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BIOINFORMATICS SEMINAR KELLY MULHOLLAND

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A COMPUTATIONAL APPROACH TO CHARACTERIZING THE AVIAN RESPIRATORY MICROBIOME

The severity and spread of many human and animal diseases are associated with specific bacterial and viral agents within the respiratory microbiome. Recent studies attempting to characterize the respiratory microbiome of poultry have focused primarily on bacteria, however elucidating the complex microbial interactions that result in disease requires the characterization of the viruses, bacteria, bacteriophage, yeast and fungi. The lack of comprehensive bioinformatics workflows and viral genome databases have limited efforts to characterize the avian virome. To address this, a comprehensive bioinformatics workflow along with host-specific viral genome databases, a bacteriophage database and a yeast and fungi database were developed. These tools, along with bacterial 16S rRNA analysis, were utilized in several studies characterizing avian microbiomes under various conditions. This talk will focus on the application of these tools in examining the evolution of the microbial ecology of the avian trachea during the growth of a commercial flock. A total of 11 viral species, 24 bacterial genera, 33 bacteriophage species, and 61 yeast and fungal species were detected. Abundance at various taxonomic levels, alpha diversity, species frequency and microbial shifts were examined for each of the microbial components. Additionally, correlations between bacteria and bacteriophage families were investigated and several highly positive correlations were identified. This study provides the first comprehensive analysis of the ecology of the avian respiratory microbiome. Further development of our bioinformatics workflow and databases into a user-friendly tool will facilitate future investigations aimed at characterizing the microbiome of various species under a variety of conditions.

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THE DATA ANALYSIS AND PREDICTION OF MAIZE BRACE ROOT TRAITS BY STATISTICAL METHODS AND DATA MINING

Maize brace roots grow from the lower stem nodes above the soil surface, and then extend into soil. The main function of brace roots also helps maize absorb water and nutrients from the soil. It also would prevent maize from falling over, which called lodging. In previous project, Erin Sparks' lab has collected samples and images for brace roots. They come from multiple plants of 53 genotypes which grown in North Carolina and Delaware in 2016 and 2017. To know whether brace roots of maize can help fight against lodging or not, it is important to figure out relationships among brace roots different phenotypes' meta-data (genotypes and phenotypes) and data. The data analysis result will support the future research between brace root phenotypes and preventing lodging function. In this project, to study the relationships among different meta-data and data about brace root, there are three main projects. Firstly, it is brace roots database building and data collection. Secondly, the data classification and data importing. The third one is that data analysis and relationships connection. This project uses different statistical methods and tools for analysis. In the future, data mining will be used for helping to predict brace root data's variation and relationships.