

**The Tempo and Mode of Evolution of Transposable Elements as Revealed by Molecular Phylogenies Reconstructed from Mosquito Genomes**

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We here present estimates of key parameters guiding transposable elements (TE) invasion dynamics as revealed by molecular phylogenies reconstructed from *Anopheles gambiae* and *Aedes aegypti* mosquito genome projects. Our analysis follows four steps: (i) mining the two mosquito genomes currently available in search of TE families; (ii) fitting, to selected families found in (i), a phylogeny tree under the general time-reversible (GTR) nucleotide substitution model with an uncorrelated lognormal relaxed clock (UCLN) and a non-parametric demographic model; (iii) fitting a non-parametric coalescent model to the tree generated in (ii); (iv) fitting parametric models motivated by ecological theories to the curve generated in (iii).

The demographic component implied by this approach is of great epidemiological interest since it can help in identifying the molecular and ecological approximate conditions under which transposable elements will spread through a host population. By exploring the analytic potential of coalescence models fitted to data generated by genome projects, we address the lack of empirical data against which putative models developed in the past could be fitted and checked.