
Effective population size does not explain long-term variation in genome size and transposable elements content variation

Alba Marino^{*1}, Gautier Debaecker², Anna-Sophie Fiston-Lavier^{1,3}, Annabelle Haudry⁴,
and Benoit Nabholz^{1,3}

¹Institut des Sciences de l'Evolution de Montpellier – Centre National de la Recherche Scientifique,
Université de Montpellier – Place E. Bataillon CC 064 34095 Montpellier Cedex 05, France

²Laboratoire d'Ecologie des Hydrosystèmes Naturels et Anthropisés – Université Claude Bernard Lyon
1, Centre National de la Recherche Scientifique – Université Claude Bernard Lyon 13-6, rue Raphaël
Dubois - Bâtiments Darwin C Forel, 69622 Villeurbanne Cedex43, Boulevard du 11 novembre
1918ENTPE3, rue Maurice Audin69518 Vaulx-en-Velin, France

³Institut Universitaire de France – Ministère de l'Education nationale, de l'Enseignement supérieur et
de la Recherche – Maison des Universités 103 Boulevard Saint-Michel 75005 Paris, France

⁴Laboratoire de Biométrie et Biologie Evolutive - UMR 5558 – Université Claude Bernard Lyon 1,
Centre National de la Recherche Scientifique – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE
CEDEX, France

Abstract

Animal genomes exhibit a remarkable variation in size, but the evolutionary forces responsible for such variation are still debated. As the effective population size (N_e) reflects the intensity of genetic drift, it is expected to be a key determinant of the fixation rate of nearly-neutral mutations. Accordingly, the Mutational Hazard Hypothesis postulates lineages with low N_e to have bigger genome sizes due to the accumulation of slightly deleterious transposable elements (TEs), and those with high N_e to maintain streamlined genomes as a consequence of a more effective selection against TEs. However, the existence of both empirical confirmation and refutation using different methods and different scales precludes its general validation. Using high-quality public data, we estimated genome size, TE content and rate of non-synonymous to synonymous substitutions (dN/dS) as N_e proxy for 807 species including ray-finned fishes, birds, mammals, molluscs and insects. After collecting available life-history traits, we tested the associations among population size proxies, TE content and genome size, while accounting for phylogenetic non-independence. Our results confirm TEs as major drivers of genome size variation, and endorse life-history traits and dN/dS as reliable proxies for N_e . However, we do not find any evidence for increased drift to result in an accumulation of TEs across animals. Within more closely related clades, only a few isolated and weak associations emerge in fishes and birds. Our analyses outline a scenario where TE dynamics vary according to lineage-specific patterns, lending no support for genetic drift as the predominant force driving long-term genome size evolution in animals.

Keywords: Genome size, Transposable elements, Mutational hazard hypothesis, Genetic drift

*Speaker