Abstract.
Pseudogenes are common in mammals but virtually absent in Drosophila. All putative Drosophila pseudogenes show patterns of molecular evolution that are inconsistent with the lack of functional constraints. The absence of bona fide pseudogenes is not only puzzling, it also hampers attempts to estimate rates and patterns of neutral DNA change. The estimation problem is especially acute in the case of deletions and insertions, which are likely to have large effects when they occur in functional genes and are therefore subject to strong purifying selection. We propose a solution to this problem by taking advantage of the propensity of retrotransposable elements without long terminal repeats (non-LTR) to create non-functional, 'dead-on-arrival' copies of themselves as a common by-product of their transpositional cycle. Phylogenetic analysis of a non-LTR element, Helena, demonstrates that copies lose DNA at an unusually high rate, suggesting that lack of pseudogenes in Drosophila is the product of rampant deletion of DNA in unconstrained regions. This finding has important implications for the study of genome evolution in general and the 'C-value paradox' in particular.

Comment in:
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