

TABLE 4. Mutation Rates in Higher Eukaryotes Estimated from Specific Loci¹

Organism	C	μ_b	G	μ_g	μ_{gs}	G_e	μ_{eg}	μ_{egs}
<i>C. elegans</i>	9.1	2.3×10^{-10}	8.0×10^7	0.018	0.16	1.8×10^7	0.004	0.036
<i>D. melanogaster</i>	25	3.4×10^{-10}	1.7×10^8	0.058	1.4	1.6×10^7	0.005	0.14
<i>M. musculus</i>	62	1.8×10^{-10}	2.7×10^9	0.49	30	8.0×10^7	0.014	0.9
<i>H. sapiens</i>	400	0.5×10^{-10}	3.2×10^9	0.16	64	8.0×10^7	0.004	1.6

NOTE: C = cell divisions per sexual generation. μ_b = mutations per base pair per genome replication. G = haploid genome size in base pairs. μ_g = mutations per genome per genome replication = $G \times \mu_b$. μ_{gs} = mutations per genome per sexual generation = $\mu_g \times C$. G_e = effective genome size (see text). μ_{eg} = mutations per effective genome per genome replication = $G_e \times \mu_b$. μ_{egs} = mutations per effective genome per sexual generation = $\mu_{eg} \times C$.

NOTE:

C = cell divisions per sexual generation. μ_b = mutations per base pair per genome replication. G = haploid genome size in base pairs. μ_g = mutations per genome per genome