Assembling mitochondrial genomes from small worms: a combined approach

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With about 1800 species formally described, Rhabdocoela MEIXNER, 1925 readily surpasses all other turbellarian taxa (i.e. non-neodermatan flatworms) in terms of species richness. Also, in terms of ecology, these animals have become highly diversified, having successfully colonised numerous niches in marine, freshwater, and even terrestrial environments. At least four different lineages have independently made the transition towards an obligate symbiotic lifestyle. The sister group-relationships of these 'shifted' lineages are in most cases firmly established. As such, symbiotic rhabdocoels form an important model to assess the molecular-genetic effects of such large evolutionary shifts at the genomic level in a comparative framework.

However, accessing these sequences has proven difficult. Considering the small size of most rhabdocoels (< 2 mm), acquiring adequate concentrations of target DNA makes up a first challenge – even in the current NGS era. The little molecular data available today also show a high degree of nucleotide diversity in the (mito)genomes of these animals, further complicating otherwise-standard procedures such as cox1-barcoding or even simple PCR protocols. The fact that no reference genome is available in this modern age speaks volumes – and only a single mitochondrial genome has been characterised to date. In this work, the first steps towards a quick and streamlined pipeline for sequencing complete mitochondrial genomes of rhabdocoels are presented. This approach can readily be customised for other meiofaunal groups. The costs and benefits of this process are considered and the resulting assemblies are discussed.

Keywords: Rhabdocoela; Platyhelminthes; Flatworms; Mitochondrion; Genomics; NGS; LR-PCR; WGA; Illumina