

Table 1 | Summary of published estimates of genomic mutation parameters in multicellular eukaryotes

Taxon/species	Method	U	ΔW	Comments	Refs
Insects					
<i>Drosophila melanogaster</i>	MA	0.01 to ~1	0.1 to 2.0	Averaged over multiple studies; most of these studies use egg-to-adult viability as a proxy for fitness	83,133
<i>Drosophila</i> spp.	KC	~0.07	NA	From three species pairs	134
<i>D. melanogaster</i>	MA, allozyme	0.1	NA	Requires assumptions about the relationship between changes in electrophoretic mobility and DNA sequence; the constrained fraction of the genome is inferred from coding loci	134,135
<i>D. melanogaster</i>	MA, sequence	1.2	NA	See text for further details	50
<i>Daktulosphaira vitifolia</i> *	MA	~0.03	>0	Average of four life-history traits	136
Nematodes					
<i>Caenorhabditis elegans</i> †	MA	~0.02	~0.1	Average of three experiments	117,137,138
<i>Caenorhabditis</i> spp.	KC	~0.02	NA	Depends on a potentially unrealistic estimate of generation time; self-compatible taxa (<i>C. elegans</i> , <i>C. briggsae</i>) are not different from an obligate outcrosser (<i>C. remanei</i>)	139
<i>C. elegans</i> †	MA, sequence	0.96	NA	See text for further details	49
<i>Caenorhabditis briggsae</i> †	MA	~0.03	0.1 to 0.3		138
<i>Oscheius myriophila</i> †	MA	0.02	0.1		77
Crustaceans					
<i>Daphnia pulex</i> *	MA	~0.6	0.2 to 2	Average of several life-history traits	140
<i>D. pulex</i> *, <i>Daphnia obtusa</i> *	DL	~0.7	NA	Average upwardly biased estimate of U from standing genetic variance in several life-history traits; DL method assumes mutation-selection balance	141
Vascular plants					
<i>Arabidopsis thaliana</i> †	MA	~0.1	~0.1	Average of two experiments; fitness estimated from several life-history traits	74,142
<i>Arabidopsis</i> spp.	KC	0.2 to 0.6	NA	Estimated from the divergence of <i>A. thaliana</i> (self) and <i>A. lyrata</i> (outcross)	143
<i>Amsinckia douglasiana</i>	MA	See REF. 144	1	ΔW estimated from flower number per plant	144
<i>Amsinckia gloriosa</i> †	MA	See REF. 144	0.5	ΔW estimated from flower number per plant	144
Endothermic vertebrates					
Quail, chicken	KC	0.49	NA		134
Sheep, cow	KC	0.9	NA		134
Dog, cat	KC	1.6	NA		134
Macaque, Old World Monkey	KC	1.9	NA		134
Mouse, rat	KC	0.91	NA	Constrained fraction of the genome was inferred from the whole-genome sequence	145
Human, chimpanzee	KC	~3	NA	Two studies; neutral mutation rate inferred from substitution rate in processed pseudogenes in REF. 48.	97,145

Values of U are underestimates, with the possible exception of those from REF. 50. *Cyclical parthenogen mating system. †Self-compatible mating system. All other mating systems are as obligate outcrossers. The 'comments' column indicates whether a study compared taxa with different mating systems. In studies that use the Kondrashov and Crow (KC) method, the constrained fraction of the genome is inferred from protein coding loci and the neutral mutation rate is inferred from the substitution rate at fourfold degenerate sites unless stated otherwise. ΔW , percentage decline per generation in mean fitness with mutation accumulation; DL, Deng and Lynch (BOX 2); MA, mutation accumulation; U , diploid genomic mutation rate for fitness.

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