



INFECTIOUS DISEASES (BACTERIAL, FUNGAL, VIRAL, PARASITIC, INFESTATIONS)

## COMPARATIVE GENOME AND TRANSCRIPTOME STUDY OF THE GENE EXPRESSION DIFFERENCE BETWEEN PATHOGENIC AND ENVIRONMENTAL STRAINS OF PROTOTHECA ZOPFII

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**Background:** The morbidity of protothecosis has increased rapidly in recent years, especially in systemic infections of patients with an impaired immune system. The infection in immunocompromised patients has a poor prognosis due to limited understanding of the pathogenesis of the disease.

**Objective:** To gain an insight into the pathogenesis of protothecosis, and to tentatively explore some possible virulence genes of the organism, we explored the genetic differences between pathogenic and environmental strains of *P. zopfii* using next-generation sequencing methods.

**Materials and Methods:** The genome of strain WLZ18125 was sequenced by SMRT technology. For RNA sample preparations, 3 µg of RNA per sample was used as input material. Sequencing libraries were generated following manufacturer's recommendations and index codes were added to attribute sequences to each sample. For each strains we created 3 biological replicates libraries. After cluster generation, the library preparations were sequenced and 125 bp/150 bp paired-end reads were generated.

**Results:** We constructed the genome of a pathogenic strain of *P. zopfii* 18125, and transcriptomes of two pathogenic strains and one environmental strain for the first time. Based on our preliminary gene expression findings, some genes in *P. zopfii* pathogenic strains are significantly up-regulated in peroxisome, metabolism pathways and pyruvate metabolism, and also genes related to RNA polymerase, spliceosome, RNA transport, ribosome biogenesis in eukaryotes, and energy metabolism.

**Conclusions:** We constructed the genome of a pathogenic strain of *P. zopfii* 18125, and





transcriptomes of two pathogenic strains and one environmental strain, by next generation sequencing methods for the first time. The differential genes such as MDH, transmembrane ATPases, and Leu1, maybe the potential virulence factors for *P. zopfii*. Furthermore, the first genome of *P. zopfii* provides some base for further studies on the pathogenesis of this species.

