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Analysis of microbial community composition based on 16S rRNA profiling via Nanopore sequencing

At the Archaea Centre in Regensburg, we routinely isolate and cultivate new archaeal organisms. However, after years of cultivation and isolation of over 1500 archaeal species, the question arises whether an environmental sample contains new archaeal species of interest and whether time-consuming cultivation attempts are justified. In order to gain information about the microbial composition (ratio bacteria to archaea) and identity of organisms in a sample prior to cultivation, we established a combined 16S rRNA-based qPCR and sequencing protocol. Notably, we employed the single-molecule long-read sequencing technology introduced by Oxford Nanopore Technologies.

Based on three case studies, I will discuss this methodological approach and show how 16S rRNA profiling by Nanopore-based sequencing provides an extremely fast and convenient means to determine the microbial composition and identity of organisms in a habitat without the necessity to isolate and cultivate these organisms.

Furthermore, I will briefly show how Nanopore-sequencing compares to other next-generation sequencing techniques when whole genome are to be sequenced and assembled. Notably, we also established native RNA-sequencing based on the Nanopore-sequencing technology, which provides unprecedented insights into the RNA biology of microbial cells and supports the genome annotation process.