Genotyping and antimicrobial resistance patterns of *Mannheimia haemolytica*, *Pasteurella multocida* and *Histophilus somni* isolated from the upper and lower respiratory tract of feedlot cattle

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Introduction

In the last 10 years, the prevalence of Pasteurellaceae resistant against drugs typically used for bronchopneumonia (BP) control has increased in feedlot cattle. Surprisingly, it is not clear whether this increase in the prevalence of multidrug resistant (MDR) bacteria is due to the spread of 1 or few multiple MDR clones among cattle during the feeding period (i.e. horizontal spread) or due to the recrudescence of MDR clones already present in the respiratory tract of cattle upon arrival at feedlots. Recently, we reported a high prevalence of MDR *M. haemolytica*, *P. multocida*, and *H. somni* isolated from cattle with BP in 4 feedlots in Western Canada. Unfortunately, as we did not genotype these isolates, it was not possible to determine whether a few or a large number of MDR clones were present in these feedlots, supporting either a horizontal spread of MDR clones among cattle or a recrudescence from carriers. Therefore, the objective was to genotype *M. haemolytica*, *P. multocida*, and *H. somni* isolates using pulsed field gel electrophoresis (PFGE).

Materials and Methods

Newly-received beef-crossed feedlot calves (arrival body-weight ± SD = 620.4 ± 61.6 lb [282 ± 28 kg]) with BRD (n = 210) and pen-matched controls (n = 107) were sampled by DNS and TTA at 4 feedlots in Western Canada. *M. haemolytica*, *P. multocida,* and *H. somni* were isolated from DNS and TTA samples and their AMR profiles were determined using broth dilution method. Isolates were then typed by PFGE and grouped into pulsotypes (≥90% similarity).

Results

In total, 195, 277, and 139 isolates of *M. haemolytica*, *P. multocida*, and *H. somni*, respectively, were isolated from DNS and TTA samples. A high proportion of *M. haemolytica* (≥ 73%) and *P. multocida* (≥ 78%) isolated from DNS and TTA were resistant against oxytetracycline (OXY) and tulathromycin (TUL). Concerning *H. somni*, there were high levels of resistance against OXY (≥ 52%) and penicillin (PEN; ≥52%) in both DNS and TTA samples. None or few isolates were resistant to florfenicol (FEE), enrofloxacin (ENR) and ceftiofur (CEF). *M. haemolytica* isolates were distributed among 20 pulsotypes and 26 singlets. However, the majority of isolates (54%) belonged to a single pulsotype, which displayed resistance to TUL and OXY. This pulsotype was isolated from 29 different pens across all 4 feedlots. *P. multocida* isolates were distributed among 9 pulsotypes and 11 singlets with the majority of isolates (67%) belonging to 1 pulsotype that displayed resistance to TUL and OXY. This pulsotype was present in 33 pens across all 4 feedlots. *H. somni* isolates were distributed among 13 pulsotypes and 28 singlets that were either susceptible to all antimicrobials tested or resistant to PEN and OXY.

Significance

The genotyping and antimicrobial susceptibility testing of Pasteurellaceae isolated from cattle recently placed at 4 feedlots showed that MDR clones of *M. haemolytica* and *P. multocida* can be shared among a large number of cattle within and between feedlots. As cattle were very likely from multiple origins, this finding suggests a horizontal transmission of these clones among cattle shortly after arrival at the feedlots.