

# Preliminary characterization of the microbiota of adult *Fasciola hepatica* from bovine and ovine hosts



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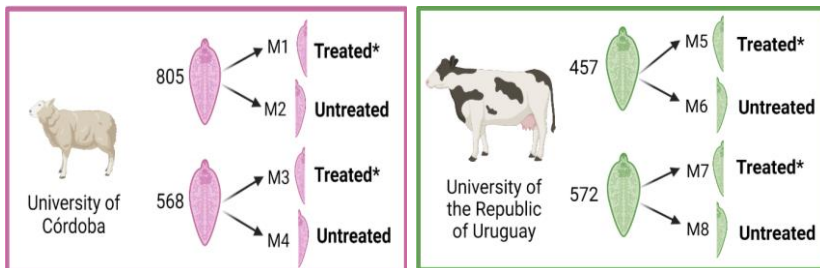


*Fasciola hepatica* is a foodborne zoonotic parasite, which is maintained in an indirect life cycle between an invertebrate and a vertebrate host. The juvenile worms are released in the duodenum of the vertebrate host following metacercariae ingestion, and rapidly penetrate the gut wall to migrate towards their definitive location, the intra-hepatic biliary ducts. During this migration, *F. hepatica* may interact not only with the host tissues, but also with its microbial communities, as it has been shown for other helminths. The present study aimed to characterize the bacterial communities associated with the adult stage of *F. hepatica*, and analyze the potential influence of the host species in its composition.

## MATERIALS AND METHODS

Four *F. hepatica* adults isolated from bovine and ovine hosts were obtained from the IRNASA-CSIC biobank, and the samples were handled as shown in Figure 1. (\*) Treated samples were incubated with antibiotics and washed in sodium hypochlorite.

Figure 1



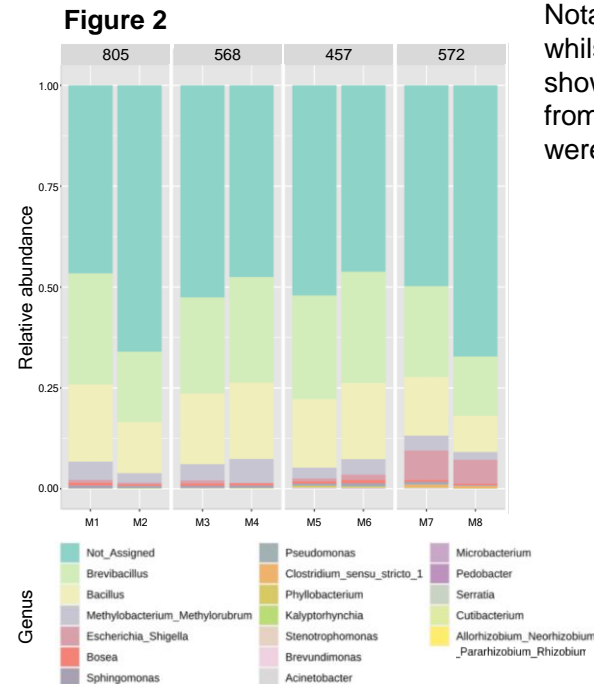
Total DNA was isolated and the MiSeq platform (Illumina) was used for the sequencing of prokaryotic 16S rRNA gene amplicons (V3-V4 region). Sequence data were processed using QIIME2, and MicrobiomeAnalyst was employed for visual representation and statistical analyses.

## CONCLUSION

Our preliminary results point towards a **possible link between the microbiota of *F. hepatica* adults and their vertebrate hosts**. However, further investigations using additional replicates are needed to confirm these findings, as well as to assess their biological meaning.

## RESULTS

Retained sequences were assigned to 4 bacterial phyla and 18 genera, whilst a substantial percentage remained unclassified (53.5%±8.4, at phylum level). The phylum Firmicutes was the most abundant in all samples (39.3%±8.2), followed by Proteobacteria (7.1%±2.6). At genus level (Figure 2), *Brevibacillus* (23.2%±4.8) and *Bacillus* (16.0%±3.6) were predominant in all samples, followed by *Methylobacterium/Methylorubrum* (3.6%±1.3) and *Escherichia/Shigella* (2.1%±2.8).



Notably, PCoA showed clustering of microbial communities by host species (Figure 3), whilst antibiotic/bleach treatment had little effect on overall microbial profiles (not shown). Moreover, microbial richness was significantly higher in specimens collected from sheep compared to those from cow (Figure 4), although no significant differences were detected in alpha diversity (Shannon index) between groups (not shown).

Figure 3

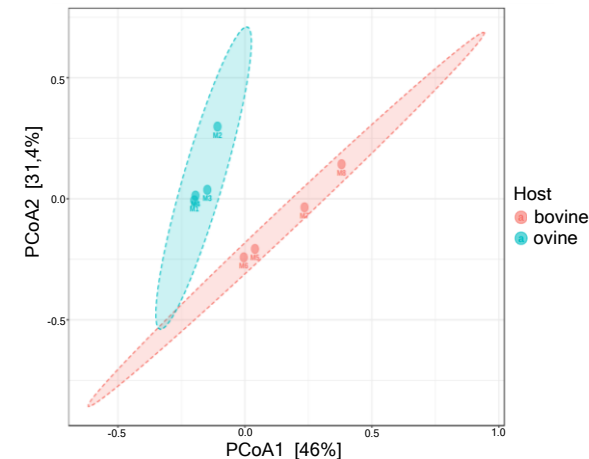


Figure 4

