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## *De novo* assembly and annotation of the genome of *Intoshia variabilis* (Orthonectida)

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Orthonectida is a group of organisms that are parasitizing a wide range of marine invertebrates. Several types of reproduction interchange in their life cycle, and the free-living stage is replaced by the parasitic stage – “plasmodium”. For a long time, the position of Orthonectida in the Metazoa system remained unclear. However, recent studies evidence that they must be members of Annelida strongly modified due to the parasitic way of life. Thus, the investigation of the Orthonectida genomes is incredibly interesting. This is possible thanks to next-generation sequencing (NGS) technology and the development of bioinformatics.

The purpose of this research is investigation of the genome of sexually mature individuals of *Intoshia variabilis*. Sequencing was performed on the Illumina HiSeq 2500 platform. We used 4 libraries of paired-end reads for our analysis. An approximate estimate of the coverage and size of the genome before assembly was done using KrATER. FastQC was used to assess the quality of libraries. Further processing of reads and the elimination of various kinds of errors were done using the BBTools program set. *De novo* genome assembly was implemented using SPAdes assembler, based on the de Bruijn graph algorithm. The quality of assembly was evaluated using QUAST, which calculates a number of important statistical parameters. The initial genome annotation was performed using Augustus, based on hidden Markov model.

As a result, *Intoshia variabilis* demonstrates the smallest genome (15,5 Mbp) and the lowest reported gene number (5,120 protein-coding genes) among Metazoa. The small genome size is a result of extreme genome reduction due to the parasitic life style, as well as to simplification and miniaturization of the free-living stages. Based on this genome assembly and annotated genes we can identify the necessary minimum for the existence of a spiral animal.

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