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## BOOK OF ABSTRACTS

## **Metchnikovellids, an evolutionary important yet poorly studied group at the root of microsporidian tree**

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Metchnikovellids are a deviated group, which is very important for untangling the early evolution of Microsporidia. All known metchnikovellids are hyperparasites of gregarines inhabiting the gut of polychaetes and some other invertebrates. Metchnikovellidean spores are devoid of the most components of canonical microsporidian extrusion apparatus; instead they possess a structure called “manubrium” and a complex of associated organelles. The life cycle of metchnikovellids is also atypical. It misses merogony and includes a division by internal budding resulted in formation of cyst-bound spores. The metchnikovellids form a robust monophyletic clade at the root of microsporidian SSU rRNA tree. Recent phylogenomic analyses confirm the early divergence of metchnikovellids. They are the most basal group that shows typical microsporidian characters, like a high rate of sequence evolution, genome reduction and an absence of mitochondrial genome. The study of metchnikovellids is hindered by hyperparasitic life style, small size and occasional occurrence in the environment. Up to now, less than 30 species of these organisms are described, most of them are known only from old descriptions. Only eight species were investigated by TEM. During the last thirty years the isolation of only five metchnikovellidean species was reported; three of them were found during our extensive screenings in the populations of the polychaete *Pygospio elegans* in the White Sea, North-West Russia. We discovered two new species – *Metchnikovella spiralis*, *M. dogieli* and reisolated *M. incurvata*, a species described hundred years ago from other locality. The biodiversity of this group is likely to be largely unexplored. To expand our yet very limited knowledge on the diversity and distribution of these hyperparasites and to sample more taxa for phylogenetic studies the long-term screenings of the populations of potential hosts combined with molecular ecological approaches are desirable.

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