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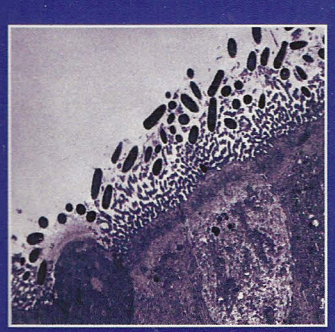

Gut Microbiology:

new insights into gut microbial ecosystems

7th Joint Symposium organised by the **Rowett Institute of Nutrition and Health,** University of Aberdeen, Scotland (UK) & the **Institut National de la Recherche Agronomique,** Clermont-Ferrand-Theix (France)

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Design of a functional DNA microarray targeting the methanogenic community of complex anaerobic ecosystems

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Methane is a potent greenhouse gas produced in the environment, e.g. natural anoxic lakes and marshes, but the most important source is due to human activity. Farm animals, particularly ruminants, produce substantial amounts of methane. In gastrointestinal tracts, methane is produced by methanogenic archaea when feeds are fermented. To improve our understanding of the rumen methanogenic community, we developed a DNA microarray based on a functional gene involved in methanogenesis. In this context, 530 oligonucleotides (24 to 59 mers) targeting the methyl-coenzyme M reductase alpha subunit gene (mcrA) were designed using Metabolic Design, HISPOD and GoArrays softwares. These dedicated softwares developed in our laboratory allowed the design of specific probes targeting known sequences and also explorative probes capable of hybridizing to sequences not yet available in databases but potentially present in complex communities. This functional microarray covers the diversity of the five known methanogenic archaeal orders: Methanobacteriales, Methanomicrobiales, Methanosarcinales, Methanopyrales and Methanococcales. It was validated using mcrA gene fragments amplified from members of the Methanobacteriales, Methanomicrobiales, Methanosarcinales and Methanococcales. Our results showed an excellent specificity and sensitivity of the designed probes towards the species tested, providing a species-specific fingerprint tool. This DNA microarray, developed to study the structure and dynamics of methanogens, can be applied to the rumen and other digestive tracts but also to a wide variety of aquatic and terrestrial methanogenic ecosystems.

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Correlation of rumen microbial community structure with milk fatty acid composition

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The conversion of dietary polyunsaturated fatty acids (PUFA) to saturated fatty acids in the rumen (biohydrogenation) is of concern because of the perceived positive implications that PUFA and conjugated linoleic acid (CLA) in ruminant products have on human health and the negative implications of saturated fatty acids. Bacteria of the *Butyrivibrio* group are thought to be primarily responsible for biohydrogenation. Other bacteria and fungi have sometimes been implicated in biohydrogenation, but the relative importance of these organisms in determining the fatty acid composition of ruminant products has never been quantified. The aim of this work was to compare milk fatty acid composition with the composition of the rumen microbial community, rumen metabolites and feed composition across 7 dairy trials carried out in MTT, Jokioinen, Finland and the University of Reading, UK. The question being asked was - "Can we relate milk fatty acid composition to the composition of the ruminal microflora, even across diets?" Cows received basal diets of maize or grass silage supplemented with concentrates and vegetable or fish oil. Total bacteria, *Butyrivibrio* spp., *Streptococcus bovis*, *Propionibacterium acnes* and *Megasphaera elsdenii* were analyzed by qPCR. All data were compiled into a common dataset comprising >100 individual parameters. A multivariate analysis 'heat-map' was constructed to illustrate correlations between measurements. Within trials, there were associations between bacterial population densities and milk fatty acid composition, but between-trial comparisons revealed a predominant influence of diet rather than microbial numbers. The unequivocal answer to the question posed above is, "No, diet is most important."