Contribution ID: **319** Type: **Oral presentation**

Phenotypic and genotypic antimicrobial resistance of Streptococcus uberis isolated from bovine mastitis in Thuringia, Germany

Wednesday, 11 October 2023 11:30 (15 minutes)

Bovine mastitis is a highly prevalent disease plaguing the dairy industry. *Streptococcus uberis* is the most predominant pathogen for bovine mastitis and is frequently isolated from milk of infected quarters. This study aimed to identify the phenotypic and genotypic antimicrobial resistance (AMR). 80 *S. uberis* were isolated from milk samples of dairy cows with clinical mastitis in Thuringia. Phenotypic AMR testing was achieved for all strains against 24 clinically relevant antimicrobial agents using a broth microdilution test. Illumina Miseq was used for genomic sequencing of 80 strains and 24 strains were further sequenced by Oxford Nanopore Technologies' MinIon. Bioinformatic analysis for AMR genes, plasmids, MLST, and virulence associated genes was performed. Phenotypic AMR against 5 antibiotic classes (β-lactams, lincosamides, aminoglycosides, macrolides, fluoroquinolones) were determined. Genetic marker for resistance against tetracyclines, lincosamides, aminoglycosides, and macrolides were detected. 21% of the strains were resistant against pirlimycin (lincosamides), while *tet(M)* associated with tetracycline resistance was the commonest detected genetic marker. 93% of the sequenced strains contain plasmid-borne sequences indicating a possible transmission of AMR genes. While the genomes of *S. uberis* generally show a high diversity, indicated by 57 detected sequence types, a few genomically highly similar strains persisted within farms or circulated between farms.

Keywords

Bovine mastitis; S. uberis; genome sequencing; AMR; virulence; MinIon; Illumina;

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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