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# Identical MALDI TOF MS-derived peak profiles in a pair of isogenic SCC*mec*-harboring and SCC*mec*-lacking strains of *Staphylococcus aureus*

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**KEYWORDS**
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**Summary** MALDI-TOF MS-based peak differences in oxacillin-resistant *Staphylococcus aureus* and oxacillin-susceptible *S. aureus* isolates have been described previously. Unfortunately, these isolates were not isogenic with respect to their *mec*A gene. Ours is the first to use a SCC*mec*-harboring parent and a SCC*mec*-lacking daughter strain, with the same genetic background, to unequivocally rule out strain-specific protein peaks. We could not show differences in the peak profiles within the preset Biotyper settings used for MALDI-TOF-based identification in this pair of SCC*mec*-harboring parent and SCC*mec*-lacking daughter strains.


## Introduction

A fast and reliable determination of the oxacillin-resistance in *Staphylococcus aureus* is crucial for therapy- and outcome of *S. aureus*-based infections. In terms of bacterial identification, a matrix assisted laser desorption/ionization time of flight mass spectrometry (MALDI TOF MS)-based identification is an accepted, fast and straightforward identification tool. In order to increase time to results it is desirable to introduce techniques, such as the MALDI-TOF MS, for a rapid and reliable oxacillin-resistance determination. MALDI-TOF MS is thought to be such a technique. A variety of recently published reports claimed that MALDI-TOF MS-based peak profiles could distinguish between oxacillin-resistant *S. aureus* (MRSA) and oxacillin-susceptible *S. aureus* (MSSA) isolates.[3,5,11,13,15] Nevertheless, for susceptibility testing MALDI TOF MS is not yet established in medical microbiological laboratory services. Recently a further study has been published, investigating a collection of *S. aureus* strains by a similar technique, the surface-enhanced (SE)-LDI-TOF mass spectrometry and artificial neural network (ANN) analysis.[12] This ANN-model also predicts MRSA by investigating the peak intensity of five different peaks. Nevertheless, a large amount of MSSA isolates were falsely identified as MRSA (Table 1). The previous studies differ with regard to mass spectrometry instruments

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**Table 1** Previous studies investigating MRSA and MSSA associated peaks by mass spectrometry.

| Study | Sample number | Sample preparation | Technology | Instrument | Protein treatment | Data acquisition | Statistical method/ model | Peak evaluation | MRSA falsely identified | Peaks associated with MRSA (Da) | Peaks associated with MSSA (Da) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Edward-Jones et al | 14 | Formic acid | Matrix-assisted | Kratos anaytical | CMBT (matrix) | 500 Da—10,000 Da | Dice coefficient >70 similarity, manually | Presence of peaks | NA | 511, 563, 640, 743, 767, 773, 854, 891, 999, 1026, 1140, 1165, 1229, 2127 | 2548.2647 |
| Du et al | 76 | None | Matrix-assisted | Micromass Ltd | CMBT and CHCA (matrix) | 500 Da—10,000 Da | Cluster analysis | Presence of peaks | 7 out of 43 | 1834, 1874, 2413, 2453, 2490 | 2093, 2308, 2345, 2547, 2585, 2686, 2723 |
| Shah et al | 99 | Lysis by urea, Lysostaphin, mechanical disruption | Surface-enhanced | Ciphergen Biosystems | Weak cation exchange array (CM10) | 3000 Da—30,000 Da | Artificial network analysis | Peak intensity | 26 out of 50 | 5709, 7694, 15,308, 18,896 | 3081, 5893, 9580 |
| Majcherczyk et al | 4 | None | Matrix-assisted | Micromass Ltd | CMBT (matrix) | NA | Manually | Presence of peaks | NA | peaks around 2450 | NA |
| Sun et al | 34 | NA | NA | NA | NA | NA | Cluster analysis | NA | None | NA | NA |

CMBT: 5-chloro-2-mercaptobenzothiazole, CHCA: $\alpha$ -cyano-4-hydrocinnamic acid, MRSA: methicillin-resistant *S. aureus*, MSSA: methicillin-susceptible *S. aureus*.