

Agreement of nasal swabs, guarded nasopharyngeal swabs, and bronchoalveolar lavage relative to transtracheal wash for the diagnosis of viral and bacterial pathogens in dairy calves with bovine respiratory disease

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Introduction

Bovine respiratory disease (BRD) is common in dairy calves, with 21.3% of mortality in preweaned calves and 50.4% of mortality in weaned heifers attributed to BRD (USDA NAHMS, 2002). Four sampling methods are used for antemortem identification of respiratory pathogens: the nasal swab (NS), guarded nasopharyngeal swab (NPS), transtracheal wash (TTW), and bronchoalveolar lavage (BAL). Each method has advantages and disadvantages. The TTW bypasses contamination from the nasopharynx, but the procedure is invasive and requires technical skill. The BAL and TTW directly sample the lower airways, but BAL, NS, and NPS can be contaminated by nasopharyngeal flora. Compared to NS, NPS provides a guarded sample of the pharyngeal recess, which may be more representative of BRD pathogens. To our knowledge, no published study has compared the results of all four of these methods in cattle with clinical BRD. The objective of this study was to compare the agreement of results obtained by NS, NPS, or BAL with those obtained by TTW for isolation of BRD pathogens in dairy calves with acute undifferentiated BRD.

Materials and Methods

Subject calves were housed on a privately owned calf rearing facility in Tulare, CA. All calves with primary naturally occurring respiratory disease in the first 90 days of life, as defined by a score of 5 or greater on the University of Wisconsin Calf Respiratory Scoring Chart, a fever of 103°F or higher, and at least 2 cm² of pulmonary consolidation identified by transthoracic ultrasound, were eligible for enrollment. Calves that had been treated for respiratory disease at any time, or calves that had been given intranasal modified live viral respiratory vaccine in the previous 30 days, were excluded. From each calf enrolled, NS, NPS, TTW, and BAL samples were collected sequentially using standard methods. All samples were tested by aerobic bacterial culture and real time reverse

transcriptase PCR (RT-PCR) for bovine respiratory syncytial virus (BRSV), bovine coronavirus (BCV), bovine viral diarrhea virus (BVDV), and bovine herpesvirus-1 (BHV-1). For each pathogen, agreement between tests and a comparison of positive results was determined by calculation of the kappa statistic and McNemar's chi-square test, respectively. Kappa values were interpreted to indicate strength of agreement as defined by Altman (1991): less than 0.20=poor; 0.21 – 0.40=fair; 0.41 – 0.6=moderate; 0.61 – 0.80=good, and 0.81 – 1.00=very good.

Results

One hundred calves were enrolled. Average calf age was 49 d, average rectal temperature was 103.8°F, average respiratory score was 10, and an average of 22.1 cm² of lung consolidation was identified by ultrasound. The prevalence of pathogens identified by TTW was: 6.6% for BCV, 17.4% for BRSV, 16.0% for *M. haemolytica*, and 59.0% for *P. multocida*. No samples were positive for BHV-1, BVDV, or *H. somni*. When *M. haemolytica* and *P. multocida* were isolated, all methods showed very good agreement relative to the TTW. When BRSV was detected, the NS had moderate agreement, the NPS had good agreement, and the BAL had very good agreement. Lastly, when BCV was detected, the NS and NPS had moderate agreement while the BAL had good agreement.

Significance

The agreement between TTW and other sampling methods differed among pathogens. All four methods yielded similar results for detection of *M. haemolytica* and *P. multocida*, while BAL had better agreement relative to swabs when compared to TTW for detection of BRSV and BCV. Future work is warranted to determine if the relative agreement among these diagnostic tests is the same for other classes of cattle with BRD.