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Draft Genome Sequence of the Mammalian Pathogen *Lagenidium giganteum* Strain MTLA-03

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Short Communication

Here we present the complete genomic sequence of *Lagenidium* giganteum, strain MTLA-03, recovered from a clinically ill canine host. This sequence information is offered to assist in clarifying the phylogenetic placement of this genus and to aid in our understanding of this organism's role as a mammalian pathogen.

Mammalian infections by members of the fungus-like phylum Oomycota were, for years, attributed to *Pythium insidiosum*. This changed in 2003, when six dogs were reported as having progressive cutaneous infections due to an organism that has both morphologic and molecular features resembling another oomycete, *Lagenidium giganteum* [1]. The genus *Lagenidium* encompasses numerous saprophytic species, as well as pathogens of algae, plants, crustaceans, and mosquito larvae [2]. *Lagenidium giganteum* is an aquatic oomycete that infects and kills mosquito larvae. There have since been multiple reports of *Lagenidium*-like organisms being associated with tissue infections, in dogs, cats and even humans [3-5]. While these isolates share many morphological features, comparison of ribosomal RNA sequences from multiple strains has identified several different genera of *Lagenidium* and one new genus *Paralagenidium* [3, 6-9]. Phylogenetic comparisons of mammalian *Lagenidium* isolates to those infecting mosquitos discovered that these two groups were closely related [6,8].

The strain *Lagenidium giganteum* MTLA-03 was isolated and collected by Drs. Leonel Mendoza and Nikki Bond from synovial fluid in a Florida dog with a subcutaneous infection. Matts of hyphae were collected 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. Genomic 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).

Sequencing was performed on the Illumina HiSeqX platform with 150-bp pair-end reads. A total of 62,723,275 pass-filter quality reads of 1.9×10^{10}-bp in length were generated, of which 89.4% had a quality score above Q30. *De novo* assembly was performed using Ray 2.3.1, which resulted in 2,440 scaffolds (>500bp) containing 13,381,848 bases with an N50 of 5,310 [10]. The longest scaffold recovered was 66,894 bases in length and the G+C content was calculated to be 54.4%. Gene predictions were made using Maker version 2.31.9 with evidence from a *Pythium ultimum* var. *sporangiiferum* proteome [11]. In addition, 10,286 protein coding genes were predicted and this set of genes possessed three virulence factors (glucan 1,3-beta-glucosidase, heat shock 70, and enolase) previously reported in *P. insidiosum* [12]. The information here will be useful in advancing our knowledge of the phylogeny of the *Lagenidium* genera and in future studies of their pathogenesis.

Accession Number

This Whole Genome Shotgun project has been deposited at GenBank under the accession PSQM00000000 (www.ncbi.nlm.nih.gov/nuccore/PSQM00000000).

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