

Towards finding new candidate genes for improvement of swine immune response

The group named "Genetic Markers in Domestic Animals" belongs to the department of Genetics, located at the University of Córdoba (Spain). The main research work carried out is about the genetic base of the immune response in swine: the characterisation of the genes that could be part of the immune response and the improvement of their immune response, is the main objective.

Different strategies used to reach this:

- Genomics:

MICROARRAYS. The genetic information present in its genome determines how the immune response of an organism will develop. There is a way to study the expression of the whole genome (the complete set of genetic information) of an organism or at least a representative sample where most of the genes of the organism are present. This is called a microarray. A DNA microarray is a collection of microscopic DNA fragments. These spots show the expression profile, monitoring expression levels for thousands of genes simultaneously.

So with a porcine DNA microarray we can study which genes are implied in a certain phenotype, in other words which genes are responsible for certain characteristics in an individual. Let's say for example that we want to find genes implied in the response to a pathogen. We would hybridize DNA segments of individuals or cellular lines that have been in the presence of the pathogen, and compare them to the ones that haven't been in contact with it. The cells infected with the pathogen and the cells not infected will have the DNA segments labelled with different colours (fluorofores). In this way we will be able to find out which genes are more / less expressed in the infected individual in comparison with the healthy one.

- Proteomics:

Instead of looking for different expressions of genes, we can also compare protein expression profiles with 2D Bidimensional electrophoresis. As in the DNA microarrays, we can compare the proteome map (map of proteins expressed by a cell) in two different situations to find proteins involved in the development of certain diseases. The "Genetic Markers in Domestic Animals group" already obtained for the first time the proteome map of alveolar macrophages of pigs (a very important immune cell of all organisms). Now proteomes of macrophages infected with a pathogen are compared with the ones that are not infected, to find proteins involved in the inflammatory immune response.

- A Single Nucleotide Polymorphism, or SNP (pronounced "snip"), is a small genetic change, or variation, that can occur within an individual's DNA sequence (relative order of nucleotide pairs): this genetic code is specified by the four nucleotide "letters" A (adenine), C (cytosine), T (thymine), and G (guanine). SNP variation occurs when a single nucleotide, such as a G, replaces one of the other three nucleotide letters—C, A, or T. An example of a SNP is the alteration of the DNA segment CGACT to CGAGT, where the fourth nucleotide "C" in the first snippet is replaced with a "G".

In our laboratory we have found SNPs (changes in the DNA sequence) in several genes involved in the immune response. Some genetic variants of the genes may confer a protective immune response against the pathogen which could be important for the development of the disease in pigs.

The discovery of new genes whose products are essential for the development of diseases and their characterisation is important since some of these gene variants may result in more resistant animals. When this strategy is used complementarily with other disease control strategies, genetic approaches will become a critical component of the sustainable control of animal disease and, hence, the provision of a safe, high quality and welfare-friendly food supply chain.