

3rd International Conference on **Epidemiology & Public Health**

August 04-06, 2015 Valencia, Spain

Molecular evidence of *Leishmania infantum* in *Sergentomyia* sand flies in Tunisia

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Introduction: Tunisia is known to be one of the most endemic areas of leishmaniasis where both visceral and cutaneous forms are reported. Cutaneous leishmaniasis (CL) is older and has a higher prevalence than visceral one (VL). It is caused by four taxa (*Leishmania* (*L.*) *major*, *L. infantum*, *L. tropica* and *L. killicki*) which are responsible for a large clinical spectrum of lesions. Phlebotomus species are known to be the transmission vectors of *Leishmania* in different areas of the world. However, some researchers have hypothesized that *Sergentomyia* (*S.*) genus phlebotomine sandflies are capable of transmitting *Leishmania* parasites. Determining whether *Sergentomyia* is a potential vector of *Leishmania* is crucial to understanding the parasite-vector transmission cycle in different areas of the world.

Materials & Methods: Sand flies were collected from south Tunisia in 2013. DNA was extracted from individual sand flies and parasite DNA was detected by PCR amplification of the ribosomal internal transcribed spacer 1 and DNA sequencing.

Results & Conclusion: *L. infantum* DNA was identified in one specimen of *S. dreyfussi*. Currently, no local data is available on infecting *Sergentomyia* spp. This is the first report of *Leishmania* DNA detection from naturally infected wild-caught *S. dreyfussi*. Our finding supports the assumption that *L. infantum* transmission via *Sergentomyia* is possible.

Biography

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