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Sequencing *Salmonella*

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There are about 16 million cases of typhoid fever throughout the world each year. In the October 25 *Nature*, Parkhill *et al.* report the complete genome sequence of the pathogenic culprit, *Salmonella enterica* serovar Typhi CT18 (*Nature* 2001, **413**:848-852). The drug-resistant strain has a genome of 4.8 Mb containing over two hundred pseudogenes, some of which correspond to virulence genes in *Salmonella typhimurium*. In the same issue of *Nature*, McClelland *et al.* report the sequence of the *Salmonella enterica* serovar Typhimurium LT2 (*Nature* 2001, **413**:852-856). This strain causes human gastroenteritis and provides a mouse model for typhoid fever. The gene differences between CT18 and LT2 may explain the human-restricted host range of *S. typhi*. CT18 has a multiple-drug-resistance plasmid and a cryptic plasmid resembling the virulence plasmid of *Yersinia pestis*. The LT2 strain also has a 94-kb virulence plasmid. The use of these sequences for comparative bacterial genomics (for example, comparisons with other *Salmonella* strains or closely-related sequenced genomes such as that of *Escherichia coli*) should identify genes related to host specificity and pathogenesis, and identify potential therapeutic or vaccine targets.

References

1. Nature , [<http://www.nature.com>]
2. *Salmonella typhi*, [http://www.sanger.ac.uk/Projects/S_typhi]
3. *Salmonella typhimurium*, [<http://genome.wustl.edu/gsc/Projects/S.typhimurium>]