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## Intestinal microbiota composition before and after probiotic treatment in dogs with diarrhoea

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Gastrointestinal problems belong to top medical conditions diagnosed in dogs for several last years (5<sup>th</sup> place - diarrhoea/intestinal upset, 6<sup>th</sup> place vomiting/upset stomach in 2017; VPI, 2018). However antimicrobial drugs are still the most frequently used treatment option, probiotic bacteria together with electrolyte replacement are sufficient in many cases of diarrhoea without long-lasting disturbance of microbiota balance observed after antibiotic administration. Our intention was to test efficacy of probiotic supplementation (*Enterococcus faecium* DSM 32820 for 7 days, the dose 109 CFU/1 ml/dog/day) in dogs (n=6) with acute diarrhoea. The faecal microbiota was detected using 16S rRNA sequencing after DNA extraction using Qiagen DNeasy PowerLyzer PowerSoil Kit. Significant improvement of faecal consistency (faecal score) was observed after 7 days of probiotic supplementation while faecal pH values were not changed. The most abundant phylum Firmicutes was stable over time (80.2 % at day 0 and 77.1 % at day 7 in average). Less abundant phylum Proteobacteria was decreased (8.6 vs 3.5 %) whereas Bacteroidetes were increased (0.4 vs 6.1 %) after probiotic application. The most common family sequenced was the Lachnospiraceae representing 25.7 % of the total taxa identified. Among other detected families, Enterobacteriaceae (8.6 vs 3.4 %), Peptostreptococcaceae (19.6 vs 12.3 %) and Coriobacteriaceae (6.8 vs 0.3 %) were decreased. In contrast, Bifidobacteriaceae (0.3 vs 2.1 %), Prevotellaceae (0.3 vs 3.6 %) and Lachnospiraceae (24.4 vs 31.0 %) were more abundant at day 7 compared to day 0. The families Clostridiaceae and Lactobacillaceae were not changed. At the genus level, predominant *Lactobacillus* genus was stable while *Escherichia-Shigella* was lower after probiotic treatment (8.4 vs 3.3 %).