

More than 7 million bacterial genes in the pig gut

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An international consortium of researchers from INRA (France), University of Copenhagen and SEGES (Denmark), BGI-Shenzhen (China) and NIFES (Norway) has now established the first catalogue of bacterial genes in the gut of pigs. This achievement is published in the latest issue of *Nature Microbiology*.

The researchers have analyzed [stool samples](#) from 287 pigs representing different breeds and selected pig lines from 11 different farms in France, China and Denmark. In total the researchers identified 7.7 million genes and identified a large number of known and unknown bacteria. The results showed clear country dependent differences, reflecting differences in farm systems and antibiotics supplementation. The results further illustrate how age, gender, and pig genetics are associated with differences in the composition of bacteria in the gut.

Importantly, the results also show how the prohibition of the use of antibiotics as growth promotants in Denmark and France seems to have reduced the load of antibiotics resistance genes in the French and Danish pigs, but still, pigs in these countries harbour genes conferring resistance to a large number of antibiotics. The detailed knowledge of the many genes in the [gut bacteria](#) will not only be of importance in order to use pigs as a model to elucidate the role of bacteria in relation to many human diseases, but will also be an important tool in the quest towards more sustainable knowledge-based pig farming with the need to combine feed efficiency with resistance to disease, while reducing the use of antibiotics, a main concern in relation to risks of [multidrug resistance](#) in

humans and animals.

More information: Liang Xiao et al. A reference gene catalogue of the pig gut microbiome, *Nature Microbiology* (2016). [DOI: 10.1038/nmicrobiol.2016.161](https://doi.org/10.1038/nmicrobiol.2016.161)

Provided by INRA

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