

Mitogenome data reveals strong differentiation among the isolated populations of *Heliconius hermathena*: a white sand ecosystem specialist.

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Abstract

Cycles of forest retraction and expansion during the Pleistocene presumably played a crucial role in the diversification of neotropical species by the formation of isolated forest refugia. Similarly, these cycles generated the strongly isolated pattern of the Amazonian white sand ecosystems: non-forest habitats with white sandy soils surrounded by forest matrix. As previously inferred by ecological and morphological data, such processes may have led to the isolation and diversification of subpopulations of *H. hermathena*, a butterfly endemic to these ecosystems with seven subspecies identified by their color patterns. Nevertheless, the genetic differentiation and structure among *H. hermathena* subpopulations are still unknown. We sequenced the mitogenomes of 71 individuals across six of the seven subspecies of *H. hermathena* from eight different localities. We then performed Bayesian phylogenetic inference and population structure analyses in order to analyze patterns of differentiation among *H. hermathena* subpopulations and their phylogenetic relationships. Most of the analysis were performed in user-friendly platforms such as Galaxy Project and Geneious 10, which implements most of the state-of-the-art bioinformatics programs. Currently, we are accessing the divergence times among these subpopulations to infer the specific mechanisms regarding the group's phylogeography and evolution. We show that two populations with equal wing color pattern (*H. h. sheppardi*) sampled from two different localities exhibit high genetic divergence and population structure. Conversely, a pair of phenotypically divergent subspecies (*H. h. vereatta* and *H. h. duckeii*) from two near sample sites in Faro, are genetically similar and have lower fixation index when compared to other sample localities. Furthermore, we found highly distinct haplogroups among *H. hermathena* subpopulations, with each haplogroup strongly structured in its own sampling locality. Our results suggest that the fragmented pattern of the white sand ecosystems may have actually played an important role in the formation and maintenance of differentiated populations and subspecies of *H. hermathena*. For this butterfly, the forest function as a barrier for free gene flow among its current populations.

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