

MINIMAL *MYCOPLASMA HYOPNEUMONIAE* GENETIC VARIABILITY WITHIN PRODUCTION

FLOWS

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Introduction

Mycoplasma hyopneumoniae (*Mhp*) diagnostic tools, such as Multiple Locus Variable number tandem repeat Analysis (MLVA) and P146 sequencing have been used to characterize this microorganism at the molecular level. Multiple variants have been identified by MLVA; however, the extent of genetic variability within production stages in swine flows has not been evaluated. The objective of this study was to assess the genetic variability of *Mhp* within swine production flows in USA.

Methods

Four *Mhp* positive production flows across various states were selected for this investigation. Within each flow, a maximum of ten laryngeal swabs were obtained from 1-3 farms per production stage (i.e. gilt developer unit, sow farm, nursery, and finisher) for up to three years. Samples were collected from pigs showing clinical signs suggestive of infection or from randomly selected pigs in the case that no clinical signs were observed. All samples were tested by PCR. MLVA typing based on characterizing Variable Number Tandem Repeats (VNTRs) of two adhesion loci, namely p97 and p146, and p146 sequencing were performed using the DNA from 1-5 *Mhp* positive samples per farm.

Results

In one production flow, a single variant (100% p146 sequence similarity and one MLVA type) was identified across all four production stages. In the remaining three flows, 1-4 MLVA types and a 98-100% sequence similarity were identified. Nevertheless, MLVA types varied by 1-2 VNTRs for either locus.

Conclusions

From a geographical standpoint, there appeared to be no relationship between location and variant distribution. Therefore, the genetic variability of *M. hyopneumoniae* within swine production flows was minimal over time and flow specific. From this study, it can be hypothesized that evolutionary pressures associated with farm management practices may not have a significant effect on genetic variability. In addition, variants across all production stages appeared to originate from vertical transmission.