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Complete Genome Sequence of *Paralagenidium Karlingii* Strain 1391

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Short Communication

Paralagenidium karlingii is a fungus-like organism in the Phylum *Oomycota* associated with mammalian infections. The organism in this study, P. karlingii 1391, was recovered from a subcutaneous dermal mass of a male Labrador retriever dog. This is the first report of a whole-genome sequence of *Paralagenidium* spp.

Oomycetes are a group of filamentous organisms that morphologically resemble fungi, but are phylogenetically distinct [1]. Their hyphal-like structures are coenocytic with cell walls containing cellulose and glucan, but not ergosterol. Many members of this phylum are pathogens of plants, crustaceans or fish, and have some association with an aquatic environment during their life cycle. For more than a century, *Pythium insidiosum* was thought to be the only species in the *Oomycota* capable of causing infections in mammals and birds. However, in 2003 a unique pathogenic oomycote was isolated from dogs in the southeastern United States that had highly invasive cutaneous lesions [2]. While the infections resembled pythiosis clinically, the isolates had morphologies and molecular characteristics resembling the genus *Lagenidium*. Since that time, other isolates similar to the original *Lagenidium* strains have been recovered from infections in dogs, cats, and humans [3-5]. Phylogenetic studies of various isolates confirmed that a new genus, *Paralagenidium*, is also associated with infections in man and animals [6].

Paralagenidium karlingii 1391 was recovered from a subcutaneous dermal mass surgically removed from a male Labrador retriever dog in Alabama in 2016. Tissue samples were plated on Sabouraud Dextrose agar and incubated at 28ºC. The isolate grew as a flat, irregular matt, white to cream colored, that strongly adhered to the agar surface. Samples of mature hyphae were removed from the agar surface and homogenized with Zirkonia beads in the presence of RNA/DNA stabilization buffer followed by a 20min incubation in a High-Pure proteinase K solution at 56°C. DNA was extracted using the High-Pure PCR Template Preparation Kit (Roche Molecular Biochemicals, Indianapolis, IN, USA) according to the manufacturer's instructions. DNA quality control, library preparation and sequencing was conducted at Hudson Alpha Genomic Services Laboratory (Huntsville, AL, USA) using an Illumina HiSeqX platform with 150bp paired-end reads. A total of 38,948,227 pass-filter quality reads, 1.2×10^{10} bp in length were generated. Approximately, 90.88% of bases resulted in sequence qualities above Q30.

De novo assembly was performed using Ray 2.3.1, which resulted in 10,613 scaffolds (>500bp) containing 49,325,952 bases with an N_{50} of 8,723 [7]. The longest scaffold recovered was 87,973 bases in length and the G+C content was calculated to be 51.3%. Using Gene Mark-ES for gene prediction, 16,537 protein coding genes were predicted [8]. This set of protein-coding genes possessed three virulence factors (glucan 1,3-beta-glucosidase, heat shock 70, and enolase) which were previously reported in *P. insidiosum* [9]. Whole genome sequencing in this study will help clarify the complex taxonomy of these oomycotic pathogens and advance our understanding of their unique ecological niches and mechanisms of pathogenesis.

Accession Number

The *Paralagenidium karlingii* strain 1391 whole genome sequence has been deposited at DDBJ/ENA/GenBank under the accession PTTM00000000 (www.ncbi.nlm.nih.gov/nuccore/PTTM00000000).

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