

ARE ANIMALS FROM THE PATIENTS' FARMS A SOURCE OF NOSOCOMIAL LA-MRSA INFECTION?



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Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most common causes of nosocomial infections, but the occurrence of livestock-associated MRSA (LA-MRSA) strains in human infections has become an emerging issue. An important risk factor for LA-MRSA infection is a direct or indirect contact with livestock, particularly pigs, which are the main reservoir of LA-MRSA. In Slovenia, there is an increasing number of humans colonised with MRSA resistant to tetracycline, which is the antibiotic resistance characteristic for LA-MRSA.

Materials and methods

- **15 Slovenian farms** – recent colonisation or hospitalisation of the family members due to LA-MRSA → epidemiological investigation → nose, throat, skin or wound swabs – all household members, nasal swabs – animals, farm environment
- **4 farms:** LA-MRSA isolates (**n=31**) from human and animals/environment → antimicrobial susceptibility testing (microdilution method - MIC for 19 antimicrobials) → *spa* typing
- **WGS:** Illumina paired-end sequencing (2×150 bp) on a NextSeq 500 platform → quality trimming with Cutadapt 1.18 and assembly into contigs with SPAdes 3.13.0 → ResFinder 3.1, VirulenceFinder 2.0, SCCmecFinder 1.2, CSI Phylogeny 1.4 (SNP analysis), MLST according to PubMLST scheme for *S. aureus* (<https://pubmlst.org/saureus/>)

Results

All isolates were of **sequence type (ST) 398**, harboured the **SCCmec type Vc** and virulence genes encoding **gamma haemolysin (*hlyABC*)** + **aureolysin (*aur*)** and were susceptible to rifampin, fusidic acid, vancomycin, linezolid, mupirocin, streptomycin and sulfamethoxazole.



Fig. 1: Maximum-likelihood SNP tree of LA-MRSA isolates, inferred by CSI Phylogeny 1.4 and RAxML 8.2. The tree is labeled with farm, origin of isolation and the presence/absence pattern of resistance genes, classified into six antimicrobial groups (aminoglycosides, beta-lactams, macrolides/lincosamides/streptogramins (MLS) group, tetracyclines, trimethoprim and chloramphenicol). Isolates from index patients are colored in red. Clusters of isolates exhibiting ≤13 SNPs are colored in red.

TIA, tiamulin; FOX, cefoxitin; CLI, clindamycin; SYN, quinupristin/dalfopristin; TET, tetracycline; TMP, trimethoprim; CIP, ciprofloxacin; GEN, gentamicin; ERY, erythromycin; CHL, chloramphenicol; KAN, kanamycin

Conclusions

Index patients were not closely related to animal and environmental isolates from the farms. Pigs from one farm were colonised with different LA-MRSA strains and indistinguishable strains were also detected in the cat and ram. These animals could be the source of LA-MRSA for human colonisation/infection, although the SNP-based analysis suggested nosocomial transmission of LA-MRSA. Long-term colonisation with the same LA-MRSA strain in index patients calls for the implementation of a regimen for successful decolonisation and/or treatment in humans, which should consider that it is also influenced by host factors.