

SWINE HEALTH

Title: Strain Variation in *Mycoplasma hyopneumoniae*; NPB #12-036
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Scientific Abstract

Mycoplasma hyopneumoniae is the causative agent of porcine mycoplasmosis and a major contributing factor in the Porcine Respiratory Disease Complex. Vaccine effectiveness against this agent has been reduced in recent years due to unknown reasons. One prevailing hypothesis is that antigenic variability in surface proteins in more recent field strains has reduced the effectiveness of bacterin-based vaccines using older strains. This project seeks to address the issue of antigenic variability by Next Generation High Throughput genome sequencing and comparing the sequences of surface antigens for amino acid variability. To this end, we subjected 17 single-colony cloned strains of *M. hyopneumoniae* to Illumina Next Generation Sequencing. Twelve of the strains were from the US Midwest and the others were from Belgium and Australia. Nextera XT kits were used for paired-end library preparation. Each library was bar coded for analysis in a single lane on an Illumina HiSeq-2000 platform. The assemblies were performed with A5 open source pipeline assembly software. In addition, a phylogenetic analysis was performed on the assembled genomes comparing the newly sequenced *M. hyopneumoniae* genomes against complete swine mycoplasma genomes in NCBI.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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