Title: Mosquito bloodmeal source diversity between disturbed and wild environments in the Americas: a review

Short title: Mosquito bloodmeal source diversity in the Americas

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INTRODUCTION

Mosquitoes (Diptera: Culicidae) transmit many pathogens to humans and other animals (Becker et al., 2010). Particularly relevant mosquito-borne diseases are malaria, dengue fever, yellow fever, zika, chikungunya, west Nile virus, lymphatic filariasis and different types of encephalitis (Tolle, 2009; Brugueras et al., 2020). Invasion of mosquito species adapted to proliferate in disturbed environments is involved in vector borne diseases expansion to new geographic areas (Brugueras et al., 2020; Cebrián-Camisón et al., 2020; Rose et al., 2020). Man-made environmental changes facilitate these invasions by modifying mosquito distribution and their bloodmeal source availability (Ramasamy & Surendran, 2016; Cebrián-Camisón et al., 2020; Rose et al., 2020; Schrama et al., 2020). Mosquito invasions can have a negative impact in both disturbed and wild environments (Cebrián-Camisón et al., 2020). Anthropogenic landscape disturbances effect in mosquito dynamics has been researched in Europe (Cebrián-Camisón et al., 2020), Africa (Rose et al., 2020; Schrama et al., 2020) and the indomalayan region (Ramasamy & Surendran, 2016).

The aim of our study is to identify mosquito bloodmeal source diversity between disturbed and wild environments in the Americas. Knowing mosquito bloodmeal sources allows for a better understanding of the zoonotic cycles of pathogens (Abella-Medrano et al., 2018), especially those carried by generalist vectors. Generalist mosquitoes have a higher chance of pathogen spread over a wide range of hosts (Abella-Medrano et al., 2018). If environmental disturbances are high, humans have an increased chance of becoming an accidental host.

MATERIALS AND METHODS

We performed an extensive literature review on the blood feeding patterns of mosquitoes in the Americas, whose bloodmeal source host had been identified through precipitin test, gel diffusion, enzyme-linked immunosorbent assay (ELISA) or other molecular techniques (Cebrián-Camisón et al., 2020). We used Clarivate Analytics Web of Science, Elsevier SCOPUS and SciELO as the main search engines to find articles identifying vertebrate hosts of mosquitoes. Throughout October 2020 we made searches with keywords including: *“mosquitoes” AND (“blood meal sources” OR “blood feeding patterns”) AND “landscape”*, *"mosquito" AND ("blood" OR "host") AND ("feeding" OR "foraging") AND ("landscape" OR "deforestation")* and *(“blood meal” OR “bloodmeal”) AND “mosquitoes”*. Additional references were obtained from the citations in these studies and pertinent articles were identified with online software ([www.connectedpapers.com](http://www.connectedpapers.com)). Overall 188 studies were obtained at a first stage. We only selected studies performed in the American continent, that had study site coordinates and bloodmeal source hosts identified. Studies that did not meet these criteria were not used. As a result we found 21 studies on the blood feeding patterns of mosquitoes in the Americas. An Excel table was created including the information of interest, such as mosquito species, decimal coordinates of latitude and longitude, host richness, total number of blood engorged mosquitoes, landscape type (i.e. disturbed or wild), bloodmeal host taxon and country where the study was developed.

RESULTS

66 mosquito species were reported amongst the 21 studies. *Culex quinquefasciatus* was the most intensively studied with 7 articles reporting this species, followed by *Aedes aegypti* (5 studies), *Ae. scapularis*, *Ae. serratus, Cx. restuans, Mansonia tittilans* and *Psorophora ferox,* these last five being mentioned in 4 studies. Only 8 studies included data from both disturbed and wild landscapes. 16 mosquito species had data for both landscapes, the rest only had data for one of the two landscapes. The top 20 species with the highest host richness corresponded to 3,517 engorged mosquitoes. Over 50% of them corresponded to two species: *Cx. erraticus* (with 1,162) and *Cx. pipiens* (636). 9 studies were conducted in the USA and 12 were developed in Latin America. Out of the 1,055 host records 82% (866 records) were identified to species level. 90 records were labeled as ‘primate’, 52 as ‘bird’, 38 as ‘non-human-primate’ and 9 as ‘monkey’.

According to the published information, 56 species were identified as vertebrate hosts of at least one of the mosquito species studied (*Cx. erraticus*), including 32 birds, 11 reptiles, 10 mammals and 3 amphibians. This *Cx. erraticus* data was reported in Tuskegee National Park, Alabama, USA, labeled as a wild landscape in our study. In contrast, only 17 hosts were reported for the same species in the disturbed landscape (Auburn city, Alabama, USA), including 9 birds, 6 mammals and 1 amphibian. *Cx. pipiens* was the species with the highest host richness in disturbed landscapes: 32 hosts reported in Chicago, Illinois, USA, including 25 birds and 7 mammals. No record of *Cx. pipiens* for a wild landscape was found in our data. The top 20 species with the highest host richness showed an ability to feed on blood from different vertebrate groups, nevertheless 53% of the bloodmeals derived from mammals and 14% from humans. The anthropophilic behavior of species like *Aedes aegypti, Psorophora albigenu* and *Aedes mediovittatus* is supported by the fact that humans represent 49-88% of the total bloodmeals sources.

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