

MICROBIOME BASED THERAPEUTICS IN COMPANION ANIMALS: DESIGN AND CREATION OF MICROBIAL COMPLEXES

Dione N.;^{1*} Jarett J.K.;¹ Jospin G.;¹ Uttarwar R.;¹ Alvarado N.;¹ Liang S.;¹ Marfori Z.;¹ and Ganz H.H.;¹

¹Animal Microbiome Analytics, Inc, Oakland, CA USA

Objectives

In companion animals, fecal microbiota transplantation (FMT) is the main microbiome-based therapeutic strategy for dysbiosis treatment. Indeed, FMT has been demonstrated as an effective treatment for chronic gastrointestinal illnesses associated with bacterial overgrowth or depletion. This phenomenon has been associated with inappropriate antibiotic therapy in both humans and animals. While its efficacy is robust, the mechanisms of the reversion of this dysbiosis have not been clearly elucidated since only part of the bacterial community in stool is known with few being isolated by culture. In this work, we developed consortia of bacteria or “microbial complexes” of diverse microbes to allow for in vivo study. These complexes will facilitate further characterization of therapeutic action and assist with the development of advanced microbiome therapies.

Methods

We established a core taxa of bacterial species associated with a healthy state for domestic cats and dogs culled from a large database (>15,000 samples) using 16S rRNA sequencing. We then designed a microbial complex by integrating these identified species along with other specific bacterial taxa known for a specific function. From this combination, we developed defined microbial complexes, target lists of bacteria and used the culturomics method for further identification.

Results and Conclusion

The core taxa for cats includes members of the genus *Ruminococcus*, *Bacteroides*, *Blautia*, *Catenibacterium*, *Clostridium*, *Collinsella*, *Dialister*, *Faecalibacterium*, *Lachnoclostridium*, *Megamonas*, *Negativibacillus*, *Peptoclostridium*, *Phascolarctobacterium*, *Prevotella* and *Sutterella*. The core taxa for dogs includes members of the genus *Blautia*, *Ruminococcus*, *Fusobacterium*, *Ruminococcus*, *Bacteroides*, *Megamonas*, *Sutterella*, *Peptoclostridium*, *Catenibacterium*, *Faecalibacterium*, *Alloprevotella*, *Phascolarctobacterium* and *Clostridium*. These microbial taxa identified open interesting prospects towards the understanding of microbial interaction, along with the construction of consortia for controlled microbiome therapies in animals with potential extension to human health applications.

Keywords: Microbiome therapy, Companion animals, Microbial complex.