

# Identification and antimicrobial resistance of *Bibersteinia trehalosi*

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## Introduction

*Bibersteinia trehalosi*, (formally *Pasteurella trehalosi* and *Pasteurella haemolytica* complex biovar T) is a known cause of disease in ruminants worldwide. Typically, *B. trehalosi* is associated with pneumonia or septicemia in sheep. Although infection with *B. trehalosi* is rare in cattle, it is a potential agent responsible for bovine respiratory disease (BRD). Anecdotal reports of increasing prevalence of *B. trehalosi* in cattle with severe disease have heightened producer and veterinary awareness.

Proper identification of *B. trehalosis* as a source of an infection is important for making treatment and prevention management decisions. Misidentification of respiratory pathogens is possible without utilization of the proper diagnostic tools. Traditionally, laboratories have relied solely on colony morphology, hemolysis patterns, and sugar fermentation to identify *B. trehalosi*. The aim of the study was to properly identify *B. trehalosi* on the basis of phenotypic and biological characterization. Additionally, evaluation of the antimicrobial susceptibility patterns of *B. trehalosi* from bovine respiratory cases were used to determine the impact of antimicrobial resistance on pathogenicity.

## Materials and Methods

A total of 19 isolates were used in this study. Ten preliminarily identified *B. trehalosi* isolates were obtained from the Iowa State University Veterinary Diagnostic Lab (VDL) by a search of the ISU-VDL Laboratory Information Management System (LIMS). Nine additional *B. trehalosi* isolates from outside sources were

also used. A 16s ribosomal RNA gene (rDNA) sequence analysis was performed on all isolates to confirm their identification.

All *B. trehalosi* isolates identified by 16s rDNA sequencing were subjected to antimicrobial sensitivity testing via TREK MIC. Isolates were ranked as highly resistant, moderately resistant, or highly susceptible. Highly resistant isolates were resistant to all but three or four antimicrobials. Moderately resistant isolates were resistant to about half of the antimicrobials evaluated. Highly susceptible isolates were susceptible to all but three or four antimicrobials.

## Results

Results of 16s rDNA analysis identified 14 of the 19 isolates as *B. trehalosi*. Three were identified as *Galibacterium anatis* and two as *Mannheimia varigena*. Seven of the 12 isolates used in biochemical analysis were *B. trehalosi*.

All isolates had similar colony morphology. Hemolytic patterns were variable among the *B. trehalosi* isolates; one sheep *B. trehalosi* isolate was  $\beta$ -hemolytic and two isolates from goats were non-hemolytic. These results are consistent with previously published data. However, four bovine *B. trehalosi* isolates in this study had variable hemolytic patterns, which contrasted with results of a previous study, in which 14 bovine isolates were non-hemolytic.

Five of 14 isolates were highly resistant to most antibiotics. One of 14 isolates had moderate resistance to about half of the antibiotics. Eight of 14 isolates were susceptible to most antibiotics.