



focus on **NRM** research

Microbiological communities in vertosol soils & aquifers

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What are you researching?

We are studying soil microbiological communities in the upper cotton soil ecosystem (Vertosol soil) from different agricultural fields and areas of native vegetation. Plus we are analysing the microbiological ecosystems in aquifers. The primary emphasis of the project is on determining the abundance and diversity of microbes involved in methane oxidation and production.

We started analysing the soil and groundwater microbiology to enable better interpretation of the air and groundwater methane surveys in the Condamine Catchment. Our preliminary results have shown that soil bacterial and archaea populations under native vegetation, traditionally fertilised irrigated cotton crops, and bio-fertilised soils are all significantly different. This raises many questions relating to soil health, disease resistance under climate variability and change, optimal nutrient uptake, and greenhouse gas production from agricultural soils.

What have you found?

Little is known about how farming practices have altered the bacterial and archaea populations in Vertosol soil. Yet the microbiological community controls soil health, plant disease resistance, nutrient uptake, and the production and consumption of greenhouse gases.

Preliminary findings:

A high diversity of aerobic methanotrophic bacteria belonging to Type 1 (Gammaproteobacteria, 2-6 percent relative abundance to the overall microbial community) and Type II methanotrophs (Alphaproteobacteria, 4-18 percent relative abundance) were observed in all soil samples. The relative abundances of single methanotrophic species

were significantly different between soil samples, whereas the composition of the overall methanotrophic community was quite similar. Furthermore, methane-producing archaea (methanogens) were detected in almost all soil samples in very low abundance (0-0.5 percent relative abundance) suggesting biogenic methane production is a negligible process in the agricultural cotton soil.

Interestingly, most of these sequences were recovered within the order Methanosarcinales and could potentially be affiliated with anaerobic methanotrophic archaea oxidising methane using e.g. nitrate, iron, or sulfate as electron acceptors. A higher abundance (7 percent relative abundance) and diversity of methanogenic archaea, mainly associated with hydrogenotrophic methanogens, were observed in the bio-fertilised soil that would contribute of methane formation and methane cycling in that soil habitat.

The irrigation water samples from every borehole sampled harboured a low-diversity methanotrophic community only associated with the order Rhizobiales with a relative high abundance of 4-12 percent to the overall microbial community. No methane-producing archaea were observed.

Where do I go for more information?

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