A draft genome of *Carpediemonas membranifera* reveals that several metabolic components were lost early in metamonad evolution, prior to the origin of diplomonad parasites.

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Carpediemonas membranifera is a free living flagellated metamonad related to diplomonad parasites such as *Giardia intestinalis* and *Spironucleus salmonicida*. To elucidate the evolutionary transitions to anaerobiosis and parasitism within metamonada, we sequenced the genome of *C. membranifera*. The genome assembly is 22.4 Mb long with 11328 predicted protein-coding genes. The genome contains 2088 introns with sizes ranging from 28 to 166 bps, with 86% of them that are less than 40 bps in length. All sequenced metamonads to date are very intron poor, and *C. membranifera* does not seem to be the exception. To date, we have completed analyses of the DNA repair pathways, stress detoxification, endomembrane system and identified proteins for mitochondrial related organelles. *C. membranifera* possesses a complete system for excision repair, the double strand break repair machinery, a complete repertoire of cell cycle checkpoints and sex-related proteins. Oxygen detoxification seems to be carried out by a nitroreductase and a FAD/FMN dependent oxidoreductase system. The genome encodes two previously described pathways for "*de novo*" synthesis of L-cysteine indicating the versatility of the species to generate precursors for protein synthesis and to maintain cellular homeostasis. The searches of putative mitochondrial genes revealed no sign of mitochondrial rRNA or protein-coding genes indicating a lack of mitochondrial genome. There is evidence of a functional *trans*-Golgi network and an endolysosomal pathway. In general, many components of the studied metabolic pathways seem to have been lost in the last common ancestor of Fornicata.