

Table 1. Direct sequencing estimates of mutation rates. Two probably accurate but indirect estimates (Nachman & Crowell 2000; Kondrashov 2003) are included for *Homo sapiens*.

species	rate of mutation per site per generation	comments	references
<i>Homo sapiens</i>	2.5×10^{-8} total (from species divergence) 1.8×10^{-8} total (phenotypic mutations analysis) 3.0×10^{-8} total (direct sequencing of Y chromosome)	indels are rare	Nachman & Crowell (2000), Kondrashov (2003), Xue <i>et al.</i> (2009)
<i>Drosophila melanogaster</i>	8.4×10^{-9} total 3.5×10^{-9} to 5.8×10^{-9} point mutations	some variation of rates between different lines; supports higher rate estimates	Haag-Liautard <i>et al.</i> (2007), Keightley <i>et al.</i> (2009)
<i>Drosophila melanogaster</i> mitochondrion	7.2×10^{-8} total 6.2×10^{-8} point mutations	high rate of G→A mutations on the major strand; higher than estimates from species divergence	Haag-Liautard <i>et al.</i> (2008)
<i>Caenorhabditis elegans</i>	2.1×10^{-8} total 9.1×10^{-9} point mutations	insertions very common; higher than previous estimates	Denver <i>et al.</i> (2004)
<i>Caenorhabditis elegans</i> mitochondrion	1.6×10^{-7} total 9.7×10^{-8} point mutations	higher than previous estimates	Denver <i>et al.</i> (2000)
<i>Saccharomyces cerevisiae</i>	0.33×10^{-9}	similar to previous estimates	Lynch <i>et al.</i> (2008)
<i>S. cerevisiae</i> mitochondrion	1.2×10^{-8} point mutations (average of two methods) 7.5×10^{-9} indels (average of two methods)		Lynch <i>et al.</i> (2008)