

Preliminary survey of fecal microbiota in Non-Hodgkin's lymphoma affected dogs

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Introduction Non-Hodgkin's lymphoma (NHL) is the most common hematopoietic malignancy in dogs. The increased lymphocyte proliferation induced by gut microbes can lead to higher chance of aberrant DNA replication, particularly in some B-lymphocytes, which are innately susceptible to genetic instability and activation. Oxidative stress caused by the intestinal microbiota either directly or indirectly through the immune system, can also affect tumorigenesis (lymphomagenesis). Optimal responses to cancer therapy require an intact commensal microbiota that exerts its effects by modulating myeloid-derived cell functions in the tumour microenvironment. We conducted a preliminary investigation of the fecal microbiome in dogs affected by NHL.

Materials and methods The microbiome in fecal samples from 6 healthy dogs, 8 NHL-affected dogs at initial presentation (or at diagnosis?), and 4 NHL-affected dogs after chemotherapy induction phase (cyclophosphamide, vincristine, and prednisolone) treated with probiotics (SivoyTM) was analyzed by qPCR assays of selected bacterial groups. Differences in microbiota between healthy and diseased dogs at presentation (diagnosis?), and between initial presentation and following chemotherapy were statistically analyzed using a t-test and Wilcoxon matched-pairs signed rank test, respectively.

Results The abundances of *Bifidobacteria* ($p=0.0001$), *Lactobacillus* ($p=0.0001$), *Faecalibacterium* ($p=0.0005$), *Bacteroidetes* ($p=0.0480$) and *Fusobacterium* ($p=0.0025$) were significantly higher in the feces of healthy versus NHL-dogs. The concentration of *Clostridium perfringens* was higher in NHL-dogs compared to healthy dogs ($p=0.0326$). No statistical differences for total bacteria, *Escherichia coli*, *Blautia* and *Ruminococcaceae* were found. The abundances of total bacteria, *Bifidobacteria*, *Lactobacillus*, *Faecalibacterium*, *Bacteroidetes*, *Fusobacterium*, *Escherichia coli*, *Blautia*, *Ruminococcaceae*, *Clostridium perfringens*) were not significantly different when compared before and after chemotherapy in 4 dogs treated with the probiotic (SivoyTM) ($p>0.01$).

Conclusions In order to reach more definitive conclusions in the microbiota of dogs treated with probiotics, larger number of pre- and post-treatment stool samples from healthy and NHL-affected dogs will be required. These preliminary data underscores the need for further investigation into the microbiota and lymphoma.