

# Comparison of sampling methods and diagnostic techniques for recovery of *Mannheimia haemolytica* from feedlot cattle

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## Introduction

Bovine respiratory disease (BRD), an economically impactful disease of feedlot cattle, is caused by interactions between host and environmental factors and pathogens. The current standard for antemortem pathogen identification is guarded deep nasopharyngeal swabbing, which is technically challenging, costly and waste generating. The objective was to compare recovery rates of *Mannheimia haemolytica* (MH) by culture and real time-quantitative polymerase chain reaction (qPCR) using guarded deep nasopharyngeal swabs (DNPS), 16-in. proctology swabs (PS) and 6-in. nasal swabs (NS).

## Materials and methods

Samples were collected from 2 groups of beef steers and bulls (n = 60 per group, mean weight = 262.2 +/- 12.5 kg). The left nostril was sampled with each swab type for culture, MALDI-TOF-MS identification, genotype classification, and antimicrobial susceptibility testing. The right nostril was sampled by each swab type for qPCR for the MH leukotoxin d gene.

## Results

Using culture, MH was recovered from 56% (203/360) of the swabs (68 NS, 67 DNPS, 68 PS); all isolates were Genotype 2. Nearly all isolates (200/203) were resistant to  $\geq 2$  drug classes (MDR); 3 isolates recovered from one animal were pansusceptible. The frequency of MH isolation and recovery of MDR isolates was not statistically different for the different swab types ( $P > 0.05$ ). Using qPCR, 76% of the swabs tested were MH positive (79% NS, 64% DNPS, 82% PS).

## Significance

Swab types provided comparable results for MH recovery. Sensitivity of qPCR was greater than culture. Use of nasal swabs or proctology swabs can provide comparable results faster, with less cost and waste than guarded swabs.

