

Poster Abstract 7th AMR Conference

Topic: **Diagnostic AMR innovations for humans and animals**

Title: **Molecular characterization of more than 700 different methicillin-resistant *Staphylococcus aureus* clones**

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The presence of antimicrobial resistance genes on mobile genetic elements spreading across different *Staphylococcus* species including *S. aureus* is an important public health issue. The study of *S. aureus* genotypes, including isolates from animals and humans, is essential to understand the global epidemiology of *S. aureus* infections. The role of livestock as reservoirs for the emergence of new virulent *S. aureus* clones with the capacity for epidemic spread also among humans is becoming increasingly important. Therefore, the study of differences between *S. aureus* (and especially MRSA) clones, particularly with regard to virulence, resistance to antibacterial agents, infectiousness, and zoonotic potential, is critical for assessing the potential risks of *S. aureus* strains.

In cooperation with InfectoGnostics researchers, we have developed an effective tool for high-resolution genotyping based on DNA microarray technology. After isolation of genomic DNA from *S. aureus* colony material, the DNA is amplified using a multiplexed linear amplification protocol. This allows a simultaneous labelling with biotin-dUTP of all target sequences that are present in the given isolate. The biotin-labeled ssDNA is hybridized to DNA oligonucleotide microarrays containing 336 probes for various genetic markers of *S. aureus* strains. These markers include a variety of species markers, virulence-associated genes for exotoxins, antibiotic resistance and SCCmec typing, MSCRAMMs, various enzymes, and other types of markers. After hybridization and subsequent washing, HRP-conjugated streptavidin binds to the labels of the bound amplicons and triggers in the next step a local dye precipitation. The resulting spots and their intensities are evaluated automatically based on a digital image of the microarray using our read-out system. The overall pattern is automatically analyzed for the presence or absence of specific markers. It is also compared with a database of strain profiles that allows assignment to about 200 clonal complexes and more than 700 *S. aureus* strains. Finally, the hybridization patterns can be used for fingerprints in order to compare isolates and to detect outbreak situations.

Major advantages of the microarray system are its high scalability and ease of adaptation. Our Genotyping Kit *S. aureus* does neither require expensive equipment nor complex bioinformatic data analysis. Thus, it is a cost-effective, rapid alternative or useful complement to sequencing.