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Linking Microbial Biofilms to Nitrate Removal in Groundwater Sediments

A fundamental goal in the field of microbial ecology is to link the activity of specific microorganisms to processes occurring within an ecosystem. This project aims to identify the drivers of community structure and succession by identifying the metabolically active fraction of microbial communities from both pure and contaminated groundwater wells. The groundwater samples include a variety of contaminants, the most important of these for this experiment being nitrate. The use of four diverse wells in conjunction with enumeration and sequencing of transnationally active microorganisms, activity assays, and geochemical measurements will allow for the explanation of the mechanisms controlling for shaping community structure and function. Multiple assay comparisons will be used to achieve an accurate characterization of the active microbial communities in the samples, and will ultimately be applied to continuous sediment cores from pure and contaminated wells. A combination of methodological approaches will be used to evaluate the active fraction of microbial communities, as well as the associated rates of activity from the pure and contaminated wells. Biolog Microbial Identification System will be used to biochemically test and identify a broad range of bacteria. The visualization and sequencing of translationally active bacterial, archaeal, and denitrifying cells was studied by applying bioorthoganol non-canonical amino acid tagging (BONCAT). For contaminated wells large proportions of the community were identified as translationally active however, specific rates of activity were low. Total cell abundances ranged from 1.11-2.07 X 10^5 cells/mL with 73-84% of the community being transnationally active.