

BBD-OP-02

TITLE

EVALUATION OF THE EXTENT OF MYCOPLASMA HYOPNEUMONIAE (MHYO) SHEDDING FROM GILTS TO THEIR PROGENY IN SEVEN MHYO ENDEMIC PIGGERIES IN AUSTRALIA

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CONTENT

Background and objectives: Mhyo is the leading cause of porcine respiratory disease complex associated with significant economic losses throughout the pig industry. Gilts are thought to play a role in Mhyo transmission, however it is widely thought that gilts stop shedding 43?46 weeks after exposure. The aim of this study is to determine the extent of Mhyo shedding in gilts to their progeny to better understand the ecology and epidemiology of Mhyo in Australia.

Material and methods: Piggeries (n=7) were selected based on replacement gilt source, i.e. in-house multiplication (IHR) closed herds versus purchased from suppliers (age ~16?22 weeks). Laryngeal swabs from gestating gilts (10?20/farm) and 3?4 week old gilt piglets (11?35/farm including 5?10 piglets per Mhyo-positive gilt) were tested using a commercial Mhyo real-time PCR assay.

Results: For Farms A?E (IHR) all samples tested Mhyo-negative in both gilts and gilt piglets. For Farm F (IHR), 20% of gilts tested Mhyo-positive at farrowing, but no gilt piglets were Mhyo-positive. For Farm H (purchased gilts) 73% of gilts (~30 weeks post arrival) and 17% of gilt piglets tested Mhyo-positive.

Discussion and conclusion: Results suggest that IHR and purchasing gilts from positive sources allows adequate Mhyo exposure to replacement gilts. On Farm F (purchased gilts from a Mhyo-negative source) 20% of gestating gilts tested Mhyo-positive, however as no gilt piglets tested Mhyo-positive, it is possible that the replacement gilts were not shedding at farrowing. Alternatively, the absence of Mhyo-positive piglets may be due to undetectable Mhyo-DNA level. On Farm H, a high proportion of gestating gilts were Mhyo-positive which did not translate to the number of Mhyo-positive gilt piglets observed. Again this may be due to Mhyo DNA below the assay detection limit. Research is planned to validate these hypotheses, through collection of longitudinal data at different farms, and across different parities.