

Session 5 - Novel approaches, methods and tools dedicated to antimicrobial resistance (detection, evolution, diagnostics, surveillance)

P85

Phenotypic and WGS-based characterization of antimicrobial resistance of *Trueperella pyogenes* clinical isolates from humans and animals in Switzerland

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Trueperella pyogenes, a commensal Gram-positive facultative-anaerobic rod of the skin and mucous membranes of animals can cause suppurative infections in animals, and rarely humans (1). These infections are commonly treated with antibiotics, posing the risk of selecting resistant bacteria through the acquisition of mobile genetic elements containing antimicrobial resistance genes (2). The objectives of the present study were to determine i) the phenotypic and genotypic antimicrobial resistance profiles of *T. pyogenes* in Switzerland, and ii) the genetic relatedness between strains of different origins.

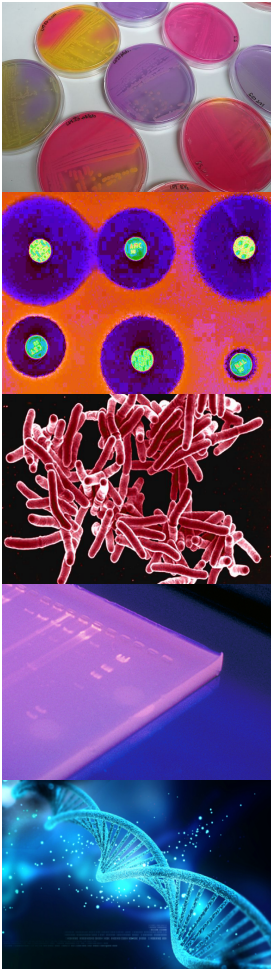
Thirty-five *T. pyogenes* isolates from animals and 8 from humans were obtained from a veterinary and a human diagnostic facility in Switzerland. The strains were cultivated on TSA-S (Becton, Dickson) under 5% CO₂ atmosphere at 37°C for 24 hours. Identification was confirmed by MALDI-TOF mass spectrometry (Bruker). Minimal inhibitory concentrations (MICs) of 19 antibiotics and 3 antiseptics were determined by broth microdilution method following CLSI recommendations. The MICs were interpreted using breakpoints derived from previously published data. Genomic DNA was extracted using Masterpure™ purification kit (Lucigen) and sequenced at the NGS Platform, University of Bern, Switzerland, using PacBio HiFi technology. Reads were demultiplexed and *de novo* assembled using Flye v.2.9.1. The 43 complete genomes were screened *in silico* for antimicrobial resistance genes using Resfinder v.4.1 (Center for Genomic Epidemiology) and CARD-RGI (McMaster University). Core genome-based MLST (cgMLST) analysis was performed for phylogenetic relatedness.

Seventeen isolates were susceptible to all tested antibiotics. Resistant test results to tetracycline (n=23), streptomycin (n=20), and sulfonamides (n=17) were common in both animal and human isolates, while resistance to erythromycin (n=4), clindamycin (n=3), trimethoprim (n=2), and chloramphenicol (n=2) was only sporadic and predominantly detected in animal isolates. The resistance genes *tet(W)*, *aadA9*, and *sulI* were the most frequently detected, reflecting the phenotypic resistance profile. Phenotypic resistance to quaternary ammonium compounds was not observed despite the frequent detection of the resistance gene *qacEAI*. Two large clusters were identified by cgMLST, revealing that human isolates were more closely related to those from cattle compared to other animal species.

The presence of genetically related *T. pyogenes* strains in humans and animals suggests that exchange of mobile genetic elements may occur. Acquired resistances to several antimicrobials indicates that judicious use of antibiotics should be made based on antimicrobial susceptibility testing.

References

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- [2] Feßler AT, Schwarz S. 2017. Antimicrobial resistance in *Corynebacterium* spp., *Arcanobacterium* spp., and *Trueperella pyogenes*. *Microbiol Spectr* 5(6) DOI: 10.1128/microbiolspec.ARBA-0021-2017



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