AVC SRLP Abstract

Title: Genomic and phenotypic traits of antimicrobial resistance in bovine respiratory bacterial pathogens

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Abstract:

Bovine respiratory disease (BRD) is one of the most significant diseases that can cause illness, mortality, and economic losses in the dairy industry. BRD can be triggered by several factors, such as bacteria, viruses, and weakened immunity, and it is one of the most common reasons for antimicrobial use in cattle. The key bacterial pathogens that cause BRD are Mannheimia haemolytica, Pasteurella multocida, and Histophilus somni, and are attributed to a high rate of antimicrobial use in cattle. Therefore, the objective of this study was to investigate the phenotypic and genomic AMR characteristics of the three bacterial pathogens isolated from nasal swabs collected from apparently healthy dairy cows across Canada. A total of 51 isolates were included in the study: 42 P. multocida, 9 M. haemolytica, and 1 H. somni. For the phenotypic analysis, all samples underwent antimicrobial sensitivity testing to determine the minimum inhibitory concentration (MIC) of 11 antimicrobials. For the genomic analysis, DNA extraction and whole-genome sequencing (WGS) were conducted using the Mk1b Oxford Nanopore system. Genome assembly and AMR gene detection were performed using the EPI2ME bioinformatic platform. All the P. multocida isolates were susceptible to all the antimicrobials except for tylosin, and three isolates of M. haemolytica were resistant to at least one antimicrobial by MIC assay. Genomic analysis revealed that two M. haemolytica isolates carried multiple AMR genes, whereas another isolate carried only the blaROB-1 gene. No AMR genes were detected in any of the other bacterial isolates.

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