Understanding Mycoplasma bovis

**Project Title:**
Investigating antimicrobial resistance (AMR) and virulence factors of Mycoplasma bovis

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**Background:**

*Mycoplasma bovis* (*M. bovis*) is associated with respiratory disease, arthritis, mastitis and ear infections in cattle. It’s not clear whether the same strains of *M. bovis* are responsible for each of these different manifestations. Developing a vaccine against *M. bovis* is difficult because it can switch which antigens it expresses on the cell surface. *M. bovis* may also becoming more antimicrobial resistant and may be able to transfer its antimicrobial resistance genes to other respiratory disease pathogens.

**Objectives:**

To gain a better understanding of *M. Bovis* and how it manifests itself in different diseases.

**What They Will Do:**

The research team will sequence the microbial genomes and characterize the upper and lower respiratory microbiomes (including all *Mycoplasma* species) of 50 cattle dying from mycoplasma pneumonia to those of 50 cattle dying from other respiratory diseases. They will examine which *Mycoplasma* species are present in the upper vs. lower respiratory tract as well as differences between calves infected with mycoplasma vs. other forms of pneumonia.

Whole genome sequencing and phenotypic antimicrobial resistance testing will be conducted on 250 *M. bovis* isolates from 2008 through 2019 to assess how antimicrobial resistance profiles have changed over time. These samples will also be used to
determine whether different *Mycoplasma* strains prefer the lung or the joints.

Since the expression of the surface proteins is so variable, the researchers will use the whole genome sequence data to look for other known virulence factors. These results will be compared to cell culture virulence assays as well as for differences in adhesion to bovine bronchial and nasal cells.

Conjugation assays will be conducted to determine whether *M. bovis* can exchange antimicrobial resistance genes with other bacteria such as *M. haemolytica*, *H. somni*, and *P. multocida*.

**Implications:**

This project will quantify changes in antimicrobial resistance patterns over time and evaluate whether *M. bovis* exchanges antimicrobial resistance genes with other bovine respiratory disease pathogens. This research will also support the development of more effective treatment regimens, as well as identify more promising vaccine candidates.

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