Furthermore, despite the general lack of crossing during sexual reproduction, P. cinnamomi excels at adapting to new environments and developing virulence to new host species through asexual growth, making it a deadly and difficult-to-control pathogen. Unravelling how P. cinnamomi is able to adapt so quickly, and remain virulent to a wide range of hosts in Australia, is an important research goal.

The currently available genome of P. cinnamomi var. cinnamomi (Joint Genome Institute (JGI); NCBI Accession no. PRJNA68241) is based on the Rans isolate from Sumatra in 1922, which has been in culture for many decades and may not be representative of the current pathogenic strains present in Australia. Here we report and make available two Australian P. cinnamomi genomes, isolated from geographically very separate areas with different available host species. After analyses of genetic differences between these two P. cinnamomi genomes, it may be that key genes or gene families under high evolutionary pressure can be identified; this may aid further studies on more effective control of this pathogen.

Sample collection and sequencing

Two isolates of P. cinnamomi were selected from areas of infection on either side of the Australian continent: one from the Brisbane Ranges in southeastern Australia (DU054, A2 mating type) and the other from southwestern Western Australia (WA94.26, A2 mating type), both Deakin University culture collection. These isolates were selected to represent possible genetic diversity of P. cinnamomi in Australia arising from geographic isolation, and possible variation of selective pressures due to different host species. Isolates were maintained on V8 agar (V8A) [50 ml unclarified V8 ‘Original’ Juice (Campbells, Australia), 0.5 g CaCO₃ and 7.5 g biological agar per 500 mL of distilled water] at 25°C in darkness, as per 5. Genomic DNA was isolated from hyphae using a DNeasy Plant Mini Kit (Qiagen), following the manufacturers protocol. Illumina TruSeq Nano library preparation and sequencing on an Illumina HiSeq 2500 platform were performed by the Australian Genome Resources Facility (Walter and Eliza Hall Institute, Parkville, Australia) generating ~154 million (2x 150bp) raw reads per isolate. Raw reads are available in the NCBI Short Read Archive (SRA) under the Bioproject Accession: PRJNA413098

Genome assembly

Raw sequencing data for each isolate was first pre-processed using Trimmomatic v0.33 with the following parameters: ILLUMINA-CLIP:TruSeq3-PE-2:fa:2:30:10:4 AVGQUAL:30 MINLEN:36, to remove Illumina adapters and filter reads based on quality scores (Phred score). Only reads with average Phred > 30 were retained. To ensure only the desired P. cinnamomi genomes were assembled, a second round of pre-processing was conducted to remove potential contaminants. MetaPhAn v2, was run with default settings and identified the Paenibacillus genus as a likely contaminant. Using BBMap v0.35 (BBMap - Bushnell. B), we mapped the Trimomatic-filtered reads to the closest species match (Paenibacillus sp., JDR-2, GenBank accession: GCA_000023585.1, with 2.7% and 2.0% of DU054 and WA94.26 reads mapping, respectively; these Paenibacillus reads were subsequently removed. The remaining reads were then mapped using BBMap to the human genome (GRCh38; NCBI accession: GCA_000001405.15), with < 0.5% (~ 430,000 reads from DU054 and ~ 630,000 from WA94.26) being mapped and subsequently removed from the data set. Thus, the final set of reads (DU054, 149 million reads; WA94.26, 151 million reads) used for the assembly contained highly quality paired-end reads not belonging to either human or bacterial contaminants.

De novo contig assembly of the two genomes was conducted independently, using IDBA-UD v1.1.0. IDBA-UD was run using the following parameters: --mink 20 --maxk 100 --step 20 --min_contig 500 --min_support 2 --min_count 3. Briefly, these conducted a multiple K-mer assembly from k = 20 up to k = 100; only assembled contigs above 500 bp and those with a minimum depth coverage ≥ 3 were kept. As heterogeneous data can increase redundancy in genome assemblies, the IDBA-UD assembled contigs were run through the Redundans pipeline v0.12c with the following parameters: -threads 4 --min_length 500. Redundans uses paired-end mapping data to reduce assembled sequence redundancy and scaffold contigs into longer less fragmented sequences. The final assembled genome of DU054 was 62.80 Mb in 14,269 scaffolds with an N50 of 9,951; the longest scaffold was 1.54 Mb in length (Table 1). For WA94.26, the final genome was 68.07 Mb in length, in 10,085 scaffolds with the largest being 1.54 Mb and an N50 of 20,813. GC content remained consistent, at ~ 53%, between both isolate genomes across both assemblies and before and after processing with Redundans. The quality, as measured by the above metrics, of the presented genomes is comparable to the previously available P. cinnamomi var. cinnamomi Rans isolate genome (JGI). The final genome assemblies are available under the NCBI Bioproject Accession: PRJNA413098.

We used the BUSCO (benchmarking universal single-copy orthologs) pipeline v1.22 with the default e-value cutoff of 0.01, to assess the completeness of the assembled genomes and compared the results to the previously available Rans isolate. Utilizing the set of 429 conserved eukaryotic single-copy orthologs (hereafter BUSCOs), the analysis indicated 82.5% and 81.8% BUSCO completeness for DU054 and WA94.26 genomes, respectively. For DU054, 335 complete BUSCOs (including single-copy and duplicated BUSCOs) and 19 fragmented BUSCOs were identified, and 333 complete and 19 fragmented BUSCOs in WA94.26 (Table 2). Overall, we find comparable levels of BUSCO completeness with the Rans isolate, suggesting our two Australian isolate assemblies are as complete references as that currently available.

Preliminary genome annotation

In the absence of any available high quality ESTs (expressed sequence tags) or transcriptome (gene expression) data for
**P. cinnamomi**, we conducted a preliminary protein-coding sequence prediction using GeneMark-ES v4.32, which utilises a self-training algorithm to identify exon, intron and intergenic regions as well as initiation and termination sites. GeneMark-ES was run using the default settings and a database of predicted gene models (i.e., predicted polypeptides) was constructed for DU054 and WA94.26 genomes. An initial 23,414 gene models were identified in DU054 and 22,573 in WA94.26. Of these, 14,735 pairs of predicted gene models appear to be orthologous between the two genomes (reciprocal best-hit Blastp, e value ≤ 1e-5). As a preliminary verification of these gene model builds, we identified orthologous counterparts to eight available *Phytophthora* genomes with more complete annotations (*P. infestans*, *P. kernoviae*, *P. lateralis*, *P. nicotianae*, *P. parasitica* (P1569_v1; Broad Institute), *P. ramorum*, *P. sojae* and *P. cinnamomi* var. *cinnamomi*). Accordingly, we used OrthoFinder v1.1.10 with default parameters, except we used DIAMOND as the alignment program with the diamond_more_sensitive flag. OrthoFinder first identifies ‘orthogroups’ (an extension of orthologues to include groups of genes descended from a single gene in the last common ancestor of a group of species) and then orthologues between each pair of species in the comparison. OrthoFinder assigned 88.5% (170,769) of the genes found in all the species to 19,089 orthogroups, and of these 50% of all the genes were contained in orthogroups, which had 10 or more genes within them. We found 2,931 orthogroups that contained genes for each of the species, and of these 1,309 orthogroups consisted entirely of single copy genes, see associated data repository. Using these single copy orthogroups gene trees were first constructed then the species tree was inferred using the distance-based implemented by fastme. The resultant species tree (see associated data repository) exhibits strong congruence to the *Phytophthora* phylogeny recently published by, providing more evidence that the genome assembly and preliminary annotation conducted here is valuable.

**Conclusions**

In summary, we present the genome assembly of two geographically separated isolates of *Phytophthora cinnamomi* from Australia, representing the first genome assembly of an Australian-isolated strain. These high-quality genomes will act as a valuable resource, particularly for the further identification and analysis of protein-encoding genes, which are expressed during plant infection, such as members of the avirulence gene families. These gene families are of specific interest in the development of novel and effective pathogen control mechanisms.
Data availability

Raw reads are available in the NCBI SRA under the Bioproject Accession: PRJNA413098

The final assemblies are available at DDBJ/EMBL/GenBank under the accessions, PDCY00000000 and PDCZ00000000 and under the Bioproject Accession: PRJNA413098.

Supporting data, including OrthoFinder analysis and BUSCO assessment results can be found in the associated data repository: doi, 10.4225/16/59d15a6917a5e1e. Data are available under the terms of the Creative Commons Attribution 4.0 International (CC BY 4.0).

Competing interests

No competing interests were disclosed.

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References

Open Peer Review

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Version 1

Referee Report 20 November 2017
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Erik Andreasson, Laura Grenville Briggs
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This data adds information about this important organism in the standard format to report a draft genome these days so it looks fine. They used hiseq and sequence coverage (BUSCO) looks appropriate and expected although there are relatively large differences between the two isolates (i.e. different final genome sizes and busco completeness scores). One suggestion is to add information on how many libraries they sequenced, and if it was only paired end and not also mate paired.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

We have read this submission. We believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Referee Report 17 November 2017
doi:10.5256/f1000research.13945.r27739
Nicolás Daniel Ayub
National Scientific and Technical Research Council, Buenos Aires, Argentina

The work was carried out professionally and resulted in good draft genomes of two pathogen strains belonging to Phytophthora genus. In my opinion, this article is an important contribution to future studies about the molecular mechanism involved in Phytophthora-plant interaction. Particularly, in the first steps of pathogen adhesion, where the virulence factors related to this are little known.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
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Competing Interests: No competing interests were disclosed.

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