

Internship form  
Course M2 GGBS 2023-24

Laboratory: CR2TI, UMR INSERM 1064

Team No: 6

Supervisor's full name: Aurelien SERANDOUR

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Prospective candidate: X

Internship Title: **METALUNG: Lung Metagenomics using nanopore sequencing to study dysbiosis.**

Summary of proposed project:

Our laboratory is interested in hospital acquired lung infections, which are very frequent and sometimes fatal. It is necessary to better characterize the dynamics of the respiratory microbiome before, during and after these infections in order to better understand the infectious process and its long-term consequences on the patient. This could eventually lead to the development of monitoring markers for clinicians and even innovative therapies such as probiotics.

Metagenomics makes it possible to identify all the micro-organisms present in a sample without any preconceived ideas. Nanopore sequencing applied to metagenomics has developed considerably over the last few years thanks to the production of long reads which greatly facilitate the assembly and identification of small genomes compared to Illumina's short read technology. In the laboratory, we currently use an external service provider who uses Illumina for metagenomics.

With the METALUNG project we have 2 operational objectives:

- to relocate metagenomics to the laboratory in order to acquire the expertise in data production and analysis.
- to move to nanopore metagenomics using our GridION in order to benefit from the added value of long reads.

We have a well-established mouse model of *E. coli* or *S. aureus* pneumonia (Roquilly et al., Nature Immunology 2020). We have also set up a murine model of bacterial colonization in the lung that allows us to study the impact of a simplified microbiome (a few bacterial families) on the response to a pathogenic bacterium. We plan to perform metagenomic analysis by full-length 16S sequencing of Specific-Pathogen-Free mouse lungs before and after bacterial colonization, and also before, during and after an induced infection, in order to identify the influence of the pulmonary microbiome on bacterial pneumonia.

The METALUNG project will allow us to acquire expertise in the production and analysis of full-length 16S metagenomic data.