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Pasteur's genome

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In the March 13 [Proceedings of the National Academy of Science](#), May *et al.* report the complete sequence of the *Pasteurella multocida* (Pm70) genome (*Proc Natl Acad Sci USA* 2001, **98**:3460-3465). *P. multocida* causes disease in birds, cattle, swine and humans, and has been studied ever since Pasteur used it in vaccine development, but the mechanisms underlying its virulence are unknown. May *et al.* used a shotgun strategy to sequence over 53,000 DNA fragments and assemble them into a [single circular sequence](#) of about 2.26 megabases. The Pm70 genome contains 2,014 predicted coding regions, accounting for 89% of the entire chromosome, as well as 6 rRNA operons and 57 tRNA genes. About 10% of the open reading frames are unique to *P. multocida*, while over half have orthologs found in closely-related *Haemophilus influenza* and in *Escherichia coli*. Comparative analysis suggests that *P. multocida* diverged from *H. influenza* around 230 million years ago and from *E. coli* around 680 million years ago. May *et al.* identified 104 putative virulence-associated genes, notably two with homology to filamentous hemagglutinin of *Bordetella pertussis*. [Microarray analysis](#) identified more than 50 genes with roles in iron acquisition and metabolism.

References

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