



EVALUATION OF SELECTED FAECAL BACTERIAL GROUPS IN DOGS SUFFERING FROM CARDIOVASCULAR DISEASES

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Gastrointestinal dysbiosis has been associated to different diseases of the GI tract (in both man and animals), but also to pathological conditions related to other organs and apparatuses [1-3]. The aim of the present study is to move a first step toward the study of faecal microbiota (selected faecal bacterial groups) in dogs presenting cardiovascular diseases (CVDs), to determine whether, similarly to human and laboratory animal medicine [4,5], interesting correlations could be found. Seven naturally voided faecal samples from 7 dogs suffering from CVD (6 valvulopathies and 1 dilated cardiomyopathy), but without gastrointestinal signs, were collected. Bacterial DNA for the study of selected faecal bacterial groups (*Lactobacillus* spp., *Bifidobacterium* spp., *Enterobacteriaceae*, *Clostridium coccoides-Eubacterium rectale* group, *Staphylococcus* spp., and *Bacteroides-Prevotella-Porphyromonas* spp.) was extracted using a modified DNA extraction method based on benzyl chloride. SYBR Green Real-Time PCR amplification were performed. For each bacterial group, the total bacterial concentration was determined using 16S rRNA gene targeted primers [6]. Our evaluation was successful in 5 out of 7 dogs, but due to the low number of patients (inclusion/exclusion criteria were very selective) it was not possible to compare statistically subgroups in our sample. However, Student's *t* test was applied to compare the mean values of bacterial concentration of each detected group in patients of the present study with those previously obtained from healthy subjects (unpublished data). *Bacteroides-Prevotella-Porphyromonas* spp. and *Bifidobacterium* spp. counts resulted significantly lower ($p < 0.05$) in the CVD dogs than in the healthy subjects, while *Lactobacillus* spp. and *Enterobacteriaceae* counts were significantly higher ($p < 0.05$). Data from our pilot study, even if very preliminary, suggest that the evaluation of faecal composition in dogs suffering from cardiovascular diseases is possible and may provide interesting insights in cardiovascular diseases' pathogenesis, prevention and treatment.

[1] Honneffer JB, et al. Microbiota alterations in acute and chronic gastrointestinal inflammation of cats and dogs, *World J Gastroenterol*, 20(44):16489-97, 2014. [2] Maranduba CM, et al. Intestinal microbiota as modulators of the immune system and neuroimmune system: impact on the host health and homeostasis, *J Immunol Res*, 2015:931574, 2015. [3] Sherwin E, et al. A gut (microbiome) feeling about the brain, *Curr Opin Gastroenterol*, 32(2):96-102, 2016. [4] Li J et al. Gut microbiota dysbiosis contributes to the development of hypertension, *Microbiome*, 5(1):14, 2017. [5] Marques FZ, et al. High-Fiber Diet and Acetate Supplementation Change the Gut Microbiota and Prevent the Development of Hypertension and Heart Failure in Hypertensive Mice, *Circulation*, 135(10):964-977, 2017. [6] Nasuti CC, et al. Changes on fecal microbiota in rats exposed to permethrin during post natal development, *Environ Sci Pollut Res Int*, 23(11):10930-10937, 2016.