

Studying marine:freshwater transitions

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Choanoflagellates are ubiquitous and one of the most important groups of heterotrophic pico- and nanoplankton. Despite their widespread distribution, the known biodiversity of freshwater choanoflagellates is surprisingly low and only a few closely related species have been described. However, the phylogeny of choanoflagellates remains poorly known and the most comprehensive phylogenies include less than 60 species (Carr *et al.*, 2017). These phylogenetic reconstructions only include a small part of the real biodiversity of choanoflagellates and some lineages are underrepresented. The biodiversity of freshwater choanoflagellates is particularly underrepresented in such phylogenies and just one major group contains all but one of the freshwater species included. Previous studies have estimated a high hidden biodiversity amongst opisthokonts, and especially amongst choanoflagellates (del Campo and Ruiz-Trillo, 2013), and most of the choanoflagellate sequences retrieved from environmental samples belong to uncultured or unknown species. The phylogenetic placement of short read sequences from eDNA provides a very useful methodology for the analysis of the real biodiversity of choanoflagellates present in an environment. We use a combination of eDNA sequencing and analysis and salinity resistance experiments to study marine:freshwater transitions, in order to study the evolutionary origin of freshwater choanoflagellates and to unravel their phylogenetic relationships.