Evolutionary genomics of *Metchnikovella incurvata* (Metchnikovellidae), an early branching microsporidian

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Metchnikovellidae are a lineage of highly specialized hyperparasites, which infect and reproduce inside gregarines (Apicomplexa) inhabiting marine invertebrates. They have been known for decades, but their phylogenetic affiliation has been under constant discussion. Confirming some early predictions, the recent analysis of the first almost complete genome for a metchnikovellid, *Amphiamblys* sp., placed them as deeply branching Microsporidia, a lineage of extremely reduced parasites that branch as sister group to rozellids (Rozellosporidia = Cryptomycota) in the Holomycota clade of Opisthokonta. We have obtained the partial genome of a second metchnikovellid, *Metchnikovella incurvata*, through single-cell genomics techniques, by isolating, whole genome amplifying, and sequencing DNA from a single infected gregarine parasitizing a polychaete of the Kandalaksha gulf in the White Sea. We have carried out phylogenomic analysis using a multigene dataset, which included *Amphiamblys sp*. Our results confirm that metchnikovellids are the earliest known branch of Microsporidia. However, although *Amphiamblys sp*. and *M. incurvata* form a unique basal group within Microsporidia, they are significantly divergent from each other. The comparative genomic analysis of these two metchnikovellids unveiled that (as most microsporidia) they lack mitochondrial genes involved in energy transduction and are incapable of synthesizing their own ATP. However, they also lack conventional microsporidian ATP transporters, which are likely products of horizontal gene transfer. We hypothesize the possibility that a family of inorganic phosphate mitochondrial carrier proteins may have evolved to transport ATP from the host to the metchnikovellid/parasite cell. We also suggest that the high evolutionary rate seen in Microsporidia is a likely consequence of the reduction and alteration of DNA repair pathways. By comparing our genome with more derived Microsporidia and their close relatives we have gain insights about how genome and functional reduction occurred during the evolution of this lineage of highly reduced parasites.