

A joint initiative of



Australian Government
Department of Agriculture,
Fisheries and Forestry



Reducing Emissions from Livestock Research Program

Methanotrophs in natural ecosystems and their role in ruminant methane mitigation

Enteric fermentation of methane by ruminant animals represents a major source of anthropogenic methane production. Methane produced in this manner is released to the atmosphere where it is highly efficient at absorbing thermal radiation, which consequently increases the global surface temperature. Although many different strategies to control ruminant methane emissions have been considered, few are currently considered viable. Obligate and facultative methane oxidising bacteria (MOB) and anaerobic methane oxidising archaea (ANME) play a fundamental role in the carbon cycle by metabolising methane before it is released into the atmosphere. Because of this, methanotrophic microorganisms represent a novel biological control agent in mitigating ruminant methane emissions.

This project aims to characterise methanotrophic microorganisms from a range of environments, and to subsequently determine the metabolic activity of these microorganisms under *in vitro* rumen-like conditions.

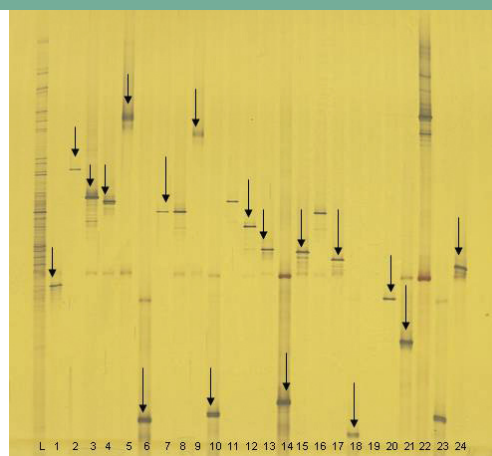


Figure 1: Denaturing gradient gel electrophoresis (DGGE) of hypothetical Type I MOB cloned inserts from the Nudgee Landfill soil 0–10cm depth. L: Nudgee Landfill soil 0–10cm community profile; 1–24: PCR products amplified from extracted plasmid DNA of individual clones. The arrows indicate clones with distinct inserts.
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The program

The Reducing Emissions from Livestock Research Program is a national collaborative program focused on developing practical on-farm options for significantly reducing emissions from livestock while simultaneously increasing productivity. The research will develop more accurate data on emissions from sheep and cattle and the levels of mitigation achieved using a range of strategies.

The Reducing Emissions from Livestock Research Program is supported by funding from the Australian Government under its Climate Change Research Program.

Project objective

Evaluate the potential for methanotrophs to reduce ruminant methane emissions.

Progress

The initial task in this PhD project was a literature review to report on:

- the impact of ruminant methane emissions on the environment
- previous control strategies designed to control these emissions
- the microbiology and metabolism of aerobic methanotrophic bacteria and anaerobic methanotrophic archaea
- preliminary data that suggest methanotrophs may exist naturally in the rumen and in the kangaroo foregut
- molecular techniques to study methanotrophic microorganisms in the environment
- a detailed overview of the basic direction the project will take over the three-year duration of the PhD

Currently, several variable samples have been collected and processed to extract microbial genomic DNA. These include planktonic water and sediment samples from a local piggery, in addition to faecal and rumen samples from cattle. Molecular diagnostic methods, such as polymerase chain reaction (PCR), have been used to detect the presence of methanotrophic DNA in the samples. Specifically, a thorough diagnostic procedure has been designed to target molecular marker genes that encode for functional enzymes associated with methanotrophy (soluble and particulate methane mono-oxygenase) and phylogenetic 16S ribosomal RNA (rRNA) marker genes.

Preliminary results from 16S rRNA gene screening suggest that aerobic methanotrophic bacteria are indeed present in the piggery water and sediment samples and DNA from DGGE gels has been cloned (Figure 1) and is in the process of being sequenced. The PCR protocols for the functional gene screening are in the process of being optimised. Future directions will identify the methanotrophic microorganisms present in these samples from their DNA sequences and an attempt will be made to obtain at least some of these bacteria in culture.

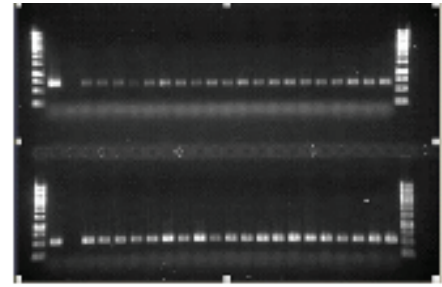


Figure 2: Gel electrophoresis analysis of Type I (top) and Type II (bottom) methanotrophic 16S rRNA genes amplified via PCR. Lanes 1 and 25: 1 kb DNA ladder; lanes 2: positive control; lanes 3: negative control; lanes 4–24: each lane corresponds to a separate environmental sample.



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