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A new microsporidian parasite, Ordospora pajunii sp. nov (Ordosporidae), of Daphnia longispina highlights the value of genomic data for delineating species boundaries

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Speciation is a complex and continuous process that makes the delineation of species boundaries a challenging task in particular in species with little morphological differentiation, such as parasites. In this case, the use of genomic data is often necessary, such as for the intracellular Microsporidian parasites. Here, we characterize the genome of a gut parasite of the cladoceran Daphnia longispina (isolate FI-F-10), which we propose as a new species within the genus Ordospora: Ordospora pajunii sp. nov (Ordosporidae). FI-F-10 closest relative, Ordospora colligata is only found in D. magna. Both microsporidian species share several morphological features. Although it is not possible to estimate divergence times for Microsporidia due to the lack of fossil records and accelerated evolutionary rates, we base our proposal on the phylogenomic and genomic distances between both microsporidian lineages. The phylogenomic reconstruction shows that FI-F-10 forms an early diverging branch basal to the cluster that contains all known O. colligata strains. Whole-genome comparisons show that FI-F-10 presents a greater divergence at the sequence level than observed among O. colligata strains, and its genomic average nucleotide identity (ANI) values against O. colligata are beyond the intraspecific range previously established for yeast and prokaryotes. Our data confirm that the ANI metrics are useful for fine genetic divergence calibration across Microsporidia taxa. In combination with phylogenetic and ecological data, genome-based metrics provide a powerful approach to delimitate species boundaries.
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