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**Title:** Land use effects on mosquito biodiversity and potential arbovirus emergence in the Southern Amazon, Brazil

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# Summary

The Amazon rainforest is considered the largest reservoir of culicids and arboviruses in the world. It has been under intense human-driven alteration, especially in the so-called "Arc of Deforestation", located in the Eastern and Southern regions. The emergence and transmission of infectious diseases are increasing, potentially due to land use change. We used landscape-scale mosquito surveillance across a forest fragmentation gradient in the Southern Amazon to evaluate the relationship between forest disturbance and the composition and structure of mosquito communities with a particular focus on the potential for arbovirus emergence in the region. Generalized Linear Models and Logistic Regression were used to associate the degree of landscape disturbance with arbovirus vectors richness and abundance. A total of 1,960 culicids, belonging to 50 species, were collected from 2015 to 2016. Among these species, 20 have been associated with the transmission of arboviruses. Our results show an association of land use, more specifically small size of forest remnants with more irregular shape and higher edge density, with the increase of arbovirus vectors richness and abundance. Six species of mosquito vectors exhibited a higher probability of occurrence in landscapes with medium or high degrees of disturbance. Our results indicate that land use change influences mosquito communities with potential implications for the emergence of arboviruses.

**Keywords:** Biodiversity; Environmental disturbance; Mosquito ecology; Vector-borne diseases; Arc of deforestation.

#### **1. INTRODUCTION**

Landscape integrity is a critical element in the maintenance of the interrelationships between environment, animals, vectors, and pathogens, which participate in the epidemiological cycle of infectious diseases. These relationships are dynamic and constantly submitted to environmental pressures, which despite tending to ecological balance, may interfere in this process (Patz and Norris, 2004; Haddad et al., 2015).

Anthropogenic disturbances, such as land use for urbanization and agriculture, leads to landscape fragmentation (Patz and Norris, 2004; Ferreira et al., 2018). Fragmentation is a degenerative process, characterized by the elimination of large contiguous areas of native

vegetation, resulting in fragments of different sizes and shapes (Vogelmann, 1995; Numata et al., 2011). The consequences of forest fragmentation include a decline in the natural ecosystems area, loss of biodiversity, changes in the hydrological regime of the river basins, soil erosion, and changes in the chemical and physical flows of the landscape, including heat, wind, water, and nutrient movements (Pedron et al., 2006), creating conditions for new ecological configurations (Guimarães et al., 2004).

Anthropogenic disturbance in sylvatic habitats may impact the distribution and abundance of hosts and vectors favoring the emergence and spread of human zoonotic infectious diseases, such as arthropod-borne viruses – the arboviruses (Keesing et al., 2010). In the past decades, arboviruses have emerged and/or re-emerged in the New World and increased their importance as human and veterinary pathogens (Marcondes et al., 2017). Arboviruses such as Saint Louis encephalitis (SLEV), West Nile (WNV), yellow fever (YFV), oropouche (OROV), and Mayaro (MAYV) are maintained in complex sylvatic cycles involving infected hematophagous vectors (such as mosquitoes) and wild vertebrates (such as mammals and birds) (Figueiredo, 2007). Humans and/or domestic animals are typically incidental or dead-end hosts but may become infected with arboviruses upon contact with infected vectors (Gould, Pettersson, Higgs, Charrel, & de Lamballerie, 2017; Vasconcelos et al., 2001).

The Amazon rainforest comprises more than a third of the world's tropical rainforests and contains the largest biodiversity reserve on the planet (Nobre, 2014). This diversity includes pathogens, parasites, and vectors, in fact the Amazon is the largest arbovirus reservoir in the world with more than 210 species isolated of which at least 40 are pathogenic to humans (Vasconcelos et al., 2001; Napoleão-Pego et al., 2014). Despite being the largest and most intact tropical rainforest on earth, the Amazon contains a 500,000 km<sup>2</sup> "Arc of Deforestation" that is expanding along the southern and eastern regions of the Brazilian Amazon to comprise the most active deforestation frontier in the world (INPE, 2021). The states of Pará (PA) and Mato Grosso (MT) have been the most active in this process of deforestation especially due to agricultural and livestock expansion (INPE, 2021).

The municipality of Sinop, MT, is located in the Arc of Deforestation and has heterogeneous habitats characterized by an urban-forest-rural landscape, which could be favorable for arboviruses emergence. In fact, Sinop has reported the co-circulation of different arboviruses, including the emergence of MAYV (Vieira et al., 2015) and SLEV (Moraes et al., 2021), which have been silently circulating during dengue outbreaks. Determining the basic ecology of mosquito

communities is crucial for understanding how deforestation and forest fragmentation influence the vector community and provides insights into where disease risk will increase (Steiger et al., 2012). Here we used landscape-scale mosquito surveillance across a deforestation gradient to determine the association of land use with the richness and abundance of mosquitoes, particularly species that are competent arbovirus vectors. We then use these results to inform the potential for regional arbovirus risk and emergence.

# **2. METHODOLOGY**

#### 2.1 Study area and collection and identification of mosquitoes

This study is part of a research network named "Land Use Change, Biodiversity, and the Community Ecology of Amazonian Vector-Borne Diseases". The studied area as well as the collection and identification of mosquitoes were previously described (Vieira et al., 2019). Briefly, mosquito collections were carried out during the dry seasons of 2015 and 2016 in 39 forest remnants located on private land within six municipalities (Cláudia, Ipiranga do Norte, Santa Carmem, Sinop, Sorriso, and Vera) in the north of the State of MT, in the Southern region of the Amazon's Arc of Deforestation (**Figure 1**). Three traps were installed at each forest remnant, 200 m apart, resulting in a total of 117 traps. CDC-UV light traps baited with CO<sub>2</sub> were installed 1.5 meters above the ground between two trees, in a shaded area. Sampling was performed during three consecutive days, each trap operating for 24 h, totaling 8,424 h of sampling effort. Mosquitoes were morphologically identified down to species level according to published taxonomic keys (Lane, 1953; Consoli and Lourenço-de-Oliveira, 1994; Forattini, 2002) and by comparing them with standard specimens from the collection of the Section of Arbovirology and Hemorrhagic Fevers, Evandro Chagas Institute, Pará, Brazil.

The sampling landscape covers approximately 10,000 km<sup>2</sup> that is primarily comprised of forest remnants, agriculture areas, and urban areas. The forest remnants were selected to cover a wide variety of forest cover and levels of disturbance gradient. Agricultural production is the main economic activity of these municipalities, which is the greatest soybeans, corn, and cotton producer in the country. The climate is tropical with an average temperature of 28 °C and annual precipitation levels of 1,900 mm. The wet season occurs from November to April and the dry season from May to October.

#### 2.2 Composition and structure of mosquito communities

Both composition and structure of mosquito communities were determined by a) abundance (Ab), measured as the total number of individuals of the same species; b) percentage of abundance (Ab%); c) frequency (F), measured as the number of points at which each species was collected; d) percentage of the frequency (F%), which is the percentage of the individuals of a species from the total of individuals collected; e) constancy (C%), i.e. the percentage of a species from the total of species collected, obtained by using the formula (p / N) x 100, where p = the number of sampling locations at which a given species was captured (points) and N = total forest remnants. Species were considered constant (C) when C> 50%, accessory (A) when C> 25-50%, and accidental (Ac) when C<25% (Silveira Neto et al., 1976); f) dominance (D%) of each species obtained by using the formula D% = (i / t) x 100, where i = total number of individuals in the species and t = total number of individuals captured. The species were considered eudominant (E) when D> 10%, dominant (D) when D between 5-10%, subdominant (Sb) when D between 2-5%, eventual (Ev) when D between 1 -2%, and rare (Rr) when D <1% (Friebe, 1983). These values were calculated for all mosquitoes collected as well as just vectors.

# 2.3 Landscape Metrics

Satellite images (Landsat 8, OLI sensor from 2015) from the Brazilian National Institute of Space Research website (www.dgi.inpe.br/CDSR) were used to generate a four-class raster map to classify the land area as forests, rivers, agricultural land or livestock areas, and bare soil or urban areas. The Semi-automatic Classification Plugin (SCP) (Congedo, 2018) in the QGIS software (QGIS Development Team, 2021) was used for landscape classification. A 1000 m radius buffer was considered for calculating patch metrics based on exploratory data analysis indicating that this buffer best explained the metric values observed (see values in Supplementary material – **Figure S1**).

We calculated landscape metrics following (Gustafson, 1998) with the Land Cover Statistics plugin (LecoS) in QGIS software (Jung, 2016). The metrics included 1) forest cover proportion; 2) mean patch area in ha; 3) number of forest patches; 4) forest core amount in ha, which is equivalent to overall forest core area based on edge depth of 30 m correspondent to our raster's

cell size; 5) core ratio, which is the ratio of total core area to total forest area; 6) edge amount in km, which is equivalent to the sum of the lengths of all edge segments involving the forests; 7) edge density, which is the ratio of edge quantity to total forest area; 8) mean patch shape index, based on patch perimeter and patch area, with values increasing as patch shape becomes more irregular; 9) forest patch cohesion index, which measures the physical connectedness of forest patches in a landscape; 10) mean time since deforestation (MTD) was determined as previously proposed (Ferraz et al., 2009). Metrics, except metrics 5 and 7, are illustrated in **Figure 2**.

# 2.4 Statistical analysis

To quantitatively describe the disturbance level of the landscape surrounding the forest remnants, we performed a principal component analysis (PCA) on all landscape metrics using the *vegan* package in R (Oksanen et al., 2018). Briefly, PCA is an orthogonal linear transformation technique that uses a coordinate system to convert a data set of observations of possibly correlated variables into a data set of values of linearly uncorrelated variables called principal components (Venables and Ripley, 2002). The first principal component of these landscape metrics was then used as a predictor in a series of quasipoisson generalized linear models (GLM) with response variables (1) overall mosquito richness, (2) overall mosquito abundance, (3) vector richness, and (4) vector abundance. These response variables were obtained using rarefaction curves. We used the quasipoisson distribution because we were modeling discrete count data with overdispersion.

In addition to the use of a composite principal component, we used quasipoisson multiple regression with each landscape metric as a predictor. We then used quasi-AIC corrected for small sample size (QAICc) to compare the support for distinct landscape metrics that might influence the abundance and richness of mosquitoes.

Finally, we used logistic regression (LRM) to test whether the degree of landscape disturbance was associated with a higher probability of occurrence of individual vector species, using presence or absence of each vector as a categorical response variable, as well as each landscape metric as explanatory variables.

All statistical analyses were performed using the computing environment R version 3.5.1 (R Development Core Team, 2021), logistic regression graphs were generated with the *popbio* package (Stubben et al., 2018), for quasipoisson GLM we used *MuMIn* package (Bartón, 2018), the coefficients of determination ( $R^2$ ) was calculated with packages *rms* (Harrell-Jr, 2018) and the

proportion of deviance explained by the GLMs (D<sup>2</sup>) was calculated with package *modEvA* (Barbosa et al., 2016).

# **3. RESULTS**

#### 3.1 Mosquito data

A total of 1,960 specimens, belonging to 50 taxonomic units and distributed in 13 genera (**Table 1**), were collected throughout the study period. Among the mosquitoes identified, *Culex Melanoconion* section (791; 40.36%) and *Cx. declarator* (229; 11.68%) were eudominant and constant species, followed by the dominant species *Coquillettidia arribalzagae* (159; 8.11%), *Anopheles triannulatus* (144; 7.35%), *Cx. coronator* (130; 6.63%), and *An. oswaldoi* (124; 6.33%). These species represented approximately 80% of the identified species (**Table 1**).

We found 20 species associated with arbovirus transmission, representing approximately 75% of all mosquitoes collected (**Table 1**). Some of them have already been considered as vectors or incriminated in the transmission of OROV (*Cq. venezuelensis, Ochlerotatus serratus, and Oc. scapularis*), MAYV (*Cq. venezuelensis, Oc. scapularis, Psorophora albipes, and Ps. ferox*), and SLEV (*Cq. venezuelensis, Cx. coronator, Cx. declarator, Mansonia titillans, Oc. serratus, Oc. fulvus, and Trichoprosopon digitatum*).

# 3.2 Mosquito-landscape relationships

A single variable represented by the first axis of the PCA explained 62% of the variance in landscape metrics. This variable, which we refer to as "landscape disturbance", was associated with lower proportion of forest cover (score = -0.39) and low amount of forest core area (score = -0.42), lower forest connectivity (score = -0.42), smaller forest patches (score = -0.43), and more patches (score = 0.23) with irregular shape (score = 0.35) (**Figure 3**). Landscape disturbance was positively associated with richness (slope= 0.28;  $R^2$ = 0.12; p<0.1) and abundance (slope= 5.51;  $R^2$ = 0.13; p<0.1) of overall mosquitoes, as well as richness (slope= 0.15;  $R^2$ = 0.10; p<0.1) and abundance (slope= 3.71;  $R^2$ = 0.15; p<0.05) of vectors (see Supplementary material – Table S1).

The most parsimonious quasipoisson GLMs as determined by QAICc supported a negative relation of overall mosquito abundance to forest cover proportion (p<0.05), as well as a strong

positive relation to mean patch shape index (p<0.01). Furthermore, there was a negative relationship of overall mosquito richness to forest cover proportion (p<0.05) (**Table 2**). Vector species abundance was strongly related to a greater number of forest patches (p<0.05), smaller forest cover proportion (p<0.01), and higher edge density (p<0.01). Vector richness was related to smaller forest cover proportion (p<0.05) and higher mean patch shape index (p<0.05) (**Table 2**; **Figure 3**).

While overall mosquito abundance and diversity were positively associated with degraded landscapes, the presence of specific species was significantly associated with specific landscape metrics (**Figure S2**) but not with PCA (result not shown).

# 4. **DISCUSSION**

Changes in land use may promote the emergence of infectious diseases due to habitat change, new distribution patterns of species, and higher contact rates between humans, vectors, and reservoir hosts (Hassell et al., 2017). We found that abundance and richness of both overall mosquitoes and vectors were higher in more disturbed forest remnants among the fragmented forest landscape around Sinop, MT in the Southern Amazon arc of deforestation. To date, this is the first study describing the association of land use, by using quantitative landscape analysis, with mosquito biodiversity.

In general, what most affected this result was the small size of forest remnants with more irregular shapes and higher edge densities. Patch size and patch quality are important characteristics that influence species persistence, coexistence, colonization, dispersal, and ecological interactions (MacArthur and Wilson, 1967; Fretwell and Lucas, 1970). As the size of forest remnants is reduced, there is an increase of transitional environments, which extend from the center of the fragment to its surrounding matrix, characteristics that directly influence local diversity interactions (Fahrig, 2003; Metzger et al., 2009). Several studies have shown that the rainforest interiors had fewer mosquito species, and different community composition compared to rainforest edges (Ewers and Didham, 2007; Steiger et al., 2012). This could be explained by changes in physical and chemical conditions, the microclimate, and the diversity of breeding sites of mosquito communities. In the tropics, cleared and forest-edge habitats are often well lit and warmer than rainforest interiors (Camargo and Kapos, 1995), characteristics that can increase mosquito larval growth, survivorship, and adult densities (Steiger et al., 2012; Hutchings et al.,

2018). Finally, other complex ecological relationships such as host availability, type of plants in the landscape, and predation could also help explain our results.

Mosquito vectors, such as *Cx. Melanoconion* section, *Cx. declarator*, *Cq. arribalzagae*, and *Cx. coronator*, were among the most abundant and dominant species in this study. Furthermore, by using LRM, it was observed that, as the degree of landscape disturbance increases, there is a greater probability of occurrence of species such as *Cx. coronator*, *Oc. serratus* (both also presenting probability of occurrence in highly preserved landscapes), *Cx. spissipes*, *Ad. squamipennis*, *Cq. arribalzagae*, *Oc. fulvus*, *Oc. scapularis*, and *Tr. digitatum*. These results indicate that land use, mainly for agriculture, might be providing a favorable environment for arbovirus vectors. In fact, some species such as *Cx. declarator*, *Cx. coronator*, and *Ochlerotatus* spp. have opportunistic characteristics, and may benefit from anthropic environmental modifications (Forattini, 2002; Gomes & Forattini, 1990; Lopes & Lozovei, 1995; Ribeiro et al., 2012; Silva, 2002; Taipe-Lagos & Natal, 2003).

Besides changes in land use, other factors such as viral genetic plasticity have contributed to arbovirus emergence and continued persistence. Since most arboviruses contain RNA as their genetic material, the mutation frequency is high, which allows them to adapt to different vertebrate and invertebrate hosts (Patz et al., 2000; Coffey et al., 2013; Cable et al., 2017). Indeed, initially, YFV, the first arbovirus described in the world, was transmitted from monkey to monkey by *Aedes africanus*, presenting a cycle restricted to the wild environment in Africa (Haddow et al., 1947). With uncontrolled urbanization, people infected in forested areas may have carried the virus to peri-urban and urban areas where there were ideal conditions for YFV maintenance, including high densities of susceptible people and infestations of competent mosquitoes such as *Ae. bromeliae* and *Ae. aegypti*, creating the urban cycle of the disease (Briscoe, 1962).

The behavioral plasticity of vectors also favors the emergence of arboviruses in humans. Some mosquito species may adapt to blood feed in a large variety of wild and domestic animals and humans (Consoli and Lourenço-de-Oliveira, 1994; Forattini, 2002), allowing them to colonize both natural and anthropogenic environments. SLEV, for example, is maintained in a bird-mosquito-bird transmission cycle (Luby, 1979; Diaz et al., 2018). In rural environments, it is generally transmitted by *Culex tarsalis* and *Cx. nigripalpus* mosquitoes and amplified by migratory bird species (Day, 2001; Diaz et al., 2018). *Cx. nigripalpus* is a widespread subtropical species and a highly opportunistic blood feeder, exhibiting either anthropophagic or zoophagic or

ornithophagic behavior (Laporta et al., 2008) that may facilitate temporal shifts from rural to urban epidemic transmission (Diaz et al., 2018).

Considering a) land use changes produce an interface between different habitats that result in greater contact between vectors and humans; b) the genetic plasticity of arboviruses; c) the behavioral plasticity of vectors and d) previous studies have shown the circulation of arboviruses in the Arc of Deforestation (Travassos-da-Rosa et al., 1998; Nunes et al., 2009; Terzian et al., 2009; Batista et al., 2011; Vieira et al., 2015), our results indicate a potential risk of arboviruses emergence to the population that lives close to forest remnants in this study, as well as to people that visit these areas for resource extraction, fishing, and tourism. Finally, infected humans could serve as arbovirus amplifiers, initiate an urban cycle and generate an epidemic. This is because, urban species with high vectorial competence for various pathogens, such as *Ae. aegypti* and *Cx. quinquefasciatus*, could serve as vectors for arboviruses (Figueiredo, 2007; N. Lopes et al., 2014; Donalisio et al., 2017). More studies, including arbovirus surveillance in culicids, are needed to identify the extent of arbovirus transmission in the Arc of Deforestation.

It is worth mentioning that the CDC-UV light traps used in our methodology favor nocturnal species such as those belonging to Anophelini and Culicini tribes (Consoli and Lourenço-de-Oliveira, 1994; Forattini, 2002; Hutchings et al., 2010), which represent more than 82% of the individuals collected in our study. Therefore, diurnal species such as those belonging to Aedini and Sabhetini tribes (*Ae. albopictus* and *Sabethes belisarioi*, respectively), which have already been associated with MAYV, OROV, and SLEV (Marcondes & Ximenes, 2016; Vasconcelos et al., 1998), had a low rate of capture. In addition, since the traps were installed 1.5 m above the ground, it was not possible to capture species that are adapted to the tree canopies, such as *Hg. janthinomys*, which is an important vector for YFV and MAYV. Future mosquito surveys in the region should include methodologies to capture diurnal species, such as Malaise and Shannon traps and mouth aspirators, as well as include the forest canopy to capture greater biodiversity (Hutchings et al., 2010). Also, in future studies, variables related to local environmental conditions may also be collected, such as tree height, the diameter of trees at breast height (DBH), canopy cover (to measure sun exposure), the presence of bromeliads, temperature, and humidity (Vezzani et al., 2005; Ruiz et al., 2010).

#### **5. CONCLUSIONS**

We verified the association of small and irregular forest remnants presenting higher edge density, with higher mosquito richness and abundance. Deforestation in the studied region, particularly for agriculture, may be contributing to an environment favorable for the higher occurrence of several mosquito vectors of arboviruses. Therefore, our study highlights that planning measures should take into account a landscape scale factors to avoid the emergence of arboviruses.

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## **Conflict of interest statement**

The authors declare that there are no conflict of interests.

#### **Ethics statement**

This study was approved by IBAMA/ICMBio (license number 47284-2).

#### Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

#### Author contribution statements

Conceptualization, design, funding acquisition, and supervision: Canale, G. R., Peres, C. A., Levi, T., Bronzoni, R. V. M.

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Methodology, analysis, and interpretation of data: Vieira, C. J. S. P., da Silva, D. J. F., Kubiszeski, São-Bernardo, C. S., Barreto, E. S., Monteiro, H. A. O., Massey, A. L., Bronzoni, R. V. M.

Formal Analysis and writing original draft: Vieira, C. J. S. P., São-Bernardo, C. S., Bronzoni, R. V. M.

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All authors agreed the work is ready for submission to this journal, gave final approval of it to be published, and accepted responsibility for the manuscript's contents.

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# Figure 1: Geographic location of the 39 forest remnants located in the north of the State of Mato Grosso, in the southern region of the Amazon's Arc of Deforestation.

Panel A: map of South America with emphasis on the Amazon and its Arc of Deforestation; Panel B: location of forest remnants in Cláudia (A), Ipiranga do Norte (F and J), Santa Carmem (B8), Sinop (B5 to B7, C, D, E and G), Sorriso (I) and Vera (H).

# Figure 2: Landscape metrics illustration.

\* Values for these metrics decrease as the disturbance degree increases; ‡ Values for these metrics increase as the disturbance degree increases; \* Values for these metrics are similar with high or low disturbance degree. The landscapes are within the black circles.

# Figure 3: Eigenvalues generated by the Principal Component Analysis (PCA).

Achieved by combining the landscape metrics within 1-km buffer around each forest remnant sampled.

Species	Ab	Ab%	D%	F	<b>F%</b>	C%	Mosquitoes associated with arboviruses
Subfamily ANOPHELINAE							
Tribe Anophelini (n: 384; 19.59%; e: 11)							
Anopheles (Anopheles) mattogrossensis Lutz & Neiva, 1911	21	1.07%	Ev	3	7.69%	Ac	-
Anopheles (Anopheles) mediopunctatus Lutz, 1903	25	1.28%	Ev	9	23.08%	Ac	-
Anopheles (Anopheles) peryassui Dyar & Knab, 1908	7	0.36%	Rr	2	5.13%	Ac	-
Anopheles (Nyssorhynchus) aquasalis Curry, 1932	2	0.10%	Rr	2	5.13%	Ac	-
Anopheles (Nyssorhynchus) argyritarsis Robineau-Desvoidy, 1827	1	0.05%	Rr	1	2.56%	Ac	-
Anopheles (Nyssorhynchus) braziliensis Chagas, 1907	3	0.15%	Rr	1	2.56%	Ac	-
Anopheles (Nyssorhynchus) darlingi Root, 1926	4	0.20%	Rr	2	5.13%	Ac	-
Anopheles (Nyssorhynchus) oswaldoi Peryassú, 1922	124	6.33%	D	7	17.95%	Ac	-
Anopheles (Nyssorhynchus) tiannulatus Neiva & Pinto, 1922	144	7.35%	D	15	38.46%	А	-
Anopheles (Stethomyia) nimbus Theobald, 1903	49	2.50%	Sd	13	33.33%	А	$PIXV^1$ ; $VEEV^1$
Chagasia sp.	4	0.20%	Rr	1	2.56%	Ac	-
Subfamily CULICINAE							
Tribe Aedeomyiini (n: 8; 0.41%; e: 1)							
Aedeomyia (Aedeomyia) squamipennis Lynch Arribalzaga, 1878	8	0.41%	Rr	4	10.26%	Ac	$V EE V^2$
Tribe Aedini (n: 99; 5.05%; e: 10)							
Ochlerotatus (Ochlerotatus) fulvus Wiedemann, 1928	10	0.51%	Rr	6	15.38%	Ac	ILHV <sup>3</sup> ; SLEV <sup>3</sup> ; UNAV <sup>4</sup> ; VEEV <sup>4</sup> ; WEEV <sup>3</sup> ; YFV <sup>3</sup>
Ochlerotatus (Ochlerotatus) scapularis Rondani, 1848	20	1.02%	Ev	11	28.21%	А	ILHV <sup>3</sup> ; MAYV <sup>5</sup> ; MUCV <sup>3</sup> ; OROV <sup>6</sup> ; ROCV <sup>7</sup> ; VEEV <sup>7</sup> ; YFV <sup>7</sup>
Ochlerotatus (Ochlerotatus) serratus Theobald, 1901	27	1.38%	Ev	10	25.64%	А	ILHV <sup>3</sup> ; MUCV <sup>3</sup> ; OROV <sup>3</sup> ; SLEV <sup>3</sup> ; UNAV <sup>3</sup> ; VEEV <sup>3</sup> ; YFV <sup>7</sup>
Ochlerotatus (Protomacleaya) argyrothorax Bonne-Wepster & Bonne, 1919	1	0.05%	Rr	1	2.56%	Ac	ILHV <sup>3</sup>
Psorophora (Grabhamia) cingulata Fabricius, 1805	6	0.31%	Rr	4	10.26%	Ac	-
Psorophora (Grabhamia) dimidiata Cerqueira, 1943	15	0.77%	Rr	8	20.51%	Ac	-

Table 1: Species of mosquitoes collected during the dry seasons of 2015 and 2016 in forest remnants of the Arc of Deforestation, Southern Amazon.

Psorophora (Janthinosoma) albigenu Lutz, 1908 (em Peryassú, 1908)	3	0.15%	Rr	2	5.13%	Ac	$EEEV^4$ ; DENV <sup>8</sup> ; UNAV <sup>4</sup> ; VEEV <sup>9</sup>
Psorophora (Janthinosoma) albipes Theobald 1907	3	0.15%	Rr	2	5.13%	Ac	ILHV <sup>3</sup> ; MAYV <sup>3</sup> ; UNAV <sup>3</sup> ; VEEV <sup>3</sup> ; YFV <sup>3</sup>
Psorophora (Janthinosoma) ferox Von Humboldt, 1819	12	0.61%	Rr	4	10.26%	Ac	EEEV <sup>9</sup> ; ILHV <sup>3</sup> ; MAYV <sup>3</sup> ; ROCV <sup>10</sup> ; UNAV <sup>3</sup> ; VEEV <sup>9</sup> ; YFV <sup>11</sup>
Psorophora (Psorophora) ciliata Fabricius, 1794	2	0.10%	Rr	2	5.13%	Ac	-
Tribe Culicini (n: 1227; 62.60%; e: 13)							
Culex (Carrolia) sp.	1	0.05%	Rr	1	2.56%	Ac	-
Culex (Culex) coronator Dyar & Knab, 1906	130	6.63%	D	14	35.90%	А	ILHV <sup>4</sup> ; MUCV <sup>12</sup> ; SLEV <sup>12</sup> ; VEEV <sup>12</sup> ; WNV <sup>13</sup>
Culex (Culex) declarator Dyar & Knab, 1906	229	11.68%	Е	25	64.10%	С	BSQV <sup>3</sup> ; SLEV <sup>3</sup>
Culex (Culex) mauesensis Lane, 1945	6	0.31%	Rr	3	7.69%	Ac	-
Culex (Culex) pinarocampa Dyar & Knab, 1908	12	0.61%	Rr	7	17.95%	Ac	-
Culex (Culex) saltanensis Dyar, 1928	39	1.99%	Ev	15	38.46%	А	-
Culex (Melanoconion) Melanoconion section Theobald, 1903	791	40.36%	Е	35	89.74%	С	$EEEV^4$ ; $VEEV^4$ ; $WEEV^3$
Culex (Melanoconion) pedroi Sirivanakarn & Belkin, 1980	2	0.10%	Rr	2	5.13%	Ac	$EEEV^4$ ; $VEEV^9$ ; $WEEV^4$
Culex (Melanoconion) portesi Sénevet & Abonnenc, 1941	1	0.05%	Rr	1	2.56%	Ac	MUCV <sup>9</sup> ; WEEV <sup>9</sup>
Culex (Melanoconion) spissipes Theobald, 1903	3	0.15%	Rr	2	5.13%	Ac	$EEEV^3$ ; $VEEV^4$
Culex (Phenacomyia) corniger Theobald, 1903	5	0.26%	Rr	1	2.56%	Ac	-
Culex sp. 1	5	0.26%	Rr	3	7.69%	Ac	-
Culex sp. 2	3	0.15%	Rr	2	5.13%	Ac	-
Tribe Mansoniini (n: 161; 8.21%; e: 3)							
Coquillettidia (Rhynchotaenia) arribalzagae Theobald, 1903	159	8.11%	D	5	12.82%	Ac	UNAV <sup>3</sup>
Coquillettidia (Rhynchotaenia) venezuelensis Theobald, 1912	1	0.05%	Rr	1	2.56%	Ac	BSQV <sup>3</sup> ; MAYV <sup>7</sup> ; MUCV <sup>3</sup> ; OROV <sup>3</sup> ; SLEV <sup>7</sup> ; WNV <sup>7</sup>
Mansonia (Mansonia) titillans Walker, 1848	1	0.05%	Rr	1	2.56%	Ac	SLEV <sup>14</sup> ; VEEV <sup>14</sup> ; WNV <sup>13</sup>
Tribe Orthopodomyiini (n: 1; 0.05%; e: 1)							
Orthopodomyia fascipes Coquillett, 1906	1	0.05%	Rr	1	2.56%	Ac	-
Tribe Sabethini ( <i>n</i> : 10; 0.51%; e: 3)							

Limatus pseudomethysticus Bonne-Wepster & Bonne, 1920	1	0.05%	Rr	1	2.56%	Ac	-
Trichoprosopon digitatum Rondani, 1848	3	0.15%	Rr	2	5.13%	Ac	BSQV <sup>15</sup> ; ILHV <sup>15</sup> ; PIXV <sup>15</sup> ; SLEV <sup>15</sup>
Wyeomyia spp.	6	0.31%	Rr	3	7.69%	Ac	-
Tribe Uranotaeniini (n: 70; 3.57%; e: 8)							
Uranotaenia (Uranotaenia) briseis Dyar, 1925	3	0.15%	Rr	1	2.56%	Ac	-
Uranotaenia (Uranotaenia) calosomata Dyar & Knab, 1907	3	0.15%	Rr	2	5.13%	Ac	-
Uranotaenia (Uranotaenia) ditaenionota Prado, 1931	2	0.10%	Rr	2	5.13%	Ac	-
Uranotaenia (Uranotaenia) geometrica Theobald, 1901	14	0.71%	Rr	5	12.82%	Ac	-
Uranotaenia (Uranotaenia) leucoptera Theobald, 1907	32	1.63%	Ev	6	15.38%	Ac	-
Uranotaenia (Uranotaenia) lowii Theobald, 1901	11	0.56%	Rr	3	7.69%	Ac	$WNV^{13}$
Uranotaenia (Uranotaenia) mathesoni Lane, 1943	2	0.10%	Rr	2	5.13%	Ac	-
Uranotaenia (Uranotaenia) pallidoventer Theobald, 1903	3	0.15%	Rr	2	5.13%	Ac	-
Total mosquito abundance	1960						
Number of mosquito species	50						

n: number of specimens; e: number of species of the tribe; Ab: abundance (number of individuals collected); D%: Dominance - E: eudominant (D> 10%); D: dominant (D> 5-10%); Sd: subdominant (D> 2-5%); Ev: occasional (D> 1-2%); Rf: rare (D <1%). F: Frequency (number of points at which the species was collected). C%: Constancy - C: constant (C> 50%); A: accessory (C> 25-50%); Ac: Accidental (C <25%).

*Alphavirus:* EEEV: Eastern equine encephalitis virus; MAYV: Mayaro virus; MUCV: Mucambo virus; PIXV: Pixuna virus; VEEV: Venezuelan equine encephalitis virus; UNAV: Una virus; WEEV: Western equine encephalitis virus.

*Flavivirus:* BSQV: Bussuquara virus; ILHV: Ilheus virus; ROCV: Rocio virus; SLEV: Saint Louis encephalitis virus; WNV: West Nile virus; YFV: Yellow fever virus. *Orthobunyavirus:* OROV: Oropouche virus.

**References:** <sup>1</sup>Travassos-da-Rosa et al., 1998; <sup>2</sup>Mitchell et al., 1985; <sup>3</sup>Reviewed by Segura & Castro, 2007; <sup>4</sup>Turell et al., 2005; <sup>5</sup>Groot, Morales, & Vidales, 1961; <sup>6</sup>Anderson, Spence, Downs, & Aitken, 1961; <sup>7</sup>Reviewed by Hutchings, Hutchings, Menezes, Motta, & Sallum, 2016; <sup>8</sup>Serra, Cardoso, Ribeiro, Santos, & Slhessarenko, 2016; <sup>9</sup>Reviewed by Hutchings, Hutchings, Menezes, Motta, & Sallum, 2016; <sup>8</sup>Calisher, 1981; <sup>11</sup>Moreno et al., 2011; <sup>12</sup>Reviewed by Consoli & Lourenço-de-Oliveira, 1994; <sup>13</sup>Unlu, Kramer, Roy, & Foil, 2010; <sup>14</sup>Reviewed by Andrews et al., 2014; <sup>15</sup>Reviewed by Zavortink, Roberts, & Iloch, 1983.

Table 2: Estimates (slope) of parameters of explanatory variables of generalized linear models (GLMs) by using quasi-poisson distribution on the richness and abundance of mosquitoes collected during the dry seasons of 2015 and 2016, in the Arc of Deforestation, Southern Amazon.

	Dee4	Number	Forest	Edee	Maan natah	Forest patch	Mean time			
Variables	Dest	of forest	cover	Luge		cohesion	since	wi	QAICc	$\mathbf{D}^2$
	models	patches	proportion	density	snape index	index	deforestation			
	1				15.84***			0.29	38.23	0.17
Overall	2				13.96**		0.03	0.24	38.59	0.19
mosquito	3		-1.11		11.88**			0.21	38.88	0.20
abundance	4		-1.17**					0.13	39.90	0.14
	5				13.98**	-1.94		0.12	39.95	0.18
Orienall	1		-0.80**					0.37	123.54	0.12
mosquito	2		-1.78**			-3.37		0.28	124.06	0.14
michnoss	3		-0.84**	95.29				0.18	124.96	0.12
richness	4		-0.64*		3.00			0.17	125.06	0.12
Vector	1		-1.97***	408.29***				0.53	48.65	0.28
obundance	2	0.19**	-1.30*					0.27	50.02	0.25
abunuance	3		-1.65**	339.63**	5.43			0.20	50.56	0.27
	1		-0.65**					0.26	154.78	0.08
	2				5.43**			0.24	154.92	0.07
Vector	3		-0.45		3.62			0.14	155.96	0.09
richness	4					-1.60		0.13	156.16	0.04
	5							0.12	156.32	0
	6				4.37	-0.98		0.10	156.62	0.07

\*p<0.1; \*\*p<0.05; \*\*\*p<0.01; \*\*\*\*p<0.001; wi = model weight; QAICc = corrected quasi-likelihood Akaike's information criterion; D<sup>2</sup> = deviation ratio explained by GLMs. In bold are the models with higher weight, all have the response variables associated with the explanatory variable "forest cover proportion" and others.



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tbed\_14154\_f2.tif

	Loading	-5 0 5 10
Patch metrics	scores	
Forest cover proportion (prop)	-0.39	
Number of patches (nump)	0.23	0 – nymp – «
Mean patch shape (shape)	0.35	S prop shape
Patch cohesion index (cohe)	-0.42	core_edg
Mean time since deforestation (mtd)	0.12	area mtd
Forest core amount (core)	-0.42	- 0
Forest edge amount (edge)	-0.29	· · · · · · · · · · · · · · · · · · ·
Mean patch area (area)	-0.43	-0.2 0.0 0.2 0.4
		PC1

