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DELLE SCIENZE VETERINARIE



ATTI LXX Convegno SISVET



**Joint
meeting**

REEV-Med
XVI Convegno S.I.C.V.
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XIII Convegno AIPVet
XIII Giornata Studio So.Fi.Vet.
III Convegno RNIV

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MAIN FECAL BACTERIAL GROUPS IN DOGS POSITIVE FOR *LEISHMANIA*

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Lamour et al. (2014) recently suggested a link between gut microbiome and *Leishmania* infection in mice. They showed that in two different mouse models of cutaneous leishmaniasis, susceptible or self-healing models, with the progression of the infection also the fecal microbiome changed, with *Clostridia* class higher in the first group and *Gammaproteobacteria* classes higher in the second one, suggesting that the intestinal microbial composition could be linked to a different response to the disease. Aim of the work: In this study we investigated the main fecal bacterial groups in dogs positive for *Leishmania* spp., with the aim of evaluating possible differences between enrolled dogs. Materials and methods: Naturally voided fecal samples were collected from 8 dogs resulted positive (exposed, infected or sick) for leishmaniasis by IFAT or ELISA (dog no. 4). In most cases dogs differed for IFAT titers and for time elapsed between positivity detection and samples collection. Five dogs (2-4, 6, 8) were not presenting any concomitant disease and were not undergoing any treatment. Four dogs (2, 3, 6, 7) were not symptomatic at the time of fecal sampling; only one dog (4) was undergoing therapy for leishmaniasis at the time of fecal sampling, and 4 dogs (2, 6-8) had been previously treated for the disease, while for the remaining three it was a first diagnosis. The samples were frozen briefly after collection. All dogs were fed on commerce diet, with the addition in dog n.1 of cooked “pasta” and meat. A Real-Time quantitative PCR (qPCR) procedure was used for the quantification of the main bacterial groups of intestinal microbiota by using specific primers as reported by Nasuti et al. (2016). DNA was extracted from dogs’ fecal samples using Stool DNA isolation kit (Norgen, Thorold, Canada). *Bifidobacterium*

spp., *Bacteroides-Prevotella-Porphyromonas* spp., *Clostridium coccoides-Eubacterium rectale* group, *Enterobacteriaceae*, *Lactobacillus* spp. and *Staphylococcus* spp. were quantified using a Mx3000P Real Time PCR based on SYBR Green detection. The more represented group in all dogs was *Clostridium coccoides-Eubacterium rectale* group with a mean value of 3.4×10^9 CFU/g of feces, while *Lactobacillus* spp. was the less present with a mean value of 3.6×10^3 CFU/g of feces. The ongoing therapy at the sampling time seemed to affect (not significantly) the log values of *Clostridium coccoides-Eubacterium rectale* group and *Lactobacillus* spp. that both were higher in the treated dog (4) compared to the mean log values of those untreated. To the authors' knowledge this is the first study on patients positive for leishmaniasis with these selected fecal bacterial groups. Even if it presents some limitations (small number of dogs, great variability within the variables), it would be interesting to deepen the possible correlation between leishmaniasis and the intestinal microbiota in the dogs suffered from this disease.

1. Lamour SD, Veselkov KA, Posma JM, et al. (2014) J Proteome Res 14, 318-329.
2. Nasuti C, Coman MM, Olek RA, et al. (2016) Environ Sci Pollut Res Int. DOI: 10.1007/s11356-016-6297-x.