

Understanding the evolution and host adaptation of the human gut microbiome

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Department/Institute: Veterinary Medicine

Research area: Bioinformatics, Microbiology, Genomics

Project outline:

The human gut microbiome represents a large and diverse ecosystem of microbial species with a wide-reaching impact in human health and disease. As the gut microbiome is now recognized as an important player in the maintenance of human health, new therapies are being developed to promote the intestinal colonization and engraftment of gut microbial species deemed beneficial to health. With this purpose in mind, there is a need to better understand the ecological and evolutionary principles that govern the assemblage and structure of the intestinal microbiome. In particular, the main factors and functional features essential for survival and successful colonization of the human intestinal tract remain largely unknown.

The aim of this project is to explore the evolution and host adaptation of the gut microbiome through a large-scale analysis of hundreds of thousands of microbial genomes from the human gut, skin and oral cavity, as well as those from other animals and environments. This will involve the development and application of bioinformatics pipelines for performing microbial genome-wide association studies, protein annotation, functional prediction and metabolic modelling. Candidate species and genes linked to human health will be further experimentally tested using microbiology and molecular biology techniques. Ultimately, this project will provide new crucial insights into the genomic adaptation of the gut microbiome that will aid the development of new strategies to improve the efficacy of targeted microbiome-based therapeutics.

BBSRC DTP main strategic theme: Bioscience for an integrated understanding of health

BBSRC DTP secondary strategic theme: Understanding the rules of life, Transformative technologies