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Unit: Arboviruses and Insect Vectors IP Department or IP: Virology

Main domains 1: Bacteria, Fungi, Insects, Parasites or Virus

# Main domain 2: surveillance and epidemiology, mechanism of resistance and

**dissemination**, biomarkers and diagnostic, new molecules, alternative strategies, technological and methodological developments.

## Attractive synopsis:

Genetically-engineered mosquitoes based a miRNA approach were developed to control arboviruses spreading.

## Research projects in relation with AMR:

The ineffectiveness of chemical control methods against mosquitoes makes urgent the need for novel vector-based approaches for controlling vector-borne diseases. Geneticallyengineered mosquitoes have been proposed as possible solutions for stopping arboviruses spreading within urban cycles. Our team has developed a miRNA-based approach that results in a dual resistance phenotype in mosquitoes to dengue (DENV) and chikungunya (CHIKV) viruses. Transgenic mosquitoes contain artificial antiviral miRNAs capable of targeting ~97% of DENV and CHIKV strains. Challenge experiments showed reductions in transmission of both viruses. Development of such strains with gene editing tools could help in designing population replacement strategies for sustainable control of multiple arbovirus diseases.

### **3 Publications**

- Atyame CM, Alout H, Mousson L, Vazeille M, Diallo M, Weill M, Failloux AB. 2018. Insecticide resistance genes affect *Culex quinquefasciatus* vector competence for West Nile virus. *Proceedings of The Royal Society B: Biological Sciences 286:* 20182273. http://doi.org/10.1098/rspb.2018.2273
- Delang L, Yen PS, Vallet T, Vazeille M, Vignuzzi M, Failloux AB. 2018. Differential Transmission of Antiviral Drug-Resistant Chikungunya Viruses by *Aedes* Mosquitoes. mSphere 3(4). pii: e00230-18.
- Yen PS, James A, Li JC, Chen CH, **Failloux AB.** 2018. Synthetic miRNAs induce dual arboviral-resistance phenotypes in the vector mosquito *Aedes aegypti. Communications in Biology* 1:11 doi: 10.1038/s42003-017-0011-5.



First Name / Last name: Louis Lambrechts Contact : louis.lambrechts@pasteur.fr

Unit: Insect-Virus Interactions IP Department or IP: Virology Secondary affiliation: Genomes & Genetics

Main domains 1: Insects, Viruses

**Main domain 2**: surveillance and epidemiology, mechanism of resistance and dissemination, biomarkers and diagnostic, alternative strategies.

## Attractive synopsis:

Our research investigates the genetic and environmental determinants of mosquito resistance to arboviruses of medical significance.

## Research projects in relation with AMR:

Our research uses experimental models and tools to (1) elucidate the genetic basis of mosquito resistance to flavivirus infection; and (2) assess the influence of the biotic environment on mosquito-arbovirus interactions. In (1), we combine gene mapping techniques and reverse genetics (including CRISPR/Cas9 gene editing *in vivo*) to dissect the genetic basis of natural mosquito resistance to dengue and Zika viruses. In (2), we use bacterial/viral metagenomics and functional experiments to examine the role of two microbiota components on mosquito-arbovirus interactions: bacterial exposure at the larval stage and co-infection with insect-only viruses.

### **3 Publications**

- Moltini-Conclois I, Stalinski R, Tetreau G, Després L, <u>Lambrechts L</u> (2018) Larval exposure to the bacterial insecticide *Bti* enhances dengue virus susceptibility of adult *Aedes aegypti* mosquitoes. *Insects* 9(4): pii: E193.
- Fontaine A, Lequime S, Moltini-Conclois I, Jiolle D, Leparc-Goffart I, Reiner RC Jr, <u>Lambrechts L</u> (2018) Epidemiological significance of dengue virus genetic variation in mosquito infection dynamics. *PLoS Pathogens* 14(7): e1007187.
- Dickson LB, Jiolle D, Minard G, Moltini-Conclois I, Volant S, Ghozlane A, Bouchier C, Ayala D, Paupy C, Valiente Moro C, <u>Lambrechts L</u> (2017) Carryover effects of larval exposure to different environmental bacteria drives adult trait variation in a mosquito vector. *Science Advances* 3(8): e17005085.