2. Experimental - Farm Trials, First Phase (Microbiota)

Treatments:
D1: Fortcell Feed® Piglets
D2: Fortcell Feed® Fattening
D3: Antibiotics
D4: Basal

Objetive

To evaluate the effect of the use of probiotic additives (D1/D2) compared to antibiotic additives (D3) and non additives (D4) on piglet productivity and its association with changes in the intestinal microbiota

Methodology

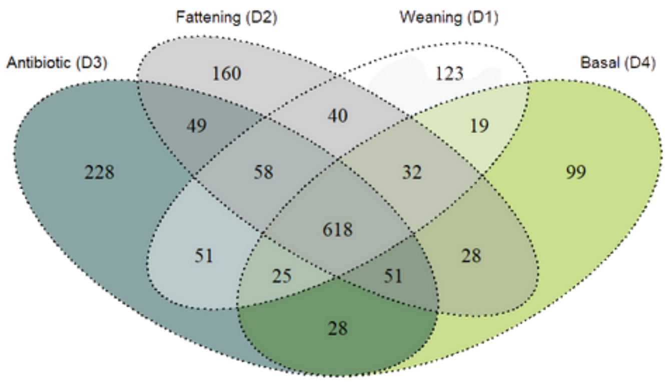
We performed 16s rRNA sequencing from fecal matter (Base Clear) to characterize the gut microbiota and explore associations with additives, age, and FCR (Feed Conversion Ratio). In total, 40 samples were collected and included 2 suckling piglets, 2 control samples and 36 samples of piglets divided among the four treatments and among the three growth phases.

Results

We found differences in alpha diversity with additives and differences in beta diversity with age and FCR.

Furthermore, the bacteria taxa used in the probiotic additives were detected in the microbiome analysis showing the efficiency of encapsulation.

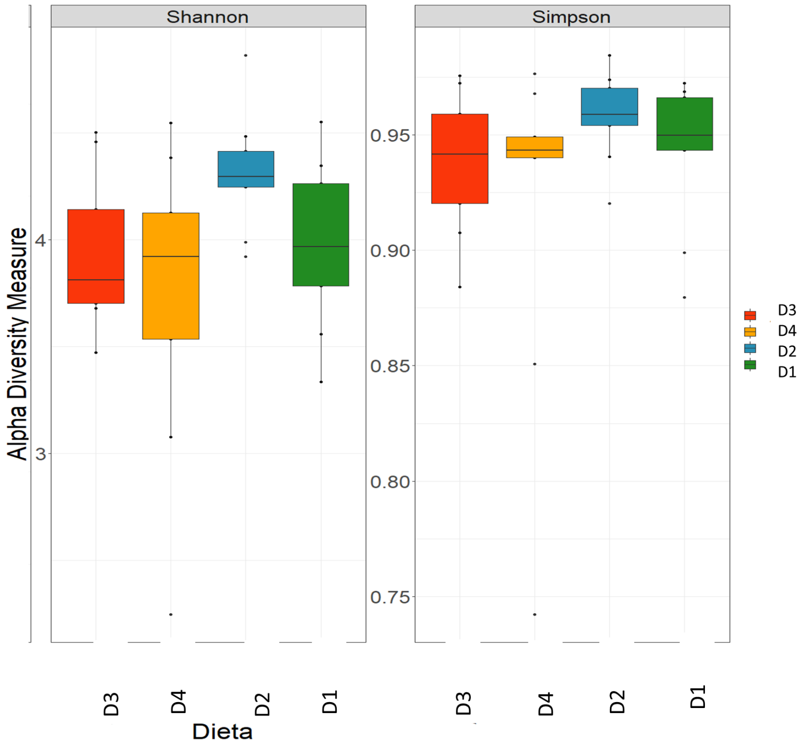
The following graph shows the number of species associated with the different additive treatments showing the variation in the microbiome and its association with the diet.



Distribution of bacteria at species level by diet

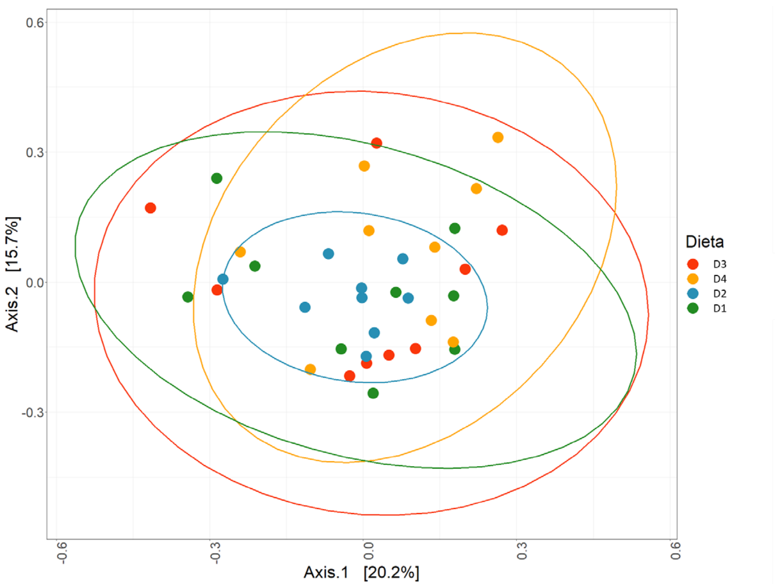
On the left, for the Shannon index, we can see that the treatments containing antibiotics had the lowest alpha diversity, followed by the control group. In contrast, diets containing encapsulated probiotics showed a higher alpha diversity.

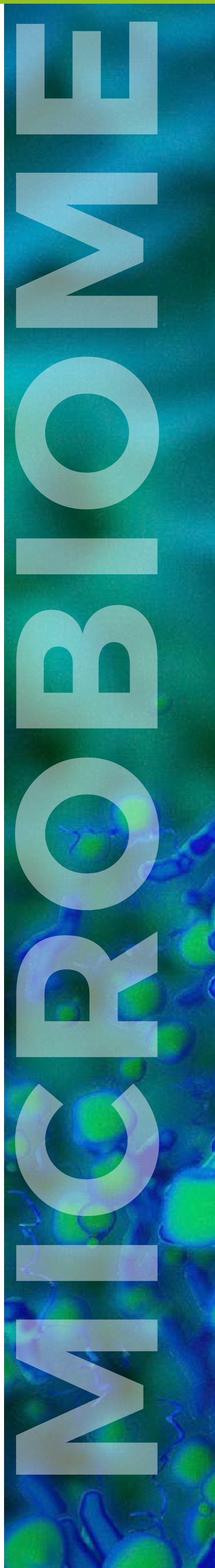
On the right, the Simpson index showed similar results to the Shannon index, with the treatments containing antibiotics having lower alpha diversity; and the treatments containing encapsulated probiotics presented a higher alpha diversity..

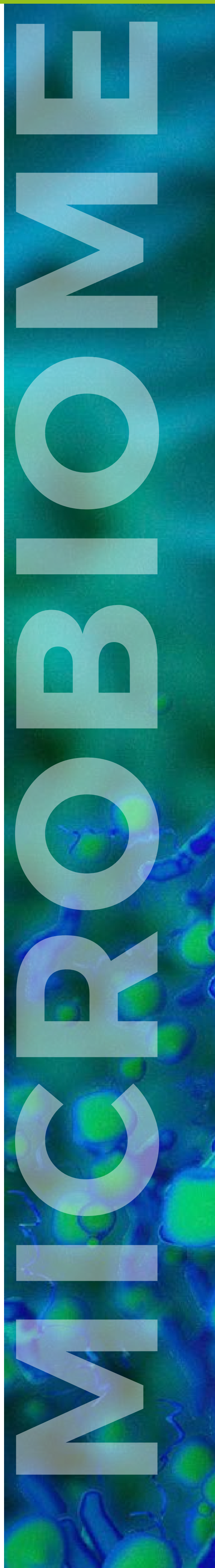


We performed Principal Component Analysis using the R software.

We compared the different treatments to check the differences in the microbiotas. As the figure shows, we found that there is small or no difference in the microbiotas regardless the supplementation in the diet.



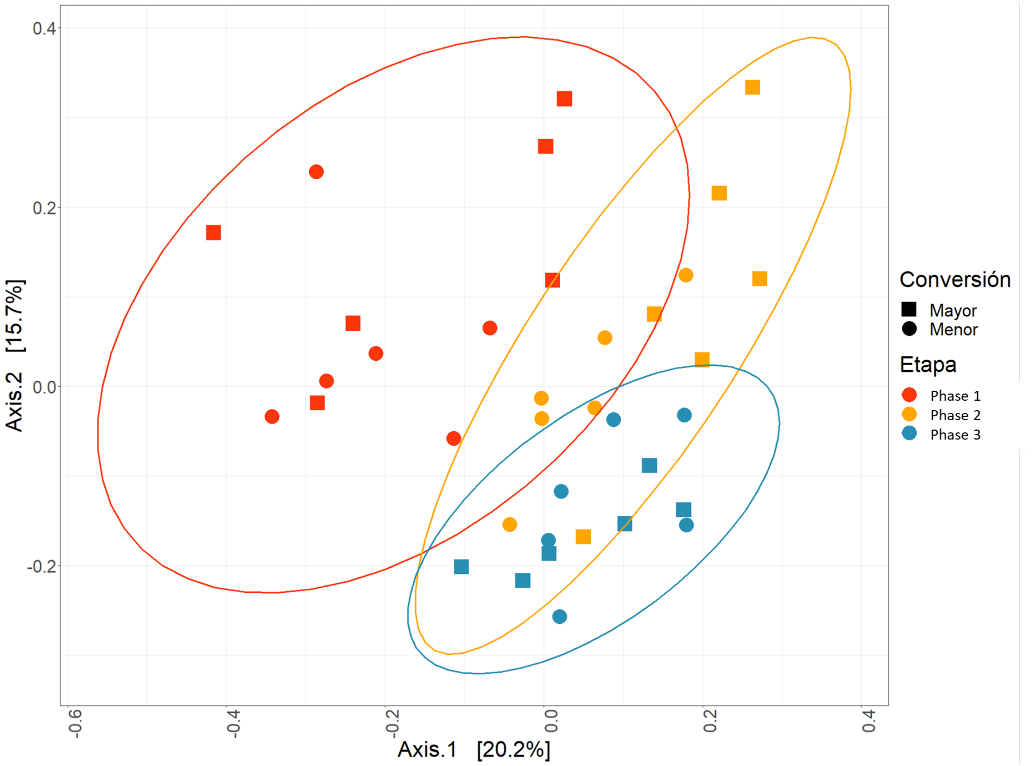




We perform a different analysis. In this case, we used the piglets' age as the comparative parameter for the microbiota analysis.

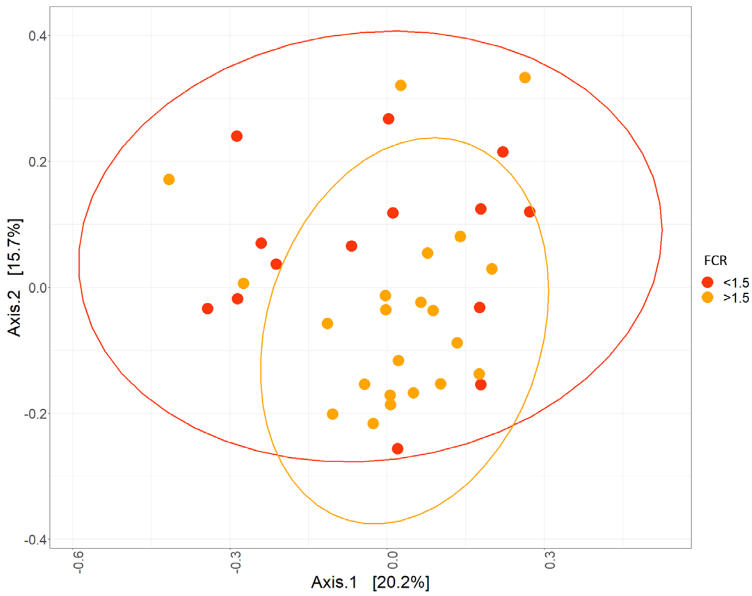
As the figure shows, there is a clear differentiation between the animal's age and the variability of the microbiotas.

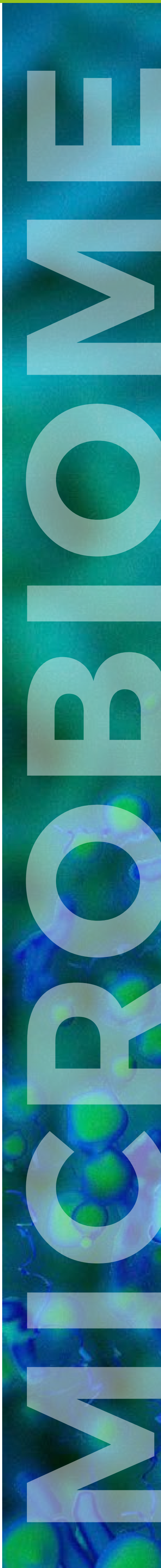
In this case, we found that the age is a factor for the change in the microbiota composition, as concluded in other researches. This variation is stronger compared with the variation in the microbiota regardless the additives supplementation



We divided the feed conversion ratio in low and high, saying that a feed conversion ratio below 1.5 is considered as a good conversion ratio in this stage of the piglets' life cycle.

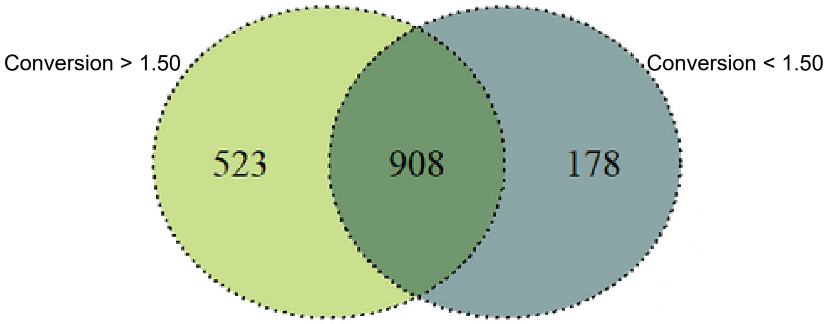
We found a trend in which there are important differences between the microbiotas, that suggest a correlation between some species and better zootechnical performance. The figure shows (in red) the low conversion ratio group. The yellow dots show the higher feed conversion ration group.





In the following graph, the microbiomes were grouped according to the conversion obtained, creating two groups: conversions below 1.5 and conversions greater than 1.5, 523 species associated with high conversions and 178 species associated with low conversions were found.

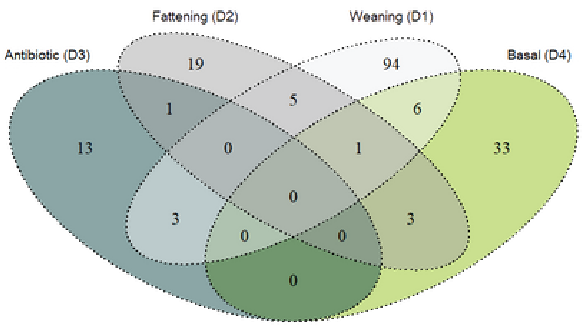
Additionally, 908 species were present in animals with both high and low Feed Conversion Ratios (FCR).



Distribution of bacteria at the species level by conversion

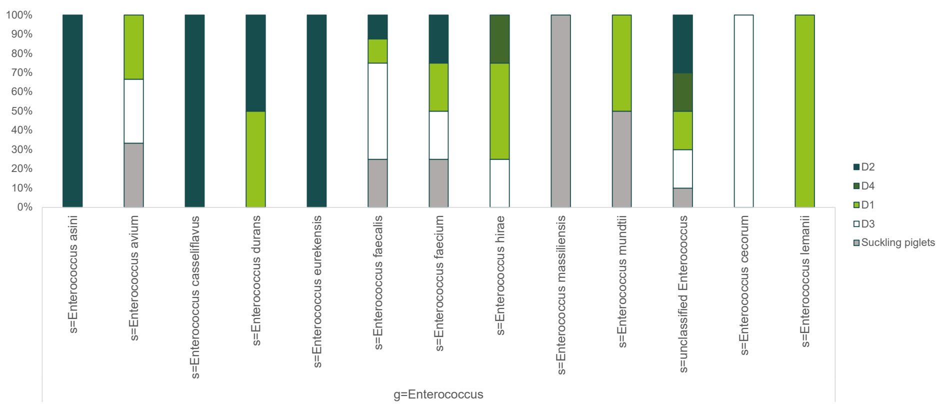
In the following graph, the 178 species associated with low FCR were evaluated by grouping them with the diets in order to evaluate if there was a predominant diet in the conformation of the microbiome with more species associated with low FCR.

The diet with probiotics D1 (Fortcell Feed® Piglets) was the one that provided more species associated with better FCR than the other diets.

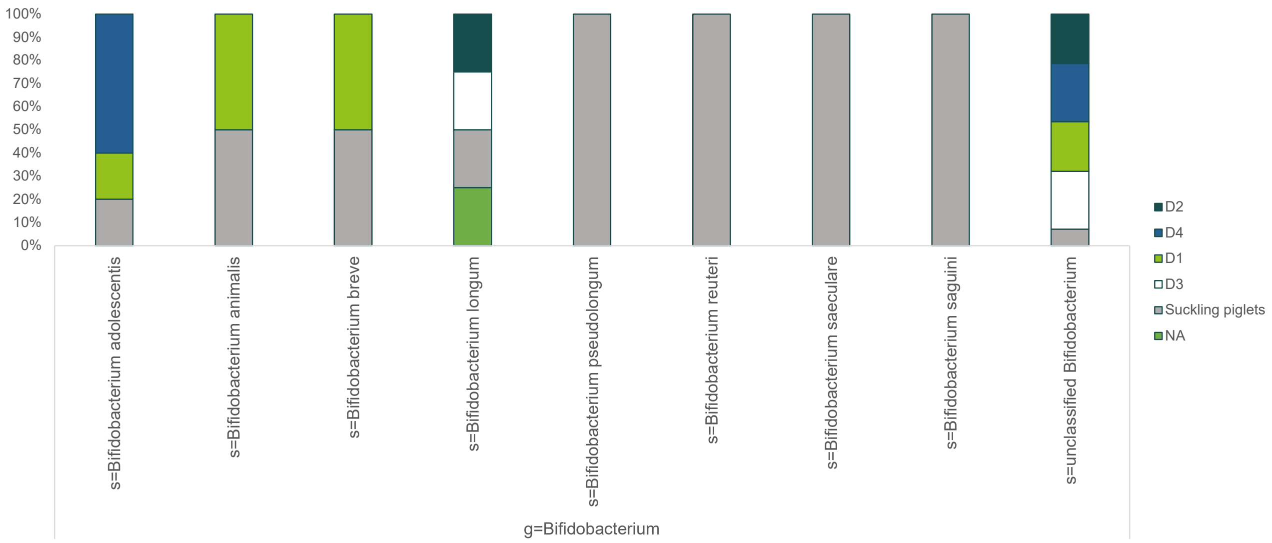


Distribution of bacteria associated with better conversion by diet

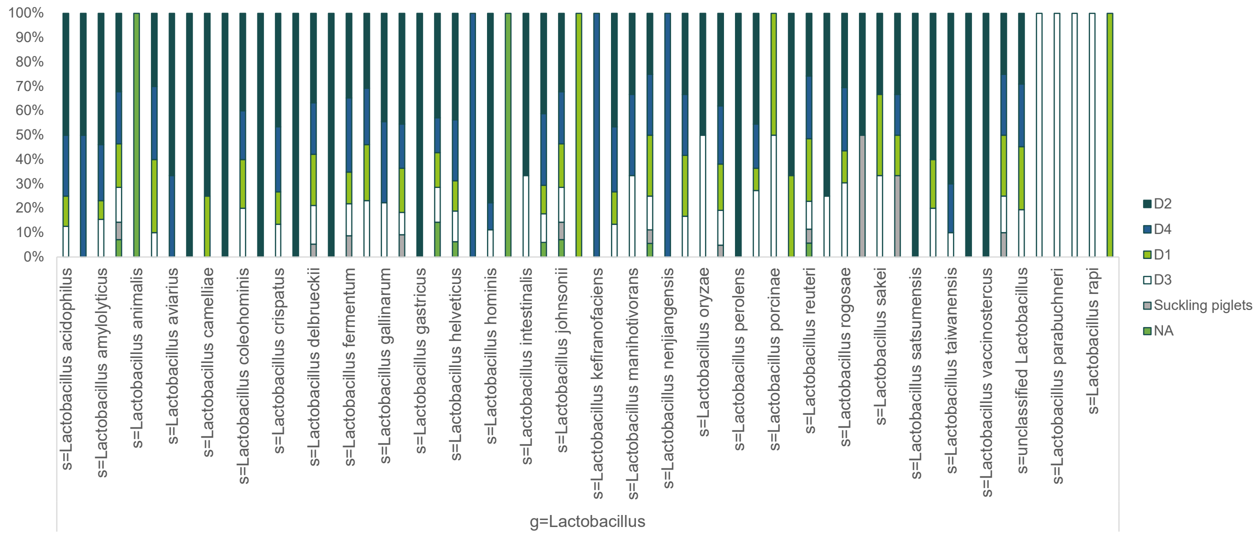
The genetic material of the encapsulated probiotic species was sequenced and classified in the animals that consumed the diet that contained them, this can be seen in the grouped column graphs where the color is associated with a specific diet, which shows the effectiveness of the patented encapsulation process and its release at the intestinal level.



Distribution of bacteria of the genus Enteroccocus by diet



Distribution of bacteria of the genus Bifidobacterium by diet



Distribution of bacteria of the genus Lactobacillus by diet

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Conclusions

Age was a stronger grouping factor than additives in PCOA analysis for Beta Diversity

Low and high FCR grouping showed significant differences in bacterial species between animals with better FCR

D1 diet with probiotics contributed the most species with the best FCR

D2 and D1 diets had the highest alpha diversity, followed by D4 basal diet, and D3 diet with antibiotics had the least diversity

Higher diversity was not associated with a better FCR.