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Daniel Crespo-Piazuelo, Lourdes Migura-Garcia, Jordi Estellé, Lourdes Criado-Mesas, Manuel Revilla, et al.. Association between the pig genome and its gut microbiota composition. *Scientific Reports*, 2019, 9 (1), 10.1038/s41598-019-45066-6 . hal-02627862

HAL Id: hal-02627862

<https://hal.inrae.fr/hal-02627862v1>

Submitted on 26 May 2020

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





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SCIENTIFIC REPORTS

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Association between the pig genome and its gut microbiota composition

Daniel Crespo-Piazuelo ^{1,2}, Lourdes Migura-García ³, Jordi Estellé ⁴, Lourdes Criado-Mesas ¹, Manuel Revilla ^{1,2}, Anna Castelló ^{1,2}, María Muñoz^{5,6}, Juan M. García-Casco^{5,6}, Ana I. Fernández⁵, Maria Ballester ³ & Josep M. Folch^{1,2}

The gut microbiota has been evolving with its host along the time creating a symbiotic relationship. In this study, we assess the role of the host genome in the modulation of the microbiota composition in pigs. Gut microbiota compositions were estimated through sequencing the V3-V4 region of the 16S rRNA gene from rectal contents of 285 pigs. A total of 1,261 operational taxonomic units were obtained and grouped in 18 phyla and 101 genera. *Firmicutes* (45.36%) and *Bacteroidetes* (37.47%) were the two major phyla obtained, whereas at genus level *Prevotella* (7.03%) and *Treponema* (6.29%) were the most abundant. Pigs were also genotyped with a high-throughput method for 45,508 single nucleotide polymorphisms that covered the entire pig genome. Subsequently, genome-wide association studies were made among the genotypes of these pigs and their gut microbiota composition. A total of 52 single-nucleotide polymorphisms distributed in 17 regions along the pig genome were associated with the relative abundance of six genera; *Akkermansia*, *CF231*, *Phascolarctobacterium*, *Prevotella*, *SMB53*, and *Streptococcus*. Our results suggest 39 candidate genes that may be modulating the microbiota composition and manifest the association between host genome and gut microbiota in pigs.

The digestive tract of animals has been evolving along the time with symbiotic microorganisms. These microbes, mostly bacteria, have adapted to thrive in such conditions forming complex and vital interactions among them and their host^{1,2}. The ecological community of these microorganisms is called microbiome, and the interactions with the host can be commensal, pathogenic or mutualistic³. In this scenario, mutualistic gut microbiota provides the host with beneficial functions that the host cannot perform, such as digesting complex polysaccharides, producing vitamins, and preventing colonization by pathogens^{2,4}. Likewise, commensal gut populations modulate hosts' immune responses which can modify the microbiota composition in order to maintain gut homeostasis⁴. Therefore, apart from the host genetics, the complexity of the interactions increases taking into account factors such as age, diet, environment, disease, or maternal seeding which are known to influence gut microbial communities⁵.

The intestinal epithelium acts as a barrier, protecting deeper tissues from bacterial entry². Supporting this defence system, the gut epithelial surface is coated with a mucous layer formed by mucin glycoproteins^{6,7}. While the small intestine has only one layer which is permeable to bacteria⁶, the mucous layer of the colon is structured in two parts: a dense inner layer firmly attached to the gut epithelium that minimizes bacterial-epithelial cell contact, and a loose outer layer that can be broken down by commensal bacteria⁷. In this outer mucous layer, the metabolites produced by these bacteria interact with the host stimulating the innate and adaptive immune responses². For instance, host innate immunity can select for a species-specific microbiota using microbicidal proteins⁸. However, the host also has mechanisms to tolerate the metabolites from non-pathogenic bacteria², just as certain bacteria trigger the host immune system for self-benefit⁹.

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In these recent years, high-throughput sequencing technologies have greatly improved the study of bacterial populations without performing microbial cultures. The microbial 16S rRNA gene sequencing is commonly used to estimate the microbiota composition, while the shotgun sequencing of DNA fragments isolated after shearing faecal or other samples is used for the metagenome (all the microbial collective genomes) characterization¹⁰. Recently, whole-metagenome sequencing has been used to obtain the reference gene catalogue of the pig gut microbiome¹¹. This study revealed that the reference catalogue of the porcine gut microbiome shared more non-redundant genes between human and pig than human and mouse¹¹, suggesting pig as a better animal model than mouse because of their similarity with humans. Both species are omnivores and have monogastric digestive tracts which are analogous in anatomy, immunology and physiology¹².

The heritability of the microbial genera composition of the pig gut has been reported to range from low to high values^{13,14}. Accordingly, host genetics has been suggested as an important factor in the determination of gut microbial composition¹⁵. However, there are limited studies measuring the contribution of inter-individual variability modulating the bacterial communities and the effect of host polymorphisms on the establishment of the microbiota¹⁶. In this context, genome-wide association studies (GWAS), which have been widely used to analyse a plethora of complex traits, are now being used to study the link between the host and its microbiota composition^{15,16}. With this approach, Blekhnman *et al.*¹⁷ were the first to describe in humans the relationship between the abundance of *Bifidobacterium* and the single-nucleotide polymorphisms (SNPs) close to the lactase gene. In this case, lactase non-persistent recessive individuals who drink milk cannot break down lactose and thus, *Bifidobacterium* thrives using this available sugar¹⁸.

Conversely, host genetics appeared to have a minor impact in the microbiota compared with age, diet or the environment¹⁹. It is not surprising, since conditions are difficult to standardize between individuals. In this regard, production pigs represent a perfect model to measure the effect of host genetics in shaping the microbiota due to their similar diet and environmental factors during their whole rearing cycle, but the relationship between the pig genome and its gut microbiota composition has not yet been fully described²⁰.

The objective of this study was to identify genomic regions that influence the gut microbiota composition through host-microbiota associations in pigs. For this purpose, the 16S rRNA gene was sequenced from rectal contents of 288 pigs genotyped with a high-throughput method.

Materials and Methods

Ethics approval. All animal manipulations were performed according to the regulations of the Spanish Policy for Animal Protection RD53/2013, which meets the European Union Directive 2010/63/EU about the protection of animals used in experimentation. Pigs were slaughtered in a commercial abattoir following national and institutional guidelines for Good Experimental Practices.

Animal material. A total of 288 healthy commercial F1 crossbred pigs (Duroc × Iberian) were used in this study. All animals were maintained in the same farm under intensive conditions and feeding was *ad libitum* with a barley- and wheat-based commercial diet. Pigs with an average weight of 138.8 kg (SD = 11.46 kg) were slaughtered in a commercial abattoir in four distinct days. Samples of rectal content and *Longissimus dorsi* muscle were snap-frozen in liquid nitrogen and later stored at −80 °C.

Microbial DNA extraction and 16S rRNA gene sequencing. For each one of the 288 samples, the DNA of 0.2 g of rectal content was extracted with PowerFecal kit (MoBio Laboratories, Carlsbad, CA, USA) following the manufacturer's recommendations. DNA purity and concentration were measured through a ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). The amplification of the V3-V4 region of the 16S rRNA gene was performed following the recommendations of the 16S *Metagenomic Sequencing Library Preparation* guide (Illumina, San Diego, CA, USA). Full description of primer sequences and methods used can be accessed at Supplementary Information S1. All the 288 amplicon pooled libraries were sequenced in three runs of a MiSeq (Illumina, San Diego, CA, USA) instrument in the Sequencing Service of the FISABIO (*Fundació per al Foment de la Investigació Sanitària i Biomèdica de la Comunitat Valenciana*, Valencia, Spain) using the MiSeq Reagent Kit v3 (600-cycle format, 2 × 300 bp paired-end reads). A mean of 104,115 reads for each sample was obtained (17.991 Gb in total), ranging from 34,186 to 218,360 reads, except for one outlier that was discarded because it had 1,758,983 reads.

Taxonomy classification and diversity studies of the gut samples. Bioinformatics analysis were performed in QIIME v.1.9.1²¹ by using the QIIME's subsampled open-reference operational taxonomic unit (OTU) calling approach and following the recommendations of Rideout *et al.*²². In brief, the *join_paired_ends.py* function in QIIME was used to merge the forward and reverse reads contained in the fastq files of the remaining 287 samples. The quality control and the filtering process was made pursuant to the considerations provided by Bokulich *et al.*²³. Therefore, the *split_libraries_fastq.py* command was used to demultiplex and filter (at Phred ≥ Q20) the fastq sequence data. After this step, OTUs were identified by using the *pick_open_reference_otus.py* function with a subsampled percentage of 10% (s = 0.1). Subsequently, chimera detection was carried on in QIIME with BLAST²⁴ and OTUs were taxonomically annotated employing the Greengenes 13.8 database²⁵. At this point, two samples did not satisfy the quality filters and were discarded. Thus, for the remaining 285 samples, a dataset containing 1,294 OTUs was obtained after filtering out singletons and OTUs representing less than 0.005% of the total number of annotated reads²³. From this dataset, 33 OTUs had missing taxonomic ranks and were discarded. Finally, 1,261 OTUs in the 285 samples were considered for further analysis (Supplementary Table S1).

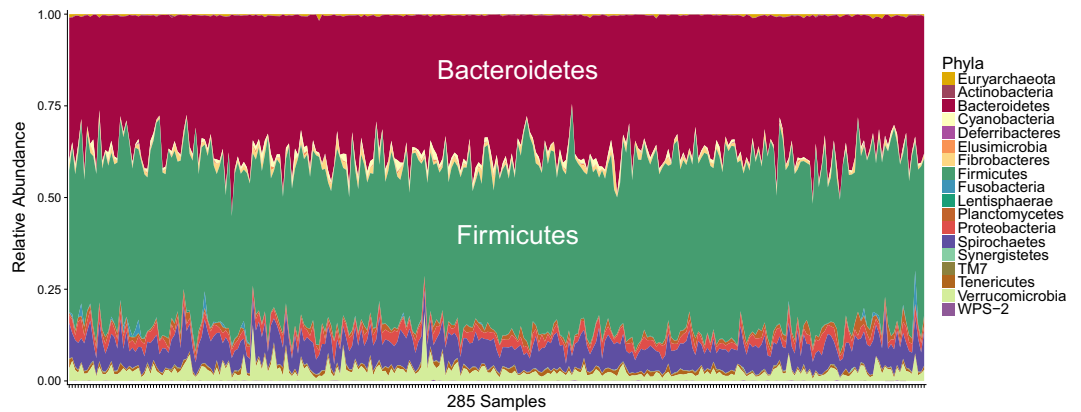


Figure 1. Stacked area plot of OTUs grouped by phyla for the 285 pig rectal samples.

The 1,261 OTUs were grouped in 18 phyla and 101 genera through the *tax_glom* method within the phyloseq package²⁶ in R (www.r-project.org). Besides, genera that belonged to a higher taxonomy rank but lacked the genus information were merged and marked as unspecified (*g__unsp*).

The analyses of α and β -diversities in the 285 samples were carried on with the vegan R package²⁷, and the non-metric multidimensional scaling (NMDS) plot was performed using phyloseq²⁶ and ggplot2²⁸. For the α -diversity study, the Shannon index was employed, whereas the β -diversity study was represented using the Whittaker index. Additionally, the dissimilarity between pairs of samples was estimated with the NMDS method using the Bray-Curtis dissimilarity²⁹.

Host DNA extraction and SNP genotyping. Pig genomic DNA was extracted from the *Longissimus dorsi* muscle of all the 288 samples using the standard phenol-chloroform method³⁰. The DNA concentration and purity was measured with a ND-1000 spectrophotometer (NanoDrop) afterwards.

A total of 288 pigs were genotyped with the GeneSeek Genomic Profiler (GGP) Porcine HD v1 (70 K) array (Illumina, San Diego, CA, USA) using the Infinium HD Assay Ultra protocol (Illumina). Genotypes were obtained with the GenomeStudio software (2011.1 version, Illumina) and filtered with the PLINK software³¹ (1.90b5 version). Further analyses were conducted using only SNPs that mapped in the *Scrofa11.1* assembly, with a minor allele frequency (MAF) >5% and missing genotypes <5%, retaining a total of 45,508 SNPs.

GWAS analysis. For the 285 samples, GWAS between the microbiota composition at genus level and the 45,508 genotyped SNPs were made. Samples were normalized in percentages based on the number of annotated reads per sample (relative abundance). To avoid errors caused by low abundant genera, GWAS were performed only in genera that comprised more than the 0.5% of the total annotated reads and were present in more than the 90% of the samples. In addition, genera marked as unspecified were excluded from the GWAS analysis. Therefore, GWAS were performed in 18 of the 101 genera found.

For the GWAS analysis, the following univariate linear mixed model was applied using the GEMMA software³² (0.96 version):

$$y_{ijkl} = \text{Sex}_i + \text{Batch}_j + u_k + \delta_k a_l + e_{ijkl},$$

where y_{ijkl} indicates the vector of phenotypic observations in the k^{th} individual; sex (two categories) and batch (4 categories) are fixed effects; u_k is the infinitesimal genetic effect considered as random and distributed as $N(0, K\sigma_u)$, where K is the numerator of the kinship matrix; δ_k is a $-1, 0, +1$ indicator variable depending on the k^{th} individual genotype for the l^{th} SNP; a_l represents the additive effect associated with the l^{th} SNP; and e_{ijkl} is the residual.

The false discovery rate (FDR) method developed by Benjamini and Hochberg³³ was applied for multiple test correction using the *p.adjust* function incorporated in R. The cut-off for considering a SNP as significant was set at $\text{FDR} \leq 0.1$. Two significant SNPs were grouped inside the same interval if the distance between them was less than 2 Mb.

Gene annotation and functional prediction. The associated regions in the pig genome were annotated at 1 Mb on each side of the previously defined intervals. The genes contained in these regions were extracted using the BioMart tool³⁴ from the Ensembl project (www.ensembl.org; release 92) using the *Scrofa11.1* reference assembly. In addition, the functional consequences of the significant SNPs were predicted through the Variant Effect Predictor tool³⁵ from the Ensembl project (release 92).

Results and Discussion

Microbiota composition and diversity. A mean of 104,115 reads per sample were obtained with a MiSeq (Illumina) after sequencing the V3-V4 region of the 16S rRNA gene from rectal contents of 288 pigs. A total of 1,261 OTUs which were grouped in 18 phyla and 101 genera were found in the 285 samples that fulfilled the quality criteria. At phylum level, *Firmicutes* (45.36%) and *Bacteroidetes* (37.47%) were the more abundant (Fig. 1 and

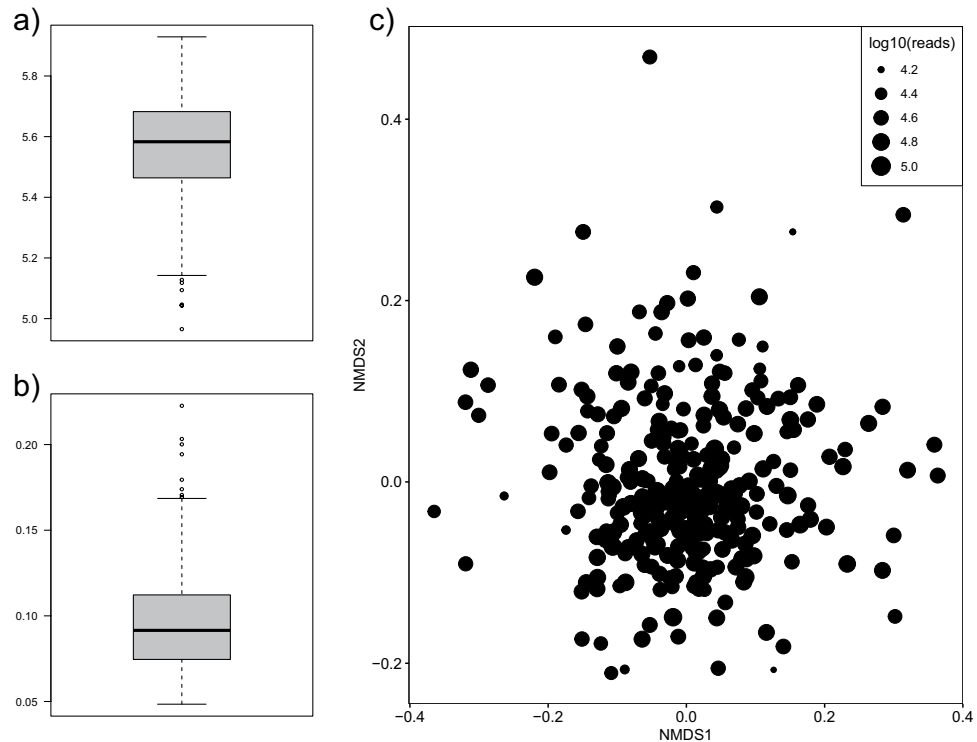


Figure 2. Plots showing the diversities and dissimilarities measured using the 1,261 OTUs found in rectal contents of 285 pigs. **(a)** Boxplot of the Shannon α -diversity. **(b)** Boxplot of the Whittaker β -diversity calculated through the Bray-Curtis dissimilarity. **(c)** Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis dissimilarities. The size of the dot is proportional to the total number of annotated reads in each sample.

Supplementary Table S2). In accordance with the literature^{36,37}, *Firmicutes* and *Bacteroidetes* are usually the most dominant phyla found in colon and faeces of pigs. The most abundant genera, not marked as unspecified, were *Prevotella* (7.03%) and *Treponema* (6.29%) (Supplementary Table S3). Accordingly, *Prevotella* spp. are frequently found as one of the most abundant genus in the lower intestine and faeces^{36,37}. However, comparisons between different studies should be made with caution, since differences in microbiota composition are conditional on the different sets of primers used in the analysis, breeds (host genetic background), age of the animals at sampling time, and environmental factors such as dietary composition^{14,38}.

To obtain a measure for the number of different OTUs and their relative abundance within each of the 285 samples, the community α -diversity was calculated through the Shannon index (Fig. 2a). The mean of the α -diversity was 5.55, ranging from 4.97 to 5.93. It is not surprising, since the distal part of the pig gut usually has a higher α -diversity than the rest of the intestine³⁷. In addition, the β -diversity was used to measure the differences between samples through the Whittaker index (Fig. 2b) obtaining a mean distance to the centroid of 0.10. Lastly, a NMDS plot was performed to observe the dissimilarities between samples employing Bray-Curtis dissimilarity (Fig. 2c). The β -diversity was closer to 0, indicating that the global microbiota composition was quite similar along the 285 samples. Furthermore, this low β -diversity was expected, since the pigs from our study have been subjected to the same diet and environmental factors during their whole rearing cycle and this uniformity is reinforced by the absence of clustering in the NMDS plot. This way, overall diversity results reinforce the appropriateness of the model to measure the effect of host genetics in shaping the microbiota.

GWAS results. GWAS were performed using 45,508 SNPs genotyped in 285 animals and the relative abundance of 18 genera; *Akkermansia*, *Bacteroides*, *CF231*, *Coprococcus*, *Fibrobacter*, *Lactobacillus*, *Oscillospira*, *Parabacteroides*, *Paraprevotellaceae* *Prevotella*, *Phascolarctobacterium*, *Prevotella*, *RFN20*, *Ruminococcus*, *SMB53*, *Sphaerochaeta*, *Streptococcus*, *Treponema* and *YRC22*. A total of 52 significant SNPs were distributed in 17 regions along the following *Sus scrofa* chromosomes (SSC): SSC3, SSC4, SSC6, SSC7, SSC8, SSC9, SSC10, SSC11, SSC13, SSC14, SSC15, SSC18 and SSCX (Supplementary Table S4). Significant association signals (FDR \leq 0.1) were found in six out of the 18 GWAS for the following genera: *Akkermansia*, *CF231*, *Phascolarctobacterium*, *Prevotella*, *SMB53* and *Streptococcus* (Fig. 3 and Table 1). No shared associated regions were found for the abundances of these six genera, albeit some of them belong to the same phyla. *CF231* and *Prevotella* are genera of the *Bacteroidetes* phylum. Within the *Firmicutes* phylum, *Phascolarctobacterium* and *SMB53* are members of the *Clostridiales* order, and *Streptococcus* is a member of the *Lactobacillales* order. Hence, our results suggest an association between chromosomal regions along the pig genome and abundance of certain bacteria genera. In the following sections, the candidate genes mapped in the genomic regions associated with the genus relative abundance of *Akkermansia*, *CF231*, *Phascolarctobacterium*, *Prevotella*, *SMB53* and *Streptococcus* are discussed in detail. The list of candidate genes is summarized in Table 1.

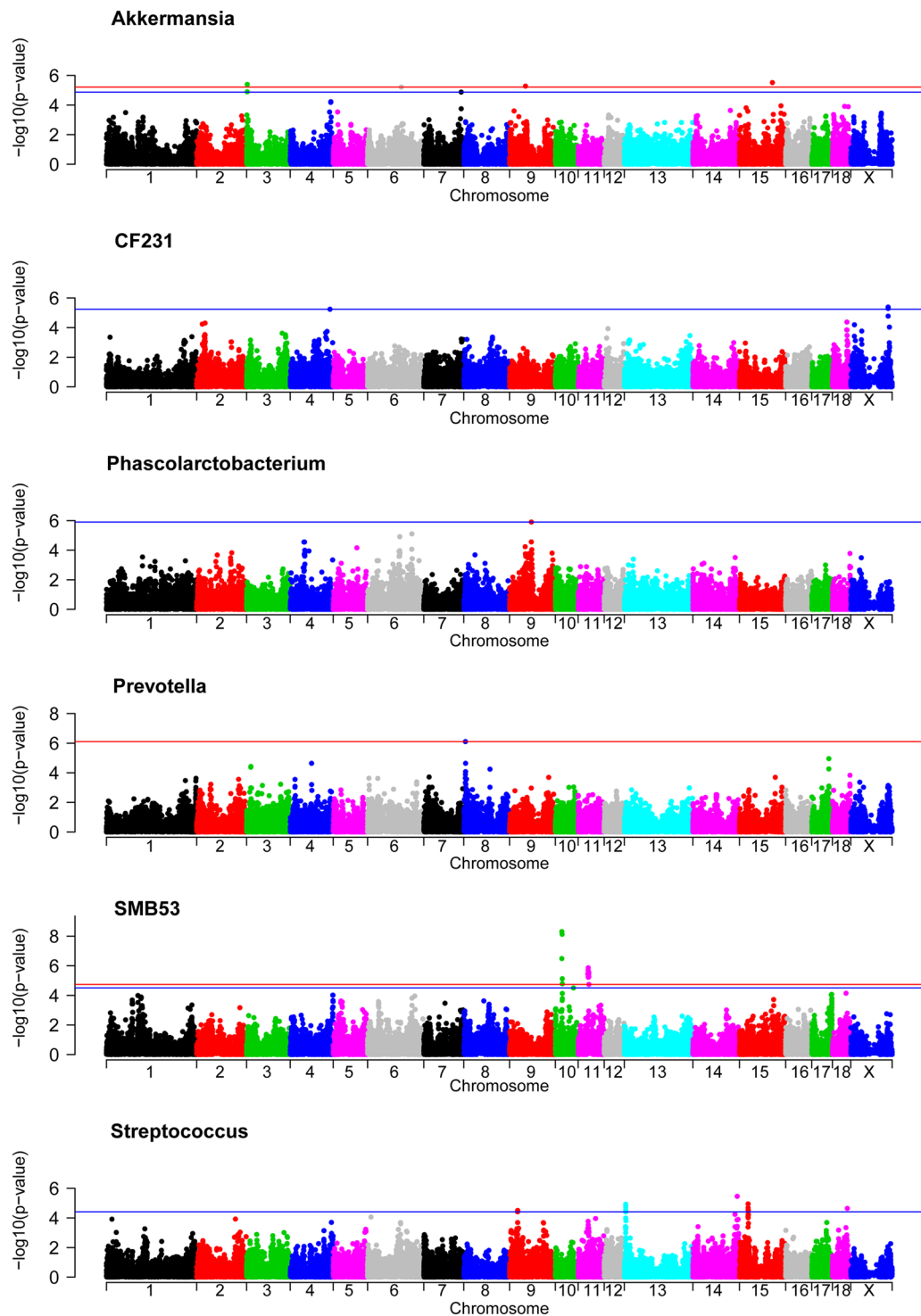


Figure 3. GWAS plot for the relative abundance of the following genera: *Akkermansia*, *CF231*, *Phascolarctobacterium*, *Prevotella*, *SMB53*, and *Streptococcus*. The red lines indicate those SNPs that are below the genome-wide significance threshold ($FDR \leq 0.05$), while the blue lines indicate those SNPs that are below genome-wide significance threshold ($FDR \leq 0.1$).

Akkermansia. The relative abundance of *Akkermansia*, a genus of the *Verrucomicrobia* phylum, was significantly associated with polymorphisms in five chromosomic regions: SSC3, SSC6, SSC7, SSC9, and SSC15 (Table 1). Within the SSC3 region (1.03–3.04 Mb), two candidate genes have been proposed, caspase recruitment domain family member 11 (*CARD11*) and carbohydrate sulfotransferase 12 (*CHST12*). *CARD11* is necessary for T helper 17 cells differentiation which are involved in the adaptive immune system and protect the body against extracellular bacteria³⁹. The *CHST12* gene is required for glycosaminoglycan biosynthesis⁴⁰. Glycosaminoglycans are

Region	Genus	Chr. ^a	Position in Mb Start - End	No. SNPs ^b	Most significant SNP	Effect (%)	p-value	FDR	Candidate genes
A1	<i>Akkermansia</i>	3	0.89–3.04	3	rs81335357; rs81246645	7.72	4.04×10^{-6}	4.58×10^{-2}	<i>CARD11</i> ; <i>CHST12</i>
A2	<i>Akkermansia</i>	6	101.46–103.46	1	rs81390429	25.85	6.06×10^{-6}	4.58×10^{-2}	<i>TGIF1</i>
A3	<i>Akkermansia</i>	7	112.61–114.61	1	rs325604118	6.56	1.33×10^{-5}	7.55×10^{-2}	<i>LGMN</i> ; <i>CHGA</i>
A4	<i>Akkermansia</i>	9	47.53–49.57	2	rs81410866; rs81410881	8.78	5.25×10^{-6}	4.58×10^{-2}	<i>ssc-mir-125b-1</i> ; <i>ssc-mir-100</i> ; <i>SORL1</i>
A5	<i>Akkermansia</i>	15	99.10–101.10	1	rs80982646	7.94	3.04×10^{-6}	4.58×10^{-2}	<i>SLC39A10</i>
B1	<i>CF231</i>	4	119.91–121.91	1	rs319005051	7.07	5.72×10^{-6}	6.48×10^{-2}	
B2	<i>CF231</i>	X	112.48–114.50	3	rs329229283	6.34	4.10×10^{-6}	6.48×10^{-2}	<i>FGF13</i> ; <i>ATP11C</i>
C1	<i>Phascolarctobacterium</i>	9	65.33–67.33	1	rs81223434	7.73	1.25×10^{-6}	5.68×10^{-2}	<i>SLC45A3</i> ; <i>RAB7B</i> ; <i>RAB29</i> ; <i>NUCKS1</i> ; <i>IKBKE</i> ; <i>MAPKAPK2</i>
D1	<i>Prevotella</i>	8	3.81–5.81	1	rs326174858	10.88	7.79×10^{-7}	3.53×10^{-2}	<i>CYTL1</i> ; <i>WFS1</i> ; <i>MAN2B2</i>
E1	<i>SMB53</i>	10	18.51–22.05	5	rs344136854	14.25	4.92×10^{-9}	1.68×10^{-4}	<i>CAPN8</i> ; <i>CAPN2</i> ; <i>SUSD4</i> ; <i>DENND1B</i> ; <i>PTPRC</i> ; <i>ssc-mir-181b-1</i> ; <i>ssc-mir-181a-1</i>
E2	<i>SMB53</i>	10	53.89–55.89	1	rs341165563	8.87	3.15×10^{-5}	7.14×10^{-2}	<i>MALRD1</i>
E3	<i>SMB53</i>	11	28.22–33.50	14	rs80835110	10.42	1.37×10^{-6}	1.47×10^{-2}	<i>PCDH17</i>
F1	<i>Streptococcus</i>	9	23.45–25.66	3	rs319168851	6.15	3.11×10^{-5}	9.41×10^{-2}	<i>FAT3</i>
F2	<i>Streptococcus</i>	13	2.97–5.15	4	rs81310237	11.88	1.20×10^{-5}	9.41×10^{-2}	<i>PLCL2</i> ; <i>GALNT15</i> ; <i>RFTN1</i>
F3	<i>Streptococcus</i>	14	133.80–135.80	1	rs337448241	10.51	3.46×10^{-6}	9.41×10^{-2}	<i>CTBP2</i> ; <i>UROS</i>
F4	<i>Streptococcus</i>	15	25.15–27.87	9	rs331341379	8.72	1.12×10^{-5}	9.41×10^{-2}	<i>ERCC3</i> ; <i>BINI</i> ; <i>MAP3K2</i>
F5	<i>Streptococcus</i>	18	44.25–46.25	1	rs334064749	7.7	2.26×10^{-5}	9.41×10^{-2}	<i>ssc-mir-196b-1</i>

Table 1. Significant genomic regions in the pig genome associated with the relative composition of genera and the candidate genes found within. ^aChromosome. ^bNumber of significant SNPs found in the region (FDR \leq 0.1).

also called mucopolysaccharides and are often found in the mucin layer together with glycans and sialic acid⁴¹. The most common species of the *Verrucomicrobia* phylum found in the gut, *Akkermansia muciniphila*, colonizes the mucus layer and it is a known mucin degrader⁴². The regulation of host genes related to glycosaminoglycans biosynthesis probably has a direct effect in the occurrence of mucin degrading bacteria. Studying further this candidate gene may help to select a genetic variant that enriches the presence of *A. muciniphila*, since this species is beneficial to the host by restoring gut barrier function and helps reducing obesity⁴³. In SSC6 (102.46 Mb), the only significant SNP (rs81390429, p -value = 6.06×10^{-6}) explained a 25% of the variance in the abundance of the *Akkermansia* genus. The candidate gene found in this SSC6 region, *TGIF1* (TGFB induced factor homeobox 1), encodes for a protein that contributes to the adaptive immunity favouring the response of T follicular helper cells⁴⁴. Additionally, two candidate genes were proposed for the *Akkermansia* spp. abundance in the SSC7 region (112.61–114.61 Mb): *CHGA* (chromogranin A) and *LGMN* (legumain). In humans, faecal levels of CHGA were associated with 61 different bacterial species including *A. muciniphila*, which was negatively associated with CHGA⁴⁵. CHGA plays a role in the innate immunity with its antimicrobial activity against bacteria⁴⁶, whereas LGMN is a cysteine protease that also has antimicrobial activity, as well as it is involved in the antigen-presenting process and Toll-like receptors (TLRs) activation⁴⁷. Thus, variations in the *CHGA* or *LGMN* genes should be affecting the microbiota composition based on the bacterial resistance to their antimicrobial activity. Inside the SSC9 region (47.53–49.57 Mb), there were three candidate genes, two microRNAs genes, *ssc-mir-125b-1* and *ssc-mir-100*, and the sortilin related receptor 1 (*SORL1*) gene. Both microRNAs are involved with the adaptive immune system: *mir-125b-1* inhibits B cell differentiation⁴⁸, while *mir-100* inhibits T cell proliferation and differentiation⁴⁹. Therefore, polymorphisms in these miRNAs genes may affect the targeting of these miRNAs or their expression, which might be associated with the abundance of *Akkermansia* spp. However, the two significant SNPs (rs81410866 and rs81410881, p -value = 5.25×10^{-6}) of the SSC9 region were located in intronic regions of the *SORL1* gene. *SORL1* is an endocytic receptor that might be affecting gut microbiota composition as it has been associated with obesity⁵⁰, and pancreatic and biliary tract cancer in humans⁵¹. Finally, a significant SNP (rs80982646, p -value = 3.04×10^{-6}) located at 100.1 Mb in SSC15 was also associated with the relative abundance of *Akkermansia* spp. In this region, we identified the *SLC39A10* (solute carrier family 39 member 10) gene which appears to be a good candidate to modulate the presence of *Akkermansia* spp., since positively regulates B cell receptor signalling pathway⁵². Hence, in accordance with our results, germ-free mice colonized with *A. muciniphila* showed an overexpression in genes related with the antigen presentation pathway and B and T cell maturation, implying its possible role as host immune system modulator⁵³.

CF231. The relative abundance of the *CF231* genus (a member of the *Paraprevotellaceae* family) was associated to genetic variations in two regions along the pig genome in SSC4 and SSCX (Table 1). While no candidate genes were found in SSC4 at 120.91 Mb, the SSCX region (112.48–114.50 Mb) contained the ATPase phospholipid transporting 11 C (*ATP11C*) and the fibroblast growth factor 13 (*FGF13*) genes. The ATP11C protein is involved in B cell differentiation past the pro-B cell stage, thus, defects in ATP11C led to a lower number of B cells and an impairment in their differentiation⁵⁴. Changes in the *ATP11C* gene may cause species-specific tolerance through the adaptive immune system and transport. Additionally, ATP11C is also involved in the metabolism

of cholestatic bile acids⁵⁵. Intestinal content of cholesterol has the potential to shape the gut microbiome⁵⁶ and the *CF231* genus might be affected by the expression of these genes, since bile acids are catabolites of cholesterol. Interestingly, an enrichment of the *CF231* genus has been detected in experiments with high fat diet-induced hypercholesterolemic rats treated with cholesterol-lowering drugs⁵⁷. On the other hand, the three significant SNPs of the SSCX region were located in an intron of the other candidate gene, *FGF13* (Supplementary Table S4). Although the biological role of the *FGF13* gene is not clear, it may be involved in the repair of the intestinal epithelial damage affecting microbiota composition. This function has been reported in another member of its gene family, *FGF2* (fibroblast growth factor 2)⁵⁸.

Phascolarctobacterium. Six candidate genes found inside the SSC9 region (65.33–67.33 Mb) may be associated with the relative abundance of *Phascolarctobacterium* spp. (Table 1). *Phascolarctobacterium* is a Gram-negative genus commonly found in human faeces able to produce short chain fatty acids (SCFAs)⁵⁹. SCFAs are absorbed and serve as a source of energy by colonocytes and peripheral tissue or can be used as substrates for lipogenesis, gluconeogenesis or regulation of cholesterol synthesis in the liver⁶⁰. Interestingly, one of the candidate genes that could be modulating the abundance of *Phascolarctobacterium* spp. was the *SLC45A3* (solute carrier family 45 member 3). *SLC45A3* is involved in the positive regulation of fatty acid biosynthetic process⁶¹. There were also two other candidate genes within SSC9 which encode GTPases that are members of the RAS oncogene family (*RAB7B* and *RAB29*). Under the induction of the lipopolysaccharides present in the Gram-negative cell wall, *RAB7B* promotes the degradation of toll like receptor 4 (TLR4) impairing the innate immune response by reducing the sensitivity of macrophages to lipopolysaccharides signalling⁶². Therefore, *RAB7B* may play an important role in the development of tolerance to Gram-negative commensal bacteria such as *Phascolarctobacterium* spp. The other GTPase, *RAB29*, is involved in bacterial toxin transport and is able to discriminate between *Salmonella enterica* serovars⁶³. The positive regulation of insulin receptor signalling pathway by the *NUCKS1* (nuclear casein kinase and cyclin dependent kinase substrate 1) gene⁶⁴ located in this SSC9 region may also be modulating the abundance of the *Phascolarctobacterium* genus, since it has been described an enrichment of this genus in diabetic animal models treated with prebiotics to alleviate glucose intolerance⁶⁰. Additionally, the two remaining candidate genes, *IKBKE* (inhibitor of nuclear factor kappa B kinase subunit epsilon) and *MAPKAPK2* (mitogen-activated protein kinase-activated protein kinase 2) might be associated with the microbiota composition because of their relationship with the immune system. *IKBKE* inhibits T cell responses⁶⁵ and *MAPKAPK2* regulates interleukin 10⁶⁶ which is crucial to maintain the gut homeostasis⁴.

Prevotella. Studies performed in humans have associated the presence of the *Prevotella* genus with a high intake of complex fibres in the diet⁶⁷. In our animal material, *Prevotella* spp. represented 7.03% of the total composition at genus level (Supplementary Table S3). In this case, only the *rs326174858* SNP located at 4.81 Mb in SSC8 was significantly associated (p -value = 7.79×10^{-7}) with the abundance of *Prevotella* spp. (Table 1). Three candidate genes were found in this SSC8 region, cytokine like 1 (*CYTL1*), wolframin ER transmembrane glycoprotein (*WFS1*), and mannosidase alpha class 2B member 2 (*MAN2B2*). *CYTL1* codes for a protein capable of chemoattracting macrophages and its activity is sensitive to *Bordetella pertussis* toxin⁶⁸. A defect in the second gene, *WFS1*, produces insulin insufficiency, causing diabetes via pancreatic β cells failures⁶⁹. Therefore, diabetic individuals would reduce glucose uptake in the gut epithelium⁷⁰. In this sense, glucose might be more available for some bacteria species, producing changes in the overall microbiota composition. In accordance with this hypothesis, the abundance of *Prevotella* spp. was reduced in diabetic children when compared to healthy ones⁷¹. The encoded protein of the last candidate gene, *MAN2B2*, is implicated in the degradation of glycans⁷². Glycans are excreted into the intestine, including those in dietary plants, animal-derived, cartilage and tissue (glycosaminoglycans and N-linked glycans), and endogenous glycans from host mucus (O-linked glycans)⁷³. The *Prevotella* genus contributes to the degradation of mucin and plant-based carbohydrates⁷⁴ and, therefore, it seems plausible that variations in a gene involved in the degradation of glycans could modulate the presence of *Prevotella* spp.

SMB53. The *SMB53* genus sequences found in swine compost were closely related with *Clostridium glycolicum*⁷⁵. The abundance of the *SMB53* genus in our pig rectal samples accounted for 1.19% of the total number of annotated reads (Supplementary Table S3), and presented three significant associated regions, two in SSC10 and one in SSC11 (Table 1). The first region of SSC10 (18.51–22.05 Mb) showed the most significant SNP (*rs344136854*, p -value = 4.92×10^{-9}). Seven candidate genes have been identified inside this SSC10 region: calpain 2 (*CAPN2*) and 8 (*CAPN8*); sushi domain containing 4 (*SUSD4*); DENN domain containing 1B (*DENND1B*); protein tyrosine phosphatase, receptor type C (*PTPRC*); *ssc-mir-181a-1* and *ssc-mir-181b-1*. Calpains are a family of proteases that are able to perform various cellular functions depending on changes in intracellular Ca^{2+} levels⁷⁶. For instance, an increase in Ca^{2+} in the intestinal porcine endothelial cells due to the *Clostridium perfringens* β -toxin triggers the calpain activation leading to intestinal cell death⁷⁷. Therefore, polymorphisms in the *CAPN2* or *CAPN8* genes may confer resistance to *Clostridium* spp. avoiding endothelial cell death and so, increasing *Clostridia* abundance in the gut. Two of the significant SNPs of this SSC10 region were located in an intron of the *SUSD4* gene, whereas other significant SNP was also located in an intron of the *DENND1B* gene (Supplementary Table S4). *SUSD4*, *DENND1B* and *PTPRC* are genes related with the immune system: *SUSD4* inhibits the complement system⁷⁸, *DENND1B* is a regulator of the T cell receptor signalling⁷⁹, and *PTPRC* is necessary for antigen receptor mediated signalling in lymphocytes⁸⁰. The last two candidate genes in this first SSC10 region were both microRNAs from the *miR-181* family. The depletion of *miR-181* causes a lack of Natural Killer T cells in the thymus as well as defects in T and B cells development⁸¹. In the second SSC10 region (54.89 Mb), the only significant SNP (*rs341165563*, p -value = 3.15×10^{-5}) was located in an intron of the *MALRDI* (MAM and LDL receptor class A domain containing 1) gene (Supplementary Table S4). This candidate gene is involved in bile acid synthesis regulation and is able to modify the gut microbiota⁸². Khan *et al.*⁵⁷ demonstrated an increase in the relative abundance of the

SMB53 genus in hypercholesterolemic rats treated with cholesterol-lowering drugs. Thus, further studies are needed to evaluate the modulation of the *SMB53* genus by the MALRD1 negative regulation of bile acid biosynthetic process. Additionally, the *SMB53* genus belongs to the *Clostridiaceae* family. Most members of this family have the capacity to consume gut mucus- and plant-derived saccharides like glucose⁸³. Interestingly, recent studies performed by Horie *et al.*⁸⁴ have detected an enrichment of *SMB53* in caecum of mice suffering type 2 diabetes, suggesting a possible role of this genus in the disease. The last region, in SSC11 (28.22–33.5 Mb), was comprised of 14 SNPs but, despite being the longest region observed (5.3 Mb), only one candidate gene (protocadherin 17, *PCDH17*) was proposed. Remarkably, the most significant SNP (rs80835110, p -value = 1.37×10^{-6}) was located in an intron of *PCDH17* (Supplementary Table S4). *PCDH17* may play a role in the colon similar to protocadherin 1 (*PCDH1*), acting as a physical barrier in the airway epithelial cells⁸⁵.

Streptococcus. There are five regions within the pig genome associated to the presence of *Streptococcus* spp., SSC9, SSC13, SSC14, SSC15, and SSC18 (Table 1). In the SSC9 region (23.45–25.66 Mb), the protein encoded by the FAT atypical cadherin 3 (*FAT3*) gene may be forming epithelial junctions that can be broken down by *Streptococcus* spp.⁸⁶. In the SSC13 region (2.97–5.15 Mb), three candidate genes were found: phospholipase C like 2 (*PLCL2*), polypeptide N-acetylgalactosaminyltransferase 5 (*GALNT15*), and raftlin, lipid raft linker 1 (*RFTN1*). Four significant SNPs were located in intronic regions of the *PLCL2* gene (Supplementary Table S4). *PLCL2* increases the thresholds of B cell activation⁸⁷ and so, it may modulate the tolerance of the adaptive immune system. On the other hand, *GALNT15* belongs to a family of proteins that are able to produce O-linked glycosylation in the mucin⁸⁸ and hence, the variations on the *GALNT15* gene might affect some mucin dwellers like *Streptococcus* spp.⁸⁹. Additionally, it is also interesting to highlight a possible link between the *RFTN1* gene, involved in the formation and/or maintenance of lipid rafts⁹⁰, and the abundance of the *Streptococcus* genus. The lipid rafts are microdomains located in the membrane surface of the cell that play an important role in cellular signaling and membrane trafficking of T and B lymphocytes^{90,91}. Furthermore, lipid rafts are also mediators of innate immune recognition of bacteria⁹². The possible association of *RFTN1* with the abundance of *Streptococci* needs further attention, since some species of *Streptococcus* are known to hijack these lipid rafts to enter the host cell causing disease⁹³. Two candidate genes were found in the SSC14 region (133.8–135.8 Mb): *CTBP2* (C-terminal binding protein 2) and *UROS* (uroporphyrinogen III synthase). The *CTBP2* gene was associated in pigs with a susceptibility to develop a bacterial respiratory disease⁹⁴. The *UROS* gene is involved in the metabolism of porphyrins including heme and uroporphyrinogen III biosynthetic processes⁹⁵. Iron in mammals is incorporated into heme; an essential component of the hemoglobin, which can be acquired by bacterial pathogens as a nutritional iron source. Several *Streptococci* species that are pathogenic to humans and animals, namely *S. pyogenes*, *S. pneumoniae* and *S. suis*, contain cell wall heme-binding proteins that allow them to scavenge heme from host's hemoglobin as a source of iron acquisition^{96,97}. Additionally, the group B *Streptococci* are able to respire in the presence of heme, enhancing resistance to oxidative stress and improving their survival⁹⁸. Our results suggest that the *UROS* gene may modulate the presence of *Streptococcus* spp. making these animals more susceptible to *Streptococci* colonization. A total of three candidate genes were identified in the SSC15 region (25.15–27.87 Mb): *ERCC3* (ERCC excision repair 3, TFIIH core complex helicase subunit), *BIN1* (bridging integrator 1), and *MAP3K2* (mitogen-activated protein kinase kinase kinase 2). The *ERCC3* gene expression was downregulated in human gastric cells after the infection with *Helicobacter pylori*⁹⁹. In the same direction as the aforementioned *GALNT15* gene, the *BIN1* gene might modulate the abundance of mucin dweller bacteria like *Streptococcus* spp. because of the attenuation of *BIN1* favours the intestinal barrier function¹⁰⁰. The protein encoded by the last candidate gene of this SSC15 region, *MAP3K2*, activates the toll like receptor 9 (TLR9) that recognizes CpG oligodeoxynucleotide motif in bacteria¹⁰¹. Finally, the last significant region (45.25 Mb) in SSC18 contained one microRNA, *ssc-mir-196b-1*, that was found upregulated in the duodenum of piglets that were resistant to *Escherichia coli* infection¹⁰².

Conclusion

This report identifies associations between the pig genome and the relative abundance of six genera (*Akkermansia*, *CF231*, *Phascolarctobacterium*, *Prevotella*, *SMB53* and *Streptococcus*). Most of the candidate genes found in the 17 associated regions of the pig genome encode for proteins that are involved in the host defence system, including the immune system, physical barriers such as the mucin layer or cell junctions, whereas other proteins participate in the metabolism of mucopolysaccharides or bile acids. Our results confirm the importance of host genomics in the modulation of the microbiota composition. However, the associations found in this study could be specific of our population, as the associated polymorphisms found may not be segregating in other populations and the gut microbiota is affected by different factors such as breed, age and diet. Therefore, further studies are warranted in different populations to determine which genetic combinations favour the enrichment of beneficial bacteria, providing the individual with the best intestinal health to avoid the entrance of potential pathogens.

Data Availability

The raw sequencing data generated by this study were deposited in the NCBI Sequence Read Archive (SRA) under BioProject accession number PRJNA540380.

References

- Nicholson, J. K. *et al.* Host-gut microbiota metabolic interactions. *Science* **336**, 1262–7 (2012).
- Caballero, S. & Pamer, E. G. Microbiota-mediated inflammation and antimicrobial defense in the intestine. *Annu. Rev. Immunol.* **33**, 227–56 (2015).
- Lederberg, J. & McCray, A. 'Ome Sweet' Omics—a genealogical treasury of words. *Scientist* **15**, 8 (2001).
- Kamada, N., Seo, S.-U., Chen, G. Y. & Núñez, G. Role of the gut microbiota in immunity and inflammatory disease. *Nat. Rev. Immunol.* **13**, 321–335 (2013).

5. Costello, E. K., Stagaman, K., Dethlefsen, L., Bohannan, B. J. M. & Relman, D. A. The application of ecological theory toward an understanding of the human microbiome. *Science* **336**, 1255–62 (2012).
6. Johansson, M. E. V. *et al.* Composition and functional role of the mucus layers in the intestine. *Cell. Mol. Life Sci.* **68**, 3635–41 (2011).
7. Johansson, M. E. V., Larsson, J. M. H. & Hansson, G. C. The two mucus layers of colon are organized by the MUC2 mucin, whereas the outer layer is a legislator of host-microbial interactions. *Proc. Natl. Acad. Sci. USA* **108**(Suppl), 4659–65 (2011).
8. Hooper, L. V., Stappenbeck, T. S., Hong, C. V. & Gordon, J. I. Angiogenins: a new class of microbicidal proteins involved in innate immunity. *Nat. Immunol.* **4**, 269–73 (2003).
9. Chu, H. & Mazmanian, S. K. Innate immune recognition of the microbiota promotes host-microbial symbiosis. *Nat. Immunol.* **14**, 668–675 (2013).
10. Human Microbiome Project Consortium. Structure, function and diversity of the healthy human microbiome. *Nature* **486**, 207–14 (2012).
11. Xiao, L. *et al.* A reference gene catalogue of the pig gut microbiome. *Nat. Microbiol.* **1**, 16161 (2016).
12. Wang, M. & Donovan, S. M. Human microbiota-associated swine: current progress and future opportunities. *ILAR J.* **56**, 63–73 (2015).
13. Estellé, J. *et al.* The influence of host's genetics on the gut microbiota composition in pigs and its links with immunity traits. in *10th World Congress of Genetics Applied to Livestock Production, Vancouver, BC, Canada* Available at: https://www.asas.org/docs/default-source/wcgalp-proceedings-oral/358_paper_9784_manuscript_952_0.pdf (2014).
14. Camarinha-Silva, A. *et al.* Host Genome Influence on Gut Microbial Composition and Microbial Prediction of Complex Traits in Pigs. *Genetics* **206**, 1637–1644 (2017).
15. Turpin, W. *et al.* Association of host genome with intestinal microbial composition in a large healthy cohort. *Nat. Genet.* **48**, 1413–1417 (2016).
16. Goodrich, J. K., Davenport, E. R., Clark, A. G. & Ley, R. E. The Relationship Between the Human Genome and Microbiome Comes into View. *Annu. Rev. Genet.* **51**, 413–433 (2017).
17. Blekhnman, R. *et al.* Host genetic variation impacts microbiome composition across human body sites. *Genome Biol.* **16**, 191 (2015).
18. Goodrich, J. K., Davenport, E. R., Waters, J. L., Clark, A. G. & Ley, R. E. Cross-species comparisons of host genetic associations with the microbiome. *Science* **352**, 532–5 (2016).
19. Spor, A., Koren, O. & Ley, R. Unravelling the effects of the environment and host genotype on the gut microbiome. *Nat. Rev. Microbiol.* **9**, 279–90 (2011).
20. Estellé, J. *et al.* Host genetics influences gut microbiota composition in pigs. in *36th International Society for Animal Genetics Conference, Dublin, Ireland*, Available at: https://www.isag.us/2017/docs/ISAG2017_Proceedings.pdf (2017).
21. Caporaso, J. G. *et al.* QIIME allows analysis of high-throughput community sequencing data. *Nat. Methods* **7**, 335–6 (2010).
22. Rideout, J. R. *et al.* Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. *PeerJ* **2**, e545 (2014).
23. Bokulich, N. A. *et al.* Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. *Nat. Methods* **10**, 57–9 (2013).
24. Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. Basic local alignment search tool. *J. Mol. Biol.* **215**, 403–10 (1990).
25. DeSantis, T. Z. *et al.* Greengenes, a Chimera-Checked 16S rRNA Gene Database and Workbench Compatible with ARB. *Appl. Environ. Microbiol.* **72**, 5069–5072 (2006).
26. McMurdie, P. J. & Holmes, S. Phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. *PLoS One* **8**, e61217 (2013).
27. Oksanen, J. *et al.* Vegan: Community Ecology Package. (2016).
28. Wickham, H. *ggplot2: Elegant Graphics for Data Analysis*. (Springer-Verlag New York, 2009).
29. Bray, J. R. & Curtis, J. T. An Ordination of the Upland Forest Communities of Southern Wisconsin. *Ecol. Monogr.* **27**, 325–349 (1957).
30. Sambrook, J., Fritsch, E. F. & Maniatis, T. Molecular cloning: a laboratory manual. In E3–E4 (Cold Spring Harbor Laboratory Press, 1989).
31. Purcell, S. *et al.* PLINK: a tool set for whole-genome association and population-based linkage analyses. *Am. J. Hum. Genet.* **81**, 559–75 (2007).
32. Zhou, X. & Stephens, M. Genome-wide efficient mixed-model analysis for association studies. *Nat. Genet.* **44**, 821–4 (2012).
33. Benjamini, Y. & Hochberg, Y. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple. *Testing. J. R. Stat. Soc. Ser. B* **57**, 289–300 (1995).
34. Kinsella, R. J. *et al.* Ensembl BioMart: a hub for data retrieval across taxonomic space. *Database (Oxford)*. **2011**, bar030 (2011).
35. McLaren, W. *et al.* Deriving the consequences of genomic variants with the Ensembl API and SNP Effect Predictor. *Bioinformatics* **26**, 2069–2070 (2010).
36. Ramayo-Caldas, Y. *et al.* Phylogenetic network analysis applied to pig gut microbiota identifies an ecosystem structure linked with growth traits. *ISME J.* **10**, 2973–2977 (2016).
37. Holman, D. B., Brunelle, B. W., Trachsel, J. & Allen, H. K. Meta-analysis To Define a Core Microbiota in the Swine Gut. *mSystems* **2**, e00004–17 (2017).
38. Zhao, W. *et al.* The dynamic distribution of porcine microbiota across different ages and gastrointestinal tract segments. *PLoS One* **10**, e0117441 (2015).
39. Molinero, L. L., Cubre, A., Mora-Solano, C., Wang, Y. & Alegre, M.-L. T cell receptor/CARMA1/NF- κ B signaling controls T-helper (Th) 17 differentiation. *Proc. Natl. Acad. Sci. USA* **109**, 18529–34 (2012).
40. Hiraoka, N. *et al.* Molecular cloning and expression of two distinct human chondroitin 4-O-sulfotransferases that belong to the HNK-1 sulfotransferase gene family. *J. Biol. Chem.* **275**, 20188–96 (2000).
41. Ouwerkerk, J. P., de Vos, W. M. & Belzer, C. Glycobiome: bacteria and mucus at the epithelial interface. *Best Pract. Res. Clin. Gastroenterol.* **27**, 25–38 (2013).
42. Ottman, N., Geerlings, S. Y., Aalvink, S., de Vos, W. M. & Belzer, C. Action and function of Akkermansia muciniphila in microbiome ecology, health and disease. *Best Pract. Res. Clin. Gastroenterol.* **31**, 637–642 (2017).
43. Everard, A. *et al.* Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity. *Proc. Natl. Acad. Sci. USA* **110**, 9066–71 (2013).
44. Leber, A. *et al.* Bistability analyses of CD4+ T follicular helper and regulatory cells during Helicobacter pylori infection. *J. Theor. Biol.* **398**, 74–84 (2016).
45. Zhernakova, A. *et al.* Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science* **352**, 565–9 (2016).
46. Briolat, J. *et al.* New antimicrobial activity for the catecholamine release-inhibitory peptide from chromogranin A. *C. Cell. Mol. Life Sci.* **62**, 377–385 (2005).
47. Dall, E. & Brandstetter, H. Structure and function of legumain in health and disease. *Biochimie* **122**, 126–50 (2016).
48. Gururajan, M. *et al.* MicroRNA 125b inhibition of B cell differentiation in germinal centers. *Int. Immunol.* **22**, 583–92 (2010).
49. Negi, V. *et al.* Altered expression and editing of miRNA-100 regulates iTreg differentiation. *Nucleic Acids Res.* **43**, 8057–65 (2015).

50. Schmidt, V., Subkhangulova, A. & Willnow, T. E. Sorting receptor SORLA: cellular mechanisms and implications for disease. *Cell. Mol. Life Sci.* **74**, 1475–1483 (2017).
51. Terai, K. *et al.* Levels of soluble LR11/SorLA are highly increased in the bile of patients with biliary tract and pancreatic cancers. *Clin. Chim. Acta.* **457**, 130–6 (2016).
52. Hojyo, S. *et al.* Zinc transporter SLC39A10/ZIP10 controls humoral immunity by modulating B-cell receptor signal strength. *Proc. Natl. Acad. Sci. USA* **111**, 11786–91 (2014).
53. Derrien, M. *et al.* Modulation of Mucosal Immune Response, Tolerance, and Proliferation in Mice Colonized by the Mucin-Degrader *Akkermansia muciniphila*. *Front. Microbiol.* **2**, 166 (2011).
54. Yabas, M. *et al.* ATP11C is critical for the internalization of phosphatidylserine and differentiation of B lymphocytes. *Nat. Immunol.* **12**, 441–9 (2011).
55. Siggs, O. M., Schnabl, B., Webb, B. & Beutler, B. X-linked cholestasis in mouse due to mutations of the P4-ATPase ATP11C. *Proc. Natl. Acad. Sci. USA* **108**, 7890–5 (2011).
56. Islam, K. B. M. S. *et al.* Bile acid is a host factor that regulates the composition of the cecal microbiota in rats. *Gastroenterology* **141**, 1773–81 (2011).
57. Khan, T. J. *et al.* Effect of atorvastatin on the gut microbiota of high fat diet-induced hypercholesterolemic rats. *Sci. Rep.* **8**, 662 (2018).
58. Song, X. *et al.* Growth Factor FGF2 Cooperates with Interleukin-17 to Repair Intestinal Epithelial Damage. *Immunity* **43**, 488–501 (2015).
59. Wu, F. *et al.* *Phascolarctobacterium faecium* abundant colonization in human gastrointestinal tract. *Exp. Ther. Med.* **14**, 3122–3126 (2017).
60. Zhang, Q. *et al.* Inulin-type fructan improves diabetic phenotype and gut microbiota profiles in rats. *PeerJ* **6**, e4446 (2018).
61. Shin, D., Howng, S. Y. B., Ptáček, L. J. & Fu, Y.-H. miR-32 and its target SLC45A3 regulate the lipid metabolism of oligodendrocytes and myelin. *Neuroscience* **213**, 29–37 (2012).
62. Wang, Y. *et al.* Lysosome-associated small Rab GTPase Rab7b negatively regulates TLR4 signaling in macrophages by promoting lysosomal degradation of TLR4. *Blood* **110**, 962–71 (2007).
63. Spanò, S., Liu, X. & Galán, J. E. Proteolytic targeting of Rab29 by an effector protein distinguishes the intracellular compartments of human-adapted and broad-host *Salmonella*. *Proc. Natl. Acad. Sci. USA* **108**, 18418–23 (2011).
64. Qiu, B. *et al.* NUCKS is a positive transcriptional regulator of insulin signaling. *Cell Rep.* **7**, 1876–86 (2014).
65. Zhang, J. *et al.* I κ B Kinase ϵ Is an NFATc1 Kinase that Inhibits T Cell Immune Response. *Cell Rep.* **16**, 405–418 (2016).
66. Ehrling, C. *et al.* MAPKAP kinase 2 regulates IL-10 expression and prevents formation of intrahepatic myeloid cell aggregates during cytomegalovirus infections. *J. Hepatol.* **64**, 380–389 (2016).
67. De Filippo, C. *et al.* Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa. *Proc. Natl. Acad. Sci. USA* **107**, 14691–6 (2010).
68. Wang, X. *et al.* Cytokine-like 1 Chemoattracts Monocytes/Macrophages via CCR2. *J. Immunol.* **196**, 4090–9 (2016).
69. Bonnycastle, L. L. *et al.* Autosomal dominant diabetes arising from a Wolfram syndrome 1 mutation. *Diabetes* **62**, 3943–50 (2013).
70. Ussar, S. *et al.* Regulation of Glucose Uptake and Enteroendocrine Function by the Intestinal Epithelial Insulin Receptor. *Diabetes* **66**, 886–896 (2017).
71. Murri, M. *et al.* Gut microbiota in children with type 1 diabetes differs from that in healthy children: a case-control study. *BMC Med.* **11**, 46 (2013).
72. Venkatesan, M., Kuntz, D. A. & Rose, D. R. Human lysosomal alpha-mannosidases exhibit different inhibition and metal binding properties. *Protein Sci.* **18**, 2242–51 (2009).
73. Koropatkin, N. M., Cameron, E. A. & Martens, E. C. How glycan metabolism shapes the human gut microbiota. *Nat. Rev. Microbiol.* **10**, 323–35 (2012).
74. Pajarillo, E. A. B., Chae, J. P., Kim, H. B., Kim, I. H. & Kang, D.-K. Barcoded pyrosequencing-based metagenomic analysis of the faecal microbiome of three purebred pig lines after cohabitation. *Appl. Microbiol. Biotechnol.* **99**, 5647–56 (2015).
75. Guo, Y., Zhu, N., Zhu, S. & Deng, C. Molecular phylogenetic diversity of bacteria and its spatial distribution in composts. *J. Appl. Microbiol.* **103**, 1344–54 (2007).
76. Kumar, V. & Ali, A. Targeting calpains: A novel immunomodulatory approach for microbial infections. *Eur. J. Pharmacol.* **814**, 28–44 (2017).
77. Autheman, D. *et al.* *Clostridium perfringens* beta-toxin induces necrostatin-inhibitable, calpain-dependent necrosis in primary porcine endothelial cells. *PLoS One* **8**, e64644 (2013).
78. Holmquist, E., Okroj, M., Nodin, B., Jirström, K. & Blom, A. M. Sushi domain-containing protein 4 (SUSD4) inhibits complement by disrupting the formation of the classical C3 convertase. *FASEB J.* **27**, 2355–66 (2013).
79. Yang, C.-W. *et al.* Regulation of T Cell Receptor Signaling by DENND1B in TH2 Cells and Allergic Disease. *Cell* **164**, 141–155 (2016).
80. Hermiston, M. L., Xu, Z. & Weiss, A. CD45: a critical regulator of signaling thresholds in immune cells. *Annu. Rev. Immunol.* **21**, 107–37 (2003).
81. Heno-Mejia, J. *et al.* The microRNA miR-181 is a critical cellular metabolic rheostat essential for NKT cell ontogenesis and lymphocyte development and homeostasis. *Immunity* **38**, 984–97 (2013).
82. Li, T. & Chiang, J. Y. L. Bile acids as metabolic regulators. *Curr. Opin. Gastroenterol.* **31**, 159–65 (2015).
83. Wüst, P. K., Horn, M. A. & Drake, H. L. Clostridiaceae and Enterobacteriaceae as active fermenters in earthworm gut content. *ISME J.* **5**, 92–106 (2011).
84. Horie, M. *et al.* Comparative analysis of the intestinal flora in type 2 diabetes and nondiabetic mice. *Exp. Anim.* **66**, 405–416 (2017).
85. Kozu, Y. *et al.* Protocadherin-1 is a glucocorticoid-responsive critical regulator of airway epithelial barrier function. *BMC Pulm. Med.* **15**, 1–12 (2015).
86. Xu, H., Sobue, T., Bertolini, M., Thompson, A. & Dongari-Bagtzoglou, A. *Streptococcus oralis* and *Candida albicans* Synergistically Activate μ -Calpain to Degrade E-cadherin From Oral Epithelial Junctions. *J. Infect. Dis.* **214**, 925–34 (2016).
87. Takenaka, K. *et al.* Role of phospholipase C-L2, a novel phospholipase C-like protein that lacks lipase activity, in B-cell receptor signaling. *Mol. Cell. Biol.* **23**, 7329–38 (2003).
88. Clausen, H. & Bennett, E. P. A family of UDP-GalNAc: polypeptide N-acetylgalactosaminyl-transferases control the initiation of mucin-type O-linked glycosylation. *Glycobiology* **6**, 635–46 (1996).
89. Homer, K. A., Patel, R. & Beighton, D. Effects of N-acetylglucosamine on carbohydrate fermentation by *Streptococcus mutans* NCTC 10449 and *Streptococcus sobrinus* SL-1. *Infect. Immun.* **61**, 295–302 (1993).
90. Saeki, K., Miura, Y., Aki, D., Kurosaki, T. & Yoshimura, A. The B cell-specific major raft protein, Raftlin, is necessary for the integrity of lipid raft and BCR signal transduction. *EMBO J.* **22**, 3015–26 (2003).
91. Alonso, M. A. & Millán, J. The role of lipid rafts in signalling and membrane trafficking in T lymphocytes. *J. Cell Sci.* **114**, 3957–65 (2001).
92. Triantafilou, M., Miyake, K., Golenbock, D. T. & Triantafilou, K. Mediators of innate immune recognition of bacteria concentrate in lipid rafts and facilitate lipopolysaccharide-induced cell activation. *J. Cell Sci.* **115**, 2603–11 (2002).
93. Toledo, A. & Benach, J. L. Hijacking and Use of Host Lipids by Intracellular Pathogens. *Microbiol. Spectr.* **3**, 637–666 (2015).

94. Huang, X. *et al.* Genome-wide association studies identify susceptibility loci affecting respiratory disease in Chinese Erhualian pigs under natural conditions. *Anim. Genet.* **48**, 30–37 (2017).
95. Tsai, S. F., Bishop, D. F. & Desnick, R. J. Human uroporphyrinogen III synthase: molecular cloning, nucleotide sequence, and expression of a full-length cDNA. *Proc. Natl. Acad. Sci. USA* **85**, 7049–53 (1988).
96. Eichenbaum, Z., Muller, E., Morse, S. A. & Scott, J. R. Acquisition of iron from host proteins by the group A streptococcus. *Infect. Immun.* **64**, 5428–9 (1996).
97. Wan, Y., Zhang, S., Li, L., Chen, H. & Zhou, R. Characterization of a novel streptococcal heme-binding protein SntA and its interaction with host antioxidant protein AOP2. *Microb. Pathog.* **111**, 145–155 (2017).
98. Franza, T. *et al.* A partial metabolic pathway enables group b streptococcus to overcome quinone deficiency in a host bacterial community. *Mol. Microbiol.* **102**, 81–91 (2016).
99. Chiou, C. C. *et al.* Helicobacter pylori infection induced alteration of gene expression in human gastric cells. *Gut* **48**, 598–604 (2001).
100. Chang, M. Y. *et al.* Bin1 attenuation suppresses experimental colitis by enforcing intestinal barrier function. *Dig. Dis. Sci.* **57**, 1813–21 (2012).
101. Wen, M. *et al.* Stk38 protein kinase preferentially inhibits TLR9-activated inflammatory responses by promoting MEKK2 ubiquitination in macrophages. *Nat. Commun.* **6**, 7167 (2015).
102. Wu, Z. *et al.* Identification of microRNAs regulating Escherichia coli F18 infection in Meishan weaned piglets. *Biol. Direct* **11**, 59 (2016).

Acknowledgements

This work was funded by the *Fondo Europeo de Desarrollo Regional (FEDER)* and the Spanish *Ministerio de Economía y Competitividad (MINECO AGL2014-56369-C2 and AGL2017-82641-R)*. D. Crespo-Piazuelo was funded by a “*Formació i Contractació de Personal Investigador Novell*” (FI-DGR) Ph.D grant from the *Generalitat de Catalunya (ECO/1788/2014)* and by the *PiGutNet COST Action (www.pigutnet.eu)* for a Short Term Scientific Mission at the GABI laboratory (INRA, France) under the supervision of J. Estellé. Contract of L. Migura-Garcia was supported by INIA and the European Social Fund. L. Criado-Mesas was funded with a FPI grant from the AGL2014-56369-C2 project. M. Revilla was also funded by a FI-DGR (ECO/1639/2013). M. Ballester was financially supported by a “*Ramón y Cajal*” contract (RYC-2013-12573) from the Spanish Ministry of Economy and Competitiveness. We acknowledge the support of the Spanish Ministry of Economy and Competitiveness for the “*Severo Ochoa Programme for Centres of Excellence in R&D*” 2016–2019 (SEV-2015-0533) grant awarded to the Centre for Research in Agricultural Genomics and the CERCA Programme/*Generalitat de Catalunya*. The authors would like to thank the Mazafrá S. L. slaughterhouse for providing access to the data and material used in this study and, specially, to Francisco Minero for the skilful veterinary assistance. We also acknowledge the contribution of Rita Benítez in the collection of samples and microbial DNA extractions.

Author Contributions

J.M.F. and A.I.F. conceived and designed the experiments; J.M.F. was the principal investigator of the project; this work is part of the PhD thesis of D.C.P. co-supervised by M.B. and J.M.F.; J.M.G.C. provided animal samples; D.C.P., M.R., M.M., J.M.G.C. and A.I.F. collected samples; D.C.P. and M.B. tested the DNA extraction protocol; D.C.P. and M.M. performed the microbial DNA extraction; L.C.M. performed the pig genomic DNA extraction; AC genotyped the samples; D.C.P. and J.E. analysed the data; D.C.P., L.M.G., M.B. and J.M.F. wrote the paper. All authors read and approved the final manuscript.

Additional Information

Supplementary information accompanies this paper at <https://doi.org/10.1038/s41598-019-45066-6>.

Competing Interests: The authors declare no competing interests.

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