Field application of *Mycoplasma hyopneumoniae* molecular characterization and analysis tools

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INTRODUCTION

Several tools have become readily available for molecular characterization and analysis of *Mycoplasma hyopneumoniae* (Mhp).

With increasing interest in control and elimination of Mhp, there was a need to better understand the epidemiology in the field.

Questions of interest included

- Evidence of Infection Chain™ versus lateral transmission in the growing pig
- Identification of variant(s) within sow herds prior to Mhp herd elimination programs to attempt to determine variant origin in the event of identification of Mhp post-elimination

MATERIALS AND METHODS

In order to begin documentation of Mhp infection/exposure between production stages, samples from known Mhp positive gilts, sows, nursery pigs and finishing pigs in the same flow were targeted for laryngeal swab sampling.

Samples from surrounding sites, with no flow similarity to the target sites, were requested to be included in the project.

Ten pigs were sampled per production stage, targeting clinical signs associated with Mhp (dry coughing and labored breathing). Pigs recently treated with Mhp sensitive antibiotics were not sampled.

In order to document lateral spread, a minimum of 20 flows were planned to be targeted with at least 100 samples analyzed.

Mhp PCR positive laryngeal swab samples with a Ct ≤ 32 were sent to the UM-VDL for P146 full sequence anlaysis and to the Mycoplasma Lab, UM for MLVA analysis. P146 full sequences and MLVA typing for each variant were uploaded into the Disease BioPortal (CADMS, UC-Davis), along with the corresponding site information for temporal-spatial genomic analysis.

RESULTS

To date molecular characterization has been successfully completed

- 6 flows
- 37 sites
- 54 sequence and typing events

The Disease BioPortal temporal-spatio-genomic visualizer, which consists of a site map linked to a phylogenetic tree, has been utilized for analysis of Mhp P146 full sequences and MLVA typing.

The authors have not identified lateral transmission of Mhp, but rather transmission has appeared to occur within the Infection Chain™/vertical within flow, as suggested by the similarity of sequences and types of variants from vertically related sites in the phylogenetic tree (Figure 1). A database has been created for variants from each site.

DISCUSSION AND CONCLUSION

Tools for molecular characterization and analysis of Mhp are available for use in the field and allow for a better understanding of the transmission of Mhp

- P146 full sequences
- MLVA typing
- Disease BioPortal

Under the conditions of this project, transmission of Mhp appears to occur within the Infection Chain™. Lateral transmission of Mhp has not been documented in this project to date.

A database has been created to help determine Mhp variant orgin in the event of Mhp identification within flows post-elimination.

Figure 1: Disease BioPortal phylogenetic tree displaying *Mycoplasma hyopneumoniae* P146 full sequences. Phylogenetic tree is rooted to a US 232 reference sequence. Mhp P146 full sequences are color coded by the flow each site is associated with.