

Near chromosome-level genome assembly of *Hamiltosporidium tvaermanniensis*

Microsporidia Fest 2023, 13.09.2023

Pascal Angst

PhD Student, Department of Environmental Sciences, Zoology,
University of Basel



@pascalangst

Microsporidia genome size variation

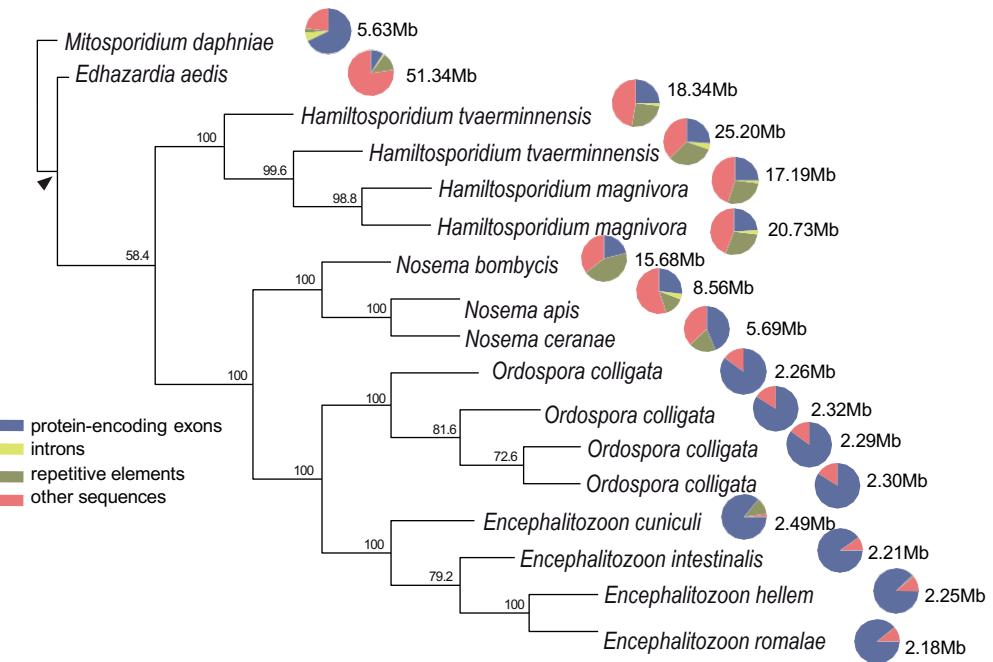
Genome reduction ...

and

Secondary genome expansion ...

... lead to high variation in

genome size (< 3 Mb to > 50 Mb)



Microsporidia genome size variation

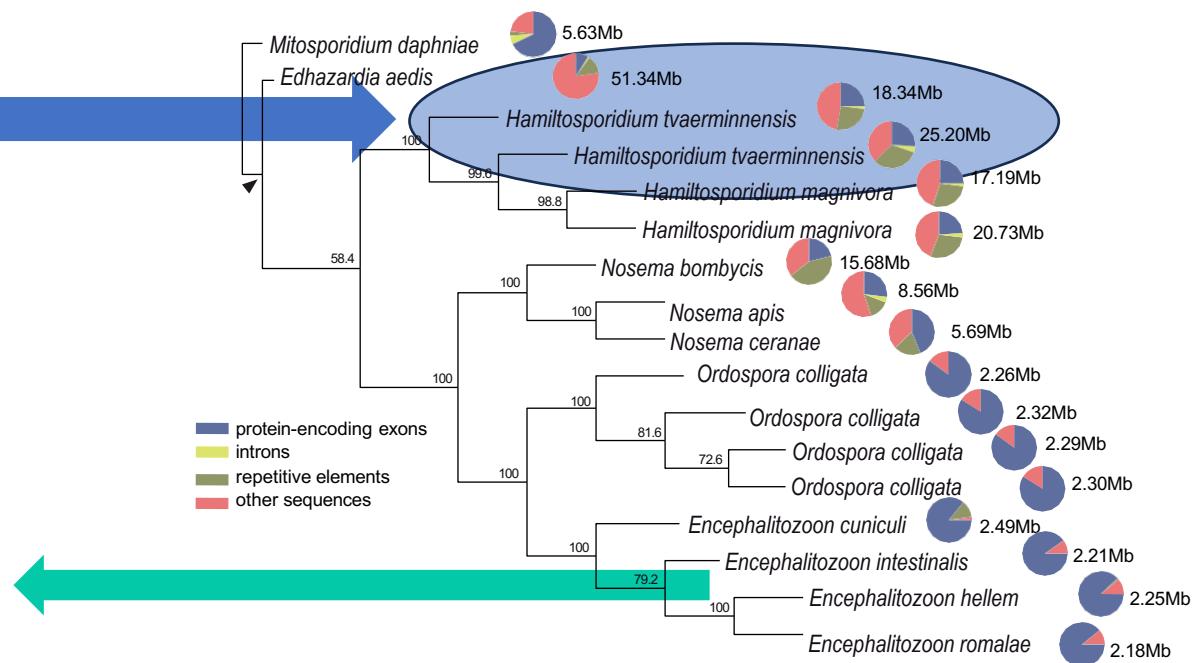
Lack in high-quality resources
from species with large genomes

RESEARCH

Open Access

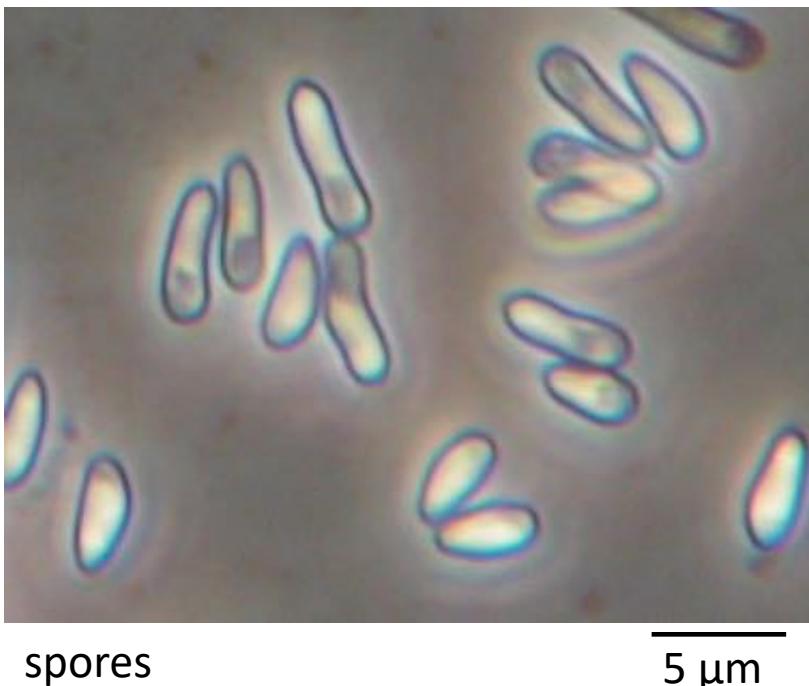
Telomere-to-Telomere genome assemblies
of human-infecting *Encephalitozoon* species

Anne Caroline Mascarenhas dos Santos¹, Alexander Thomas Julian¹, Pingdong Liang¹, Oscar Juárez¹ and
Jean-François Pombert^{1*}



Hamiltosporidium tvaermanniensis

- Transmission: Vertical and horizontal
- Asexual
- Fat body, ovaries



infected *D. magna*

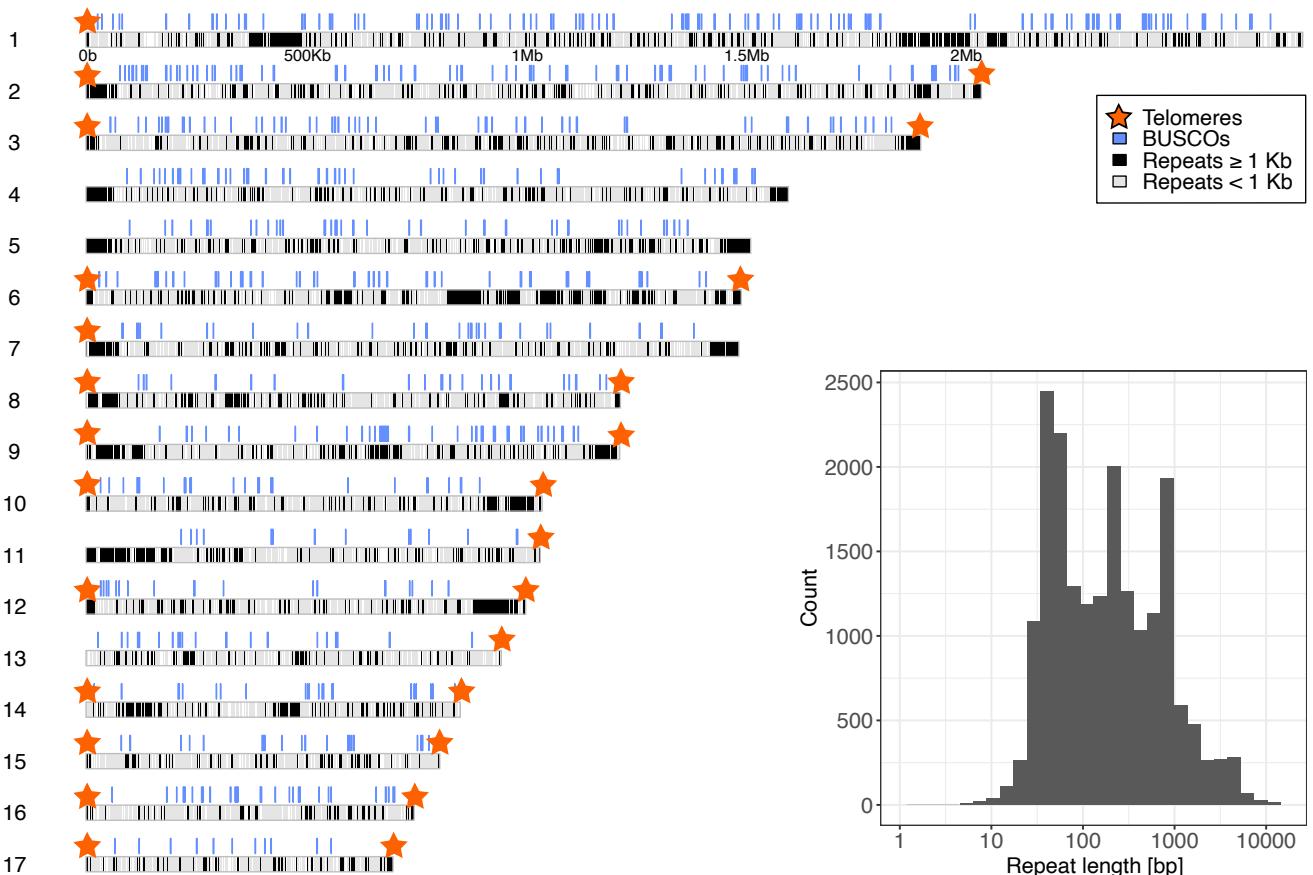
Pictures: Ebert (2005)

Materials and Methods

- Genome assembly: PacBio, Oxford Nanopore, and Illumina sequencing
- Annotation: PacBio Iso-Seq to sequence full-length transcripts, providing reliable isoform information without assembly steps

Final assembly

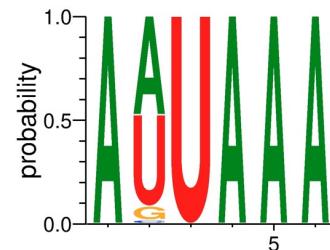
- 21.64 Mb
 - N50 1.44 Mb
- BUSCO score 94 %
- 39.56% interspersed repeats
 - retroelements 7.07%
 - DNA transposons 7.04%
 - other 25.45%



Iso-Seq (full-length transcript data)

- Number of protein-coding genes in 21.64 Mb: 3,573
Encephalitozoonidae: genome size 2-3 Mb, ~2,000 genes
- We observed Alternative PolyAdenylation (APA), which could be a potential mechanism for gene regulation in microsporidia

The motif for cleavage of protein-coding mRNA is shared with other Metazoans:



Conclusion

- Genome size variation in microsporidia can potentially be explained by repetitive sequence content:
 - > comparative genomic analyses aiming to understand the evolution of genome reduction and expansion should focus on understanding how and why repetitive sequence is purged or aggregated in the studied species.

Thank you!

Ebert Group

Dieter Ebert

Peter Fields

and Jean-François Pombert



University
of Basel



Swiss National
Science Foundation

JOURNAL ARTICLE ACCEPTED MANUSCRIPT

Near chromosome-level genome assembly of the microsporidium *Hamiltosporidium tvaerminnensis* ③

Pascal Angst ✉, Jean-François Pombert, Dieter Ebert, Peter D Fields Author Notes

G3 Genes|Genomes|Genetics, jkad185, <https://doi.org/10.1093/g3journal/jkad185>

Published: 11 August 2023 Article history ▾

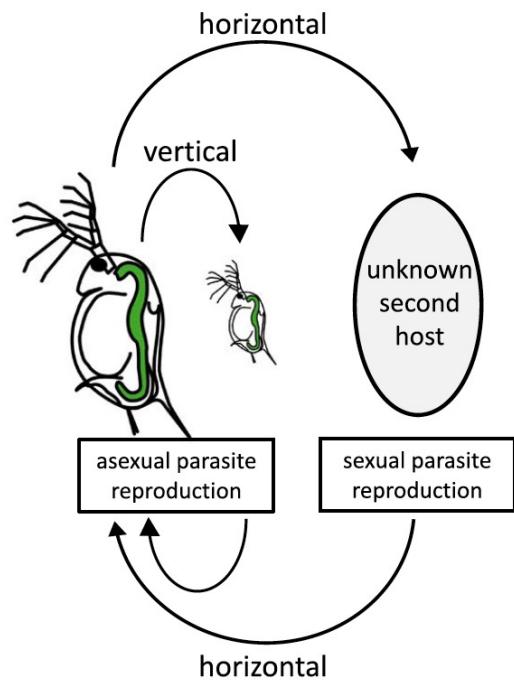


@pascalangst

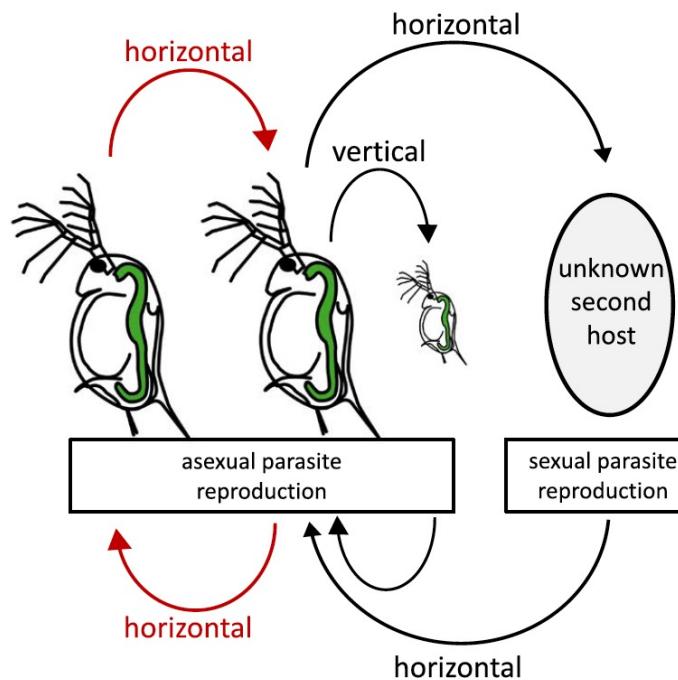
Assembly	
Total length (Mb)	21.64
GC content (%)	26.60
Contig N50 (Mb)	1.44
Contig number	17
BUSCO completeness score (%)	94
Annotation	
Total length of repeats (Mb)	8.56
Number of protein-coding genes	3,573
Mean gene length (bp)	1,391
Number of predicted introns	98
Number of Iso-Seq confirmed introns	17
Number of genes with confirmed introns	15
Mean intron length (bp)	28

1) Ancestral lifecycle

(as in *H. magnivora*)

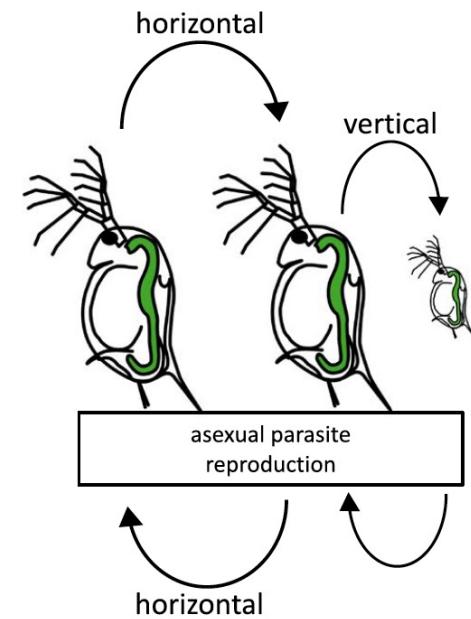


2) New feature



3) Absence of second host

(as in *H. tvaerminnensis*)



- *H. magnivora* depends on two hosts
- vertical transmission to offspring
- horizontal transmission to second host (and back)
- sexual reproduction in the second host

- New feature additionally allows to transmit horizontally amongst *D. magna*

- *H. tvaerminnensis* can colonize areas where the second host is absent
- sexual reproduction is absent

FIGURE 4 Putative evolutionary change in the *Hamiltosporidium* life cycle. (1) The ancestral life cycle of *Hamiltosporidium* might have involved asexual vertical transmission to offspring and transmission to a second host where sexual reproduction could take place, as is the case for *Hamiltosporidium magnivora*. (2) However, a novel transmission strategy arose wherein horizontal transmission amongst the host *Daphnia magna* without sexual reproduction (3) allowing this derived *Hamiltosporidium* group to colonize geographical regions where the second host is absent, as is the case for *Hamiltosporidium tvaerminnensis*. Sexual reproduction would then only be possible in the presence of the now facultative second host. This figure illustrates our hypothesis and is a speculation based on our results

Angst et al. (2022)

