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Decay in the leprosy genome

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Leprosy, which has been described since biblical times, is caused by the obligate intracellular pathogen *Mycobacterium leprae*. In the February 22 *Nature*, Cole *et al.* report the sequencing of the entire *M. leprae* genome (*Nature* 2001, **409**:1007-1011). Pairwise comparison with the genome sequence of the closely related *M. tuberculosis* revealed that the *M. leprae* genome has undergone considerable reduction during evolution. The 3.27 megabase *M. leprae* genome contains less than half the number of genes found in the tubercle bacillus (1604 compared to 3959), but has many more pseudogenes (1116 compared to 6). This extensive genome downsizing has been accompanied by the loss of genes important for envelope biogenesis, lipolysis and energy metabolism. Genome decay may explain some unusual characteristics of the leprosy bacillus, such as its exceptionally long doubling time (about 14 days).

References

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2. *Mycobacterium leprae*, [http://www.sanger.ac.uk/Projects/M_leprae]
3. Leproma, [<http://genolist.pasteur.fr/Leproma>]
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