Genetic characterization of *Anastrepha zenildae* Zucchi (Diptera: Tephritidae) populations within the *fraterculus* group

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Introduction

*Anastrepha zenildae* infests about 30 hosts in Brazil and is the most frequent species in the Semi-Arid region. This species belongs to the *fraterculus* group and has been misidentified as *Anastrepha fraterculus* for a long time. The aim of this study was the genetic characterization of *Anastrepha zenildae* within the *fraterculus* group by the sequencing of mitochondrial and nuclear DNA regions.

Methods

Populations of *Anastrepha zenildae* and some species within the *fraterculus* group collected in Brazil, Mexico, Peru, and Venezuela were studied (Figure 1). We sequenced the mitochondrial regions COI and ND6 and the nuclear regions *period* and *ITS1*.

Figure 1. Map of locations where samples of *Anastrepha zenildae* and some species of *fraterculus* group used in this study were collected.

Results

Phylogenetic analysis revealed that *A. zenildae* populations clustered together in a monophyletic group for all the gene regions studied (Figure 2). In the COI analysis, it was verified that *A. zenildae* and *A. coronilli* are genetically closer. The period analysis was not adequate to resolve the phylogenetic relationships among these closely related species. The results indicate that *A. zenildae* is closer to the *A. fraterculus* Peruvian morphotype and *A. fraterculus* Mexican morphotype than to *A. fraterculus* Brazilian morphotypes.

Figure 2. Phylogenetic reconstruction using Bayesian inference method for the COI gene using Markov Chain (MCMC) to 10 million Generation. Posterior probability values (PP) are indicated in knots.

Conclusion

*A. zenildae* is closer to the *A. fraterculus* Peruvian and *A. fraterculus* Mexican morphotypes than to *A. fraterculus* morphotypes Brazilian 1 and Brazilian 3.

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