Whole genome sequences of the raspberry and strawberry pathogens *Phytophthora rubi* and *P. fragariae*

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Abstract

Phytophthora rubi and *P. fragariae* are two closely related oomycete plant pathogens that exhibit strong morphological and physiological similarities, but are specialized to infect different hosts of economic importance, namely raspberry and strawberry. Here, we report the draft genome sequences of these two *Phytophthora* species as a first step towards understanding the genomic processes underlying plant host adaptation in these pathogens.

Genome announcement

More than 150 species of oomycete plant pathogens are harbored in the genus

Phytophthora (1, 2). These organisms are highly diverse in lifestyle, host preference, and

economic importance (1). Whole-genome sequences of various species in the genus

Phytophthora have recently been published, yielding novel insights into the molecular basis of

plant disease such as the identification of effector proteins that can disrupt the physiology of

the host (3, 4). Here, we present the whole-genome sequences of two soil-borne *Phytophthora*

sister species, *P. fragariae* and *P. rubi.* These are highly similar in morphology and physiology,

but infect different hosts. Sequencing the genomes of these species will advance our

understanding of the genomic mechanisms underlying host adaptation and knowledge of

molecular mechanisms of plant pathogenicity (5).

Genomic DNA was extracted from *P. rubi* strain "pd0101050015038" (isolated in the

Netherlands by K. Rosendhal from red raspberry) and *P. fragariae* strain CBS 209.46 (isolated in

England by C.J. Hickman from strawberry). Genomes were sequenced by the Beijing Genomics

Institute (BGI, Beijing, China) using the Illumina HiSeq2000 platform (Illumina, San Diego, CA)

using TruSeq libraries (paired end reads, insert size of 500 bp, average read length of 90 bp).

Assemblies were performed using SOAPdenovo2 (kmer size of 36) (6). Transcriptomes of both

species were also sequenced by BGI using the Illumina HiSeq2000 technology (paired end reads,

insert size of 500 bp, average read length of 90 bp). To obtain high quality gene calls, the

transcriptomes were assembled using Trinity (7) and translated into amino-acid sequences

using TransDecoder (8). To generate a reference database, gene prediction and annotation for

the nuclear genomes of both species were performed using MAKER (9) trained with gene calls

from other *Phytophthora* genomes including *P. ramorum*, *P. sojae*, and *P. infestans* (10, 11). The assembled transcripts were used as RNA evidence in MAKER to improve the quality of the called gene models.

The predicted gene models were annotated using InterproScan 5 (12). The *P. fragariae* assembly was estimated to be 74 MB in size, assembled into 8,511 scaffolds with an N50 of 18,987 bp. The *P. rubi* genome was assembled into 9,434 scaffolds spanning a total length of ~74 Mbp and a N50 of 16,735 bp. A total of 20,448 and 23,476 gene models were found for *P. fragariae* and *P. rubi*, respectively. Both species show a high abundance of Gene Ontology terms for DNA integration, nucleic acid binding, protein binding, peptidase/helicase and hydrolase activities, integrases, endonucleases, repeats, and transporter domains.

The genomes of *P. fragariae* and *P. rubi* will provide a unique resource for these closely related soil-borne oomycete plant pathogens and the molecular mechanisms associated with plant pathogenicity. Whole-genome data have been submitted to NCBI BioProject (PRJNA375089).

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