Chromosomal inversions as drivers of ecological adaptation and diversification in a grasshopper species complex

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Abstract

The study of inversion polymorphisms along environmental gradients has long attracted the attention of evolutionary biologists. Currently, the application of genomic approaches has provided new evidences about the role that these rearrangements might have played as drivers of ecological adaptation and speciation. The grasshopper Trimerotropis pallidipennis is considered a "species complex" composed of several genetic lineages distributed from North to South America in arid and semi-arid high-altitude environments. The southernmost lineage, Trimerotropis sp., bears inversion polymorphisms whose frequencies vary along environmental gradients. These polymorphisms may have allowed this grasshopper to adapt to more temperate environments. Herewith, we analyze chromosomal, mitochondrial and genome-wide SNP markers in 19 populations of Trimerotropis sp. mainly distributed along two altitudinal gradients. We show that populations across Argentina are formed by two main chromosomally differentiated lineages: one distributed in the southernmost border of the "Andes Centrales", adding evidence for a differentiation hotspot in this area; and the other widely distributed in Argentina. Within the latter, footprints of secondary contact between divergent populations were detected, probably leading to incipient speciation through selective disadvantages of heterozygous individuals and asymmetrical gene flow. We demonstrated the stability of inversion polymorphisms for more than 30 generations and the occurrence of non-neutral markers associated with environmental and chromosomal gradients. These results confirm the adaptive nature of the chromosomal gradients and provide a framework to future investigations about candidate genes that may be implicated in the rapid adaptation to new environments.

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