

ABSTRACT

Mitochondrial endosymbiosis was a key event in the evolution of eukaryotes. Its proteome evolved into a unique combination of inherited bacterial components as well as novel eukaryotic inventions. Today, mitochondria show a huge variety across eukaryotic species – from aerobic mitochondria with cristae and complex protein apparatus for maintaining its own genome to hydrogen-producing hydrogenosomes and tiny anaerobic mitosomes without their own genome and with only a single metabolic pathway.

Comparing the existing spectra of mitochondria is beneficial for studying their evolution. The only ubiquitous and unifying features are double membrane, ISC pathway for iron-sulfur cluster synthesis and the core of protein import pathway. Therefore, these features could be considered as truly ancestral and essential to mitochondria. Mitosomes of various parasitic protists have evolved independently from complex mitochondria, since they are present in completely unrelated species and yet their evolution led in a surprisingly similar composition of protein import pathway. These retained components are thus believed to be functionally essential and for some reason hard to be replaced by alternate proteins. Mitosomal import pathways were considered very minimalistic for a long time. Nevertheless, the latest research shows, that some of them possess many unique lineage or even species-specific proteins, which likely substitute the loss of canonical components of this pathway.

Mitosomes of *Giardia intestinalis* are one of the most reduced mitochondrial forms discovered so far. However, with the improvement of bioinformatic tools, many distant homologues of proteins involved in protein import pathway such as Tom40, Tim44 and Tim17 were discovered over the last years. Moreover, with the identification of many new *Giardia*-specific proteins, novel unique functions and pathways are likely yet to be discovered.