

## **Applications of metagenomics to gut microbial communities**

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Complex anaerobic microbial communities are responsible for the breakdown of otherwise non-digestible plant material in the gut of farm animals and man. In herbivores, especially ruminants, these communities provide most of the energy obtained from the diet, while in humans the large intestinal community plays an important role in mediating the effects of diet upon health. The extreme diversity and oxygen sensitivity of micro-organisms within these communities make them obvious targets for metagenomic approaches. Major sequence-based projects on human gut metagenomes, funded by the EU and in the USA, have produced new information on the relationship between microbiota diversity, metabolic health and gut health. Meanwhile functional screening approaches, although more demanding of time, have the potential to reveal new genes and activities, while metagenome data can also be linked with targeted analyses and analyses of gene products (eg. metaproteomics). The decreasing costs and increasing speed of nucleic acid sequencing offer great opportunities for the analysis of gut samples, but it should be noted that interpretation and annotation of sequence data continues to rely critically on knowledge obtained from cultural microbiology and biochemistry.