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## GILT FLOW AND ACCLIMATION AS DRIVERS OF *MYCOPLASMA HYOPNEUMONIAE* SOW HERD STABILITY

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### Introduction

The objective of this study was to characterize the *Mycoplasma hyopneumoniae* (*Mhp*) colonization and seroconversion pattern in negative gilts, which had been recently introduced to three positive farms.

### Materials

Farms practiced different types of replacement gilts' flow. Two of the three farms (A and B) practiced continuous flow, where gilts were co-housed with older gilts exhibiting coughing immediately post-entry, and shared the same air space, regardless of age. The remaining farm (C) practiced an all-in/all-out flow, where gilts were housed in separate air space from older gilts, and were co-housed with coughing culling sows at 130 days of age. Two replicates, of 35 gilts each, were randomly selected per farm and followed longitudinally. All gilts were sampled by blood collection and laryngeal swabs four/ five times every 60 days, approximately. Samples were assayed for *Mhp* antibodies and genetic material using a species-specific ELISA and real time PCR. The last sampling event took place peri-farrowing in all 3 farms, and 60 suckling piglets were sampled in Farms B and C to evaluate sow-to-piglet transmission. Moreover, *Mhp* genetic variability was evaluated in gilts at all farms using a MLVA typing method. The results showed a similar detection pattern of *M. hyopneumoniae* by PCR, as well as a similar seroconversion pattern.

### Results

No difference in the detection or seroconversion pattern was observed at farms regardless of the flow type. *Mhp* genetic material was not detected in the last sampling event (prior to farrowing), including in gilts introduced to the farm at 130 doa.

### Discussion

No sow-to-piglet transmission was detected. However, 30.9% of the gilts were not detected positive by PCR during the study, which may have resulted from a possible acclimation failure. Additionally, the genetic variability analysis revealed a limited number of *Mhp* variants in gilts at the three different farms.