

Accumulation of mutations in nonsense alleles of *Drosophila melanogaster*

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Mutations are the sine qua non of evolution; they also shape variation. Even deleterious mutations may segregate within a population for multiple generations if selection against them is not too strong. Point mutations in coding regions of genes may be synonymous if they don't change the encoded amino acid; nonsynonymous if they change it; or nonsense if they result in a premature stop codon. As a nonsense mutation pseudogenizes the gene, it effectively disables negative selection at a gene, making subsequent accumulation of nonsynonymous mutations at other positions of the same gene neutral. Therefore, in the absence of recombination, post-nonsense nonsynonymous mutations are expected to accumulate at the same rate as synonymous mutations. Here, we verify this hypothesis using genomes of 162 inbred lines *Drosophila melanogaster*. We identified 960 genes with 1202 nonsense mutations. On average, each line carries 63 nonsense mutations in 59 genes. The number of nonsynonymous mutations nested within nonsense alleles may be used to estimate the age distribution of such mutations, and therefore, the period of time for which they segregate in the population.