

## PROGRAMME START – Fellowships funding scheme

### Masters scholarships – The ANRS MIE International network

#### Two internship offers as part of the 'Brazil Partner site' partnership

##### Offer B\_01

**Internship title/subject:** Screening bacteria with DENV-blocking phenotype in mosquitoes

**Home institution:** Institut Pasteur, Paris

**Laboratory/Team:** Arboviruses and Insect Vectors Unit

**Country :** France

**Scientific supervisor (Tutor):** Dr FAILLOUX Anna-Bella, head of the Arboviruses and Insect vector unit

**Internship site(s):** Institut Pasteur, Paris, France

**Disciplines / areas of training:** viral transmission, mosquitoes, bacteria, Amazonian Basin

##### **Main internship objectives:**

mosquito collections and identification; isolation, identification and cultivation of bacteria from mosquito midguts; experimental infection of mosquitoes.

##### **Description of the internship:**

Mosquito gut microbiota plays a complex role in determining the vector competence for arboviruses. The emblematic example is *Wolbachia* which is an intracellular bacteria detected in 65% of all insect species. This bacterium manipulates host reproduction through male killing, feminization parthenogenesis, and more commonly, cytoplasmic incompatibility (CI). CI phenotype became the basis for *Wolbachia* release programs aiming for mosquito population suppression or replacement. This pathogen blocking effect coupled with efficient spread has contributed to the use of *Wolbachia* as vector control agent for a safe dengue biocontrol. **Our project has the ambition to expand the panel of bacteria playing a similar pathogen-blocking effect in *Aedes aegypti*.** More precisely, we will: (i) collect wild mosquitoes by placing traps in dengue-free areas in the Amazonian Basin (to be determined) during a 2-month period coinciding to the period of highest dengue transmission (based on previous records), (ii) identify mosquitoes and pool according to species, location and period, (iii) after surface sterilization, dissect midguts from each pool and homogenize in PBS, (iv) identify bacteria by 16SRNA gene sequencing, (v) isolate bacteria on two different media (brain heart infusion (BHI) broth or Luria-Bertani (LB) broth), (vi) inoculate selected bacteria into the main dengue vector *Aedes aegypti* rendered germ-free after antibiotic treatments, and (vii) determine if inoculated mosquitoes are able to transmit dengue virus. The steps further for a thesis will be to decipher (i) the molecular mechanisms at the origin of virus inhibition, (ii) the mode of bacteria transmission (trans-stadial *versus* vertical) and (iii) determine the prevalence of the bacteria in low-dengue areas *versus* dengue-endemic regions.

##### **Expected profile:**



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- **Candidate profile/training:** skills in bacteriology
- **Type of master to be considered:** Master 2 on pathogen-host interactions
- **Languages spoken:** English
- **Techniques / tools required:** bacteria isolation, cultivation, identification
- **Computer software skills:** analyse 16S sequences, determine diversity and abundance
- **Availability:** from January 2026

## Offer B\_02

**Internship title/subject:** Screening and characterizing flavivirus insectiviruses in mosquitoes

**Home institution:** Aix-Marseille university, France

**Laboratory/Team:** Unité des Virus Émergents [in collaboration with the Arboviruses and Insect Vectors team, Institut Pasteur, Paris, France]

**Country :** France

**Scientific supervisor (Tutor) :** Pr Xavier DE LAMBALLERIE, Unit manager

**Internship site(s) :** Aix-Marseille university, Marseille, France

**Disciplines / areas of training:** virus discovery, mosquitoes

### **Main internship objectives:**

Mosquito collection and identification ; identification and isolation of flavivirus insectiviruses ; genomic characterization and evolutionary analysis.

### **Description of the internship:**

Flavivirus-related insectiviruses are viruses that replicate only in mosquitoes and have been described mainly in *Aedes* and *Culex* mosquitoes, although they are likely to be present in a much wider variety of mosquitoes. These common but intriguing viruses are of great scientific interest. In particular, 1) they are an informative link of the evolutionary diversification of flaviviruses; 2) they have the potential to interfere with the replication of arboviral flaviviruses in the body of mosquitoes; 3) they may display pathogenic phenotypes in mosquito species different from the species from which they were isolated; 4) they can be used to construct flaviviral vaccine chimeras ; 5) some of them can produce genomic DNA forms, episomic or integrated in the mosquito genome.

Taking advantage of mosquito collections organized in collaboration with the Arboviruses and Insect Vectors team, [Institut Pasteur] in the Amazonian region :

- we will use molecular detection techniques to screen different sylvatic mosquito species for the presence of flavivirus-related insectivirus RNA and DNA sequences,
- we will sequence them using Next Generation Sequencing techniques,
- whenever possible, we will isolate the corresponding viruses in mosquito cell cultures,
- we will proceed to phylogenetic and taxonomic analyses based on the sequences obtained.

This virus discovery step will allow further analyses (for a PhD) aiming at characterising the flavivirus diversity and evolution, the mechanisms underlying DNA synthesis of flavivirus genomes, the potential of these sylvatic viruses to infect other mosquito species and the impact of infection on arbovirus transmission and mosquito fitness.

### **Expected profile:**

- **Candidate profile/training:** skills in virology
- **Type of master to be considered:** Master 2 on Biological and Health Sciences
- **Languages spoken:** English



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- **Techniques / tools required:** virus isolation, molecular diagnostics, genomics
- **Computer software skills:** analyse virus sequences, determine diversity and abundance
- **Availability:** from January 2026