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.
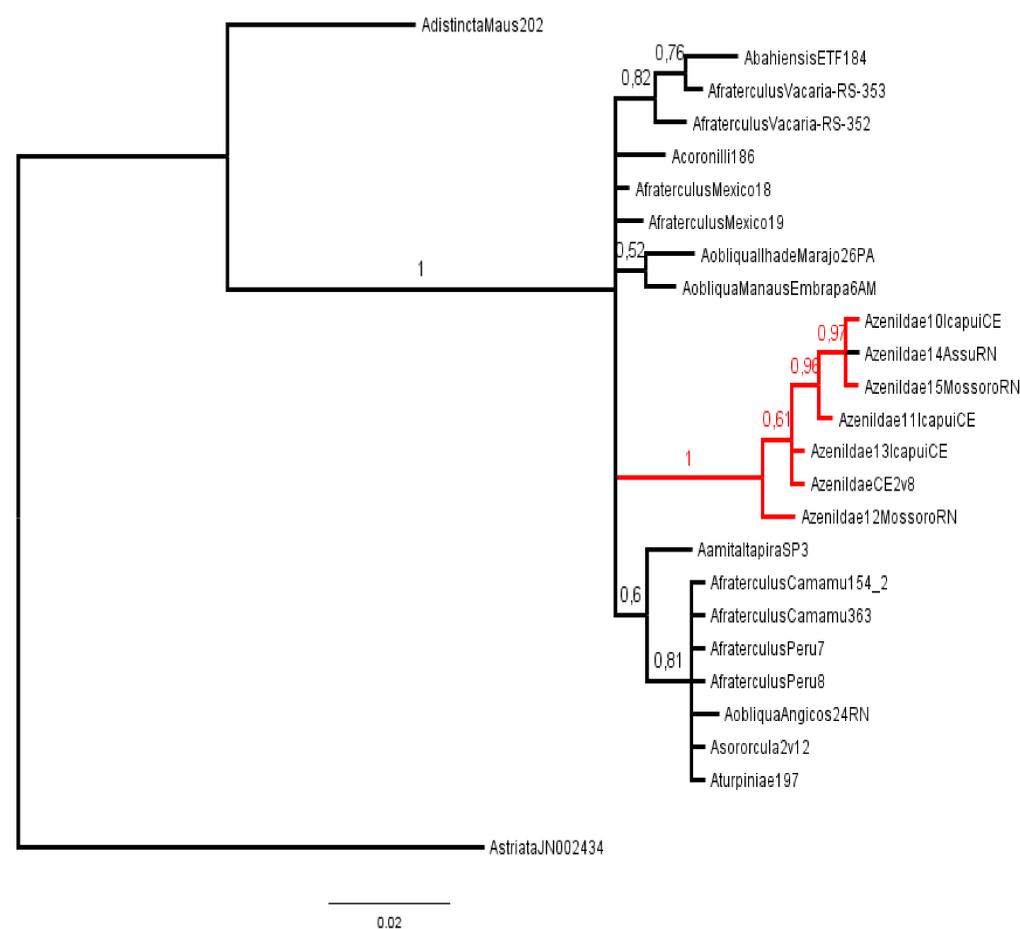
Methods

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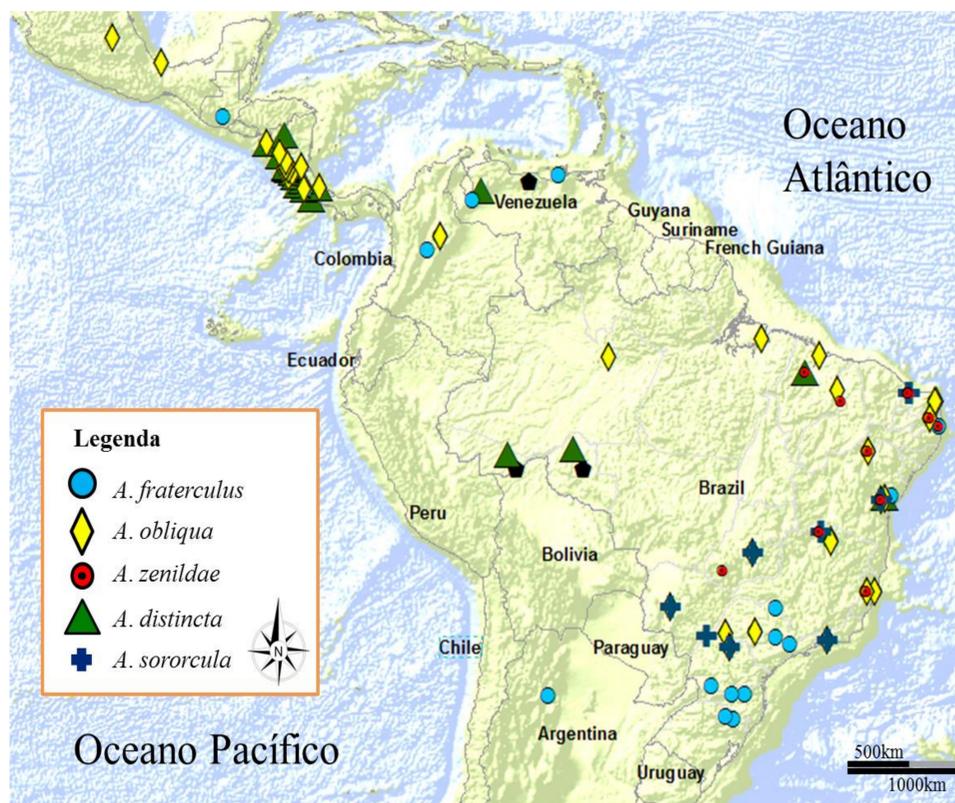
Figure 1. Map of locations where samples of *Anastrepha zenildae* and some species of *fraterculus* group used in this study were collected.

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.