OC.05_148 - ROLE OF XENOSIALIZATION IN THE PATHOGENESIS OF COLITIS IN THE CANINE MODEL; POSSIBLE POSITIVE EFFECTS OF NEW PROBIOTIC BLENDS

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Objective:
Inflammatory bowel disease (IBD) is a heterogeneous state of chronic intestinal inflammation with no exact known cause. In dogs, IBD is expressed histologically with lymphoplasmacytic inflammation (LPL) of gastrointestinal tract. The study evaluates the possible correlation between microbiota, dietary absorption, enteric expression of N-glycolylneuraminic acid (Neu5Gc) (xenosialization) and intestinal inflammation (xenosialitis) in dogs with IBD. Neu5Gc is indeed synthesized from its N-acetyl precursor (Neu5Ac) by cytidine-5'-monophospho-N acetylneuraminic acid hydroxylase (CMAH), absent in humans, and polymorphic in dogs.

Methods:
105 dogs (divided by breed into 3 groups) with lymphoplasmacytic enterocolitis, compared with 10 healthy dogs (control). Neu5Gc in stools of healthy and enteropathic dogs (20 + 20) was evaluated by ELISA, before and after 30d of administration a probiotic mixture (FSG6822) rich in live bifidobacteria with sialic acid cross-feeding activity. Neu5GC was highlighted with specific antibody (Creative Diagnostic, DMABH-C003). The distribution of desializing bacteria was performed using two different sequencing techniques for different regions of the 16S rRNA gene on 127 + 167 dogs (healthy vs enteropathic).

Results:
Neu5Gc was associated with severe colitis ($p<0.005$), with no relationship to race. In enteropathic dogs there is a higher prevalence of Clostridiales and Bacteroidales ($p=0.0011$), without difference of Bifidobacteria.

Conclusions:
In dogs, the severity of colitis correlates with Neu5Gc and with an increase in Clostridiales and Bacteroidales. In the absence of an increase in desializing bifidobacteria this predisposes to xenosialitis. Actually, (FSG6822) probiotic mixture, shows good levels of reduction in fecal elimination of Neu5Gc, and could reduce xenosialization.

OC.06_167 - A MECHANISTIC APPROACH TO HARNESS THE HYBRID TWO-COMPONENT SYSTEM OF THE HUMAN COLONIC BACTEROIDOTA AS BIOMARKERS FOR MANIPULATION OF HOST HEALTH

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Objective:
The human colon is inhabited by trillions of microorganisms that impact host health. The majority of dietary polysaccharides flowing into the colon is fermented by the Bacillota and the Bacteroidota phyla. Thus, we hypothesized that by harnessing the polypeptide designated the Bacteroidota Hybrid Two Component System (HTCS), a regulator of nutrient metabolism, we will uncover biomarkers amenable to manipulation of the colonic microbiome.

Methods:
Amino acid sequences of the sensor modules in 2,348 HTCS were extracted for multiple sequence alignment and phylogenetic tree construction. To functionally annotate the tree, total RNA and culture supernatants of Bacteroides species, grown on different dietary polysaccharides, were subjected to RNAseq and metabolomic analysis, respectively. Isothermal titration calorimetry was then used to further confirm substrate specificities of the sensors and computational analyses employed to extract the metabolites associated with fermentation of each polysaccharide.

Results:
The sensor phylogenetic tree yielded 10 major clusters, with multiple sub-clusters. Transcriptional analysis (RNAseq), recombinant protein expression, and biophysical approaches (ITC) enabled identification of the clusters representing pectin, arabinan, and arabinoxylan sensors, while metabolomic analyses linked metabolism of dietary polysaccharides, especially complex arabinoxylans, to diverse compounds with antioxidant/anti-inflammatory, neurotransmitter, and antibacterial properties.

Conclusions:
The HTCS sensors constitute biomarkers in the colon for metabolism of different polysaccharides. These biomarkers, designated the Polysaccharide Sensing and Degradation Signature (PSDS), are proxies informing the capacity of an individual to metabolize different dietary polysaccharides. By linking the PSDS to metabolite production, rational manipulation of the colonic microbiome can be implemented through probiotics/prebiotics/synbiotics for health benefits.