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The Pig's other genome: a reference gene catalogue of the gut microbiome as a new resource for deep studies of the interplay between the host and its microbiome

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Up to 400 words (360 words)

The pig is a major species for livestock production and is also extensively used for biomedical research. A reference catalogue of gut microbial genes would clearly complement the recently established pig genome sequence. We established a comprehensive catalogue of gut microbial genes from 287 pigs from France, Denmark and China. Deep sequencing of fecal DNA samples generated 1,758 Gigabases (Gb) of high quality data with an average of 6.125 Gb per sample. The dataset allowed us to identify 7,685,872 non-redundant (NR) genes with an average contigN50 length of 1.89 Kilobases, together with 719 metagenomic species (MGS). 50% of the NR genes could be taxonomically classified, and of these more than 98% could be assigned to the Bacteria super kingdom. At the phylum level, Firmicutes was the most abundant followed by Bacteroidetes. At the genus level, *Prevotella* was the most abundant followed by *Bacteroides*, *Clostridium*, *Ruminococcus* and *Eubacterium*. We identified a common set of 4,430 NR genes, 36 MGS and 3,463 related annotated functions shared by

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100% of the 287 pig samples, suggesting the existence of a core of genes, species, and functions in the gut microbiome in pigs. The pig and human catalogues share 12.6 % and 9.3 % of their genes, respectively, a higher proportion than that shared between the mouse and human catalogues. Importantly, 78 % and 96% of the functional pathways are shared, underscoring the potential use of pigs for biomedical research. The pig metagenome exhibited a higher alpha diversity than both the human and mouse microbiomes, and lower beta diversity than the human metagenome at the gene, genus, and KEGG levels. We show that gender, age and host genetics markedly influence the pig gut microbiome. We report a common set of antibiotic resistance genes (ARGs) found in all pigs, regardless the country of origin or the supplementation with antibiotics, but show a significantly greater ARG load in animals continuously fed antibiotics. Thus, our data confirmed the efficiency of eliminating antibiotics from animal diet to reduce the risk of dissemination associated with farming systems. The pig microbiome gene catalogue reported here provides a straightforward new resource for metagenomics-based research in biomedicine and for sustainable knowledge-based pig farming.

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