

Genome analysis will reveal how bacteria in our guts make themselves at home

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Researchers from the Institute of Food Research and The Genome Analysis Centre have published the genome sequence of a gut bacterium, to help understand how these organisms evolved their symbiotic relationships with their hosts.

The relationship between [gut bacteria](#) and the [gastrointestinal tract](#) is one of IFR's main research areas. Key to understanding the role of bacteria in establishing and maintaining gut health is knowledge of how the very close relationship between the bacteria and their hosts has evolved to be mutually beneficial to both.

One [bacterial species](#), *Lactobacillus reuteri*, has been used as a model for studies in this area, and TGAC, a partner of IFR on the Norwich Research Park, has sequenced its genome, funded by the Biotechnology and Biological Sciences Research Council (BBSRC). The collaboration between the two institutes will provide new insights into the genomic basis for host adaptation of *L. reuteri* to the gut.

L. reuteri inhabits the gastrointestinal tract from a large host range, from humans to rodents and birds. Previous work had shown that each [host species](#) has its own subpopulation of *L. reuteri* strains. These strains differ slightly, and are host specific, and the differences between them are driven by evolutionary pressures from the host.

In close collaboration with IFR scientists, TGAC sequenced and assembled the genome of a *L. reuteri* strain obtained from pig to a high

quality draft standard and also provided a full annotation. The annotation is needed to identify which genes carry out which functions in the sequence. Comparisons between different strains of *L. reuteri*, which have already been made available in the major international sequence databases, helped identify a set of genes unique to this particular strain.

The IFR and TGAC researchers are now hoping to use this information to elucidate exactly what it is that restricts certain *L. reuteri* strains to specific hosts.

L. reuteri confers certain health benefits, and has a role in modulating the immune system. A greater understanding of how *L. reuteri* host adaptation will help in efforts to exploit these health benefits, for example in the production of new probiotics.

The gastrointestinal tract contains many millions of bacteria, known collectively as the microbiota. IFR is also developing a model microbiota that is representative of the human colonic microbiota. This will become a powerful tool for investigating the function and interplay of the microbiota within the gastrointestinal system. It will also become an integral part of studies investigating the extent, diversity and function of metabolic diversity in the microbiota.

More information: Genome sequence of a vertebrate gut symbiont *Lactobacillus reuteri* ATCC 53608, Heavens et al, *Journal of Bacteriology* [doi:10.1128/JB.05282-11](https://doi.org/10.1128/JB.05282-11)

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