■ Table 2 Base-substitution rates estimated from evolution experiments with whole-genome data

Study	Bacterial Strain	Clones	Cumulative Generations	Synonymous Sites (bp)[a]	Synonymous Mutations	$\mu \times 10^{-11}$ (per bp per generation)[b]
This study	Escherichia coli B REL606	19	300,000	941,000	25 (52)[c]	8.9 [5.7–13]
Conrad et al. (2009) Lee and Palsson (2010)	Escherichia coli K-12 MG1665	12	10,700	930,000	5	50 [16–120]
Kishimoto et al. (2010)	Escherichia coli W3110	4	13,850	945,000	2	15 [1.9–55]
Lind and Andersson (2008)	Salmonella typhimurium LT2	1	5000	990,000	2	40 [4.9–150]
Velicer et al. (2006)	Myxococcus xanthus DK1622	1	1000	2,140,000	1	47 [1.2–260]

For these calculations, we used only independently evolved end-point clones, and we pooled data from replicate lineages started from the same ancestral strain.

[a] The effective synonymous target size was calculated from the ancestral genome sequences (see *Materials and Methods*).

[b] The mutation rate μ (per bp per generation) was calculated as the number of observed synonymous mutations divided by the product of the total number of generations and the effective number of synonymous target sites. Brackets indicate 95% confidence limits estimated from a binomial distribution. These estimates do not take into account base composition or changes in genome size.

[c] For comparison with the other datasets, we used only the first clone sequenced at the latest nonmutator time point from each of the eight long-term populations: 20K-A for Ara-1,40K for Ara-3, and 40K-A for the other six populations (Table 1). There were 25 synonymous mutations in these clones and 52 overall in the dataset. A more accurate estimate of μ and its uncertainty for the long-term lines takes into account the multiple clones sequenced from the same population, the pseudo-replication of clones from the same population, the base signatures of the mutations, and changes in genome size. That comprehensive analysis yields 8.9 [4.0–14] $\times 10^{-11}$ per bp per generation (see text).

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