RESILMARKER

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Summary

During their productive life, pigs are exposed to multiple viral or bacterial pathogens, some of which cannot be controlled with current disease control measures. These pathogens may increase production costs due to productivity drop and veterinary costs.

Selection for **genetic markers for disease resilience**, can be an effective strategy to reduce the impact of disease on the production system.

Resilient animals present more robust (and better predicted) phenotypes, and cope better with internal and external challenges such as viral and bacterial pathogens. In this proposal, we aim at building a panel of genetic markers associated to health resilience in pigs that could be used in selection programs, without compromising productivity and meat quality traits in pig.

Research team members

- Romi Pena (PI)
- Lorenzo Fraile (PI)
- Ramon Armengol
- Isabel Blanco-Penedo
- Houda Laghououata
- Ana Stoian
- Rayner González-Prendes (external member, University of Wageningen)

- Sabine Hammer (external member, University of Vienna)
- Elena Novell (external member, GSP-Lleida)
- Jordi Baliellas (external member, GSP-Lleida)

Tasks

The project is organised in seven tasks.

Task 1 - FIELD POPULATIONS

Three commercial populations will be monitores in this project.

- **Population 1.** Samples and data of producing sows from a previous experiment (project COMRDI16-1-035) will be used to discern sows which show a resilient behaviour during PRRSV outbreaks.
- **Population 2.** Samples for DNA isolation were being collected from 10 pig farms undergoing natural outbreaks with PRRSV + Actinobacillus Pleureopneumoniae or PRRSV + Streptococcus suis. All the outbreaks have been confirmed by serological/molecular and microbiology assays.
- **Population 3.** The **UdLGIM database**. Over the last 15 years, the research group for Pig Breeding at the University of Lleida (UdL) has collected samples and data from >2,000 pigs from a commercial Duroc line. Pigs are genealogically connected and their productionand meat quality data constitutes the UdLGIM biobank

Task 2 - EXPERIMENTAL INFECTIONS

During this project, the following experimental infections will take place:

1. Infection of **young pigs** with PRRSV + Actinobacillus pleuropneumoniae
2. Infection of **young pigs** with a high-virulent PRRSV strain
3. Infection of **pregnant sows** with a high-virulent PRRSV strain

All the infections will take place in animal experimental facilities and have been issued with a suitable license from the relevant authorities. The **purpose** of the experiments are two fold: First, to describe the pathogenesis of the infections and second to identify individual variability in the response to the infection that can lead us to discover DNA markers associated to more resilient responses,

Task 3 - DISCOVERY OF NEW DNA VARIANTS ASSOCIATED WITH RESILIENCE

Populations 1 and 2 (Task 1) will be used to investigate the DNA variants associated with (partial) resistance to the infections. With this aim, total genomic **DNA will be sequenced** at a depth of 6X to identify new DNA variants by means of a genome-wide association study (GWAS). A list of candidate variants will be generated to be validated in Task 4.

Task 4 - VALIDATION ON DNA MARKERS

Cross-population association analysis will be performed to validate the effects detected in one population and also to study the extend of the association with other pathogens and the age of the animal.

Task 5. ASSOCIACION ANALYSIS WITH PRODUCTION TRAITS

between resilience DNA markers and production and meat quality traits.

Task 6. DESIGN OF A PANEL OF MARKERS FOR RESILIENCE

Task 7. INTERNATIONALIZATION AND DISSEMINATION OF RESULTS