

Publication

High-throughput sequencing of litter and moss eDNA reveals a positive correlation between the diversity of Apicomplexa and their invertebrate hosts across alpine habitats

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Author(s) Singer, David; Duckert, Clement; Hedenec, Petr; Lara, Enrique; Hiltbrunner, Erika; Mitchell, Edward A. D.

Author(s) at UniBasel [Hiltbrunner, Erika](#) ;

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A high diversity of Apicomplexa was recently found in tropical soils presumably reflecting the diversity of their invertebrate hosts, but such patterns have not been explored in colder regions. We analysed the diversity of Apicomplexa and their potential metazoan hosts in litter and mosses collected in 11 different alpine habitats using an eDNA metabarcoding approach. The abundance and diversity of Apicomplexa phylotypes and of their potential invertebrate hosts were positively correlated. This confirms that eDNA metabarcoding is a useful tool to explore the unknown biodiversity of free-living eukaryotes, as well as potential host-parasite interactions. Future studies should aim at describing this diversity using a combination of morphological and molecular approaches.

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