Seminar: Unraveling the role of Antimicrobial Resistance in Bovine Respiratory Disease

Bovine respiratory disease (BRD) is the most prevalent disease in North American feedlot cattle, accounting for 65–80% of feedlot morbidities and 45–75% of mortalities costing the global cattle industry over $3 billion annually. It arises from a multifactorial interaction of stressors, animal susceptibility, and respiratory pathogens, with Mannheimia haemolytica, Pasteurella multocida, Histophilus somni and Mycoplasma bovis being the primary causative agents. Antimicrobial therapy is a valuable tool for preventing, treating, and controlling BRD, but its efficacy is compromised by the emergence of antimicrobial resistance and a lack of new generation antimicrobials. Bacterial members of the BRD complex respond to antimicrobials by developing or acquiring resistance genes or resistance-mediated mutations. Mobile genetic elements (MGEs), such as plasmids, transposons, or integrative conjugative elements (ICE) carry resistance genes and play a key role in the dissemination and persistence of resistance within the Pasteurellaceae. ICE accumulate antimicrobial resistance genes (ARGs), with some elements carrying 12 or more ARGs conferring resistance to all antimicrobials approved for the treatment of BRD. ICEs can also harbor genes associated with host survivability, environmental fitness (e.g., heavy metal, acid, heat, or phage resistance), metabolism and virulence. We have found that ICE are transferred to other bacterial species. This presentation will outline the numerous factors that contribute to AMR within the bacterial BRD complex and shed light as to why BRD continues to be a devastating disease to the North American feedlot industry.