



Phylogenetic analysis of *Anastrepha obliqua* (Macquart) populations in Brazil

Joseane Fernanda Passos¹, Roberto Antonio Zucchi², Beatriz Ronchi-Teles³, Raul Ruiz-Arce⁴, Norman B. Barr⁴, Bruce A. McPherson⁵, Elton Araujo⁶, Ricardo Adaime⁷, Janisete Gomes Silva¹

¹Universidade Estadual de Santa Cruz, Rodovia Jorge Amado, km 16, Salobrinho, Ilhéus, Bahia, Brazil, ²Escola Superior de Agricultura “Luiz de Queiroz”, Universidade de São Paulo, Piracicaba, São Paulo, Brazil, ³Instituto Nacional de Pesquisa da Amazônia, Manaus, Amazonas, Brazil, ⁴United States Department of Agriculture, Texas, USA, ⁵Ohio State University, Ohio, USA, ⁶Universidade Federal Rural do Semi-Árido, Mossoró, Rio Grande do Norte, Brazil, ⁷Empresa Brasileira de Pesquisa Agropecuária, Macapá, Amapá, Brazil

joseanefernanda@bol.com.br

Introduction

The West Indian fruit fly, *Anastrepha obliqua*, is a major pest of tropical fruits infesting a wide variety of hosts and in Brazil it is the second most frequent species in the genus. Molecular analyses have shown that *A. obliqua* does not represent a monophyletic group. This would suggest the need for more detailed studies about population structure. We sequenced a portion of genomic regions COI, ITS, Period and ND6 from *A. obliqua* gathered in Brazil.

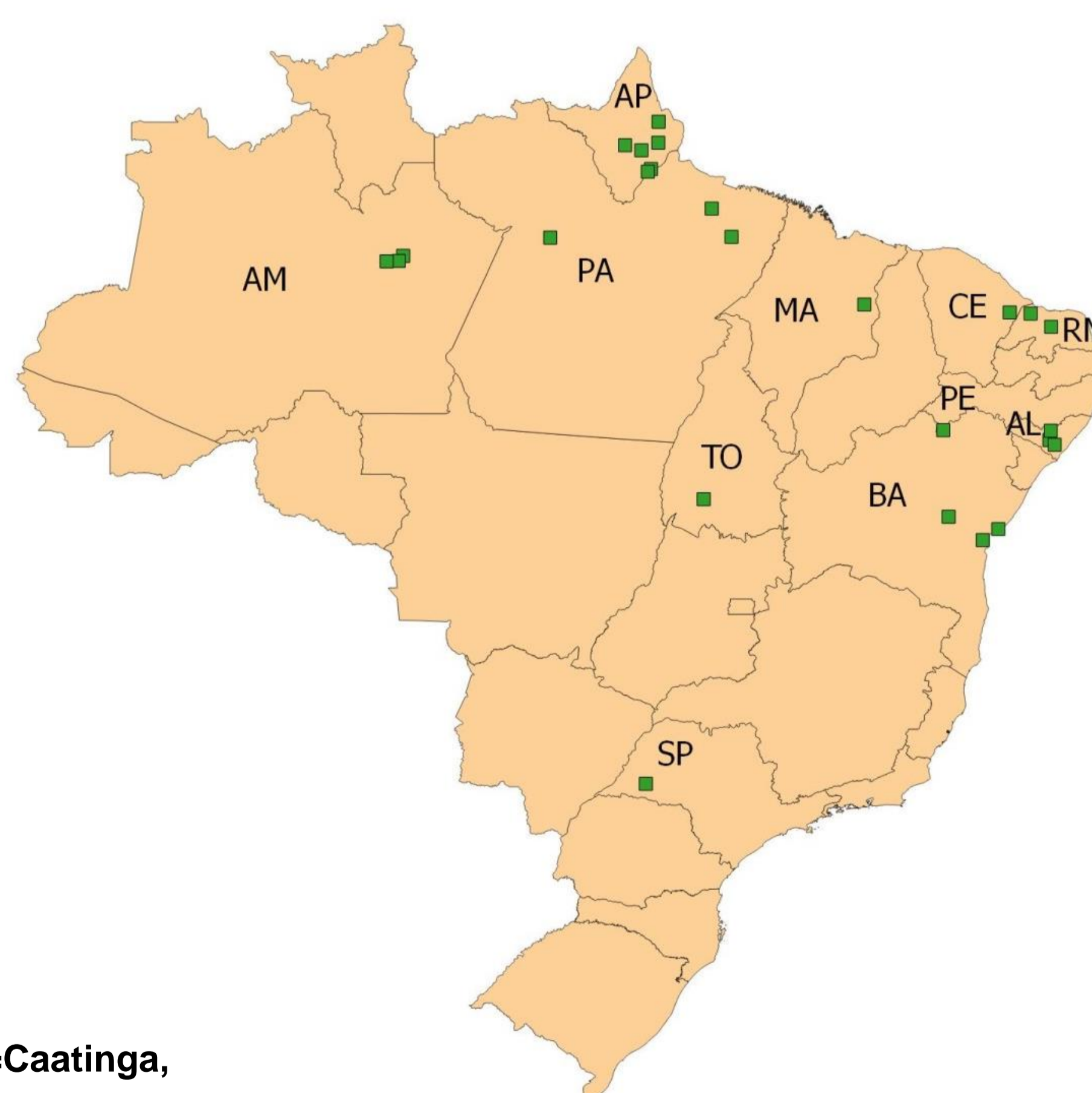
Methods

Forty two specimens were collected from fruits and traps from 25 geographic sites in eleven states in Brazil (Table 1 and Figure 1). DNA was isolated and a partial fragment of each genomic region was amplified by the Polymerase Chain Reaction, then sequenced. The sequences were concatenated in a sequence matrix. We performed partition analysis for each genomic region to choose the best evolution model. A Bayesian phylogenetic tree was constructed and analyses for population structure and demographics were estimated.

Table 1. Information on *A. obliqua* specimens used in this study.

Localidade	N	Estado	Bioma
Cariri	2	TO	FA
Petrolina	2	PE	CA
Caxias	2	MA	CE
Indiana	1	SP	MA
Salvador	3	BA	MA
Itaberaba	1	BA	CA
Valença	1	BA	MA
Mossoró	2	RN	CA
Angicos	2	RN	CA
Limoeiro do Norte	1	CE	CA
Irاندuba	1	AM	FA
Manacapuru	1	AM	FA
Manaus	4	AM	FA
Junqueiro	1	AL	MA
Arapiraca	4	AL	CA
Palmeira dos Índios	2	AL	MA
Macapá	1	AP	FA
Porto Grande	1	AP	FA
Pracuuba	2	AP	FA
Santana	1	AP	FA
Serra do Navio	1	AP	FA
Cutias	1	AP	FA
Santarém	2	PA	FA
Ilha de Marajó	1	PA	FA
Tomé-Açu	2	PA	FA
Total	39		

FA = Floresta Amazônica, CE=Cerrado, CA=Caatinga, MA= Mata Atlântica



0 500 1000 km

Figure 1 . Geographic locations of the 23 collection sites of *A. obliqua* in South America.

Results

A fragment of 2,184 bp contained 78 variable sites e genetic distance of 2.8% between clades. A total of 33 haplotypes (designated H1-H33) were observed with haplotype diversity of 0.9884. We observed two clades (Figure 2). Clade I consisted of mostly Northeastern collections and clade II of collections from the Northern. We saw that haplotypes recovered from individuals gathered in Para and Amapá showed in both clades.

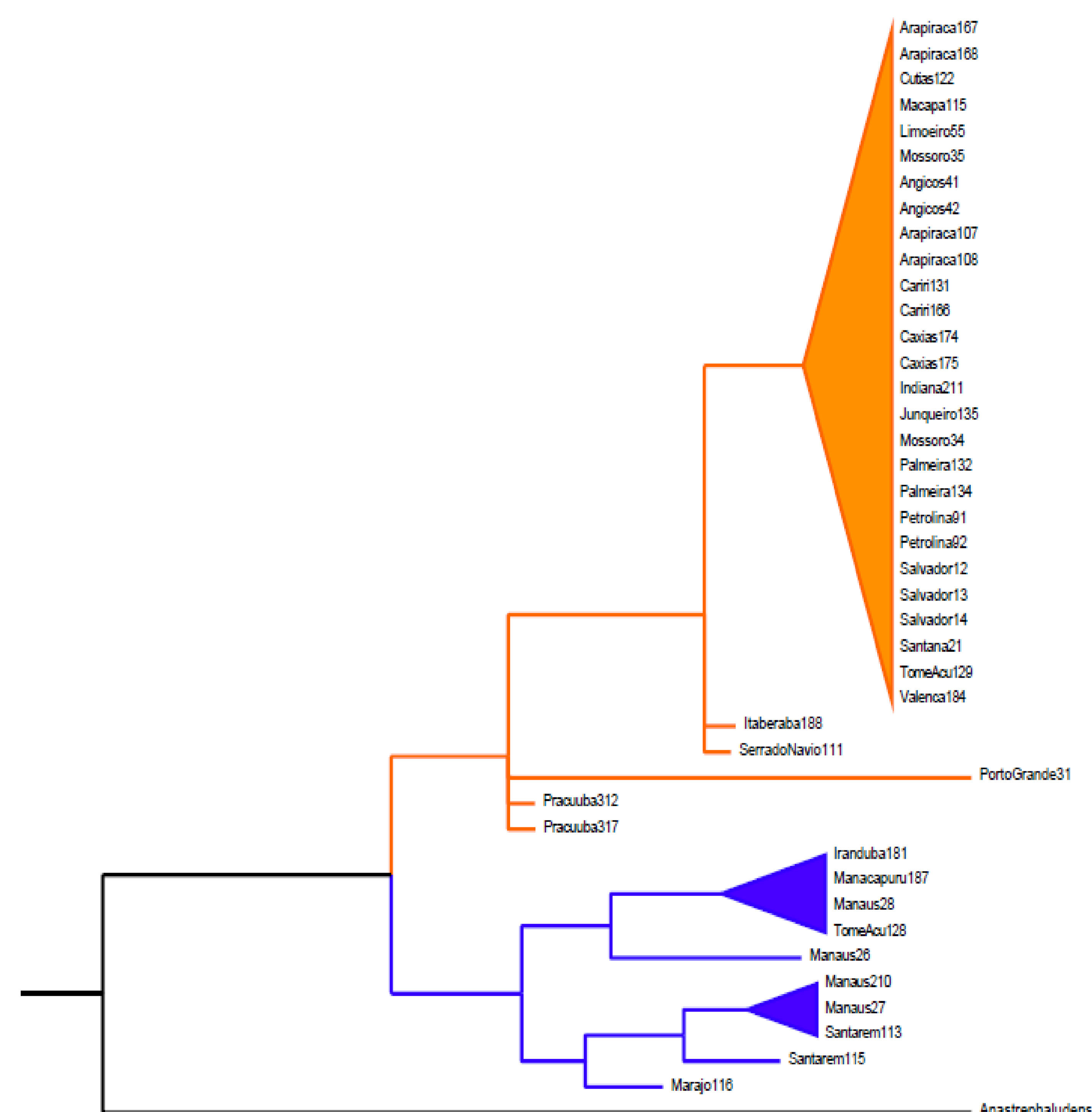


Figure 2. Bayesian phylogeny of *A. obliqua* haplotypes using mitochondrial genes (ND6 and COI) and nuclear regions (ITS1 and Period). *Anastrepha ludens* was used as an outgroup.

Conclusion

Our results show high haplotype diversity and two clusters of *A. obliqua* in the phylogenetic tree with exclusive haplotypes in each region, which can have resulted from a decrease in gene flow between populations due to geographic distance.

Financial Support

