

Exploring the anaerobic adaptations of the mitochondrion-related organelles of *Blastocystis*

Lyto Yiangou¹ and Anastasios D. Tsaousis¹

1. *Laboratory of Molecular and Evolutionary Parasitology, RAPID group, School of Biosciences, University of Kent, Canterbury, Kent, UK*

Blastocystis is an obligate anaerobic unicellular eukaryote that belongs to Stramenopiles and can inhabit the gastrointestinal tract of both humans and animals. However, its pathogenicity still remains a controversial subject. *Blastocystis* was considered to be a member of normal intestinal flora in the past but reports about its pathogenicity vary greatly amongst different geographic areas. *Blastocystis* can live in the gastrointestinal tract for weeks or years and symptoms can include abdominal pain, weight loss and diarrhoea. However, despite its occurrence as a parasite/organism in various hosts, there is still very little known about its host specificity, geographic distribution, genetic diversity and cell biology. *Blastocystis* has adapted to its anaerobic environment by acquiring, for example, a functional cytosolic sulphur utilisation factors' (SUF) system from non-pathogenic archaea to synthesize Fe/S clusters under oxygen stress. Other unorthodox characteristics of *Blastocystis* involve its organelles and more specifically the diminished mitochondrion-related organelles (MROs). As a result, *Blastocystis* seems to lack the classic aerobic mitochondrial pathways. Nevertheless, *Blastocystis* MROs unconventionally contain enzymes found in normal mitochondria as well as enzymes typically found in hydrogenosomes, which are normally present in anaerobic protists. Recent studies have shown that *Blastocystis* possesses pathways of an incomplete oxidative phosphorylation chain, a partial Krebs cycle, amino acid and fatty acid metabolisms and an iron/sulphur (Fe/S) cluster assembly. Transcriptomic and genomic analysis have predicted the presence of 115 and 750 proteins respectively involved in those pathways. However, despite these only a few proteins have been successfully localised in *Blastocystis* MROs. The purpose of this project is to investigate the evolutionary adaptations of *Blastocystis* and its MROs under various environmental conditions. Using proteomic studies will try to characterise the key pathways involved in *Blastocystis* MROs and identify the presence or absence of mitochondrial-related proteins. Furthermore, will try to confirm these proteins by cloning and expressing them in complementary yeast studies. These data will present the first comprehensive investigation on the unique anaerobic adaptations of *Blastocystis* mitochondria.