Mycoplasma hyopneumoniae surveillance – a production system approach for health management decision making

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INTRODUCTION

Mycoplasma hyopneumoniae (M. hyo) is a common etiologic agent that causes economic losses in all production stages of our system.

The pathogenesis of disease is unknown and variable across the 38 sow flows.

The goal in this project was to develop a surveillance program to successfully classify the *M. hyo* status and strain within three distinct production flows.

By routinely testing the gilt development units (GDU), sow farms, and downstream pigs of each flow, we can determine the timing of *M. hyo* colonization and infection dynamics within the system to develop systematic intervention methods to reduce or eliminate the clinical impact.

MATERIALS AND METHODS

Historical wean-to-finish (wtf) diagnostics identified three sow farms experiencing clinical *M. hyo*.

Each sow farm represents one of three distinct genetic flows.

At each sow farm, 30 laryngeal swabs were collected from gilts entered into the sow farm 8 weeks prior from the GDU, at expected peak *M. hyo* shedding, to prove *M. hyo* instability.

Swabs were tested individually by real-time PCR at the BIVI HMC, Ames, IA. Positive PCR samples were sent to the University of Minnesota VDL for sequencing and a comparative dendrogram developed.

After baseline sow farm sampling, additional laryngeal swabs were tested at the gilt grow-finish, GDU, and wtf at approximately 8 weeks placed.

RESULTS

Gilts in Flow A
- Tested negative for *M. hyo* at the grow-finish and GDU
- 27 % of gilts tested positive at the sow farm
- No wtf pigs have tested positive for *M. hyo*, but sampling is ongoing

Gilts in Flow B
- Tested negative for *M. hyo* at the grow-finish and GDU
- 27 % of gilts tested positive at the sow farm
- 24 % of wtf pigs were positive

Gilts in Flow C
- Tested negative for *M. hyo* in grow-finish
- 40 % of gilts tested positive at the GDU
- The sow farm and wtf both tested negative

Sequence results showed each multiplication flow has a unique *M. hyo* strain with 99 % + homology consistent across each production stage.

The three flows are 97 % homologous, but each flow has a distinct dendrogram cluster.

CONCLUSION AND DISCUSSION

The results have led to discussion about *M.hyo* stabilization and elimination programs.

The keys to successful implementation will be:
- Early gilt acclimation
- 250+ day cool down to clear active infection before first farrowing

The previously described surveillance strategy utilizing laryngeal swabs will be used to confirm the cessation of *M. hyo* shedding prior to gilt entry into the sow farms.

Sequencing and dendogram development have been helpful epidemiological tools that allow agent tracking and support the system approach.