



Thesis

2022–2025



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Funding

50% INRAE
50% Centre-Val de Loire
Region

Antibiotic resistance gene variants in animal and human gut microbiota

The emergence of multidrug-resistant organisms poses a very real threat to our healthcare system. This phenomenon is mainly caused by the transfer of mobile resistance genes between bacteria.

It is widely accepted that human and livestock microbiota are reservoirs of mobile resistance for pathogens. Research on microbiota using metagenomic approaches has shown that many resistance genes considered to be mobile are broadly shared between human or animal individuals, and even between different species, which suggests significant interpopulation and interspecies transfers.

However, these findings do not take into account the nucleotide diversity of these genes (the variants), which provides more specific information about their inter-relationships.

The aim of the thesis project will be to reanalyse existing metagenomes of human and animal microbiota at the scale of resistance gene variants and to map these variants in different populations and/or species.

The findings will make it easier to determine the genes that are actually shared between animal and human gut microbiota, and to explore the mobile nature of some of these genes.