



Coordinator

Claire ROGEL-GAILLARD
claire.rogel-gaillard@inrae.fr

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INRAE unit

GABI - GeMS
GABI - Plateforme BRIDGe
GenPhySE
GENESI - porc
MICALIS - MIHA
MGP -
INFOBIOSTAT



ENTEROTYPIG

Enterotypes of the porcine gut microbiota: fine characterisation and influence of host genetics to assemble the holobiont

The EnterotyPig project is part of axis 1 of the metaprogramme dedicated to the study of the mechanisms of assembly and interaction within holobionts, "farm animals" component, pig species. In particular, it aims to analyse the genetic determinism of the host in the construction and evolution of the holobiont during life and the differential functional analysis of the two enterotypes (i.e. types of microbiota) found to be dominant in farming conditions.

In animals, and in particular mammals, studying the influence of host genetics on the composition of the gut microbiota is hampered by the difficulty of accurately separating the variability of the microbiota due to genetic effects and environmental effects linked in particular to the transmission of maternal microbiota at birth. A formal demonstration of the possibilities of host-microbiota (holobiont) evolution by directional selection over several generations will allow progress to be made on this question.

Objectives

Our objective is to study, in pigs, the role of host genetics on their intestinal microbiota, considered not as a simple phenotype but as a dynamic ecosystem that will co-evolve with its host, thus relying on the holobiont concept. We propose to exploit and develop a study model based on the constitution of contrasting lines of pigs for two enterotypes in order to:

- Study the intergenerational transmission of enterotypes and their association with breeding traits.
- Study the influence of the peri-postnatal maternal environment by cross-adoption.
- Characterise the fine taxonomic composition of the two enterotypes by quantitative metagenomic analyses using the pig gut microbiota gene catalogue.
- Evaluate the feasibility and usefulness of a rapid and reliable test that allows the classification of animals by enterotype.



- Determine the evolutionary dynamics of enterotypes between 60 and 120 days. The results will enable the study model to be consolidated with at least one publication on the genetic determinism of the composition of the microbiota, and will be the basis for submitting a project to the ANR on the links between phenotype, genome and metagenome at the holobiont level, taking into account the coupling between health, welfare and production traits.

Partners

INRAE division	INRAE unit	Expertise
GA Animal Genetics	GABI - GeMS	Pig genetics and genomics, study of host-gut microbiota interactions, computational biology, metagenomics, animal experimentation and experimental unit sampling, faecal DNA extraction
	GABI - Plateforme BRIDGe	MiSeq sequencing
	GenPhySE	Quantitative genetics, estimation of genetic parameters, management of pig lines with referral to the Poitou-Charentes ethics committee
	GENESI - porc	Production of animals from both lines; semen freezing
MICA Microbiology and the Food Chain	MICALIS - MIHA	Microbiology, molecular biology, strain and microbiota functionality, bioinformatics, genomics
	MGP - INFOBIostat	Statistics and bioinformatics, microbiota/health relationships