

ANALYSIS OF GENES EXPRESSED IN  
LUTZOMYIA LONGIPALPIS MALE ANTENNAS

Dias, DBS<sup>1,2</sup> Azevedo, R. V.<sup>1</sup> Mazzoni, C.J.<sup>1</sup>, Albano, R.M.<sup>3</sup>,  
Dávila, A.M.<sup>1</sup>, Peixoto, A.A.<sup>1</sup>

<sup>1</sup>Laboratório de Biologia Molecular de Insetos, Instituto Oswaldo Cruz, Rio de Janeiro; <sup>2</sup>Departamento de Biologia Celular e Genética; <sup>3</sup>Departamento de Bioquímica, Universidade do Estado do Rio de Janeiro, Brazil

The attraction of major disease vectors towards their hosts and the detection of airborne odorants are mediated by a large number of olfaction molecules. The sandfly *Lutzomyia longipalpis* (Diptera, Psychodidae) is the main vector of American Visceral Leishmaniasis. Males of this vector species are attracted to hosts where they aggregate and produce pheromones that help attracting females. We are interested in characterizing sandfly genes involved in olfaction. Although different genes and proteins involved in the olfactory process have already been described in *Drosophila melanogaster* and *Anopheles gambiae*, little is known about *L. longipalpis*. In this initial analysis we have sequenced a *L. longipalpis* cDNA library from male antennas using sandflies from Lapinha Cave (MG), Brazil. The sequences were used to construct an Expressed Sequence Tag (EST) database using the GARS system (Dávila et al, 2005). The database consists of 1765 ESTs, which were assembled into 127 contigs and 1,081 singlets. Sequence analysis revealed candidate odorant binding proteins and other genes putatively involved in olfaction.

This work was supported by HHMI, CNPq and FIOCRUZ

key words: *L. longipalpis*, sandfly, olfaction, leishmaniasis.