

Título: MICROBIOME OF THE GASTRIC MUCOSA OF SWINES WITH AND WITHOUT ULCER OF THE PARS ESOPHAGEA

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Resumo:

Advances in DNA sequencing technology have revealed the complexity of bacterial communities living in the gut of humans and animals, but we still have limited knowledge about microbiome characterization of the stomachs. This study aimed to characterize the composition of the microbiota of eight porcine stomachs (four with and four without ulcer of the *pars esophagea*), obtained from an industrial abattoir, using next generation sequencing technology. Fragments from the gastric mucosa (antrum and corpus) of each stomach were taken with 5 mm biopsy punches for DNA extraction and amplification with primers targeting the hypervariable V4 region of the bacterial 16S rRNA gene. Ion PGM platform was used for sequencing and sequence data were processed using QIIME, with OTUs (Operational Taxonomic Units) calculated at 97% similarity level using the closed-reference based protocol. A total of 696,947 quality-filtered and classified reads were obtained. Forty-three phyla were identified, but 92.8% of all reads were affiliated to only two bacterial divisions: Proteobacteria and Firmicutes. Helicobacteraceae was the most abundant family of Proteobacteria, and Lactobacillaceae predominated among the Firmicutes. Although the samples revealed similar bacterial phylum-level representation, differences in community composition were observed at finer taxonomic resolution. The antrum of stomachs with ulcer showed higher Shannon diversity indices than that of stomachs without ulcer ($p = 0.007$). Analyses of bacterial communities at the genus and species levels showed that other *Helicobacter* species than *H. suis* were present, although in much lower abundance, including *H. pylori*, *H. pullorum* and *H. rappini*. Differences in species diversity and richness of swine gastric microbiota may play an important role in health and disease.

Palavras-chaves: Gastric microbiome, swine, ulcer of the *pars esophagea*, gastric mucosa.

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