Fecal microbiota differences in Non-Hodgkin Lymphoma (NHL) affected dogs: preliminary results.

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Animal models play an essential role in understanding the importance of gut microbiome in immune development and composition, and play a key role to reinforce the relationship between the microbiome and health and disease [3]. Non-Hodgkin Lymphoma (NHL) is the most common hematopoietic malignancy in dogs, caused by clonal proliferation of lymphocytes in solid organs [2]. Whether microbes influence immune cells directly, indirectly, or both, increased lymphocyte proliferation can lead to a higher chance of aberrant DNA replication, particularly in some B lymphocytes which are innately vulnerable to genetic instability and activation. Oxidative stress caused by intestinal microbiota, either directly or indirectly through the immune system, can also affect tumorigenesis, thus, the microbiota can affect several pathways associated with lymphomagenesis [4]. The optimal responses to cancer therapy require an intact commensal microbiota that mediates its effects, by modulating myeloid derived cell functions in the tumour microenvironment [1].
In our study design we analysed the microbiome (by using 16S rRNA gene 454-pyrosequencing and qPCR assays) of naturally voided fecal samples from 6 healthy dogs, 8 NHL dogs before and 4 NHL (of the eight) dogs after induction phase of chemotherapy (cyclophosphamide, vincristine, and prednisolone) plus probiotics (Sivoy ^{TM}).
Several statistical significances were observed compared the fecal microbiome of healthy dogs *vs*NHL dogs before chemotherapy. In particular, differences were observed for *Bifidobacteria* (p=0.0001), *Lactobacillus* (p=0.0001), *Faecalibacterium* (p=0.0005), *Bacteroidetes* (p=0.0480), and *Fusobacterium* (p=0.0025), which concentrations were higher in healthy dogs compared to NHL dogs. On the contrary, the concentration of *Clostridium perfrigens* was greater in NHL dogs compared to healthy dogs (p=0.0326). No statistical differences for total bacteria, *Escherichia coli*, *Blautia,* and *Ruminococcaceae* were found. Microbiome shift (total bacteria, *Bifidobacteria*, *Lactobacillus*, *Faecalibacterium*, *Bacteroidetes*, *Fusobacterium*, *Escherichia coli*, *Blautia*, *Ruminococcaceae*, and *Clostridium perfrigens*) of fecal samples were also compared before and after induction phase of chemotherapy plus probiotics (Sivoy ^{TM} probiotic mix Slab51, containing 8 strains of lactic acid bacteria and bifidobacteria dosed at 200 billion per stick) but no statistical significance was found.
In order to understand microbiome's changes in NHL affected dogs treated with standard protocol plus probiotics, a larger number of stool samples before and after treatment, from a greater number of animals, should be investigated. The fact that an increased number of lymphomas are becoming associated with bacterial infections underscores the need for more studies involving microbes and lymphoma and about the use of probiotics to restore normal microbiota in affected dogs.

References

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