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INTESTINAL MICROBIOTA IN LYMPHOMA: A COMPARISON IN HEALTY DOGS AND DOGS WITH NON HODGKIN LYMPHOMA

Alessandra Gavazza[1], Rossi Giacomo[1], George Lubas[1], Matteo Cerquetella[1], Jan Suchodolski[2],

[1]School of Biosciences and Veterinary Medicine, University of Camerino, Italy, Department of Veterinary Sciences, University of Pisa, Italy
[2]Gastrointestinal Laboratory, Texas A&M University, College Station, TX, USA

agavazza@vet.unipi.it

Background and objectives
Animal models play a key role in understanding the importance of gut microbiome in immune development and composition as well as to reinforce the relationship between the microbiota and health and disease. Intestinal bacteria have been implicated in several types of cancer. Regardless, microbes influence immune cells directly, indirectly, or both, and increased lymphocyte proliferation can lead to a higher chance of aberrant DNA replication. This particularly occurs with some B lymphocytes which are innately vulnerable to genetic instability and activation.

Methods
We analyzed the microbiome (by using 16S rRNA gene sequencing and qPCR assays) of naturally voided fecal samples from 12 healthy and 12 Non Hodgkin Lymphoma (NHL) dogs in order to evaluate the microbiota composition using a dysbiosis index. An index value greater than 2 indicates dysbiosis, while below 0 indicates normal microbiota.
Results. Significant differences were observed when comparing the fecal microbiota structure of all healthy dogs vs NHL dogs (ANOSIM; $P<0.05$). Specifically, differences were observed for Faecalibacterium ($P<0.001$) with concentrations higher in healthy vs NHL dogs. The dysbiosis index was significantly lower ($p=0.007$) in healthy vs NHL dogs (mean, SD: -2.6, 2.0 vs 1.7, 3.2), respectively.

Conclusion
Interestingly, lower levels of Fecalibacterium prausnitzii were recently found in humans with some chronic colonic conditions as well as colorectal cancer ($P < 0.001$) compared with healthy subjects. This study showed that NHL have a increased dysbiosis index, indicating dysbiosis. Animal models of cancer can be critical in order to demonstrate a link between the microbiome and carcinogenesis.