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Plague genome

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Yersinia pestis is a Gram-positive bacterium that has wreaked havoc for centuries by causing plague pandemics such as the Black Death. Threats that *Y. pestis* could be used as a biological warfare agent suggest that it will continue to provide a healthcare challenge in the future. In the October 4 *Nature*, Parkhill *et al.* from [The Sanger Centre](#) report the complete genome sequence of the *Y. pestis* strain CO92 (*Nature* 2001, **413**:523-527). The killer genome consists of a 4.65 megabase chromosome and three plasmids (of 96.2, 70.3 and 9.6 kb). Anomalies in GC composition bias in the *Y. pestis* genome suggest frequent intragenomic recombination events, and there is ample evidence for lateral transfer and horizontal gene acquisition from other bacteria and insect parasites. Genes whose function has been lost during evolution (leading to pseudogene accumulation) include those for motility, lipopolysaccharide biosynthesis and characteristics of enteropathogenicity. Parkhill *et al.* suggest that comparative genomic analysis will reveal what determines the evolution of virulent pathogens such as *Y. pestis*.

References

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