INVERTEBRATE-DERIVED DNA (iDNA) TO IDENTIFY SANDFLIES' BLOODMEAL.

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Metabarcoding data obtained by Next Generation Sequencing (NGS) has been used to determine the species in mixed biological samples, like DNA obtained through the gut content of invertebrates that feed on vertebrates (invertebrate-derived DNA, iDNA).

In the present study, we identified the vertebrate species from iDNA samples of female sand flies using the metabarcoding approach. We also compared the results among a mammal-specific (16SrRNA), broader vertebrate-specific (12SrRNA) mini-barcodes, and a barcode of the *CytB* mitochondrial gene.

Phlebotomine sand flies were collected in an endemic area of Cutaneous Leishmaniasis (CL) located in the Cacao Region, southeastern of Bahia, Brazil. We analyzed forty female sand flies distributed in thirteen samples of seven different sand fly species including CL vectors in Brazil.

The Operational Taxonomic Units (OTUs), obtained after metabarcoding sequencing, were compared with the sequences available in the GenBank NCBI® for species identification. The criteria of high percentage of matches (98%-100%) was used for OTU assignment at species level, combined to reference databases of the expected species occurrence in the study area.

Metabarcoding results revealed twenty-one OTUs of vertebrate's species, distributed in forty GenBank® sequences, including primates (four OTUs), rodents (four) and ungulates (six). Surprisingly, non-mammals' species, such as reptiles (one OTU) and amphibians (three) were also detected. The mini-barcode 16SrRNA identified twelve OTUs in 69 detections, 12SrRNA and CytB eleven OTUs in 30 and 38 detections, respectively.

Canis lupus, *Equus asinus*, *Equus caballus* and *Homo sapiens* were the sandflies' bloodmeal identified by the three targets used, presenting the highest ratio of detection.

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