

Exploratory project
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metagenomics,
metatranscriptomics

Participating INRAE units

GABI
ISP
MaIAGE
MGP

Partners

University of Surrey
(United Kingdom)

ANSES (France)



MIMISIPI

Metagenomics and metatranscriptomics of gut microbiota within the context of dysbiosis induced by *Salmonella* super shedding in pigs

The super shedding of *Salmonella* is a health problem in the pig industry. In a previous study (PMID:36629432), researchers showed that the holobiont disruption specific to high- and low-shedder pigs follows a complex scenario. First, the host animal presented an inflammatory peak; next, a disruption of the gut microbiota was observed, including functions linked to anaerobic respiration; finally, a peak in *Salmonella* shedding, exacerbated in super shedders, was observed.

Our theory is that changes in the gut microbiota at the functional level ultimately determine whether a pig becomes a low or high shedder. This is why we want to study this phenomenon with an approach that combines metagenomics (potential/predicted functions) and metatranscriptomics (expressed functions). For this study, we will reanalyse the samples already collected for the PMID:36629432 study to perform a metagenomic and metatranscriptomic characterization of the time points before and immediately after infection.

We will also perform an integrated data analysis to determine which of the metagenomic species expresses crucial functions, and specifically those linked to the inflammatory response and *Salmonella* colonization.

This project will provide a valuable addition to current knowledge of *Salmonella* super shedding and underpin work to modulate the gut microbiota to reduce the impact of *Salmonella* on this holobiont.

Objectives

The objective of MiMiSiPi is to develop an approach involving the combined metagenomic and metatranscriptomic characterization of complex samples (e.g. gut microbiota).

We are proposing an interdisciplinary programme for bioinformaticians, mathematicians and microbiologists, based on three separate events:

1. A seminar for people from INRAE working on or interested in combined metatranscriptomic and metagenomic characterization to study complex samples, such as those from the gut microbiota;

2. A workshop focusing on the interest, tools and future applications of this approach, especially those related to the association between metagenomic species and the metatranscriptomic functions expressed, using biostatistics and mathematical modelling;
3. A second-year master's internship with joint supervision focusing on the taxonomic reconstruction of metagenomic species and their association with expressed functions.

Partners

INRAE unit	Expertise	INRAE division
GABI	Pig metagenomics; metatranscriptomics	GA
ISP	<i>Salmonella</i> and salmonellosis; metagenomics	MICA
MaIAGE	Mathematics; modelling; data analysis	MATHNUM
MGP	Pig metagenomics; functional annotation	/
Partner	Expertise	
ANSES (France)	<i>Salmonella</i> in pig production	
University of Surrey (United Kingdom)	<i>Salmonella</i> in pig production; metagenomics	