M. hyopneumoniae outbreaks: what you need to know to aid in your investigation

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Key points

- Molecular characterization tools such as p146 sequencing for *Mycoplasma hyopneumoniae* (*M. hyopneumoniae*) can provide insight towards investigating elimination failures or new introductions within swine herds

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What do we know about eliminating *M. hyopneumoniae*?

Within the swine industry, *M. hyopneumoniae* elimination programs, involving herd closure and strategic medication, have been successfully conducted .[1,2] In some cases, *M. hyopneumoniae* has been detected after the program has been completed calling into question whether the pathogen was eliminated or re-introduced.

M. hyopneumoniae outbreaks

An investigation was conducted on six sow farms within one production system that had a history of *M. hyopneumoniae* activity occurring unexpectedly after the elimination program had been conducted. The objective was to determine whether the *M. hyopneumoniae* outbreaks occurred via elimination failures or new introductions by employingmolecular characterization tools and investigating transportation records and diagnostics. To identify variant(s) origin, p146 sequencing was performed from the genetic material of *M. hyopneumoniae* positive laryngeal or bronchial swabs. Sequences obtained pre- and post-elimination efforts were analyzed using BioPortal and sequence analytic tools.

Informative findings

- Sequences obtained pre- and post-elimination efforts were 98.3% similar. In our experience, this % similarity in conjunction with other factors in the case, suggest a new variant on the six sow farms when compared to the original variants (Figure 1).
- All six farms had identical sequence suggesting that *M. hyopneumoniae* was introduced by a common source (Figure 1).
- A gilt development unit (GDU) sourced all six farms approximately 2.5 months prior to detecting *M. hyopneumoniae* post-elimination. Thirty gilts per gilt group were tested prior to sow farm entry and were negative for *M. hyopneumoniae* seroconversion via ELISA.

What does this mean?

The use of molecular characterization tools can be a vital component of an elimination program to aid veterinarians in the investigation of *M. hyopneumoniae* activity and variant origin. We used this tool and concluded that the co-sourced GDU was the most probable source of *M. hyopneumoniae* introduction in this case. We believe the gilts tested negative by ELISA due to the low sensitivity of the testing protocol.[3] It is vital to question the accuracy of the gilt "screening" protocols set in place to detect early *M. hyopneumoniae* infections.

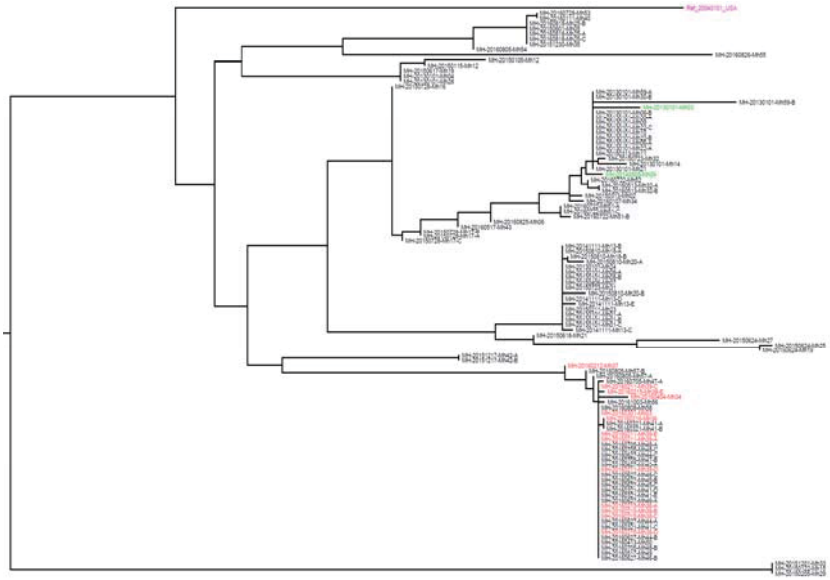

Figure 1. Comparison of p146 sequences obtained prior to and/or after *M. hyopneumoniae* outbreaks
*Green=sequences obtained prior to *M. hyopneumoniae* elimination program from one sow farm and a GDU that co-sourced all six sow farms; red=sequences obtained post completion of the *M. hyopneumoniae* elimination program from all six sow farms; pink=*M. hyopneumoniae* 232 reference strain; black=sequences obtained from other farms within the system.

References:
1) Holst S, et al. Elimination of *Mycoplasma* hyopneumoniae from breed-to-wean farms: A review of current protocols with emphasis on herd closure and medication. Journal Swine Health and Production. 2015; 23(6): 321-330.

2)Yeske PE. Economic impact of *M. hyopneumoniae* eliminations. Conference proceedings from 23rd International Pig Veterinary Society Congress. 2014. 256

3) Roos L, et al. A model to investigate the optimal seeder-to-naïve ratio for successful natural *Mycoplasma hyopneumoniae* gilt exposure prior to entering the breeding herd. Journal of Veterinary Microbiology. 2016. 51-18.

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