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Molecular quantification of chytrid fungi from gut content of freshwater zooplankton

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Earlier studies identified small phytoplankton as the only important food source for freshwater crustacean zooplankton. However, recent findings suggest that zooplankton taxa have much broader diets, including diverse prey groups, such as bacteria, aquatic fungi, pollen, heterotrophic flagellates, protozoans, rotifers and nauplia. Such pronounced omnivory should have profound consequences for the food web structure and ecosystem functioning. Yet, no quantitative data exists on the relative importance of all these alternative prey in freshwater planktonic food webs. Our research has focused on the recently discovered Mycoloop – a link between chytrid fungi and zooplankton, where chytrids grow on food sources that cannot be used by zooplankton directly. Chytrids produce free-swimming zoospores, which are considered to be a high-quality food source for zooplankton due to their high content of poly-unsaturated fatty acids (PUFAs). The Mycoloop consists of two main pathways: (1) saprotrophic chytrids mediate energy transfer to zooplankton from seasonal terrigenous inputs of organic matter into lakes, such as pollen and leave litter; (2) chytrid parasites of large inedible phytoplankton convert phytoplankton biomass to ingestible zoospores and/or make it available via fragmentation. We have developed and validated quantitative real-time PCR assays to quantify chytrid zoospores from gut content of the most common zooplankton groups: daphnids and copepods. This method enables for the first time to quantitatively assess the contribution of chytrid fungi to zooplankton diet using field-collected samples.

Key words: freshwater zooplankton; trophic interactions; zooplankton diet; quantitative real-time PCR; gut content analysis; aquatic fungi

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