

Detection of Yellow fever virus (YFV) in different species of mosquito (Diptera: Culicidae) captured during the entomological surveillance in São Paulo State, Brazil

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Yellow Fever Virus (YFV), belonging to *Flavivirus* genus within the *Flaviviridae* family, is currently endemic in some parts of Africa and America, causing periodic outbreaks in South America. Yellow Fever has a great impact on Public Health, once YFV may cause a severe disease in humans that can progress to a lethal hemorrhagic fever. In Brazil, YFV is maintained in a sylvatic transmission cycle among non-human primates (NHP) as vertebrate hosts and acrodendrophilic mosquitoes (*Haemagogus* and *Sabethes* genus). Humans can be infected in a spill over event when they encroach areas with viral circulation. The urban cycle, that involves *Aedes aegypti*, was eradicated in 1942. Recently, beginning in 2016, the largest sylvatic outbreak within decades occurred in the southeastern Brazilian region, including São Paulo State, the most populous one. The aim of this study is to investigate YFV in mosquitoes collected during entomological surveys in areas of circulation in the State of São Paulo. Mosquitoes were captured by SUCEN (Superintendence of Endemic Control of the State of São Paulo) in different municipalities at ground level between 9 am and 3 pm, by using an entomologic net and bottle-type manual vacuums in woods and green areas, and Nasci's Aspirator in urban dwellings; they were identified morphologically, grouped into pools according to their taxonomic category. Later, pools were sent to Adolfo Lutz Institute for YFV detection. A specific RT-qPCR using primers targeting the 3' UTR region was used, with a threshold cycle (Ct) cut off  $\geq 38$ . Only non-engorged mosquitoes were sent for analysis. A total of 3,936 pools from 177 municipalities were analyzed, of which 48 (1,21%) were YFV positive distributed in 21 municipalities. These specimens belong to 10 species distributed in *Aedes*, *Haemagogus*, *Psorophora* and *Sabethes* genus, with Ct values varying from 16 to 38. Although species that have already been incriminated as vectors were detected naturally infected, *Aedes* mosquitoes were also positive. Although no *Aedes aegypti* were found positive, and no urban case was detected, more studies are needed to better understand the role of other Culicidae species on YF cycle, in order to shed light on the recent transmission dynamics and the potential risk of future Yellow Fever outbreaks in the region.

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