Differences in the intestinal microbial composition of cats and dogs

Ronnie Gueta¹, Francesco Cian²,
Anton Heusinger¹, Petra Kühnlein¹,
Ines Langbein-Detsch¹,
Elisabeth Müller¹

¹ Laboklin GmbH & Co. KG, Bad Kissingen, Germany

² Batt Laboratories Ltd, Coventry, United Kingdom

OBJECTIVES

Imbalances in the microbial composition of the intestinal microbiome are associated with various gastrointestinal diseases. Recent studies have identified distinct bacterial groups that are significantly altered in animals with gastrointestinal symptoms in comparison to healthy individuals and may be used as biomarkers for dysbiosis. Aim of the study was to analyze the intestinal microbiota from clinically healthy cats and dogs in comparison to animals with acute diarrhea.

METHODS

DNA from fecal samples of cats and dogs (n = 20) with acute diarrhea and clinically healthy control animals (n = 20) was extracted during veterinary routine diagnostics. Animals positively tested for enteropathogenic bacteria, viral diseases and endoparasites were excluded from this study. Subsequently qPCR assays targeting 16S rRNA genes for seven different bacterial groups (*Faecalibacterium prausnitzii*, *Fusobacteria*, *Blautia*, *Turicibacter*, *Escherichia coli*, *Clostridium hiranonis* and total bacteria) were performed.

RESULTS

The intestinal microbiota of clinically healthy cats and dogs vary in their composition. When comparing animals with acute diarrhea, mucosa-protective bacteria like *F. prausnitzii* were decreased 100-fold in both dogs and cats. In contrast, proteolytic bacteria like *Fusobacteria* were increased up to 100-fold in cats and decreased up to 100-fold in dogs. This suggests, that certain bacterial compositions in the intestines have beneficial as well as negative effects depending on the host type.

STATEMENT (CONCLUSIONS)

This study indicates that the intestinal microbial composition differs between cats and dogs. Furthermore, we demonstrate, that the analysis for dysbiotic shifts in the intestinal microbiome yields valuable information for the differential diagnosis of gastrointestinal symptoms with unclear genesis and may give additional information for treatment options.