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**<https://udel.zoom.us/j/91240820848>  
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## BIOINFORMATICS SEMINAR JUNIPER LAKE

*PhD Student, Department of AFS UNIVERSITY OF DELAWARE*

### MOLECULAR INSIGHTS INTO WOODEN BREAST IN BROILER CHICKENS SUGGEST SIMILAR PATHOMECHANISM TO DIABETES MELLITUS

Wooden breast is a major myopathy of fast-growing broilers which continues to threaten global poultry production due to its severe impact on meat quality. Tightly associated with economic traits such as growth rate, feed efficiency, and breast muscle yield, wooden breast presents an exceptional challenge to producers, as dietary or management strategies generally impair performance. An understanding of its genetic basis is therefore critical for developing a long-term solution. To this end, a genome-wide association study was conducted using Cobb500 broilers, a common commercial crossbred meat-type chicken. Results indicate that variation in genes involved in insulin secretion is likely a major contributing factor to phenotypic variation in wooden breast severity. Several of these genes were also supported as candidate genes for wooden breast based on their differential expression in early stages of the disease.

## ZACH SCHREIBER

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### UTILIZING THE GENOTYPIC FEATURES OF PHAGE REPLICATION MODULES TO MAKE SENSE OF VIRAL DARK MATTER

Microbes play an important role across all ecosystems and viruses influence these communities by acting as ecological drivers while also providing a large source of genetic diversity. Deep sequencing across whole microbial communities has yielded a reservoir of information; however, results often show a lack of homology among environmentally sampled sequences when compared to known databases. This lack of annotated viral genes has been classified as viral dark matter and can occur in more than half of the surveyed sequences throughout reference and environmental data sets. Although sharing little to no homology in current reference databases, characterization of viral dark matter across environmental metagenomes has proven useful. We have observed unknown proteins in reference data sets sharing significant homology when compared to environmental metagenomes and aim to shed light on unclassified reference and metagenomic viral proteins' functions by assuming gene neighbors often share complementary functions. The overall concept is driven by a network based analysis on predicted peptide open reading-frames (ORFs) that are positioned along assembled contiguous reads (contigs). Various methods are applied to the sequence data in order to relate unassigned proteins to known neighbors therefore, implicating possible functional attributes demonstrating viral dark matter to be more than just random noise.

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