The human gut contains a vast number of microorganisms that have been collectively characterized as the ‘gut microbiota’ through the use of high-throughput DNA sequencing technologies. All three kingdoms of life, Archaea, Bacteria, and Eukarya, are represented in the gut microbial community. An estimated $10^{11}$ individual bacteria belonging to over 1,000 species reside in the mammalian gut with a collective genome predicted to be 150-fold greater than that of its host. Humans have coevolved to exist with our gut microbiota in a mutualistic relationship, where we provide a uniquely suited environment in return for physiological benefits provided to us by our gut microbiota. Despite its importance in maintaining the health of the host, growing evidence suggests the gut microbiota may also be an important factor in the pathogenesis of various diseases, a number of which have shown a rapid increase in incidence over the past few decades such as diabetes, inflammatory bowel diseases, colon cancer, atherosclerosis, and asthma. The composition of the gut microbiota has been shown to be ‘dysbiotic’, with an alteration in community structure, in a number of diseases, although studies are still required to demonstrate that dysbiosis plays a role in the pathogenesis of human disease rather than simply being a result of the disease process. Nevertheless, evidence in animal models suggests that the former may be true, at least under certain circumstances.

Factors including age, genetics, and diet may influence microbiota composition. Of these, diet is easiest to modify, and presents the simplest route for therapeutic intervention. In studies to be presented, we used diet inventories and 16S rDNA sequencing to characterize fecal samples from 98 individuals [1]. Fecal communities clustered into previously described enterotypes [2] were distinguished primarily by levels of *Bacteroides* and *Prevotella*. Enterotypes were associated with long-term diets, particularly protein and animal fat (*Bacteroides*) versus simple carbohydrates (*Prevotella*). Although the distinction of enterotypes as either discrete clusters or a continuum will require additional investigation, numerous studies...
have demonstrated the coexclusion of the closely related *Prevotella* and *Bacteroides* genera in the gut microbiota in healthy human subjects [3], where *Prevotella* appears to be a discriminatory taxon for residence in agrarian societies [4, 5]. A controlled feeding study of 10 subjects showed that microbiota composition changed detectably within 24 h of initiating a high-fat/low-fiber or low-fat/high-fiber diet, but that enterotype identity remained stable during the 10-day study. Thus, alternative enterotype states are associated with long-term diet. Interestingly, we have also shown that diet is also associated with alteration of the human gut virome that is primarily composed of bacteriophage [6].

Having demonstrated the impact of diet on human gut microbiota composition, we are now focusing on the impact of a dietary intervention known to be effective in the treatment of Crohn's disease, namely a defined formula diet, on the composition of the human gut microbiota. The results of these studies may help to identify bacterial taxa that play a role in the pathogenesis of Crohn's disease and/or serve as biomarkers that may help to predict response to therapeutic interventions. Ultimately, it is hoped these, and other studies, will help to define the 'healthy diet' for individuals genetically predisposed to the development of chronic inflammatory diseases such as inflammatory bowel disease.

References