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ABSTRACTS

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P302 Response to selection on fecal microbiota composition in Large White piglets. C. Larzul^{*1}, M. Borey², Y. Billon³, M.-N. Rossignol², G. Lemonnier², J. Estelle², and C. Rogel-Gaillard², ¹Université de Toulouse, INRAE, ENVT, GenPhySE, Castanet-Tolosan, France, ²Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France, ³INRAE, GenESI, Surgères, France.

Pig gut microbiota displays high interindividual variability and it remains an open question to determine to what extent its taxonomic composition relies on host genetic determinism and not only on environmental conditions. We carried out a study to demonstrate coevolution of the host and its gut microbiota established 1 mo post-weaning, by directional selection over 2 generations. The gut microbiota was characterized by sequencing the V3-V4 variable region of the 16S rRNA gene from fecal samples collected on 60-d-old Large White piglets. Amplicon sequence variants were inferred from amplicon data and the microbial community was further studied at the genus level. Based on the stratification of the initial population (generation G0) according to the 2 major pig enterotypes, characterized by relative overabundance of either *Prevotella* and *Mitsuokella* or *Ruminococcus* and *Treponema*, we used the relative abundance of these 4 genera as selection criteria. From the G0 population of 317 piglets, we selected 6 males and 30 females per line and produced 2 successive generations (G1 and G2) of approximately 130 pigs per line. We consistently confirmed a moderate heritability for each of the selected genera ($h^2 = 0.3$ to 0.4). We also estimated the heritability values of the relative abundances for 64 additional bacterial genera, which ranged from 0.1 to 0.5. We showed significant differences between the 2 lines in the relative abundance of the 4 bacterial genera at G1 ($P < 0.001$, from 0.6 genetic standard deviation for *Treponema* to 1.3 for *Prevotella*). In the following generation G2, response to selection was maintained for *Prevotella* and was even increased for the 3 other genera. The observed contrasts were in the expected direction for the genera under direct selection, and we extended the analysis to the 64 other bacterial genera with estimated heritabilities higher than 0.1. All these results confirm a significant influence of host genetics on the composition of gut microbiota at 60 d of age in pigs, and a capacity of directional selection over generations that will be further explored together with early and late host traits.

Key Words: pig, microbiomics, heritability, genetic improvement

P303 The impact of host genetics, independently of environmental factors, on porcine gut microbiota composition. A. Heras-Molina^{*1}, J. Estellé², A. López-García¹, J. L. Pensantez-Pacheco^{1,3}, S. Astiz¹, C. Garcia-Contreras¹, M. Vazquez-Gomez^{4,5}, B. Isabel⁴, A. Gonzalez-Bulnes⁶, and C. Ovilo¹, ¹INIA (CSIC), Madrid, Spain, ²Université Paris-Saclay, INRAE, AgroParisTech, GABI, Jouy-en-Josas, France, ³School of Veterinary Medicine and Zootechnics, Faculty of Agricultural Sciences, University of Cuenca, Cuenca, Ecuador, ⁴Faculty of Veterinary Medicine, UCM, Madrid, Spain, ⁵Nutrition and Obesity: Systemic Approaches Research Unit (NutriOmics), INSERM, Sorbonne Université, Paris, France, ⁶Departamento de Producción y Sanidad Animal, Facultad de Veterinaria, Universidad Cardenal Herrera-CEU, Valencia, Spain.

Pig microbiota is associated with the host's breed, with lean and fatty breeds showing relevant differences in their productive parameters. However, in previous studies aiming to investigate the microbiota differences between both breed groups, involved animals were gestated in their corresponding lean or fatty mother, leading to maternal influences. The present study aimed to elucidate the importance of host's genotype on the gut microbiome composition without maternal confounding factors. Sixteen Iberian (IB; fatty breed) sows were inseminated with heterospermic semen (from Iberian and Large White [LW; lean breed] boars). Offspring was sampled at 60 d old ($n = 36$; 22 IB×IB and 14 IB×LW) and at 210 d old ($n = 31$; 18 IB×IB and 13 IB×LW) to obtain fecal microbiota composition which was analyzed by sequencing the 16SrRNA gene (V3-V4 amplicon) in an Illumina MiSeq. Bioinformatic analyses were done with QIIME2, and biostatistics analysis were performed using

phyloseq and metagenomeSeq R packages. Firmicutes and Bacteroidetes were majority at the phylum level, while *Prevotella* and *Treponema* were the most abundant genera. Observed α diversity was only affected by age ($P < 0.0001$; higher at 210 d). For β diversity there was a genotype \times age interaction ($P < 0.01$) and at 210 d, IB×IB animals showed higher β diversity than IB×LW ($P < 0.05$). The differential abundance analysis showed 156 significant ($q < 0.05$) over-abundant amplicon sequence variants (ASVs) in IB×IB animals and 71 in IB×LW. At the genus level, *Anaerovibrio* and *Lachnospiraceae* were more abundant in IB×LW. At 60 d, most over-abundant ASVs observed in IB×IB animals belong to *Ruminococcus* genus, and at 210 d, IB×LW had the most over-abundant ASVs belonging to *Prevotella*. At the genus level, *Agathobacter*, *Parasutterella* and *Lachnospiraceae* were more abundant at 60 d old and *Ruminococcus* at 210 d old, all in IB×IB. These different abundant bacteria are involved in adipogenesis, feed efficiency, digestibility and inflammation, and could be related to breeds' phenotypic differences. Thus, the host genotype affected pig's gut microbiota composition, in a model that exclude maternal confounding factors.

Key Words: pigs and related species, metagenomics, breed diversity, pregnancy, meat production

P304 Assessment of the fecal microbiota from sow to piglet and the impact of different ratios of dietary polyunsaturated fatty acids. M. Cau^{*1,2}, A. Agazzi³, T. X. Nguyen³, M. McLaughlin², and A. S. Bonastre¹, ¹Departament de Ciència Animal i dels Aliments, Facultat de Veterinària, Universitat Autònoma de Barcelona (UAB), Bellaterra, Barcelona, Spain, ²College of Medical, Veterinary and Life Sciences, School of Veterinary Medicine, University of Glasgow, Glasgow, UK, ³Department of Health, Animal Science and Food Safety "Carlo Cantoni" (VESPA), Università degli Studi di Milano, Lodi, Italy.

The microbiome can influence animal production and changes in the intestinal microbial status can lead to a deterioration or improvement of the animal's health status and therefore its quality as a food product. These changes can occur due to various factors including stress, antibiotics and diet. In the current study, we hypothesized that: 1) alteration in the fatty acid composition of the diet influence the gut microbiota of the sows, modify their milk and/or gut microbiota composition; 2) the milk from the sows influence the microbiota profile of the piglets; 3) the fatty acid composition and seaweed derived supplements of the solid diet, post weaning, can influence the microbiota of piglets over a longitudinal period (0–21 d). Microbial 16S DNA from 270 fecal samples from sows and their piglets were extracted and sequenced using the MiSeq system (Illumina) and analyzed with QIIME2. Sows were fed with a diet containing poly unsaturated omega fatty acid (PUFAs) at a ratio of $\omega 6:\omega 3 = 4$ (low ratio diet, LR) and one group fed with a ratio $\omega 6:\omega 3 = 13$ (control ratio diet, CR). At post weaning, piglets were subdivided and one group received additional dietary supplement derived from seaweed (*A. nodosum*), which can promote animal health and development. Statistically significant differences (q -value < 0.05) were found in the evenness of the microbiome profile in the LR-fed sows at time points 0 and 14, and 0 and 21; a longitudinal change was not detected in CR-fed sows. With regard to piglets, there was no statistical evidence comparing piglets from LR and CR sows at time point 0 (after one week of lactation); this may suggest that the milk feeding did not influence the offspring's microbiota. A statistical difference is observed in piglets that received seaweed supplementation (SW) from sows of both diets during time point 7. We are currently examining the fecal metabolome of the cohorts of sows and piglets that demonstrate altered microbiome to gain further insight into the impact of diet on the mother and offspring gut composition and physiology. The results from this study form part of the European Joint Doctorate in Molecular Animal Nutrition (MANNA).

Key Words: microbiota, microbiome, pig, 16S, bioinformatics