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Single Cell Genomics and Transcriptomics for Unicellular Eukaryotes

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Despite their small size, unicellular eukaryotes have complex genomes with a high degree of plasticity that allow them to adapt quickly to environmental changes. Unicellular eukaryotes live with prokaryotes and higher eukaryotes, frequently in symbiotic or parasitic niches. To this day their contribution to the dynamics of the environmental communities remains to be understood. Unfortunately, the vast majority of eukaryotic microorganisms are either uncultured or unculturable, making genome sequencing impossible using traditional approaches. We have developed an approach to isolate unicellular eukaryotes of interest from environmental samples, and to sequence and analyze their genomes and transcriptomes. We have tested our methods with six species: an uncharacterized protist from cellulose-enriched compost identified as *Platyophrya*, a close relative of *P. vorax*; the fungus *Metschnikowia bicuspidate*, a parasite of water flea *Daphnia*; the mycoparasitic fungi *Piptocephalis cylindrospora*, a parasite of *Cokeromyces* and *Mucor*; *Caulochytrium protosteloides*, a parasite of *Sordaria*; *Rozella allomycis*, a parasite of the water mold *Allomyces*; and the microalgae *Chlamydomonas reinhardtii*. Here, we present the four components of our approach: pre-sequencing methods, sequence analysis for single cell genome assembly, sequence analysis of single cell transcriptomes, and genome annotation. This technology has the potential to uncover the complexity of single cell eukaryotes and their role in the environmental samples.