

A novel method for estimating neutral rates and patterns of DNA evolution in *Drosophila* takes advantage of the propensity of non-LTR retrotransposable elements to create nonfunctional, transpositionally inactive copies as a product of transposition. For many LINE elements, most copies present in a genome at any one time are nonfunctional "dead-on-arrival" (DOA) copies. Because these are off-shoots of active, transpositionally competent "master" lineages, in a gene tree of a LINE element from multiple samples from related species, the DOA lineages are expected to map to the terminal branches and the active lineages to the internal branches, the primary exceptions being when the sample includes DOA copies that are allelic or orthologous. Analysis of nucleotide substitutions and other changes along the terminal branches therefore allows estimation of the fixation process in the DOA copies, which are unconstrained with respect to protein coding; and under selective neutrality, the fixation process estimates the underlying mutational pattern. We have studied the retroelement Helena in *Drosophila*. An unexpectedly high rate of DNA loss was observed, yielding a half-life of unconstrained DNA sequences approximately 60-fold faster in *Drosophila* than in mammals. The high rate of DNA loss suggests a straightforward explanation of the seeming paradox that *Drosophila* has many fewer pseudogenes than found in mammalian species. Differential rates of deletion in different taxa might also contribute to the celebrated C-value paradox of why some closely related organisms can have very different DNA contents. New data presented here rule out the possibility that the transposition process itself is highly mutagenic, hence the observed linear relation between number of deletions and number of nucleotide substitutions is most easily explained by the hypothesis that both types of changes accumulate in unconstrained sequences over time.