

TOPIC (choose ONE of these 10 topics; erase the rest):

3) Leishmaniasis

APPROACH (choose ONE of these 4 approaches; erase the rest):

2. Vector biology and eco-epidemiology

Title: Sandfly's (Diptera: Psychodidae: Phlebotominae: *Lutzomyia*) taxonomic diversity in a leishmaniasis endemic zone in northern Colombia

Keywords: leishmaniasis; vector biology; eco-epidemiology; sandfly's; taxonomic diversity.

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The Montes de María region is one of the most important leishmaniasis macro hotspots in Colombia, with the municipality of El Carmen de Bolívar stands out for having high prevalence rates of visceral leishmaniasis. This municipality has fragments of tropical dry forest with abundant wildlife, incriminated as reservoirs of *Leishmania* and affected by fruit tree crops, providing optimal ecological conditions for the circulation of some phlebotomine sandflies species with epidemiological antecedents. Recently, 20 species of *Lutzomyia* were recorded for this municipality, which added to the presence of *Lu. evansi*, vector of *L. infantum chagasi*, etiologic agent of visceral leishmaniasis and *Lu. gomezi* and *Lu. panamensis*, vectors of *L. braziliensis* and *L. panamensis*, etiological agents of cutaneous leishmaniasis. As an aim, it was proposed to analyze the spatiotemporal variation of phlebotomine assemblage in El Bledo, El Carmen de Bolívar, a leishmaniasis endemic area in northern Colombia. Phlebotomine were collected during five samplings between January 2018 and April 2019, using CDC traps in the domestic, peridomestic and sylvatic ecotopes, during three consecutive nights/sampling, between 18:00 -06:00 h. *Lutzomyia* species were identified according to Young and Duncan (1994), taxonomic diversity and spatial variation was estimated, obtaining Hill numbers (richness $q=0$, typical species $q=1$ and abundant species $q=2$) in each ecotope with 95% confidence. A total of 8,784 individuals of the genus *Lutzomyia* distributed in eight species was collected, of which *Lu. evansi* (74.39%), *Lu. panamensis* (19.2%) and *Lu. gomezi* (6.31%) showed the highest abundances. According to the rarefaction/extrapolation curve based on sample size, the richness values for $q=0$ were not significant between peridomestic, domestic and sylvatic ecotopes, but if between domestic and sylvatic ecotopes, meaning that some species in peridomestic ecotope may have a wider range of distribution reflected in migrations between ecotopes. For orders $q=1$ and $q=2$, no significant differences were found, indicating that typical species were the most abundant in the ecotopes. Rarefaction/extrapolation curves revealed that in domestic and

sylvatic ecotopes the greatest number of species was covered, while in peridomestic ecotope the number of possible species to be sampled was not reached, perhaps because some of them were cryptic. The accumulation curves per sampling revealed similarities in the diversities of the different ecotopes, in relation to the typical and dominant species present among them, with a notable decrease in richness during the first three samplings. The diversity orders in peridomestic ecotope remained constant in most of the samplings, varying only in the last sampling. In conclusion, the assemblages of the three ecotopes are similar (although the peridomestic ecotope has higher richness) because the typical and dominant species of the ecotopes are shared among them.