Relaxed purifying selection is associated with an accumulation of transposable elements in flies

Vincent Merel[1,2], Théo Tricou[2,3], Nelly Burlet[2], and Annabelle Haudry*[2]

[1]Department of Ecology and Evolution [Lausanne] – Biophore - CH-1015 Lausanne, Suisse
[2]Laboratoire de Biométrie et Biologie Evolutive - UMR CNRS 5558 – Université Claude Bernard Lyon 1 – France
[3]Unité Mixte de Recherche d'Épidémiologie des maladies Animales et zoonotiques – VetAgro Sup - Institut national d'enseignement supérieur et de recherche en alimentation, santé animale, sciences agronomiques et de l'environnement, Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement – France

Résumé

Although the mechanisms driving genome size evolution have not yet been fully deciphered, one potentially important factor is the dynamic of accumulation in mobile selfish genetic elements named transposable elements (TEs). Because the majority of these sequences are neutral or slightly deleterious, a negative correlation between genome size and selection efficacy is expected, as formalized by Lynch and Connery (2003). Nevertheless, previous studies relying on empirical data from closely related species have yielded inconsistent conclusions, leaving this matter contentious.
Here, we provide an original experimental design to properly test Lynch and Connery's theory on a large set of closely related species of flies, with comparable biology. Using an extensive dataset of Drosophilid genomes, including some that are novel, we present a detailed guide to testing the underlying question, taking into account confounding factors, which may have contributed to variability in previous empirical studies. We reconstructed a phylogeny based on whole genome data (2,242 genes) for 82 lineages representing 77 Drosophilid species and studied correlations between genome size, TE content and measures of selection efficacy. We highlighted a strong phylogenetic inertia on genome size, and confirmed that TEs are the major components of the genome size.

The study's meticulous control for shared history enhances our understanding of genome size evolution by providing evidence of a positive correlation between genome size, TE content, and a measure of the intensity of genetic drift. Indeed, we found a strong positive correlation between genome-wide ratios of non-synonymous to synonymous divergence (dN/dS) and genome size, particularly for GC-poor genes, providing valuable insights into the impact of genetic drift and reduced purifying selection on TE dynamics.

In addition, we reviewed previous studies and highlighted that the lack of evidence of TE accumulation in association with increased genetic drift may be due to secondary effect of changes in life history trait (in particular to asexuality) on TE dynamics.
In a nutshell, this work provides evidence for TE proliferation in the genome of flies when

---

*Intervenant

purifying selection is reduced and the genetic drift increases. It clarifies the existing debate, supporting the Lynch and Connery's theory and provides a new understanding of the role of nearly neutral elements and genetic drift on the evolution of genome architecture using a systematic approach.

Mots-Clés: genome size evolution, genetic drift, purifying selection