

Comparison of whole-genome sequencing and pulsed field gel electrophoresis for characterizing relationships in *Mannheimia haemolytica*

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Introduction

It has long been presumed that cattle developing BRD tend to become sick from their own native strains of *Mannheimia haemolytica*. Previous work by others has demonstrated that the diversity of *Mannheimia haemolytica*, as evaluated by PFGE, within a pen of cattle remains high during BRD outbreaks. Prior to the development of whole genome sequencing (WGS), pulsed field gel electrophoresis (PFGE) had been considered the gold standard for characterizing outbreaks of bacterial disease. Recently, many studies from the human literature have raised question regarding the accuracy of PFGE as WGS has become more widely implemented. Studies investigating *Acinetobacter baumannii*, *Clostridium difficile*, and vancomycin resistant *Enterococci* outbreaks in hospitals have shown WGS to have superior discernment and more accurately classify strains when compared to PFGE. Considering the superiority of WGS in characterizing outbreaks in all of these species, it may be that relationships inferred in *Mannheimia haemolytica* based on PFGE could be inaccurate. It is therefore our goal to compare the discernment ability of PFGE and WGS for *Mannheimia haemolytica* isolates collected from beef cattle.

Materials and Methods

A total of 48 *Mannheimia haemolytica* isolates collected from lightweight beef cattle that had been collected as part of another study were submitted for PFGE. An identity cutpoint

of 90% was used to cluster the isolates, and a dendrogram was generated. Whole genome sequences of the same 48 isolates that had been sequenced as part of another study were submitted to the CSI Phylogeny web interface for alignment. The resulting alignment file was used to create a maximum likelihood tree using RAxML version 8.2.11 in Geneious, using a GTR GAMMA nucleotide model and running 1,000 bootstrap replicates.

Results

The tree produced by PFGE found the isolates falling into 11 different clusters. The tree produced by WGS placed the isolates into a total of 4 different clusters. Multiple isolates that had been grouped together by WGS were not grouped together by PFGE.

Significance

As has been seen in the human literature, the results of this study suggest that PFGE may not accurately classify *Mannheimia haemolytica* isolates when compared to the results from WGS. This study furthermore suggests that PFGE may imply greater diversity in isolates than is actually present based on WGS.