

# **Ancient adaptive lateral gene transfers in the symbiotic *Opalina* - *Blastocystis* lineage in Stramenopiles**

**Naoji Yubuki<sup>1</sup>, Guillaume Reboul<sup>1</sup>, Purificación López-García<sup>1</sup>, Nicolas Pollet<sup>2</sup> and David Moreira<sup>1</sup>**

<sup>1</sup> *Unité Ecologie Systématique Evolution. CNRS - Université Paris-Sud, France*

<sup>2</sup> *Laboratoire Evolution Génomes Comportement Ecologie. CNRS - Université Paris-Sud, France*

Lateral gene transfer (LGT) is very common and evolutionarily important in bacteria and archaea and can play an important role for adaptation to new environments. In eukaryotes, the role of LGT remains highly debated, but recent research supports that gene transfer from bacteria to a wide diversity of eukaryotes may be much more common than previously appreciated. However, most of this research was focused on animals and there is room for improvement to better understand the true phylogenetic and functional impact of bacterial genes in neglected protist groups.

Eme et al. (Curr Biol 2017, 27:807-820) recently reported 74 cases of LGT from prokaryotes to the human parasitic stramenopile *Blastocystis* sp. and suggested that the new functions acquired by LGT facilitated the adaptation to the human gut. Although several of those genes were inferred to have been transferred to a common ancestor of several *Blastocystis* lineages, the time of their acquisition remained unclear due to the poor taxon sampling available for non-photosynthetic stramenopile lineages. Ribosomal RNA phylogenetic analyses suggest that *Blastocystis* is related to the symbiotic slopalinida, represented by genera such as *Opalina*, found in intestines of frogs and toads. The Slopalinida-*Blastocystis* assemblage is probably sister to Placidida, a lineage including small free-living marine flagellates such as *Wobblia* and *Placidia*. Here we report the first transcriptome sequences of an Slopalinida species; *Opalina* sp. from the frog *Xenopus tropicalis*. Using phylogenomic approaches, we identified at least seven genes transferred from prokaryotes to a common ancestor of *Opalina* and *Blastocystis*, including a gene functioning in anaerobic metabolism in a mitochondria related organelle. These data suggest a very early origin for some gene transfers from bacteria and that LGT probably facilitated to explore animal gut environments before the divergence of Opalinata and *Blastocystis* from a free-living ancestor.