

Impact of early life feeding management on fattening calves ruminal metagenomeS. Costa¹, G. De La Fuente¹, M. Blanco², J. Balcells¹, I. Casasús² and D. Villalba¹¹University of Lleida, Av. Alcalde Rovira Roure, 191, 25198, Lleida, Spain, ²CITA, Av. Montañana, 930, 50059, Zaragoza, Spain; scosta@ca.udl.cat

The aim of this work (GENTORE H2020) was to study the impact of feeding management in early life on fattening calves ruminal metagenome. Eight *Parla de Montaña* male calves were raised with their dams from birth to weaning (156 days [d] of age); they were fed on their dams' milk and had free access to hay and straw (DAM). Ten Holstein male calves were separated from their dam at birth and they received milk replacer and a starter concentrate until weaning (56 d of age) (REP). From weaning, they were fed cereal-based concentrate and barley straw *ad libitum*. Ruminal fluid was obtained via oesophagus tube twice: in growing (GRO; 172 d of age, 241 kg body weight [BW]) and finishing periods (FIN; 295 d of age and 438 kg BW). Rumen bacterial and archaeal community composition was analysed by taxonomic profiling of 16S ribosomal RNA V3-V4 variable regions. Venn diagram, Shannon index values, multivariate analysis and Adonis test were obtained and analysis of variance of microbial abundance data (including treatment, period and their interaction as effects) was performed. Core bacterial/archaeal community (shared taxa by all individuals) was comprised of 87 OTUs (out of 459), which gathered the 92.0% of analysed sequences. Contrarily, specific OTUs of each treatment and period clustered few sequences (between 0.06-0.25%, within groups). Ruminal biodiversity, in terms of Shannon index values, was affected by treatment by period interaction ($P=0.003$) and it was higher in DAM animals in both GRO (2.45 in DAM vs 1.03 in REP) and FIN (2.32 in DAM vs 1.86 in REP), showing different microbial development in both groups. Multivariate analysis plot showed clear clustering of animals according to treatment and period, which was confirmed by the Adonis test ($P<0.001$). *Bacteroidetes*, *Firmicutes*, and *Actinobacteria* were the main phyla in both treatments. DAM animals had higher titers of *Selenomonas*, *Olsenella* and *Methanobrevibacter* genus, whereas REP ones had more abundant *Prevotella* and *Agathobacter* genus. The feeding management in early life clearly affected the calves' ruminal metagenome and this effect lasted over all their fattening period.

Effects of dietary capsicum supplementation on growth performance and gut microbiota of weaned pigsJ.H. Cho¹, R.B. Guevarra¹, J.H. Lee¹, S.H. Lee¹, H.R. Kim¹, J.H. Cho², M. Song³ and H.B. Kim¹¹Dankook University, Department of Animal Resources Science, Cheonan, 31116, Korea, South, ²Chungbuk National University, Department of Food and Animal Sciences, Cheongju, 28644, Korea, South, ³Chungnam National University, Department of Animal and Dairy Science, Daejeon, 34134, Korea, South; hbkim@dankook.ac.kr

Dietary capsicum has been scientifically recognized to improve the gut health of weanling pigs due to its anti-inflammatory functions, which may reduce the negative effects of pathogen infection. Nowadays, it is urgent to develop alternatives to antimicrobials in livestock to address the problem of antimicrobial resistance. However, there have been no reports to observe the composition of the gut bacterial communities in response to feeding dietary capsicum extracts in weanling pigs. Therefore, the current study was conducted to determine the effects of capsicum on growth performance and intestinal microbiota of weaned piglets using high-throughput next generation sequencing. A total of 12 Landrace-Yorkshire-Duroc (LYD) pigs at 4 weeks of age were randomly assigned to 2 dietary treatments (2 pigs/pen; 3 pens/treatment). The dietary treatments were: (1) control diet based on corn and soybean meal (CON); and (2) capsicum group (CAP) (CON + 300 ppm capsicum extract). Faecal samples were collected at 0 and 6 weeks after feed supplementation. Total DNA extracted from fresh faecal samples were used to amplify the 16S rRNA gene for Illumina MiSeq sequencing. Sequence quality filtering was performed using Mothur and analysis of the faecal microbiota was performed using the QIIME pipeline. Data for growth performance was analysed using the PROC GLM procedure of SAS. Capsicum extracts showed an increase in average daily gain (ADG) (14 to 29 g/day) and feed efficiency (0.591 vs 0.631 g/g) as compared with CON group throughout the experimental period. Taxonomic analysis revealed a higher relative abundance of *Prevotella* and *Methanobrevibacter* in capsicum fed piglets than in the CON group. Principal coordinate analysis (PCA) showed clear separation of the microbiota from the CAP group at week 6 as compared to CON. In conclusion, dietary capsicum extracts can improve the growth performance by shifting the gut microbial community composition of weaned piglets.

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Impact of early life feeding management on fattening calves ruminal microbiota

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Introduction

- Feeding management during early life is different between dairy and beef cattle.
- We aimed at studying the impact of feeding management during early life on ruminal microbiota, in fattening calves fed high concentrate diets.

Materials and methods

Animals and diets



	REP	DAM
Animals	10 Holstein male calves	8 Parda de Montaña male calves
Rearing system	Separated from their dams at birth	Raised with their dams
Weaning	56 days of age	156 days of age
Diet before weaning	Milk REPLACER and free access to concentrate and straw	DAM's milk and free access to hay and straw
Diet after weaning	Corn-based concentrate and barley straw	

Ruminal microbiota data

Ruminal fluid was sampled via oesophagus tube twice: in growing (GRO; 172 days of age, 241 kg body weight [BW]) and finishing periods (FIN; 295 days of age and 438 kg BW).



Bacterial and archaeal community composition was analysed by taxonomic profiling of 16S ribosomal RNA V3-V4 variable regions.

Results

- Bacteroidetes, Firmicutes and Actinobacteria** were the main phyla.
- Shannon index** values were higher in DAM animals in GRO (2.45 in DAM vs. 1.03 in REP, $P < 0.001$) but not in FIN (2.32 in DAM vs. 1.86 in REP, $P = 0.160$).

Results

They had a lot in common...

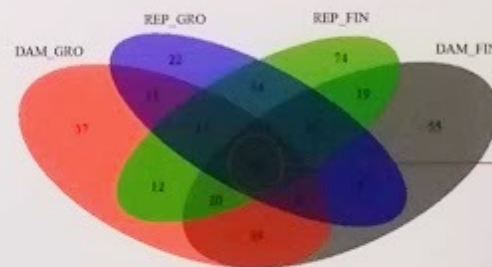


Fig. 1 Venn diagram showing the number of OTUs shared or unshared by treatments and periods, depending on overlaps.

Core microbial community gathered 92% of analysed sequences.

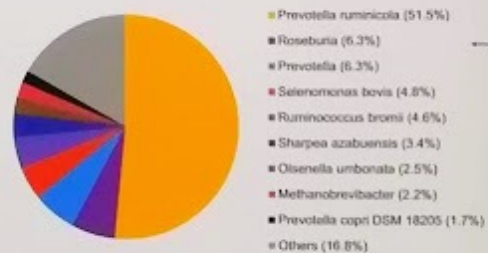


Fig. 2 Pie chart showing core bacterial and archaeal composition within the four groups.

... but they were still different!

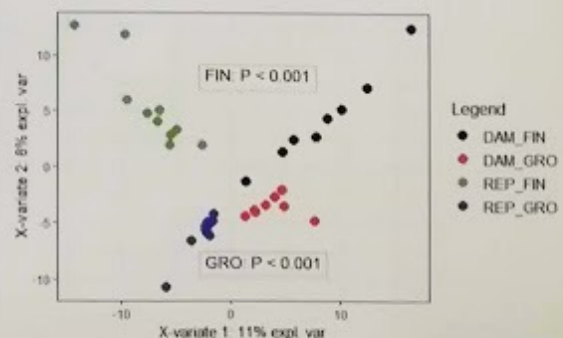


Fig. 3 PLS-DA on ruminal fluid microbiota. P-values corresponding to Adonis test results are also included.

Conclusions

Feeding management in early life clearly affected calves' ruminal microbiota and this effect lasted over all their fattening period.

