Analysis of Equine Gut Microbiota by Living Environment

Tittel, Lauren (School: Oregon Episcopal School)

The gastrointestinal tract microbiome is vital for proper nutrition, balanced metabolism, and a healthy immune system and is foundational for understanding diseases and ailments related to microbiota imbalance. This project analyzed the diversity of the equine gut microbiome by living environment to better understand the external factors that influence gut bacterial species and thus impact animal health. Manure samples were collected from horses (n=30 total) in three unique living situations: full turnout on pasture grass, partial turnout, and no turnout where horses live in box stalls. Bacterial DNA was extracted and the V3/V4 regions of the highly conserved 16S gene were amplified via PCR. Ten out of the thirty original samples exhibited sufficient DNA, as established by gel electrophoresis, and 16S metagenomic sequencing was performed. Data cleaning, quality control, and alpha diversity analyses were performed with mothur and QIIME2 software. Complete microbial composition, including species abundance, was visualized and summarized at different taxonomic levels. Equine manure samples from partial and full pasture groups demonstrated very diverse gut microbiomes. However, no statistically significant differences in bacterial diversity across groups were found. Further investigation into equine gut microbiota diversity can suggest optimal living environments and diets to enhance horse health.

Awards Won:
University of Arizona: Renewal Tuition Scholarship