



Genetic diversity in Brazilian populations of *Anastrepha obliqua* (Macquart) based on mtDNA

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Introduction

Anastrepha obliqua (Macquart), the West Indian fruit fly, is the second most polyphagous species within the genus in Brazil and therefore one of the most economically important pest species. It infests an extensive range of hosts, at least 60 species. *Anastrepha obliqua* ranges from northern Mexico to southern Brazil also including the Caribbean Islands.

Methods

The specimens of *A. obliqua* were either reared from fruit and traps in 33 geographic sites in Brazil (Table 1 and Figure 1). We sequenced a fragment of the mitochondrial gene COI to estimate population structure and genetic diversity of *A. obliqua* geographic collections in Brazil.

Table 1. Frequency and distribution of mitochondrial haplotype from each geographic site.

Population	Localidade	Haplótipo (número)
AM	Manaus	H6(2) H11(4), H16(1), H17(3)
AM	Irlanduba	H11(2)
AM	Rio Preto da Eva	H6(1) H4(2) H11(2)
AM	Manacapuru	H11(1)
AM	Ferreira Gomes	H6(1) H5(2)
AM	Cutias	H1(8), H6(1)
AM	Pracuuba	H9(2)
AM	Porto Grande	H8(2)
AM	Macapá	H1(6), H2(1), H4(1), H5(1)
AM	Serra do Navio	H1(4), H2(1), H3(1)
AM	Pedra Branca	H7(1)
AM	Tartarugalzinho	H4(2)
AM	Santana	H1(5), H4(1), H6(2)
AM	Santarém	H4(1), H13(1), H14(1)
AM	Tomé-Açu	H1(2), H11(1)
AM	Ilha de Marajó	H4(1), H6(1), H12(2)
Ce	Cariri do Tocantins	H1(5)
Ce	Indiana	H1(4), H20(1)
Ce	Caxias	H1(5)
Ce	Teresina	H1(2)
Ca	Limoeiro do Norte	H1(9), H19(1)
Ca	Angicos	H1(8), H18(1)
Ca	Mossoró	H1(8)
Ca	Petrolina	H1(5)
Ca	Itaberaba	H1(2)
Ca	Arapiraca	H1(3), H10(3)
Ce	Palmeira dos Índios	H1(6)
FA	Anadia	H1(1)
FA	Maceió	H1(5)
FA	Junqueiro	H1(2)
FA	Valença	H1(2)
FA	Salvador	H1(5)
FA	Vitória da Conquista	H1(4), H15(1)

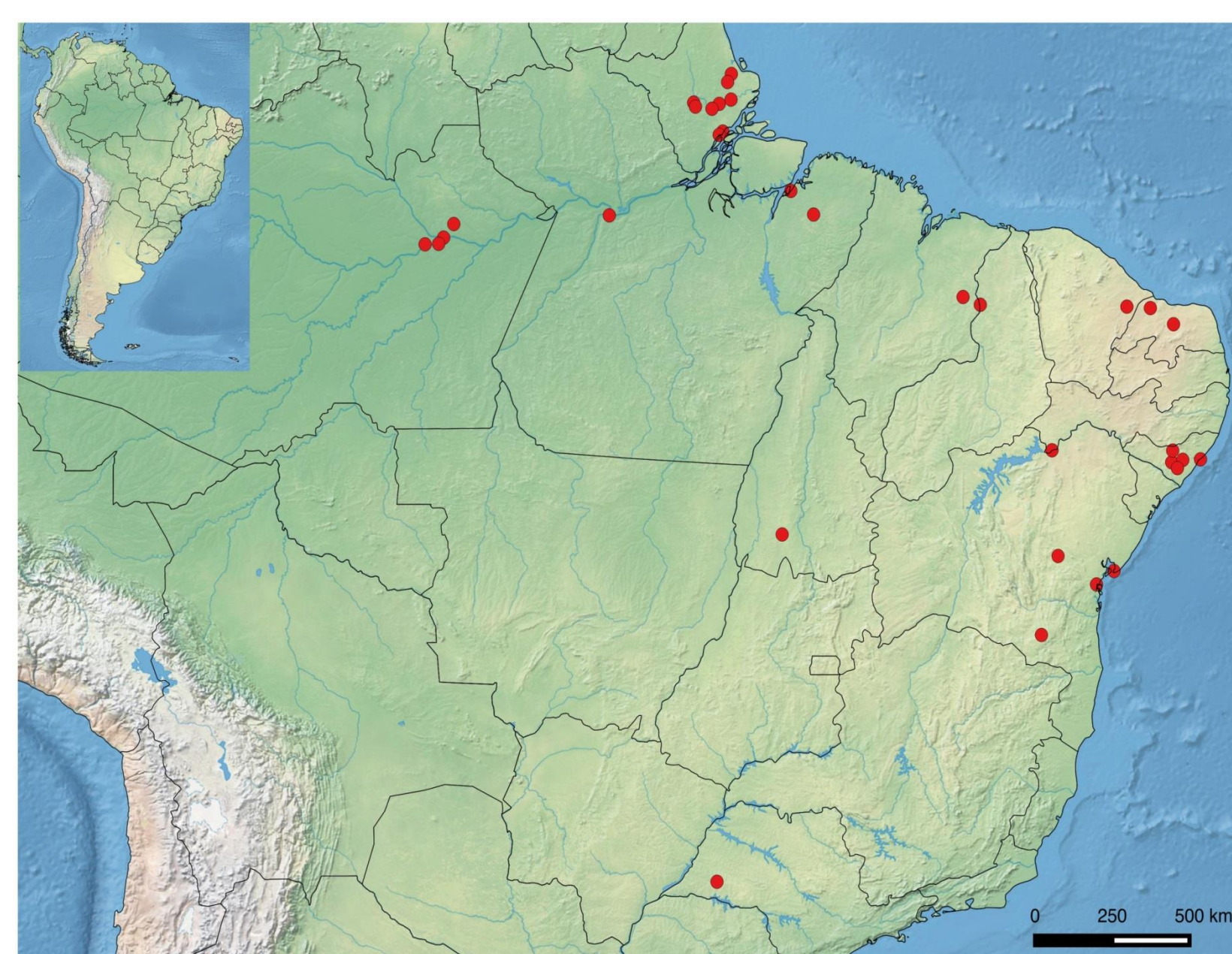


Figure 1. Map with the sampled localities

Results

A total of 153 specimens from the Amazon Forest, Atlantic Rainforest, Cerrado, and Caatinga were analyzed. A total of 20 haplotypes were found. The highest diversity levels were observed in collections from the Amazon Forest (Table 2). AMOVA and Fst tests showed evidence of genetic structure allowing us to delineate two groups of *A. obliqua* populations. This groups were observed in haplotype network (Figure 2). The Mantel tests were not significant indicating a weak correlation between genetic and geographic distances. Mismatch distributions and Neutrality Tests suggest that the Caatinga, Cerrado and Atlantic Forest populations have experienced a recent population expansion.

Table 2. Statistic summary for COI analysis of *A. obliqua* populations.

Populações	n	h (±S.D.)	π (±S.D.)	D	Fs	R ₂
AF	26	0.1000 (0.70)	0.00016(0.0011)	-1.15559	-1.09352	0.19230
CA	40	0.2048(0.86)	0.00034(0.00015)	-1.43092	-2.68408	0.07642
CE	17	0.1176(0.101)	0.00019(0.0016)	-1.16387	-0.74844	0.23529
AM	70	0.8298(0.038)	0.00847(0.0045)	0.46575	-0.05912	0.11897
Total	153	0.556(0.048)	0.00542(0.00055)	-0.86391	-3.46712	0.06149

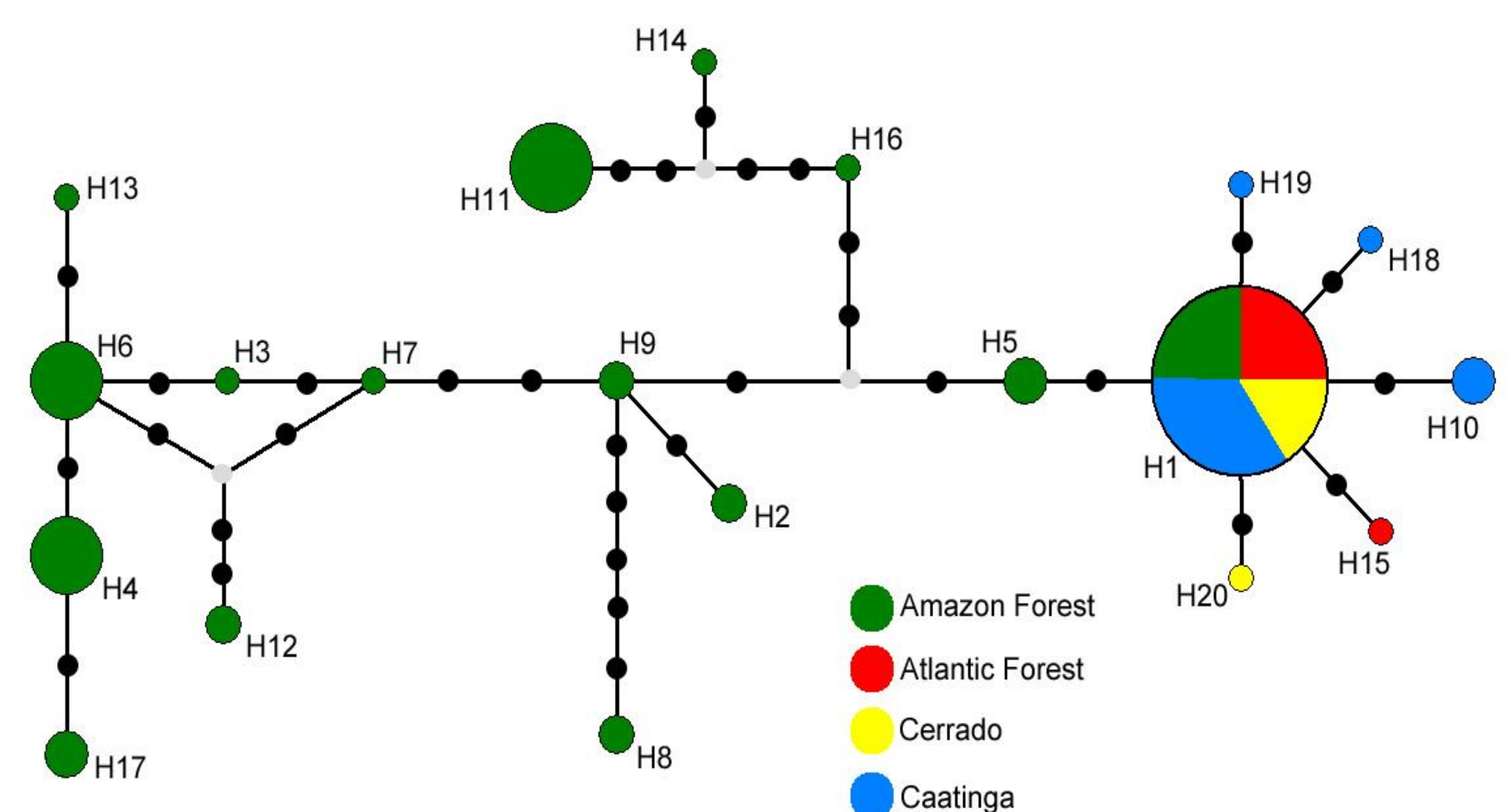


Figure 2. Haplotype network of COI sequences of *A. obliqua*. Sampled haplotypes are indicated by colored circles and missing or unsampled haplotypes are indicated by small solid gray circles. Haplotypes are colored according to biomes.

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

Conclusion

Populations in the Amazon Forest showed high genetic diversity when compared to the other biomes and the demographic parameters indicated a recent expansion of *A. obliqua* in Brazil.

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