

**L-19**  
**MODULATION OF *LEISHMANIA* INFECTION IN SAND FLIES BY INSECT'S MIDGUT MICROBIOTA**

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The midgut microbiota of insect vectors has been recognized as a critical factor influencing the transmission dynamics of vector-borne pathogens<sup>1–3</sup>. Sand flies (Diptera: Phlebotominae), tiny blood sucking insects, are best known for their role in the transmission of parasitic protists of the genus *Leishmania*, the causative agents of leishmaniases, a disease ranked among the top 10 neglected tropical diseases globally<sup>4</sup>. Within sand flies, bacteria of genus *Asaia* constitute an integral part of both the insect's dietary intake and its midgut microbiome<sup>3,5,6</sup>.

To investigate the interactions between *Asaia* bacteria and *Leishmania* protist within sand flies, we established a laboratory model to monitor the development of these bacteria and their impact on *Leishmania* infection and growth within the sand fly vector.

Two wild type *Asaia* species, *Asaia siamensis* and *A. krunghthepensis*, were introduced to the midgut of *Phlebotomus duboscqi* females via sugar meals. These bacteria successfully colonized the sand fly midgut for up to 8 days and were vertically transmitted to the next generation through contamination of the egg surface. However, when sand flies infected with *Asaia* were subsequently exposed to *Leishmania major* promastigotes via membrane feeding of infected blood, no significant impact was observed on *Leishmania* infection parameters, namely infection rate, parasite load, localization of infection. (Fig. 1).

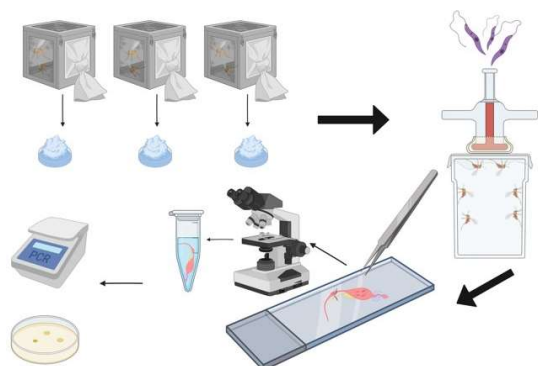


Fig. 1. Experimental superinfection of *Leishmania major* and *Asaia* sp. in *P. duboscqi*

Furthermore, we evaluated an engineered strain of *Asaia* expressing a surface protein from *Wolbachia* (WSP)<sup>7</sup>, given that *Wolbachia*-mediated activation of insect immunity has been shown to play a role in vectorial capacity<sup>8</sup>. This modified strain of *Asaia* also readily colonized the midgut of *P. duboscqi*. However, similarly to the wild-type strains, this modified bacterium did not appear to affect leishmania infection in sand flies.

In conclusion, our findings suggest that in *L. major* – *P. duboscqi* model, bacteria of genus *Asaia* do not significantly affect the course of *Leishmania* infection. Nevertheless, our experiments are ongoing, and further studies are needed to fully understand the complex interactions between the sand fly microbiome and pathogen transmission.

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