How an Agr system controls the expression of two bacteriocin clusters in a human symbiont?

Keywords
Human gut, Bacteriocins, Quorum-sensing, Colonization resistance, Sactibiotic, Lantibiotic

Summary
In this project, we propose to better understand how *Ruminococcus gnavus*, a dominant Gram-positive bacterium of the human gut, senses its environment and uses host-specific signals to regulate the expression of genes encoding functions dedicated to facilitating adaptation to the ecosystem and to protecting it against pathogens. Agr systems are known to play a key role in the regulation of virulence factors through quorum-sensing, in various pathogenic bacteria such as *Staphylococcus aureus* or *Clostridium difficile*. Here, complementary approaches (i.e. anaerobic microbiology, molecular biology, microbial genetics and biochemistry) will allow us to determine if and how a symbiotic human bacterium uses an Agr-like system to drive, under the control of a specific signal from the intestinal environment, the expression of two genetic clusters responsible for the biosynthesis of bacteriocins from two different classes (i.e. lantibiotics and sactibiotics). These two bacteriocins, recently-well described for their activities against mains pathogens and multi-resistant bacteria, are also of significance for preserving the microbiome homeostasis[1-6]. Furthermore, as such bacteriocin genetic clusters are widely spread in the gut microbiota, there is a considerable interest in understanding the mechanism behind the production of these natural antimicrobial molecules in situ which by extension could potentially lead to control their expression in the natural producing organism[7, 8].

References:
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Locations
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Expected profile of the candidate
The candidate should have a good background in microbiology, molecular genetics and biochemistry. Previous experience in antimicrobial peptides or microbial ecology of the gut would be a strong advantage.