Deep metagenomic sequencing of multiple ruminant guts reveals species-specific microbiomes

Mick Watson (1) and John Wallace (2) 1.   ARK-Genomics, The Roslin Institute, Easter Bush, University of Edinburgh, EH25 9RG 2. Rowett Institute of Nutrition and Health, Greenburn Road, Bucksburn, Aberdeen, UK

Ruminant species such as cattle, sheep, deer, goats and reindeer represent a fascinating opportunity to study gut function and metagenomics. With a solely vegetarian diet, the gut microbiome of ruminants is perfectly adapted to digest and gain energy from plant material. However, different animals have different diets (e.g. grass vs lichen) which require different microbes to digest. We have deep-sequenced the rumen gut microbiome of several ruminant species using the Illumina HiSeq 2000 system, generation several hundred gigabases of sequence data in the process. Here we describe bioinformatic investigations into these data, including assembly into large contigs, prediction and annotation of genes and taxon assignment. We show that the vast majority of sequence data comes from as-yet uncharacterized bacterial species, representing huge potential for discovery of novel enzymes. Finally, we show that ruminants can be clustered together according to their gut microbiome structure and species abundance. Bio would be: Mick Watson is an established bioinformatician, with 15 years' experience in industry and academia. He was involved in the implementation and management of pipelines for functional genomics at GlaxoWellcome, SNP discovery at Incyte Genomics and Target Discovery at Paradigm Therapeutics, before joining the Institute for Animal Health as Head of Bioinformatics in 2002. He has been Director of ARK-Genomics since July 2010, and has won several grants to create a bioinformatics research group allied to the ARK-Genomics facility. His group's research focuses on the use of computational and mathematical techniques to understand genome function with an emphasis on systems of relevance to animal health and food security. Publications include both primary bioinformatics research papers and collaborative research in a variety of technical and scientific journals. The outputs from his research have included novel algorithm development, as well as the application of bioinformatics techniques to microbial and meta-genomics. Amongst other projects, he is Roslin PI on a Technology Strategy Board project to use NGS to discover biomass-degrading genes from rumen gut microbiota. To date, the project has generated 300Gb of sequence data, the assembly of which has produced over 3.6 million novel proteins. Cheers Mick