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Report to Pennsylvania Soybean Promotion Board

Title: Influenza D Virus in Pennsylvania Cattle
Mid-term report: August 15, 2019
Principal Investigator: Dr Suresh Kuchipudi

Objectives:

The aim of this project was to isolate and characterize IDVs from PA cattle to evaluate the prevalence and genetic diversity of these viruses.

Progress to date:

During this funding period, we identified additional influenza D virus (IDV) in four archived lung tissue samples from cattle with respiratory disease. Of all tissue samples screened, only about 2% tested positive for IDV. This is lower than what we obtained from nasal swab samples. Although IDV has periodically been found by other researchers in lung following experimental infection with IDV, IDV primarily causes upper respiratory infection in cattle. Future studies could examine if other sample locations (i.e. trachea) could also be useful for IDV testing. Sequencing of the IDV isolates from lung is ongoing.

Expanded phylogenetic analysis of whole-genome sequences of our IDV isolates from PA and surrounding states in 2017 indicated that these isolates are closely related to a swine isolate also from 2017 from Kentucky. These sequences are the most recent genetic characterization of IDV in the US.

When initiating an infection, IDVs bind to cells through interaction cell surface receptors with a viral surface protein called hemagglutinin-esterase fusion (HEF) protein. Differences in the amino acid sequences of HEF from various IDVs are used to categorize IDV isolates into "lineages." When we analyzed the amino acid sequences of the HEF proteins from previous isolates of IDV as well as those from PA, Kentucky, and other

states in 2017, we discovered that the receptor binding site of HEF differs significantly between IDV of different lineages. We analyzed the predicted structure of the HEF protein that these differences would provide and found that these changes in HEF between IDV lineages alter the conformation of the RBS. All 2017 IDV isolates demonstrate a unique amino acid sequence in the receptor binding site that is not seen in isolates from previous years. We suspect that these variations in the binding site may affect the ability of IDV to bind specific cells in the bovine respiratory tract. Changes in IDV's ability to bind to upper and lower respiratory tract cells could have major implications to virus transmission and development of respiratory disease, respectively. We hope to explore this in future studies.

Sincerely,

Suresh Kuchipudi

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