

Trash DNA is what gets thrown away: high rate of DNA loss in *Drosophila*.

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ABSTRACT.

We have recently described a novel method of estimating neutral rates and patterns of spontaneous mutation (Petrov et al., 1996). This method takes advantage of the propensity of non-LTR retrotransposable elements to create non-functional, 'dead-on-arrival' copies as a product of transposition. Maximum parsimony analysis is used to separate the evolution of actively transposing lineages of a non-LTR element from the fate of individual inactive insertions, and thereby allows one to assess directly the relative rates of different types of mutation, including point substitutions, deletions and insertions. Because non-LTR elements enjoy wide phylogenetic distribution, this method can be used in taxa that do not harbor a significant number of bona fide pseudogenes, as is the case in *Drosophila* (Jeffs and Ashburner, 1991; Weiner et al., 1986). We used this method with Helena, a non-LTR retrotransposable element present in the *Drosophila virilis* species group. A striking finding was the virtual absence of insertions and remarkably high incidence of large deletions, which combine to produce a high overall rate of DNA loss. On average, the rate of DNA loss in *D. virilis* is approximately 75 times faster than that estimated for mammalian pseudogenes (Petrov et al., 1996). The high rate of DNA loss should lead to rapid elimination of non-essential DNA and thus may explain the seemingly paradoxical dearth of pseudogenes in *Drosophila*. Varying rates of DNA loss may also contribute to differences in genome size (Graur et al., 1989; Petrov et al., 1996), thus explaining the celebrated 'C-value' paradox (John and Miklos, 1988). In this paper we outline the theoretical basis of our method, examine the data from this perspective, and discuss potential problems that may bias our estimates.