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## Members of the gut community

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The human gut is home to an astonishing number of [microorganisms](#) - 500 to 1000 bacterial species. Many of these live at peace with their host, providing essential functions for metabolism and the immune system, and they offer an attractive model to study symbiotic evolution. In the March 28 *Science* two groups report genome sequences of members of the human intestinal community.

Jian Xu and colleagues at the [Washington University School of Medicine](#) sequenced the complete 6.26 Mb genome of the Gram-negative anaerobe *Bacteroides thetaiotaomicron*, a dominant gut microbe (*Science* 2003, **299**:2074-2076). It has a predicted proteome of 4779 proteins over half of which have predicted functions. It has an expansion of genes involved in polysaccharide uptake and degradation, as well as environment-sensing systems. There are more glycosylhydrolases than in any other bacteria and this explains the species' role in degrading indigestible dietary polysaccharides. Mechanisms for sensing changes in the gut environment suggest an intimate interaction with the host and other members of the intestinal community.

Paulsen and co-workers at [The Institute for Genome Research](#) in Maryland, sequenced a rogue bug, the vancomycin-resistant *Enterococcus faecalis* (*Science* 2003, **299**:2071-2074). *E. faecalis* is a resilient, Gram-positive bacterium that is resistant to many antibiotics, including vancomycin, and presents a serious healthcare threat. The bacterial chromosome and three plasmids encode 3337 predicted proteins. Over a quarter of the genome is made up of mobile elements and foreign DNA that possibly contributed to virulence and drug resistance. One of these elements appears to confer vancomycin resistance, while another represents a large pathogenicity island. Virulence factors and surface proteins encoded by the genome will be future drug targets.

The availability of host and bacterial genomes will provide more insights into how we interact with our intestinal tenants - for good and for bad.

## References

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