
RESOLUTION NUMBER: 36 **Approved**

SOURCE: **COMMITTEE ON SHEEP, GOATS AND CAMELIDS**

SUBJECT MATTER: **To Urge the Establishment of Accurate Testing Protocols for *Mycoplasma ovipneumoniae* (*M. ovipneumoniae*), to Include Differentiation Between *M. ovipneumoniae* and a Newly Identified Respiratory-associated *Mycoplasma* Species (*Mycoplasma* nov. sp.¹) and to Urge Completion of Phylogenetic Analysis of Full-length Sequences of *M. ovipneumoniae* Isolated from Multiple Species.**

BACKGROUND INFORMATION:

Mycoplasma ovipneumoniae (*M. ovipneumoniae*) is endemic in wildlife species (captive and free-range), in addition to domestic sheep and goats.

Many published polymerase chain reaction assays used for *M. ovipneumoniae* detection are not specific for *M. ovipneumoniae*, rather indiscriminately detect *Mycoplasma* nov. sp. in addition to *M. ovipneumoniae*, therefore resulting in the potential for false positive results when testing for *M. ovipneumoniae*.

This novel species of mycoplasma has not been an identified cause of disease. It would be beneficial to both domestic and wildlife species to ensure accurate testing that differentiates *M. ovipneumoniae* and *Mycoplasma* nov sp.

RESOLUTION:

The United States Animal Health Association (USAHA) urges the United States Department of Agriculture (USDA), Animal and Plant Health Inspection Service and USDA, Agriculture Research Service (ARS) to establish accurate testing protocols for *M. ovipneumoniae* that include differentiation between *Mycoplasma ovipneumoniae* and other *Mycoplasma* spp., including the recently identified *Mycoplasma* nov. sp.

Further, USAHA urges USDA-ARS to complete phylogenetic analysis of full length sequences of multiple *M. ovipneumoniae* isolates from different species to fully understand the genotypes,

¹ Herndon DR, Beckmen KB, Highland MA. Draft Genome Sequence of a Novel *Mycoplasma* Species Identified from the Respiratory Tract of an Alaska Moose (*Alces alces gigas*). Microbiol Resour Announc. 2021 Feb 25;10(8):e01371-20. doi: 10.1128/MRA.01371-20. PMID: 33632866; PMCID: PMC7909091.

phylogeny, and pathogenesis of this bacterium that has been identified in multiple domestic and wildlife species.

RESPONSE:

Mycoplasma species differentiation requires in-depth knowledge of the sequences for both Mycoplasma species present in the United States. This is because current PCR based methodologies will eventually become obsolete due to the high sequence variability of Mycoplasma strains and the emergence of new strains. PCR tests are currently available for purchase through the Kansas State Veterinary Diagnostic Laboratory at Kansas State University.

To overcome the lack of sequence data, ARS scientists developed a multi-locus sequence typing (MLST) analysis to differentiate bacterial species. MLST sample analysis is available for purchase through the Washington Animal Disease Diagnostic Laboratory (WADDL) at Washington State University. However, WADDL scientists believe that current MLST analysis may be providing false positives and false negatives for *Mycoplasma ovipneumoniae*. To improve the phylogenetic analysis of full-length sequences, ARS researchers are currently preparing bacterial genomic DNA to sequence 20 *M. ovipneumoniae* genomes isolated from domestic sheep. Isolates chosen for sequencing are based on their phylogenetic distance in the MSLT markers and ARS is aware of other scientists also working to improve MLST analysis.