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## The Pig's other genome: a reference gene catalogue of the gut microbiome

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The pig is a major species for livestock and biomedicine. A pig reference genome was recently published. Here we report on the first gene catalogue of the pig gut microbiota based on faecal samples of 287 pigs from France, Denmark and China. More than 7.6 million non-redundant genes representing 719 metagenomic species were identified by deep metagenome sequencing. Results highlight substantially more similarities with the human than with the mouse catalogue. The pig and human catalogues share 12.6 and 9.3 % of their genes, respectively, but 78 and 96% of their functional pathways. Notably, the pig gut microbiota is influenced by gender, age and breed. Analysis of the prevalence of antibiotics resistance genes (ARGs) confirmed the efficiency of eliminating antibiotics from animal diet to reduce the risk of ARG dissemination due to farming systems. This first gene catalogue of the pig gut microbiota creates a substantial resource for whole metagenomics-based research in biomedicine and for sustainable knowledge-based pig farming.

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