Contribution of transposable elements to the host shift in cactophilic Drosophila species

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Abstract

Insects that use plant hosts as feeding and breeding sites rely on this interaction for their survival. In the process of exploring different hosts and particularly when host shift occurs, successive adaptations might initiate reproductive isolation between populations, as a result of divergent selection. Therefore, host shift has been considered an important hallmark for ecological speciation. The adaptations underlying shifts have been attributed to both genomics and transcriptomics variation in many species. Despite the well-known contribution of transposable elements (TEs) as foremost engine for genome evolution, extensively contributing to local adaptation between species/populations, the extent of TEs' contribution to host shift remained unexplored. Cactophilic *Drosophila* species are an excellent model to investigate the genetic background underlying host shift since many species have different primary hosts. In this work, we selected seven cactophilic *Drosophila* species with different host preferences and incipient reproductive isolation to investigate the role of TEs on their divergence. Using long reads sequencing technology, we observed differential expansion of TE families among species, as well as a high prevalence of TE copies in the promoter region of genes associated with host location. Several insertions are likely to harbor transcription factor binding sites, highlighting their potential adaptive role. In addition, our transcriptomics analyses from head and larvae tissues have shown the presence of polymorphic TE insertions generating transcripts derived from genes and TEs (chimeric transcripts), including genes associated with host shift. Taken together, our results demonstrate that TEs have substantial contribution to both genomic and transcriptomic variability of cactophilic *Drosophila* species, even between recently (_˜200,000 years) diverged subspecies, reinforcing their role in rapid evolution. Our combined genomics and transcriptomics approaches provide new insights regarding the role of TEs in the evolution of host shift, and ultimately their contribution to ecological speciation.

Keywords: host shift, ecological speciation, chimeric transcripts

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