Master project 2024-2025

Personal Information

Supervisor	Florencia Correa Fiz
Email	flor.correa@irta.cat
Institution	institute of agrifood research and technology
Website	https://www.irta.cat/en/animal-production/animal-health/
Group	Endemic respiratory bacteria and antimicrobial resistance

Project

Computational genomics

Project Title:

Cornerstone nasal microbiota for respiratory disease control in pigs

Keywords:

Bioinformatics, 16s-microbiome, Python, bash, antimicrobial-resistance

Summary:

The worldwide ability to treat common infections is continuously being threat, due to the emergence of drug-resistant pathogens. Antimicrobial usage in farm animals contributes to the emergence of resistant bacteria that can be transferred to humans through direct contact, the food chain or the environment. Antimicrobial resistance is a complex problem with socio-economic burden that requires a multisectoral approach from a ‘One Health’ perspective. In Spain, pig production is a strategic sector that represent 14.8% of the total agriculture production and 39.2% of the animal production. Spain is the second producer in the EU and 4th in the world. Bacterial diseases in livestock, including pigs, are still frequently controlled with antimicrobial treatments. Although in a better position now, Spain is still the 4th country (out of 31) in Europe in sales. The nasal microbiota plays a relevant role in controlling pathogen colonization at the mucosae and stimulating the correct maturation of the immune system. A deep understanding of how the nasal microbiota is established and the specific members involved in its early establishment is essential for the control of pathogens that use the nasal cavity as entry way for infection. In this context, the hypothesis of this proposal is that if newborn piglets are colonized by the cornerstone microbiota, this early microbiota can determine the future microbiota, the health and the performance of pigs. The establishment of a proper nasal microbiota can have an impact in neonate vaccination, by ensuring the correct immune development and therefore an optimal response to early-life vaccines. It is mandatory to obtain scientific knowledge to support the reduction of the use of antimicrobials in animals by providing new tools for controlling diseases to improve the general health status of the animals by stimulation of the immune system, providing disease resistance, and therefore reducing the need for antimicrobials and improving the welfare of the animals. We offer the possibility for two students to join us in the context of this project: 1) The specific objective is to identify taxa from the nasal microbiota associated to a better outcome to pathogen infection and higher response to the selected vaccines. To accomplish that, bioinformatics characterization of the nasal microbiota through 16S analysis in QIIME2 from Mycoplasma hyorhinis (Mhyo) and porcine circovirus type 2 (PCV2) experimental inoculations already performed will be done to expand the knowledge on the effect of the microbiota composition on Mhyo and PCV2 disease outcome and their vaccines efficacy. The correlations between taxa from the nasal microbiota and lesion scores and level of antibodies in the case of Mhyo, or the associations with viremia and level of antibodies for PCV2 will be analyzed by a multivariable model analysis. Moreover, LEfSe will be used to detect potential bacterial markers responsible for the differences between groups. Relevant functions linked to vaccine response will be detected using PICRUSt2, and STAMP programs. 2) The specific objective is to understand the origin of piglet nasal microbiota. We will analyze the contribution of different microbiota niches from the sows to newborn piglets and the stability of the acquired bacterial community until weaning. Moreover, the microbiota intimately associated to the nasal mucosa will be explored and compared to the information obtained from the standard swabbing procedure. DNA from colostrum samples, nasal mucosa and nasal swabs from piglets and sows will be submitted to 16SrRNA metagenomic sequencing and analyze using QIIME2. To analyze the relative contributions of different sources from the mother environment on the initial colonization of newborn’s nasal microbiota, we will use the Bayesian approach implemented in SourceTracker (Knights et al. Nat Methods 8(9):761-3; 2011). Moreover, the ASVs detected at birth will be compared to those found at weaning, to understand the dynamics of the initial microbial components of the microbiota through piglets’ lives. The final aim will be to compile all this in-silico information to select taxa associated to health and good response to vaccines. The students will be incorporated in a pioneer research group in the study of the nasal microbiota of pigs representing an exceptional opportunity for training since integrates different aspects of research in a topic, the microbiota, whose relevance is increasing in many ambits of human and animal health. These projects will be done in a multidisciplinary environment, including bioinformatics and next generation sequencing, organ-on-chip technology, cell biology, immunology in the Catalan Research Institute for technology in food and agriculture, IRTA. The development of IRTA's research activity follows the European Charter for Researchers and, as a result, in 2015 IRTA was awarded with the HR Excellence in Research Award.

References:

Blanco-Fuertes et al. Anim Microbiome 5:53 (2023). Bonillo-Lopez et al. Vet Res 54(1):112 (2023) Blanco-Fuertes et al. Pathogens 10(5):603 (2021). Correa-Fiz et al. Sci Rep.9(1):6545 (2019) Correa-Fiz et al. BMC Genomics 17:404 (2016). Obregon-Gutierrez et al. Pathogens 10(6):697 (2021). Correa-Fiz et al. Vet Microbiol.198:116-20 (2017) López-Serrano et al. Vaccines 9(5):534 (2021). Correa-Fiz et al. Sci Rep.10(1):20354 (2020). Obregon-Gutierrez et al. Vet Sci 9(9):463 (2022).

Expected skills:

Team working is a must. The student will develop his/her project as part of a team at IRTA and in collaboration with other students in the group. Desidered skills include: - Linux and programming (python and/or other languages) - Team working & love learning - Talented and enthusiastic - Persistance and resilience - Good organizational skills

Possibility of funding:

To be discussed

Possible continuity with PhD:

To be discussed

Comments:

We offer: -IRTA-CReSA has the infrastructure necessary for the correct development of this Project. Microbiota sequencing (Illumina) will be performed using external services or with Oxford nanopore sequencing available at CReSA (MinIONTM). -For effective analysis of the massive sequences, we have access to the supercomputing server of CSUC (Consorci de Serveis Universitaris de Catalunya). In addition, local analyses will be performed in a workstation with high performance capacities already available. -Great environment with transdisciplinary team -Active participation in seminars -Active participation in congresses -Possibility to continue with PhD thesis -Possibility of remote work Please, do not hesitate to contact us for further enquires!