

# Mosquitoes Mobilome

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Genomes of living organisms are composed of stable (genes) and unstable components (mobile genetic elements or transposable elements (TEs)). In the last years an increasing amount of evidence highlights the importance of TEs as major players in the genome evolution providing raw material for natural selection. Such elements have been shown to reshape the host genomes in a multitude of ways as generating chromosome rearrangements, rewriting of transcription networks and also being co-opted for a new advantage features for the host species. Although much is known about TEs, such knowledge is restrict to few model organisms, for most of currently available genomes poor information exists even at the mobilome characterization level which reflects the almost absence of data about TE impact on these genomes. Mosquito genomes are available for some time from now and its mobilome annotation has both extremes: *Anopheles gambiae* genome with well characterized mobilome, *Aedes aegypti* and *Culex quinquefasciatus* with some degree of characterization and the other new 16 Anophelinae genomes available in 2016 with only partial description of TEs. Based on the reasoning presented above the main goal of this study was to evaluate the TE impact on mosquito genomes by re annotating it using recently developed and powerful pipeline for mobilome characterization making use of information from mosquitoes genomes and transcriptomes. REPET package was used for genome-wide TE characterization in seven genomes so far. Our preliminary results shows that this pipeline detected a higher TE content (20%) in the *Anopheles gambiae* genome than previously reported in the literature (17%). A different TE proportion also was found for all other 6 species: *A. arabiensis* (9,59%), *A. coluzzii* (10,41%), *A. merus* (9,6%), *A. melas* (4,71%), *A. epiroticus* (5,51%) and *A. christyi* (0,81%). In addition, we also performed a deeper analysis for each TE superfamily and could detect a different dynamics of those superfamilies both inside of each genome as well as among them. Some families being old components of the genome probably not transposing anymore and other probably highly active families which may have a deeper impact on a shorter evolutionary scale. In summary, our data shows the need of standardized and deeper mobilome characterization of the mosquitoes genomes and that TEs experienced different expansion time and extent inside of each genome. Moreover mosquito mobilome are evolving under different selection constraint among those related species studied.