

Genomic evolution of *Helicobacter pylori* within a host

Background

The bacterial species *Helicobacter pylori* lives in the stomach of half of the human population, causing gastric ulcers and cancer. A high level of genetic diversity and inconsistency was found when comparing genomes of *H. pylori* harboured by different human hosts. This presumably indicates frequent mutation and recombination, but prevents a clear understanding of the properties of the evolutionary forces involved. A potentially more revealing approach consists in comparing genomes extracted at timed intervals from the same patient. Such data has recently been acquired and needs analysing.

Objectives

The aim of this project is to analyse genetic data from *H. pylori* genomes sampled at timed intervals from the same patient. When comparing two such genomes, it should be possible to pinpoint exactly where mutation and recombination has happened, thus bringing a better understanding of the mode of evolution of *H. pylori* within a host.

Research plan

The first task will be to look at the distribution of polymorphism along a pair of genomes. This should suggest a stochastic model for the evolution of the genome of *H. pylori*. This model will then be applied to the data, using for example Hidden Markov Model (HMM) and/or Monte-Carlo Markov Chain (MCMC) techniques.

References

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Suerbaum and Josenhans, 2007 *Helicobacter pylori* evolution and phenotypic diversification in a changing host, *Nature Reviews Microbiology* 5:441-52