PennState

Department of Veterinary and Biomedical Sciences
The Pennsylvania State University
115 William L. Henning Building
University Park, PA 16802-3500 USA

814-865-7696
Fax: 814-863-6140
vbs.psu.edu

Suresh V Kuchipudi, DVM, MVSc, PhD, DACVM,
Clincial Professor and Section Head of Microbiology,
Associsate Director, Animal Diagnostic Lab (PADLS-PSU),
Emai: skuchipudi@psu.edu, Direct: 814-863-5737

Dated 10/3/2019

Report to Pennsylvania Soybean Promotion Board

Title: Influenza D Virus in Pennsylvania Cattle
Final Report: October 3, 2019
Principal Investigator: Dr Suresh Kuchipudi

Objectives:

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

Research Progress:

Through the course of this multi-year study, we screened over 580 lung and nasal swab samples for presence of IDV genomic RNA. IDV was not identified in calves and was detected in 6.7% of samples from cattle >6 months old. A subset of the cattle (n=192) were healthy subjects, and the prevalence of IDV detection in the healthy cattle (7.8%) was not appreciably different from that in cattle with BRD symptoms (5.9%). This is a significant finding that suggests IDV infection itself does not correlate with BRD symptoms. It instead implies that IDV infection may cause sub-clinical BRD and/or affect the cattle immune system to increase susceptibility to co-infection with other BRD-causing pathogens. We intend to explore these possibilities in future research. Another observation was that healthy female PA cattle had lower IDV detection rates (2.7%) than males (9.0%), which is similar to what we observed in a separate study of cattle in western and mid-western US. Scientists have frequently observed this sex-specific pattern of infection, and the implications of this result in the context of IDV will be interesting to explore.

Full genome sequencing of 13 IDV isolates was attempted, and complete genomes were obtained for 9 (plus one partial genome). These sequences, from samples obtained in 2017, are the first IDVs from Pennsylvania and the first cattle-origin US IDV sequences since 2014. Phylogenetic analysis of the major viral surface protein revealed a sequence which may significantly impact the ability of IDVs to bind to host tissue surfaces. This

sequence is only found in one other recent IDV sequence, also from 2017. We suspect that the unique structural changes this sequence creates may correspond to unique effects that the PA IDVs have on cells when compared with historical IDVs from other parts of the US, particularly the ability to induce cytopathic effect on HRT-18G cells. Overall, PA IDVs were closely related to one another with limited genetic diversity within PA, but there is strong evidence of PA IDVs being part of an emerging distinct genetic cluster of IDV.

The results of this project have provided novel insights into the viruses threatening PA cattle. Since even healthy PA cattle demonstrated IDV infection, we are now convinced that a better understanding of how IDV affects cattle immunity can lead to insights in overall cattle health. Further monitoring of IDV in PA cattle is warranted to examine possible mutations that develop which increase transmission or virulence.

Sincerely,

Suresh Kuchipudi