

# More than just bacteria: The importance of microbial diversity in gut health and disease

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The gut microbiota contains a vast number of microorganisms from all three domains of life, including bacteria, archaea and fungi, as well as viruses. These interact in a complex way to contribute towards both health and the development of disease—interactions that are only now being elucidated thanks to the application of advanced DNA sequencing technology in this field.

"Using novel metagenomic approaches, scientists are at last beginning to characterize the taxonomic abundance and community relationships not only of bacteria, but also the other microbes that inhabit the gut environment,"<sup>1</sup> says Professor Gary Wu, University of Pennsylvania, Philadelphia. "This exciting work is bringing us one step closer to understanding the importance of microbial diversity in intestinal [health](#) and disease and could ultimately lead to new ways of diagnosing and treating gastrointestinal (GI) disease."

His talk was one of the topics presented at the Gut Microbiota for Health World Summit in Miami, FL, USA. On March 8-9, 2014, internationally leading experts discussed the latest advances in [gut microbiota](#) research and its impact on health.

The microorganisms that inhabit the gut can be broadly divided into prokaryotes (bacteria and archaea), bacteriophages (viruses that infect prokaryotes), eukaryotic viruses, and the meiofauna (microscopically small benthic invertebrates that live in both marine and fresh water environments—primarily fungi and protozoa).<sup>1</sup> Of these, bacteria have

been the most extensively studied. The gastrointestinal tract is now considered one of the most complex microbial ecosystems on earth and understanding how the multiple communities interact presents both opportunities and challenges.

"We have known for some time that the bacteria in the gut play an important role in both health and disease," says Prof. Wu. "It is also now becoming clear that the non-bacterial microbiota interacts in a complex way with the bacterial microbiota to contribute to these processes."

### **Viruses in the gut**

The most common viruses in the gut are the bacteriophages. These rapidly-evolving viruses can outnumber bacteria by a factor of 10 to one; they infect and destroy bacterial cells and have the ability to transfer genetic material from one bacterium to another, with potentially profound implications for GI health and disease.

"There is a predator–prey relationship between bacteriophages and bacteria that may play a role in altering the bacterial microbiota in conditions such as inflammatory bowel diseases (IBD)," says Prof. Wu. "The fact that bacteriophages induce immune responses in bacteria and may also transmit genomic material into bacteria that may alter their function makes these [viruses](#) extremely important and we need to know much more about them."

### **Meiofauna in the microbiota**

DNA sequencing techniques have also confirmed the presence of commensal meiofauna in the GI tract that may be important in promoting health and disease.<sup>1</sup> Certain types of meiofauna (e.g. helminths and *Blastocystis*) are thought to protect against IBD by suppressing inflammation, and others believe that increased fungal

diversity may contribute to GI diseases, including IBD.

"Decreases in fungal diversity have been shown to correlate with an increase in healthy bacterial colonisation following probiotic therapy, suggesting niche competition between fungi and [bacteria](#)," says Prof. Wu. "This effect is also evident in the development of mucosal *Candida* infection following antibiotic treatment."

### **Non-bacterial microbes and the future**

Prof. Wu and others believe that the importance of trans-domain interactions in health and disease are only just beginning to emerge. By studying the complex relationships between bacterial and non-bacterial microbes in the [gut](#), it is hoped that a greater understanding of pathogenic mechanisms will be gained, leading ultimately to novel approaches to diagnosis and treatment.

**More information:** <sup>1</sup> Norman JM , Handley SA , Virgin HW. Kingdom-agnostic Metagenomics and the Importance of Complete Characterization of Enteric Microbial Communities. *Gastroenterology*. 2014 Feb 5. pii: S0016-5085(14)00154-1. [DOI: 10.1053/j.gastro.2014.02.001](#). [Epub ahead of print]

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