Searching for genomic elements of sexual reproduction in a microsporidian pathogen

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The adaptive value of sex in eukaryotic unicellular pathogens is a matter of intense debate, and the genetic mechanisms involved in sexual reproduction of these organisms are largely unknown. Differences in reproduction systems could help explaining differences in modes of transmission, host range amplitude, and response to environmental changes, all tightly related to pathogenicity and virulence of such pathogens. This work aims to identify genomic elements that could be associated with modes of reproduction and transmission, and further elucidate the role of sexual cycles in a microsporidian parasite. Microsporidia belong to a phylum of unicellular intracellular pathogenic Fungi. These parasites are found in virtually all types of animals, being of importance to health and agriculture. *Hamiltosporidium tvaerminnensis* is a microsporidian shown to be asexual and being both vertically and horizontally transmitted to its host, the microcrustacean *Daphnia magna*. *H. tvaerminnensis* possesses a sister species, *Hamiltosporidium magnivora*, which differs by being sexual and only vertically transmitted. Our work uses as reference a newly assembled draft genome of *H. tvaerminnensis*. It is an unusually large genome for a microsporidian, estimated to contain 25 Mb of sequence. Additionally, we rely on deep sequencing reads from two recently resequenced lineages of *H. magnivora*, one from Belgium and another from Israel, as well as a set from *H. tvaerminnensis*, from Finland, using technology newer than the reference. Our sequence assembly yielded 11.87 Mb for the genome of *H. tvaerminnensis* Finland strain, with a GC content of 27.29%, and at least 10-fold reduction in contig number comparing to the reference. Assemblies of *H. magnivora* isolates from Belgium and Israel yielded 17.42 Mb and 18.03 Mb respectively, both with a GC content of 32.78%. Continuing on, we plan to use two approaches in our study: (1) Comparing overall gene contents and searching for point mutations or indels in reproduction related genes, by mapping the reads of each Hamiltosporidium isolate onto contigs containing meiosis and cell division candidate genes. We are currently annotating those genes on the assemblies. (2) Searching for larger rearrangements in the Hamiltosporidium genomes, by aligning the assembled genomes.

We acknowledge the Brazilian Coordination for the Improvement of Higher Education Personnel (CAPES) for providing funding, and Dr Dieter Ebert for supporting this work.