

Soil naked amoeba in rare environments: Enormous diversity of mostly unknown species

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Abstract

Naked amoeba (*Gymnamoeba*) occupy key positions in soil food webs; they are the major consumers of bacterial production in soil due to their amoeboid morphology, small size, high abundance and fast turnover rates. Despite their important functions for nutrient cycling as the base of the heterotrophic eukaryotic food web in soil we only have a vague idea on the identity of the dominant taxa. This lack of knowledge is caused by methodological difficulties in cultivation and quantification in the opaque soil environment as well as a lack of taxonomic expertise. However, recent developments in molecular techniques now promise to reduce this methodological gap on this largely unknown trophic link in the soil food web.

We aim to combine morphological and molecular methods to increase the knowledge on *Gymnamoeba* in soils as part of the EU-project EcoFINDERS.

We investigated the diversity of *Gymnamoeba* in high altitude soils from Tibet, provided by the University of Beijing as a satellite partner. We established parallel enrichment cultures of four different soils to cultivate and enumerate *Gymnamoeba*. Cultures were microscopically grouped into morphotypes supplemented by more detailed molecular information, i.e. sequences of the 18s rDNA.

Conditions in the soils investigated were extreme in many respects; first, soils were investigated only after one year; second, soil water contents were very low, generally below 10 percent; third, samples were taken from very high altitudes of up to 5033 m. Consequently, the abundance of *Gymnamoeba* was low with a general average of 1407 amoeba g⁻¹ dry soil. However, the diversity of *Gymnamoeba* extracted was enormous: Most known morphotypes of soil *Gymnamoeba*, roughly representing phylogenetically related organisms, were recovered. However, sequences revealed that almost all cultures represent species new to science. This study suggests that a plethora of new amoeba still await discovery, not even mentioning distinct functional differences.