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Data Article

Draft genome sequences of the oomycete *Pythium insidiosum* strain CBS 573.85 from a horse with pythiosis and strain CR02 from the environment

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ABSTRACT

Pythium insidiosum is an aquatic oomycete microorganism that causes the fatal infectious disease, pythiosis, in humans and animals. The organism has been successfully isolated from the environment worldwide. Diagnosis and treatment of pythiosis is difficult and challenging. Genome sequences of *P. insidiosum*, isolated from humans, are available and accessible in public databases. To further facilitate biology-, pathogenicity-, and evolution-related genomic and genetic studies of *P. insidiosum*, we report two additional draft genome sequences of the *P. insidiosum* strain CBS 573.85 (35.6 Mb in size; accession number, BCFO00000000.1) isolated from a horse with pythiosis, and strain CR02 (37.7 Mb in size; accession number, BCFR00000000.1) isolated from the environment.

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Specifications Table

Subject area	Biology
More specific subject area	Microbiology, Genomics
Type of data	Genome sequence data
How data was acquired	IlluminaHiSeq 2000 and IlluminaHiSeq 2500 Next Generation Sequencing Platforms
Data format	Assembled genome sequences
Experimental factors	Genomic DNA was extracted from the *Pythium insidiosum* strains CBS 573.85 (an animal isolate) and CR02 (an environmental isolate).
Experimental features	Genome of the *P. insidiosum* strains CBS 573.85 and CR02 were sequenced and assembled.
Data source location	*Pythium insidiosum* strain CBS 573.85 was isolated from a horse in Costa Rica, and strain CR02 was isolated from the environment in Thailand.
Data accessibility	The draft genome sequences of *P. insidiosum* have been deposited in the DNA Data Bank of Japan (DDBJ) under the accession numbers: BCFO00000000.1 (strain CBS573.85; https://www.ncbi.nlm.nih.gov/nuccore/BCFO00000000.1) and BCFR00000000.1 (strain CR02; https://www.ncbi.nlm.nih.gov/nuccore/BCFR00000000.1).

Value of the data

- Previously, only genome sequence data of *P. insidiosum* isolated from humans is available in the public databases.
- The first draft genome sequences of *P. insidiosum* isolated from a non-human animal with pythiosis and from the environment are now made available.
- The additional genome data will facilitate biology-, pathogenicity-, and evolution-related studies of *P. insidiosum*, through comparative genomic studies of *Pythium* species and related species.

1. Data

Pythium insidiosum is an aquatic oomycete microorganism that causes the lethal infectious condition, pythiosis, in humans and other animals [1,2]. The organism has been isolated from the environment in Australia, Thailand, Brazil and the United States [3–6]. Genome sequences of *P. insidiosum*, isolated from humans, are available and accessible in public databases [7,8]. We report two additional draft genome sequences of the organism isolated from a horse with pythiosis, as well as from the environment.

2. Experimental design, materials and methods

2.1. Genome sequencing and assembly

Genomic DNA samples were extracted from *P. insidiosum* strain CBS573.85 (from an infected horse in Costa Rica) and strain CR02 (from an agricultural area in Thailand), using the conventional extraction method described by Lohnoo and co-workers [9]. rDNA sequence analysis was performed to confirm the identity of the organism [10–12]. The extracted genomic DNA of each of these two strains was subjected to preparation of a paired-end library for genome sequencing, using the IlluminaHiSeq 2500 (strain CBS573.85) or IlluminaHiSeq 2000 (strain CR02) platform (Yourgene Bioscience, Taiwan). Quality trims of the raw reads were executed by CLC Genomics Workbench