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INRAE

Thesis
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Improving resistance to colonisation of the intestinal microbiota against vancomycin-resistant enterococci: proof of concept in a preclinical mouse model and search for mechanisms

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The gastrointestinal tract is a reservoir of opportunistic pathogens or pathobionts, which benefit from an imbalance in the gut microbiota or dysbiosis to proliferate in susceptible patients. Vancomycin-resistant enterococci (VRE) originate in the gastrointestinal tract, where their proliferation precedes dissemination into the bloodstream and lymphatic system and infection.

Understanding the mechanisms responsible for resistance to intestinal VRE colonisation is essential to control infections and limit the spread of antibiotic resistance. Recent studies have shown the effectiveness of using commensal bacteria as a strategy to improve resistance to colonisation of the gut microbiota against enterococci.

The project aims to elucidate the mechanism(s) of resistance to colonisation against enterococci by commensal bacteria in a preclinical murine model. To achieve this objective, we will combine high-throughput sequencing, mathematical modelling and microbial ecology techniques of the dynamics of the gut microbiota in a murine model. The knowledge gained will allow us to propose commensal bacteria as alternatives or complements to antibiotics and as markers of risk of antibiotic-induced pathobiont proliferation.

Métaprogramme
HOLOFLUX

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