



Structure and function of archaeal communities in natural and agriculturally used soil ecosystems

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Since the 1990ies Archaea (formerly called *Archaebacteria*) are considered as an independent domain in the biosphere which occur exclusively in extreme environments (e.g. cold/hot; acidic/alkaline; anoxic). With the advent of cultivation-independent, molecular techniques the picture of Archaea has changed: Archaea could be detected in various natural and anthropogenically influenced terrestrial ecosystems, such as arable, grassland and forest soils, hence Archaea can be considered as ubiquitous soil organisms and are involved in many nutrient cycles, mainly carbon and nitrogen transformations.

We are applying a phospholipid biomarker approach based on phospholipid etherlipids (PLEL) to estimate archaeal biomass in soils and to assess the proportion of Archaea of total microbial biomass. It turned out that Archaea accounted up to 10% of the microbial biomass in cultivated, oxic soils and are therefore important members of soil microbial communities. By using molecular techniques based on community DNA and RNA it could be shown that methane fluxes are highly correlated with archaeal activities.

In this contribution we will present data obtained from studies dealing with natural and agriculturally used soil ecosystems. The objectives were to analyze the effects of a) soil type b) plant vegetation c) organic matter quantity and quality d) fertilisation levels on archaeal communities and function (C-fluxes: methane, organic matter

degradation).