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## Tropheryma whippleigenome

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Whipple's disease is a rare multisystem chronic infection, causing weight loss, arthralgia, diarrhea, and abdominal pain and is caused by the poorly understood Gram-positive actinomycete *Tropheryma whipplei*. In the February 22 Lancet, Stephen D Bentley and colleagues at The Wellcome Trust Sanger Institute, Cambridge, UK, describe the complete *T. whipplei* genome sequence, which may provide insights into the etiology of Whipple's disease (*The Lancet*, **361**:637-644, February 22, 2003).

Bentley *et al.* sequenced a *T. whipplei* strain TW08/27 isolated from the cerebrospinal fluid of a patient diagnosed with Whipple's disease. They observed that the bacterium genome is 925,938 bp long and contains a predicted 784 genes. About 5% of the genome was composed of repeated DNA sequences, used to boost variation. The sequence analysis revealed a family of large surface proteins, some associated with large amounts of non-coding repetitive DNA. In addition, they observed that *T. whipplei* lacks the genes for many core functions such as a major energy-generating system (the TCA cycle) and synthesis of key amino acids (arginine, tryptophan, histidine).

"The genome reduction and lack of metabolic capabilities point to a host-restricted lifestyle for the organism," suggest the authors.

"Unlike its closest known relatives which are soil-oriented organisms, *T. whipplei* has chosen a lifestyle that is based upon an intimate relationship with humans. In revealing its genetic blueprint we learn a great deal about the particular strategy chosen by *T. whipplei* for establishing this kind of relationship, and why it has been so difficult to cultivate in the absence of human cells, as well as novel mechanisms for generating genetic variability and unexpected features of actinomycete evolution," they conclude.

## References

- 1. Whipple's disease
- 2. *The Lancet*, [http://www.thelancet.com]
- 3. The Wellcome Trust Sanger Institute, [http://www.sanger.ac.uk/]