

## SWINE HEALTH

**Title:** Assessment of *Mycoplasma hyopneumoniae* strain variability and relationship to virulence - **NPB #02-126**

**Investigator:** F. Chris Minion

**Institution:** Iowa State University

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**Abstract:** The objective of this proposal is to assess variability of low-passage, field strains of *Mycoplasma hyopneumoniae*. Five strains were evaluated in a pig challenge model by comparing lung lesion scores with virulent strain 11. In addition, we studied the feasibility of using microarrays and other molecular techniques to assess genetic differences in twelve field strains.

**Introduction:** *M. hyopneumoniae* infection of swine has been universally established as among the most important diseases in the swine industry. Economic losses attributed to mycoplasma pneumonia in the U.S. swine industry easily exceeds \$2 per pig or approximately \$200 million annually. Loss occurs as a consequence of reduced average daily gain and efficiency of feed utilization, prophylactic and therapeutic interventions, and mortality. Prevalence of lesions of enzootic pneumonia in swine at slaughter has been very high (>70%) for many years and does not seem to have abated over the past 40 years. During recent years, swine practitioners and diagnosticians have noted an increased occurrence of severe pneumonia, referred to as Porcine Respiratory Disease Complex (PRDC). *M. hyopneumoniae* is an integral component of PRDC in association with other swine pathogens such as PRRSV and SIV. In combination with other respiratory pathogens such as PRRSV, however, pneumonia due to the second pathogen is significantly enhanced. Vaccination against *M. hyopneumoniae* neither prevents colonization of the swine respiratory tract nor protects sufficiently against disease. In addition, vaccination does not obviate the potentiating role of *M. hyopneumoniae* in dual infection with other pathogens. In the absence of effective intervention strategies to reduce disease, improved vaccines are essential if we are to reduce economic losses due to mycoplasma pneumonia.

An important problem that has not received adequate study is the possibility of genetic variability in *M. hyopneumoniae* field strains and the impact that would have on virulence. Genetic variability can significantly alter disease progression and complicate control measures by changing the surface architecture of *M. hyopneumoniae* and its presentation to the host's immune response. The extent of genetic variability in *M. hyopneumoniae* is not known.

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**For more information contact:**

**National Pork Board, P.O. Box 9114, Des Moines, Iowa USA**

800-456-7675, **Fax:** 515-223-2646, **E-Mail:** [porkboard@porkboard.org](mailto:porkboard@porkboard.org), **Web:** <http://www.porkboard.org/>