Posters

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Polymicrobial Etiology of Bacterial Pneumonia Associated with the Bovine Respiratory Disease Complex

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Introduction

The bovine respiratory disease complex (BRDC) is currently recognized as the most costly infectious disease problem for beef producers in North America. The BRDC is associated with severe and often fatal bacterial pneumonia. The most common and virulent bacterial pathogen associated with BRDC is Mannheimia (M.) haemolytica. However, other pathogens are sometimes isolated from pneumonic tissue. In this project, we completed a quantitative and qualitative characterization of the organisms associated with fatal cases of BRDC.

Materials and Methods

In the first study, 20 lungs from calves with acute and fatal pneumonia were subjected to quantitative and qualitative analysis. The calves from which these lungs were selected died prior to antimicrobial treatment. Bacterial identification was completed using standard diagnostic methodology. In addition, tissue samples were processed through mesh screens for serial dilution to quantitate bacteria per gram of pneumonic tissue by serial dilution and subsequent plate counts of colony forming units. Antimicrobial sensitivity testing was completed by Kirby-Bauer testing and in some cases confirmed by broth dilution testing. An additional set of 225 case submissions of BRDC were also evaluated to confirm the polymicrobial nature of BRDC.

Results

The most common bacterium isolated was M. haemolytica (95% of the cases) and it was present from 2 X 10^3 to 5 X 10^8 cfu per gram of affected lung tissue. The lung tissue at the periphery of the consolidated tissue was predominantly infected with M. haemolytica. However, Pasteurella (P.) multocida, P. trehalosi, Histophilus somni and other bacteria were isolated from 16 of 20 lungs, most often from the center of the consolidated tissue as well as from within the conductance zones. Multiple phenotypes of M. haemolytica were isolated from individual lungs. The predominant phenotype was mucoid, resistant to tetracyclines and expressed patterns of restricted carbon source utilization. From a broader set of isolates from lungs of BRDC cases (n=225 cases), a similar distribution of expressed phenotypes was observed. The large majority (>95%) were susceptible to commonly used antimicrobial agents but were resistant to ampicillin, tetracyclines and erythromycin. In a secondary set of cases (n=42) where tissues were available to test for infection by possible translocation from the lung, similar patterns were observed except that a significant number of isolates were also resistant to florfenicol (28%) and/or tilmycosin (12%).

Significance

The continued recognition that the bacterial pneumonia of the BRDC is polymicrobial could have significant impact on therapeutic strategies as well as clinical outcomes. The total numbers of bacteria present in an infected lung are are high but consistent with other forms of bacterial pneumonias in other mammalian species. These observations reinforce the necessity of early diagnosis and treatment. The polymicrobial and polyclonal nature of the infections may also increase the likelihood of systemic inflammatory distress syndromes. It is also clear that the density and diversity of the infections characterized are great enough in magnitude to reach the thresholds of spontaneous mutant generation. Therefore, antimicrobial therapeutic doses should ideally be above mutant prevention concentrations.

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