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GENETIC STRUCTURE, GLACIAL REFUGEES AND PHYLOGEOGRAPHY OF *RHAGIO MYSTACEUS* (DIPTERA, RHAGIONIDAE), A CONTINENTALLY DISTRIBUTED SPECIES

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Evolução e Filogeografia/Oral

Continuous and continentally distributed species rise questions about the processes promoting genetic lineage diversification. The absence of explicit geographic barriers leads to other microevolutionary processes to comprehend the spatial distribution of genetic diversity. The snipe fly species *Rhagio mystaceus* is distributed on the middle-eastern portion of North America. However the absence of barriers promoting disjunctions of its range rises questions about its actual genetic structure and the forces acting to promote its genetic diversity. In this study we investigated the genetic population structure, estimating historical demographic dynamics, recognizing potential refuge areas during the Last Glacial Maximum (LGM, ~21kya) from which the species might have colonized and achieved its actual distribution range. Two different genetic clusters were reconstructed using mitochondrial gene sequences available in GenBank from previous studies. These two clusters don't correspond to any recognizable geographic break, been formed 150kya. Demographic and neutrality tests show that these populations are experiencing a population expansion in the last 12,000 years, corresponding to a genetic diversification observed in the dated gene tree. Despite the actual distribution range of the species, two areas were reconstructed as potential refugees during the LGM, one on the East Coast of the United States and one in the Beringia and the Western portion of the Yukon Territory. The species might have expanded from these two localities colonizing the areas actually occupied. Analyses using model-based methods to compare different evolving scenarios might cast more light over the diversification drivers acting on *R. mystaceus*.

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