

TABLE 1
Parameters used in describing the mutation process

Parameter	Definition
Abbreviations	
b	Base or base pair
kb	Kilobase or kilobase pair
Parameters	
C	The variously calculated ratio of total mutations to observed mutations
f	Mutant fraction in a population
G	Genome size in bases or base pairs (haploid unless otherwise indicated)
G_e	Effective genome size (portion in which most mutations are deleterious)
h	Dominance coefficient associated with a typical detrimental mutation
ΔM	Rate of decline per generation of the mean of a quantitative fitness trait
N	Population size
\bar{s}	Mean reduction in trait value of a single mutation when homozygous
\bar{s}	Mean selection coefficient against a heterozygous deleterious mutation
U	Rate of deleterious mutations per genome per sexual generation
U_c	U for a chromosome
U_d	U for the diploid genome
U_h	U for the haploid genome
ΔV	Increase in variance of a quantitative fitness trait in parallel lines
δ	Reduction in mean fitness of inbred versus randomly mated diploids
μ_b	Mutation rate per base pair per replication
μ_g	Mutation rate per genome per replication
μ_{eg}	Mutation rate per effective genome per replication
μ_{egs}	Mutation rate per effective genome per sexual generation
μ_{lin}	Mutation rate under conditions of linear replication in RNA viruses
μ_{bin}	Mutation rate under conditions of binary replication in RNA viruses
μ_m	$(\mu_{lin} + \mu_{bin})/2$ for RNA viruses