Genomic characterization of Salmonella Dublin recovered from Ohio cattle

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Introduction

Multidrug-resistant (MDR) Salmonella enterica is a threat to animal and human health. Salmonella Dublin, a bovine-adapted S. enterica serotype, causes severe outbreaks among calves that frequently result in high mortality. Additionally, S. Dublin causes invasive infections in people, and the incidence of S. Dublin infections in people has been increasing over the past decade. Recovered isolates are frequently resistant to antimicrobials necessary for the treatment of invasive infections in calves and people. The transmission pathways of virulent Salmonella serotypes are not well characterized. Genomic characterization of recovered strains can be used to elucidate the genetic relatedness and identify potential routes of transmission. Therefore, the objective of this study as to characterize the genetic relatedness and genomic antimicrobial resistance determinants of S. Dublin recovered from cattle in Ohio.

Materials and Methods

Twenty-four S. Dublin isolates recovered from samples submitted to the Ohio Department of Agriculture from sick cattle were selected for whole-genome sequencing (WGS) with Illumina MiSeq. Genotypic analysis of AMR determinants and plasmid replicons in each assembly was performed through Center for Genomic Epidemiology (https://cge.cbs.dtu.dk/services/) and nucleotide BLAST analyses. The webtool CSIPhylogeny 1.4 was used for phylogenetic reconstruction to determine S. Dublin relatedness.

Results

All isolates were multilocus sequence type (MLST) ST-10 and showed close clustering in single nucleotide polymorphism (SNP) phylogenetic analyses, demonstrating the circulation of a single clonal strain. Additionally, WGS efficiently characterized genomic determinants of resistance. All genomic determinants of resistance were plasmidmediated, and the majority of identified resistance genes were located on plasmid incompatibility group IncA/C2; however other plasmid replicon groups (IncFII(S) and IncX1) were also present. Among fluoroquinolone resistant isolates, WGS identified chromosomal point mutations, but no plasmid-mediated quinolone resistance genes were identified.

Significance

Strains of Salmonella Dublin recovered from Ohio cattle were highly genetically related, demonstrating on-going circulation of single clonal complex. Additionally, WGS was useful to comprehensively identify the genomic-mediators of the previously identified resistance phenotypes and their genomic location. Genes mediating resistance to critically important antimicrobials were located on horizontally transmissible plasmids. Regardless, further characterization of the transmission pathways for S. Dublin and other virulent serotypes Salmonella serotypes is necessary to identify optimal prevention practices and reduce the incidence of disease in animals and people.