

Analysis of Microbial Communities from Deep Aquifers using DNA Sequence Data

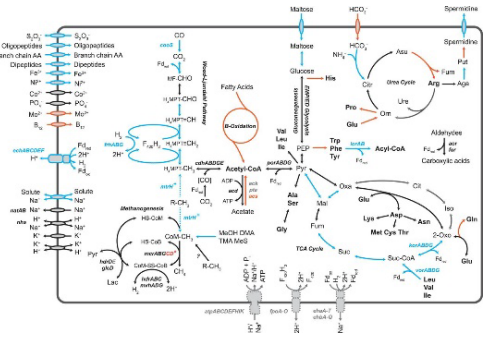
Background

Microbial communities in deep aquifers consist mainly of bacteria and archaea adapted to extreme conditions like high pressure and low nutrients. Their slow metabolism and physical adaptations help them survive over long timescales. Studying these communities enhances our understanding of subsurface life and groundwater quality. Microbial communities in coal bed methane (CBM) aquifers play a crucial role in methane production by breaking down organic material in coal through microbial consortia. Their activity is influenced by factors such as water chemistry, temperature, and nutrient availability. Understanding these microbial processes is essential for optimising methane recovery and managing groundwater quality in CBM reservoirs.



Techniques

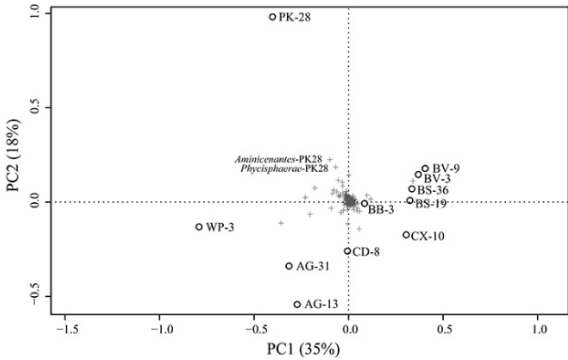
Studying these deep aquifer microorganisms is challenging due to their inaccessibility, low biomass, and extreme environmental conditions. Traditional culturing techniques are inadequate because many subsurface microbes are slow-growing or have yet to be cultured in the lab. While taxonomic gene sequence data (types of microorganisms) provides insight into microbial diversity, is often biased towards highly abundant and lacks metabolic information (potential growth substrates), making it insufficient for understanding microbial community dynamics.



Metagenomics (sequencing of the entire microbial community’s DNA) overcomes these challenges by enabling the direct extraction and sequencing of environmental DNA, providing a comprehensive view of microbial diversity and function. This approach allows us to identify unculturable microbes, analyse their metabolism, and understand microbial interactions within these aquifers. By bypassing cultivation barriers and taxonomy gene limitations, metagenomics enhances our ability to study and characterise these hidden microbial ecosystems.

Deep Aquifer Systems

We have previously used microbial analysis techniques to study the microbiomes of deep aquifers across several Australian geologic formations, including the Surat and Bowen basins, to understand community structure and metabolic capabilities. In these aquifers, we identified previously unknown microorganisms and characterized their metabolic potential using bioinformatics techniques (Evans et al., 2015; Robbins et al., 2016). Through this research, we provided a biological basis for methane generation in these environments and demonstrated the ability of microbial communities to metabolise substrates introduced into the deep aquifers (Robbins et al., 2016).



Additionally, we compared microbial communities across sampling sites using a metagenomic approach to assess changes resulting from substrate amendments (Robbins et al., 2016). Beyond reconstructing microbial communities that inhabit depths of approximately 800 metres below the surface, we have also produced industry reports from monitoring wells to distinguish microbial communities affected by surface water contamination.

Microbial Community Analyses Service

We offer sample collection, in house DNA sequencing, in house data analysis and report writing, specifically

- Collection of biological materials either by filtration or bulk sample collection
- Barcode sequencing of the microbial community to identify community structure
- Metagenomic DNA sequencing to identify microbial community structure and function
- Informatic comparisons of microbial communities to identify structural and metabolic differences
- Expert report writing of microbial community characteristics linked to ecological significance

## **Publications**

Examples of our work using metagenomic techniques to study microbial communities from Australian aquifers:

PN Evans, DH Parks, et al. (2015). Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. *Science* 350: 434-438

SJ Robbins, PN Evans, et al. (2016) Genome-centric analysis of microbial populations enriched by hydraulic fracture fluid additives in a coal bed methane production well. *Frontiers in Microbiology* 7:731

## **Contact**

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