Characterization of the Shelter Feline Gut Microbiota and Optimization of Sample Collection Techniques

Kelly A. Bosco1, Jennifer L. Howard2, Amanda N. Burling3, Aaron C. Ericsson4, Craig L. Franklin5

1,2Veterinary Research Scholars Program; 3Department of Veterinary Medicine and Surgery; 4,5Department of Veterinary Pathobiology & MU Metagenomics Center, College of Veterinary Medicine, University of Missouri

Background

• The microbiome refers to the collection of organisms, their genomes, and the surrounding environmental conditions.
• Past research has explored the relationship between the gut microbiota (GM) and host health in humans, however, study of the feline microbiome is still in its infancy and more research is needed to investigate how environmental factors and disease influence the GM.
• We hypothesize that (1) felines exposed to related environments and disease states will have similar GM composition and (2) cat litter contains PCR inhibitors that are detrimental to obtaining quality metagenomics data.

Objectives

• The purposes of the present study are to:
  I. characterize the GM of shelter and feral cats to determine what environmental or host health factors influence composition
  II. assess whether litter contains components that interfere with the ability to obtain quality metagenomics data

Methods

• Fecal samples were collected and DNA was extracted with a commercially available PowerFecal® kit, amplified by PCR using conserved bacterial primers and subjected to next generation sequencing.
• Shelter and feral cats were assessed for parameters including shelter location, fecal score, and sex.
• To evaluate the impact of litter contamination, house cat fecal samples obtained from paper towel-lined litter pans are being spiked with litter and metagenomics data compared to that of unspiked samples.
• OTU’s with reads <10,000 were excluded from the data.

Shelter Associated Differences in Fecal GM

Differences between groups in beta diversity were determined via one-way permutational multivariate analysis of variance (PERMANOVA) of Bray-Curtis and Jaccard distances using Past 3.15.

Conclusions & Future Directions

• There was marked variation in fecal GM across all samples.
• GM composition was influenced by shelter and sex with the latter showing the most dramatic influence.
• OTU’s with reads <10,000 were excluded from the data.
• Differences between groups in beta diversity were determined via one-way permutational multivariate analysis of variance (PERMANOVA) of Bray-Curtis and Jaccard distances using Past 3.15.
• Stipend supported by the University of Missouri College of Veterinary Medicine Office of Research.
• Project support for KB provided by Franklin discretionary funds.
• We would like to thank several shelter locations and owners willing to provide access to their cats.

Acknowledgements

• Stipend supported by the University of Missouri College of Veterinary Medicine Office of Research.
• Project support for KB provided by Franklin discretionary funds.
• We would like to thank several shelter locations and owners willing to provide access to their cats.
• Special thanks to Becky Dortmund, Giedre Tumer, and the MU DNA Sequencing and Bioinformatics Cores for technical assistance, as well as sample and data processing.