

Supplementary Table 1. Estimated tMRCA and clock rate for various bacterial pathogens

Lineage	Disease	tMRCA (years ago)	Mean clock rate (substitution per bp per year)	Citation
<i>Salmonella enterica</i> serovar Typhi H58	Typhoid fever	27	$1.4 \times 10^{-7}$	[1]
<i>Staphylococcus aureus</i> EMRSA-15	Epidemic MRSA	30	$1.3 \times 10^{-6}$	[2]
<i>Vibrio cholerae</i> (7th pandemic)	Epidemic cholera	60	$8.3 \times 10^{-7}$	[3]
<i>Salmonella enterica</i> serovar Agona	Food poisoning	80	$9.3 \times 10^{-8}$	[4]
<i>Streptococcus equi</i>	Equine strangles	106	$5.2 \times 10^{-7}$	[5]
<i>Vibrio cholerae</i> (epidemic)	Epidemic cholera	200	ND	[6]
<i>Salmonella enterica</i> serovar Paratyphi A	Enteric fever	450	$1.3 \times 10^{-7}$	[7]
<i>Shigella sonnei</i>	Dysentery	350	$6.0 \times 10^{-7}$	[8]
<i>Mycobacterium tuberculosis</i> (Lineage 4)	Tuberculosis	1,600	$5.0 \times 10^{-8}$	[9]
<i>Mycobacterium leprae</i>	Leprosy	3,100	$6.1 \times 10^{-9}$	[10]
<i>Yersinia pestis</i>	Plague	5,000	$8.6 \times 10^{-9}$	[11,12]
<i>Mycobacterium tuberculosis</i> Complex	Tuberculosis	5,200	$4.9 \times 10^{-8}$	[9,13]
<i>Helicobacter pylori</i>	Gastritis, ulcers	100,000	$3 \times 10^{-4}$ (short term) – $2.6 \times 10^{-7}$ (long term)	[14-18]

## Reference List

1. Wong, V. K. *et al.*. 2015 Phylogeographical analysis of the dominant multidrug-resistant H58 clade of *Salmonella* Typhi identifies inter- and intracontinental transmission events. *Nature Genet* 47, 632-639.
2. Holden, M. T. G. *et al.*. 2013 A genomic portrait of the emergence, evolution and global spread of a methicillin resistant *Staphylococcus aureus* pandemic. *Genome Res* 23, 653-664.
3. Didelot, X., Pang, B., Zhou, Z., McCann, A., Ni, P., Li, D., Achtman, M., and Kan, B. 2015 The role of China in the global spread of the current cholera pandemic. *PLoS Genet* 11, e1005072.
4. Zhou, Z., McCann, A., Litrup, E., Murphy, R., Cormican, M., Fanning, S., Brown, D., Guttman, D. S., Brisse, S., and Achtman, M. 2013 Neutral genomic microevolution of a recently emerged pathogen, *Salmonella enterica* serovar Agona. *PLoS Genet* 9, e1003471.
5. Harris, S. R., Robinson, C., Steward, K. F., Webb, K. S., Paillot, R., Parkhill, J., Holden, M. T., and Waller, A. S. 2015 Genome specialization and decay of the strangles pathogen, *Streptococcus equi*, is driven by persistent infection. *Genome Res* 25, 1360-1371.
6. Devault, A. M. *et al.*. 2014 Second-pandemic strain of *Vibrio cholerae* from the Philadelphia cholera outbreak of 1849. *N Engl J Med* 370, 334-340.

7. Zhou, Z., McCann, A., Weill, F. X., Blin, C., Nair, S., Wain, J., Dougan, G., and Achtman, M. 2014 Transient Darwinian selection in *Salmonella enterica* serovar Paratyphi A during 450 years of global spread of enteric fever. *Proc Natl Acad Sci U S A* 111, 12199-12204.
8. Holt, K. E. *et al.*. 2012 *Shigella sonnei* genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. *Nature Genet* 44, 1056-1059.
9. Kay, G. L. *et al.*. 2015 Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. *Nat Commun* 6, 6717.
10. Schuenemann, V. J. *et al.*. 2013 Genome-wide comparison of medieval and modern *Mycobacterium leprae*. *Science* 341, 179-183.
11. Cui, Y. *et al.*. 2013 Historical variations in mutation rate in an epidemic pathogen, *Yersinia pestis*. *Proc Natl Acad Sci USA* 110, 577-582.
12. Rasmussen, S. *et al.*. 2015 Early divergent strains of *Yersinia pestis* in Eurasia 5,000 years ago. *Cell* 163, 571-582.
13. Bos, K. I. *et al.*. 2014 Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis. *Nature* 514, 494-497.
14. Linz, B., Windsor, H. M., McGraw, J. J., Hansen, L. M., Gajewski, J. P., Tomsho, L. P., Hake, C. M., Solnick, J. V., Schuster, S. C., and Marshall, B. J. 2014 A mutation burst during the acute phase of *Helicobacter pylori* infection in humans and rhesus macaques. *Nat Commun* 5, 4165.

15. Didelot, X., Nell, S., Yang, I., Woltemate, S., van der Merwe, S., and Suerbaum, S. 2013  
Genomic evolution and transmission of *Helicobacter pylori* in two South African families. *Proc Natl Acad Sci U S A* 110, 13880-13885.
16. Maixner, F. et al.. 2016 The 5300-year-old *Helicobacter pylori* genome of the Iceman. *Science* 351, 162-165.
17. Morelli, G., Didelot, X., Kusecek, B., Schwarz, S., Falush, D., Bahlawane, C., Suerbaum, S., and Achtman, M. 2010 Microevolution of *Helicobacter pylori* during prolonged infection of single hosts and within families. *PLoS Genet* 6, e1001036.
18. Moodley, Y. et al.. 2012 Age of the association between *Helicobacter pylori* and man. *PLoS Pathog* 8, e1002693.