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Learning from the locals: marsupials and metagenomics

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Australia's 'model' marsupial, the Tammar wallaby *(Macropus eugenii),* may provide clues as to why marsupials are thought to produce less greenhouse gas emissions, according to recent CSIRO research in the new field of 'metagenomics'.

The Tammar wallaby may be Australia's 'model' marsupial

The agricultural sector accounts for some 16 per cent of Australia's total greenhouse gas emissions, 67 per cent of which are methane emissions from livestock. Much Australian research on anthropogenic methane emissions has therefore focused on sheep and cattle. However, scientists at CSIRO's Division of Livestock Industries (CLI) are now excited about the 'new' microbiology they've found in the foregut of the Tammar wallaby.

The digestive systems of macropods (kangaroos and wallabies) are often compared to those of domesticated livestock, especially sheep and cattle, because both groups have evolved to subsist on grasses and shrubs with a large cellulose, and hence fibre, component.

Their key adaptation is the microbiology that supports the deconstruction and fermentation of this food in large, specially designed compartments. This foregut environment tends to be anaerobic, maintains a constant temperature and pH suited to the microbial processes it harbours, and moves gut contents through peristalsis.

However, there are key differences between the two types of animals in terms of digestive anatomy and processes. Plus, macropods generate less methane during digestion than ruminant herbivores. In one study, methane production accounted for about one per cent of macropod digestible energy intake, compared with about 10 per cent for sheep. [1]

The CLI project [2] , lead by Professor Mark Morrison and Chris McSweeney, emphasises metagenomics, which combines DNA sequencing with molecular and computational biology to better understand the structure and function of complex microbial communities. The Tammar wallaby research aims to characterise the genomic content of the foregut's consortium of microbes, or 'microbiome'.

The team wants to know how these microbes break down plant fibre. Methanogens – microbes that produce methane – are important to this process, because they are believed to be hydrogen scavengers. They produce methane using the molecular hydrogen generated by other microbes during rumen fermentation as a source of energy.

Previous research has suggested that macropod microbiomes might possess unique protozoa, bacteria and archaea (single-celled organisms in the Archaea taxonomic domain). But, as Prof. Morrison explains, 'our knowledge of the evolutionary adaptations of Australia's native herbivores to their environment has been compromised until now, because we have had virtually no understanding of their gut microbiomes and the genetic potential supporting their nutrition and well being.'

The CSIRO team have compared metagenomic libraries of the Tammar wallaby foregut microbiome with those of ruminants, and hashave identified several unique bacterial lineages.

'The repertoire of microbial enzymes responsible for breaking down complex carbohydrates in the Australian macropods is different from those of ruminant livestock, says Prof. Morrison. 'And, it appears that the number of methane-producing archaea in the Tammar wallaby is less than what we typically see in sheep and cattle.'

Prof. Morrison says future research may include metagenomic studies of the host–microbe relationships in other Australian herbivores.

'Australia's native herbivores are some of our nationally unique and greatest natural resources, which must be protected,' he says. 'These types of metagenomics studies are therefore important facets of CSIRO's biodiversity research, and might also contribute novel biotechnologies relevant to future agribusiness and bioindustry, including:

1. enzymes that support a more rapid and extensive deconstruction of plant biomass in support of fuel ethanol production or other types of industrial fermentations
2. microbes that might be used as probiotics to improve feed digestion and nutrient retention
3. enzymes and/or microbes that provide specialised biotransformations of polyphenolic compounds and lignins'.

[1] Von Englehardt W, Wolter S, Lawrenz H and Hemsley JA (1978). Production of methane in two non-ruminant herbivores. *Comparative Biochemistry and Physiology*, **60**, 309–311. Pergamon Press.

[2] The CLI project is a collaboration with the US Department of Energy, and is supported by CSIRO's Chief Executive Office Science Team and Transformational Biology Capability Platform

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