Plasmid-Encoded Transferable mecB-Mediated Methicillin Resistance in Staphylococcus aureus

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During cefoxitin-based nasal screening, phenotypically categorized methicillin-resistant Staphylococcus aureus (MRSA) was isolated and tested negative for the presence of the mecA and mecC genes as well as for the SCCmec-orX junction region. The isolate was found to carry a mecB gene previously described for Macroccocus caseolyticus but not for staphylococcal species. The gene is flanked by β-lactam regulatory genes similar to mecR, mecl, and blaZ and is part of an 84.6-kb multidrug-resistance plasmid that harbors genes encoding additional resistances to aminoglycosides (aacA-aphD, aphA, and aadK) as well as macrolides (ermB) and tetracyclines (tetS). This further plasmidborne β-lactam resistance mechanism harbors the putative risk of acceleration or reacceleration of MRSA spread, resulting in broad ineffectiveness of β-lactams as a main therapeutic application against staphylococcal infections.

Staphylococcal cassette chromosome mec (SCCmec)—mediated β-lactam resistance resulting from production of an additional penicillin-binding protein (PBP) 2a drastically limits the treatment options in cases of hospital- and community-related infections by staphylococci, leading to increased illness, death, and socioeconomic costs (1,2). Besides methicillin-resistant coagulase-negative staphylococci, notorious for foreign body–associated infections, methicillin-resistant Staphylococcus aureus (MRSA) strains are a global public health priority, despite some countries in Europe reporting stabilizing or decreasing MRSA rates (3–5). Since the initial reports of MRSA in 1961, several epidemic waves have resulted in threats of healthcare-, community-, and livestock-associated MRSA (6–9).

For staphylococci, 2 PBP 2a-encoding genes, mecA and mecC, including several allotypes, have been described as chromosomally located genetic bases for phenotypic methicillin resistance (10–14). In contrast, mecB, originally described as mecA∗, was reported as part of a probable primordial form of a methicillin resistance gene complex often found in a transposon mec complex (Tn6045) in Macroccocus caseolyticus, a colonizer of animal skin (15,16). Just recently, a mecD gene, most closely related to mecB, has been detected in bovine and canine M. caseolyticus isolates (17).

The impact of plasmidborne resistance for staphylococci is abundantly demonstrated for β-lactamase–mediated penicillin resistance. Resistance rates are >60% in human S. aureus isolates from the general population and >90% from hospital-related cases, regardless of the clinical background (18,19). In contrast to frequent interstrain and interspecies transmission of resistance plasmids by conjugation or transduction, only a relatively low rate of spontaneous horizontal transfer of SCCmec elements is assumed, resulting in still-manageable and controllable MRSA rates if prevention measures are adequate (20–24). However, transferable methicillin resistance might bear the consequence of an almost complete loss of β-lactam drugs as the most efficient class of antibacterial drugs for treatment of staphylococcal infections. Here, we report both a plasmid-encoded, and thereby transferable, methicillin resistance encoded by mecB and the occurrence of this gene in an isolate of the genus Staphylococcus.

Methods

Strain Detection and Identification

At the University Hospital of Münster, Germany, MRSA is generally cultured, identified, and differentiated by routine microbiological diagnostic methods using dextrose broth enrichment; chromID MRSA selective agar (bioMérieux, Marcy-l’Étoile, France), which contains cefoxitin; VITEK 2 automated system (bioMérieux) applying the antimicrobial susceptibility test card AST-P632; PBP2a detection kit (PBP2a Culture Colony Test, Alere, San Diago, CA, USA); S. aureus–specific PCR targeting mecA/mecC (GenoType MRSA, Hain-Lifescience, Nehren, Germany); and matrix-assisted laser desorption/ionization
time-of-flight mass spectrometry (Microflex-LT system, MALDI-Biotyper 3.0; Bruker Daltonik, Bremen, Germany). In February 2016, an *S. aureus* isolate (which we numbered UKM4229) was recovered during routine MRSA screening. The isolate displayed a β-lactam–resistant phenotype without carrying the methicillin resistance genes *mecA* or *mecC*. For further characterizations, isolate UKM4229 was stored at –80°C and was cultivated on chromID MRSA agar (bioMérieux) at 37°C.

**Genetic Analysis**

We extracted genomic DNA from *S. aureus* isolate UKM4229 using the QIAamp DNA Mini Kit (QIAGEN, Hilden, Germany) according to the manufacturer’s instructions. We isolated plasmid DNA with the PrepEase Mini Spin Plasmid Kit (Affymetrix USB, Santa Clara, CA, USA) following the protocol standards. For both plasmid and genomic DNA, we applied lysostaphin (20 µg/mL) (Wackerchemie, Steinbach, Germany) for bacterial cell lysis. We performed multilocus sequence typing and spa gene typing initially as described elsewhere (25,26) and confirmed our results later by analysis of whole-genome sequencing (WGS) and DNA microarray data (discussed later in this article). We analyzed DNA sequences using RidomStaphyType and SeqSphere+ (Ridom GmbH, Münster, Germany). Applying DNA microarray analysis (IdentiBAC Microarray; Alere Technologies GmbH, Jena, Germany), we identified resistance and virulence determinants and checked genotyping results.

**Molecular Confirmation of Methicillin Resistance**

Using PCR, we tested for the presence of methicillin resistance genes *mecA* and *mecC* (27,28) as well as *mecB*. DNA sequences of PCR oligonucleotides are given in Table 1. Oligonucleotides for *mecB* were made on basis of the plasmid pMCCl2 of *M. caseolyticus* (GenBank accession no. NC_011996.1). We performed PCR reactions using the following protocol for *mecA*: 5 min at 95°C; 40 cycles of 0.5 min at 95°C, 0.5 min at 55.5°C, and 0.75 min at 72°C; and final elongation of 7 min at 72°C. The protocol for *mecB* was 5 min at 95°C; 35 cycles of 0.5 min at 95°C, 0.5 min at 57°C, and 2.5 min at 72°C; and final elongation of 7 min at 72°C. The protocol for *mecC*: 5 min at 95°C; 40 cycles of 0.5 min at 95°C, 0.5 min at 59.3°C, and 2 min at 72°C; and final elongation of 7 min at 72°C.

**Antibiotic Drug Susceptibility Testing**

We determined the MIC of cefoxitin for *S. aureus* isolate UKM4229 by the reference broth microdilution method according to the International Organization for Standardization (ISO) 20776-1 guideline (https://www.iso.org/standard/41630.html), as required by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and the Clinical and Laboratory Standards Institute (CLSI). Cefoxitin (Sigma Aldrich, Taufkirchen, Germany) was tested in 2-fold concentrations (0.25–128 µg/mL). We subcultured the isolate and incubated it overnight before testing.

We investigated the susceptibility profile of UKM4229 by determining MICs of various β-lactam and non–β-lactam antibiotic drugs (Table 2) using the gradient diffusion method (Etest; bioMérieux) according to the manufacturer’s instructions. As recommended, the inoculated plates were incubated at 35°C for 18 ± 2 hours. In addition, we tested oxacillin using conditions for increased expression of methicillin resistance, as reported for *mecA* isolates (30): Mueller-Hinton agar supplemented with 2% saline, incubation at 30°C, and prolonged incubation up to 48 h. We investigated the applicability of a commercial automated susceptibility testing device to recognize methicillin resistance due to presence of *mecB* in *S. aureus* by using the VITEK 2 system. We evaluated the in vitro activity of the endolysin HY-133 against UKM4229 using the broth microdilution method in accordance with ISO 20776-1 guidance (https://www.iso.org/standard/41630.html), as described elsewhere (31,32). In brief, we tested 2-fold final concentrations of HY-133 ranging from 0.06 µg/mL to 8 µg/mL using 1–5 × 10⁶ CFU/mL suspension of UKM4229 in cation-adjusted Mueller-Hinton broth. The MICs were read after incubation at 35°C for 18 ± 2 h.

We performed all experiments in triplicate on different days and calculated the median MIC values. We used *S. aureus* ATCC 29213 as a quality control strain on every testing day. For the antibiotic drugs we used, the MICs for the quality control strain were within acceptable limits throughout the testing.

**Whole-Genome Sequencing**

For the PacBio RS II platform (Pacific Biosciences, Menlo Park, CA, USA), we extracted staphylococcal DNA using the Genomic-tip 20/G Kit (QIAGEN) according to the manufacturer’s instructions, except that we

| Table 1. Oligonucleotides used in study of methicillin resistance genes in *Staphylococcus aureus* |
|---|
| **Gene** | **Oligonucleotide** | **Nucleotide sequence, 5′→3′** | **Melting temperature** | **Source** |
| *mecA* | mec5 | AAATTCGATGTTAAGGTTGCG | 55°C | (29) |
|  | mec6 | AGTTTGCCAGTACCGGGATTGTCG |
| *mecC* | mecAL3 | TCAYTGGATTTCATTATCA | 59.3°C | This study |
|  | mecAL4 | AACATGGTTATTCGAAAGATGACGA |
| *mecB* | mecB-for | TTAACATATACACCCTGG | 57°C | This study |
|  | mecB-rev | TAAAGTTCAATTAGGACCTCC | | |

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applied lysostaphin (20 µg/mL) (Wakchemie) for bacterial cell lysis. We sequenced the extracted high-quality, double-stranded DNA (5 µg) using P6-C4 chemistry on the PacBio RS II instrumentation using 4-hour movie collection and 110 pmol/L of complexed 20-kb SMRTbell library. We performed the initial de novo assembly using the HGAP3 v2.3.0 Assembler (Icahn Institute for Genomics and Multiscale Biology, Icahn School of Medicine at Mount Sinai, New York, NY, USA). We annotated the assembled genome through the GenDB pipeline (33). We verified questionable sequences within the plasmids by applying PCR (LA-Taq-DNA-Polymerase; Takara, Frankfurt am Main, Germany) and Sanger sequencing (Eurofins Genomics, Ebersberg, Germany).

### Results

During routine MRSA screening, we recovered an *S. aureus* isolate UKM4229 from a combined nasal-throat swab of a 67-year-old male cardiology inpatient who had no signs of infection. We isolated colonies with typical appearance for presumptive MRSA from a chromogenic MRSA selective agar and identified them as *S. aureus* by VITEK 2, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, and PCR. Discrepancies between phenotypic detection of methicillin resistance by VITEK 2 and negative results of a PBP2a detection kit, as well as negative mecA and mecC test results, by commercial and in-house PCRs led to the detection of a mecB-encoded methicillin resistance.

*S. aureus* isolate UKM4229 showed a median MIC of 32 µg/mL for cefoxitin, as determined by broth microdilution and gradient diffusion tests. The MICs of other antibiotics, as well as correspondent interpretative categories, are shown in Table 2; the resistance gene profile is given in online Technical Appendix Table 1 (https://wwwnc.cdc.gov/EID/article/24/2/17-1074-Techapp1.pdf). Optimal oxacillin testing conditions previously reported to increase expression of methicillin resistance in mecC isolates (30) unexpectedly led to lower oxacillin MIC values for UKM4229 (Table 2). A novel anti–*S. aureus* agent in development, the recombinant phage endolysin HY-133 (Hy-Fusidic acid Mupirocin Gentamicin Trimethoprim/sulfamethoxazole Tetracycline Tetracyclines Tigeclycline Folate pathway inhibitors Trimetoprim/sulfamethoxazole Aminoglycosides Gentamicin Pseudomonic acids Mupirocin Fusidines Fusidic acid Bacteriophage endolysins HY-133

| Antimicrobial class and agent | Median MIC, µg/mL | Category |
|------------------------------|-------------------|----------|
| β-lactams                    |                   |          |
| Penicillins                  |                   |          |
| Benzylpenicillin             | 1.5               | R        |
| Ampicillin                   | 3                 | R        |
| Ampicillin/sulbactam         | 2                 | R        |
| Piperacillin                 | 6                 | R        |
| Piperacillin/tazobactam      | 3                 | R        |
| Oxacillin                    | 12                | R        |
| Oxacillin†                   | 4/4               |          |
| Cephalosporins              |                   |          |
| Cefoxitin                    | 32                | R        |
| Cephalothin                  | 2                 | R        |
| Cefuroxime                   | 3                 | R        |
| Ceftriaxone                  | 24                | R        |
| Cefepime                     | 6                 | R        |
| Ceftobiprole                 | 2                 | S        |
| Ceftarolone                  | 0.5               | S        |
| Carbapenems                  |                   |          |
| Imipenem                     | 0.032             |          |
| Non-β-lactams                |                   |          |
| Glycopeptides                |                   |          |
| Vancomycin                   | 1                 | S        |
| Lipoglycopeptides            |                   |          |
| Telavancin                   | 0.012             | S        |
| Lipopeptides                 |                   |          |
| Daptomycin                   | 0.19              | S        |
| Fluoroquinolones             |                   |          |
| Levofloxacin                 | 0.19              | S        |
| Macrolides                   |                   |          |
| Erythromycin                 | >256              | R        |
| Lincosamids                  |                   |          |
| Clindamycin                  | >256              | R        |
| Oxazolidones                 |                   |          |
| Linezolid                    | 1                 | S        |
| Rifamycins                   |                   |          |
| Rifampin                     | 0.008             | S        |
| Phosphonic acid derivatives  |                   |          |
| Fosfomycin                   | <0.064            | S        |
| Streptogramins               |                   |          |
| Quinupristin/dalfopristin    | 0.5               | S        |
| Tetracyclines                |                   |          |
| Tetracycline                 | 12                | R        |
| Glycylcyclines               |                   |          |
| Tigeclycline                 | 0.125             | S        |
| Folate pathway inhibitors    |                   |          |
| Trimethoprim/sulfamethoxazole| 0.047             | S        |
| Aminoglycosides              |                   |          |
| Gentamicin                   | 24                | R        |
| Pseudomonic acids            |                   |          |
| Mupirocin                    | 0.19              | S        |
| Fusidines                    |                   |          |
| Fusidic acid                 | 0.094             | S        |
| Bacteriophage endolysins     |                   |          |
| HY-133                       | 0.25              |          |

*Tested by using the gradient diffusion method. S, susceptible; R, resistant (according to EUCAST [www.eucast.org] for antibiotic drugs with available breakpoints).†Conditions: 2% NaCl, 30°C; 18 h/48 h. MIC at regular reading after 18 ± 2 h/MIC after 48 h.
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From other *mecB* database entries, the highest nucleotide identity was shared with the sequence of *mecD* (68.7%), whereas the reported allotypes of *mecC* and *mecA* were more distantly related (online Technical Appendix Figure 1). WGS revealed that the UKM4229 genome consists of a 2,851,374-bp circular chromosome and 2 different plasmids, a 20,725-bp plasmid (pSAWWU4229_2) and an 84,599-bp plasmid (pSAWWU4229_1; Figure); the latter carried *mecB* (GenBank accession no. PRJE19527). The pSAWWU4229_1 plasmid backbone showed the highest similarity with the plasmid pMCLL2 of *M. caseolyticus* JCSC5402 (GenBank accession no. AP009486.1; blastn [https://blast.ncbi.nlm.nih.gov/Blast.cgi] 2.7.0+ maximum score 27,835; query coverage 71%; identity 99%) (33). These 2 plasmids shared 73.3% nucleotide identity (global alignment using Stretcher [Emboss], Matrix EDNAFULL; gap penalty 16, extend penalty 4). Whole plasmid comparative analysis of the sequences of pSAWWU4229_1 and pMCLL2 showed homologous regions between the mec gene complex, the downstream part of the mec complex, and the other antibiotic drug resistance genes (online Technical Appendix Figure 2).

Within the pSAWWU4229_1 plasmid, *mecB* was flanked by β-lactam regulatory genes similar to *mecR*, *mecI*, and *blaZ* (nucleotide identities: 99.9%, *mecRm* from *M. caseolyticus* JCSC7096; 100%, *mecIm* from *M. caseolyticus* JCSC7096 and 100%, *blaZm* from *M. caseolyticus* JCSC7096). pSAWWU4229_1 contained additional antibiotic drug resistance genes encoding resistance to aminoglycosides (*aacA-aphD*, *aphA*, and *aadK*), as well as macrolides (*ermB*), tetracyclines (*tetS*), and streptothricin (*sat*), all located in the same gene section. This particular region of the plasmid showed similarities with the transposon Tn551 of *S. aureus* 4578 (Genbank accession no. LC125350.1; blastn 2.7.0+ maximum score 11,064; query coverage 10%; identity 99%) (34). The sequences shared 48.9% nucleotide identity (global alignment using Stretcher [Emboss], Matrix EDNAFULL; gap penalty 16, extend penalty 4). Mating-pore genes or genes responsible for the DNA transfer suggesting self-transmission or mobilization properties of pSAWWU4229_1 were not detected. Genotyping revealed that *S. aureus* isolate UKM4229 belonged to multilocus sequence typing type ST7 and spa-type t091 (spa-CC 091).

**Figure.** Circular map of the mecB-carrying plasmid pSAWWU4229_1 from *Staphylococcus aureus* isolate UKM4229, obtained from a 67-year-old cardiology inpatient who had no signs of infection, Münster, Germany. Arrows indicate annotated genes: the mec-complex is noted in green, antibiotic resistance genes in red, transposase/integrase genes in orange, other genes with known function in violet, and other genes with unknown function in gray.
DNA microarray analysis and WGS revealed the isolate possessed the leucotoxin genes lukF, lukS, lukD, lukE, lukX, and lukY. The isolate belonged to capsule type 8, and the biofilm-associated genes icaA, C, and D were detected. Furthermore, the hlb-converting bacteriophage of immune evasion cluster type G comprising the enterotoxin encoding genes sep, sak, and scn was present in the genome. Additional information about the virulence profile of this isolate is given in online Technical Appendix Table 2.

Discussion
Recent studies have shown that mobile SCCmec elements have been imported more frequently by different S. aureus clonal lineages than previously assessed (35). Nevertheless, in contrast to the huge diversity of non-MRSA S. aureus clonal lineages (36), comparatively few clonal lineages still dominate the global MRSA population (37). However, an increased transferability of methicillin resistance by a plasmid-encoded course of action would have the capacity to drastically change the MRSA epidemiology. In staphylococci and other members of the phylum Firmicutes, plasmids have contributed enormously to the emergence and spread of antimicrobial resistance, and plasmid-encoded penicillin resistance has reached or exceeded 80% of clinical staphylococcal isolates (38).

In M. caseolyticus, mecB genes have been found within the chromosome as part of an SCCmec element as well as on a plasmid (15,16,39). For S. aureus UKM4229, it was shown that the mecB carrying plasmid pSAWWU4229_1 was distantly related to a macrococcal plasmid (pMCLL2 of M. caseolyticus JCS5402), substantiating a possible gene transfer between the two genera. Because macrococcal and staphylococcal species may share the same hosts, mammalian skin and food, an exchange of mobile genetic elements between members of both closely related genera is likely and transmission to mammal-adapted staphylococci is generally to be feared (3). Genotyping of S. aureus UKM4229 revealed spa type t091, which is relatively common, as 0.92% of the >370,000 submitted spa sequences assigned to ≈17,000 spa types (as of February 2017) of the RIDOM SpaServer database (http://spa.ridom.de/spatypes.shtml) belong to this spa type.

Routine phenotypic methods for susceptibility testing cannot distinguish between methicillin resistance determinants; thus, mecB-encoded methicillin resistance can remain undiscovered. Moreover, mecB detection is not part of molecular screening approaches. Certain clonal lineages of S. aureus, including MRSA, have emerged as zoonotic pathogens colonizing farm and wild animals (40). Tetracycline resistance frequently observed in staphylococci associated with husbandry is another indication for a possible livestock origin of the isolate (41). A putative livestock source of the mecB-encoding plasmid underlines the importance of the One Health concept in combating the spread of antimicrobial drug resistance.

Although the mecB isolate has been tested susceptible toward several agents of non–β-lactam antibiotic drug classes, the generally increased risk, compared to that of a SCCmec transfer, should be taken into consideration in that a mecB-encoding plasmid will be transmitted through horizontal gene transfer to other staphylococcal strains, even to already multidrug-resistant strains. In S. aureus, 2 major means of horizontal gene transfer for plasmids have been described: conjugation and bacteriophage transduction. Here, pSAWWU4229_1 did not harbor the typical genes responsible for conjugation or mobilization, which is, however, a common lack in S. aureus, affecting ≈95% of plasmids (42). In contrast, for most staphylococcal plasmids, a transfer through bacteriophage generalized transduction has been suggested (43,44). Further studies are warranted to underpin this putative threat and to investigate how a plasmidborne methicillin resistance would affect the SCCmec-based methicillin resistance. For UKM4229, the WGS data revealed that the SCCmec chromosomal attachment site (attB) locus and the neighboring orfX (rlmH) gene were intact, and no integration of an SCCmec element was found.

The mecB isolate was tested to be susceptible to cefotibiprole and ceftaroline. Although cephalosporins with anti-MRSA activity are still active against the majority of MRSA isolates, nonsusceptibility has been already associated with certain MRSA lineages ranging between 3.9% and 33.5% of all MRSA isolates (45–48).

The discovery of plasmid-encoded methicillin resistance in S. aureus of probably macrococcal origin in a healthcare setting reveals a novel level of risk of the transfer of broad β-lactam resistance in staphylococci. Further studies are needed to clarify the real prevalence of mecB-caused methicillin resistance among MRSA and methicillin-resistant coagulase-negative staphylococci in human and animal populations, whether mecA and mecC genes could be found integrated on plasmids, and how the answers to these questions may affect human and animal health.

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Plasmid-Encoded Transferable *mecB*-Mediated Methicillin Resistance in *Staphylococcus aureus*

Technical Appendix

Technical Appendix Table 1. Resistance profile of *S. aureus* UKM4229 determined by microarray and whole genome sequencing

| Gene        | Description†                           | Microarray | UKM4229 genome | pSAWWU229-1 | pSAWWU229-2 |
|-------------|----------------------------------------|------------|----------------|-------------|-------------|
| *mecA*      | Alternate penicillin binding protein 2, defining MRSA | –          | –              | –           | –           |
| *mecB*      | Beta-lactam-inducible penicillin-binding protein | ND†        | –              | +           | –           |
| *mecC*      | Novel *mecA* homologue, also associated with beta-lactam resistance | –          | –              | –           | +           |
| *mecD*      | Beta-lactam-inducible penicillin-binding protein | ND†        | –              | –           | –           |
| *blaZ*      | Beta-lactamase gene                     | +          | –              | +           | +           |
| *blaZ-SCCmecXI* | Beta-lactamase gene associated with SCCmec XI elements | –          | –              | –           | –           |
| *blaI*      | Beta lactamase repressor (inhibitor)     | +          | –              | –           | +           |
| *blaR*      | Beta-lactamase regulatory protein        | +          | –              | –           | +           |
| *erm(A)*    | rRNA methyltransferase associated with macrolide/lincomamide resistance | –          | –              | –           | –           |
| *erm(B)*    | rRNA methyltransferase associated with macrolide/lincomamide resistance | +          | –              | +           | –           |
| *erm(C)*    | rRNA methyltransferase associated with macrolide/lincomamide resistance | –          | –              | –           | +           |
| *lnu(A)*    | Lincosaminide nucleotidyltransferase (=lnA) | –          | –              | –           | –           |
| *msr(A)*    | Macrolide efflux pump                    | –          | –              | –           | –           |
| *mep(A)*    | Macrolide efflux protein A               | –          | –              | –           | –           |
| *mph(C)*    | Macrolide phosphotransferase II (=mpbBM) | –          | –              | –           | –           |
| *vat(A)*    | Virginiamycin A acetyltransferase        | –          | –              | –           | –           |
| *vat(B)*    | Acetyltransferase inactivating streptogramin A | –          | –              | –           | –           |
| *vga(A)*    | ABC transporter conferring resistance to streptogramin A and related compounds | –          | –              | –           | –           |
| *vga(A) (BM 3327)* | vga(A) allele from strain BM 3327 | –          | –              | –           | –           |
| *vqB(A)*    | Virginiamycin B hydrolase (=vgb)        | –          | –              | –           | –           |
| *aacA-aphD* | Aminoglycoside adenyl-/phosphotransferase (gentamicin, tobramycin) | +          | –              | +           | –           |
| *aadD*      | Aminoglycoside adenyltransferase (neo-/ kanamycin, tobramycin) | –          | –              | –           | –           |
| *aphA3*     | Aminoglycoside phosphotransferase (neo-/ kanamycin) | +          | –              | +           | –           |
| *sat*       | Streptothricin acetyltransferase         | –          | –              | +           | –           |
| *dfrS1*     | Dihydrofolate reductase mediating trimethoprim resistance (=dfrA) | –          | –              | –           | –           |
| *fusB*      | Fusidic acid resistance gene (=farA)    | –          | –              | –           | –           |
| *fusC*      | Fusidic acid resistance gene (=Q6GD50)  | –          | –              | –           | –           |
| *mupA*      | Isoleucyl-tRNA synthetase associated with mupirocin resistance (=mupR) | –          | –              | –           | –           |
| *tet(K)*    | Tetracycline efflux protein              | –          | –              | –           | –           |
| *tet(M)*    | Ribosomal protection protein associated with tetracycline resistance | –          | –              | –           | –           |
| *tetS*      | Tetracycline resistance protein TetS     | ND         | –              | +           | –           |
| *cat* (total)| Chloramphenicol acetyltransferase       | –          | –              | –           | –           |
| *clf*       | 23S rRNA methyltransferase (phenicols, lincomamides, oxazolidinones, pleuromutilins, streptogramin A ) | –          | –              | –           | –           |
| *faxA*      | Chloramphenicol/florfenicol exporter     | –          | –              | –           | –           |
| *fosB*      | Metallothiol transferase                | –          | –              | –           | –           |
### Technical Appendix Table 2: Virulence profile of *S. aureus* UKM4229 determined by microarray and whole genome sequencing

| Gene     | Description† | Microarray | WGS | PSUWWU4229-1 | PSUWWU4229-2 |
|----------|--------------|------------|-----|---------------|---------------|
| *fusB* (plasmid) |  | - | + | - | - |

**Resistance genotype: efflux systems**

| Gene     | Description | Result by |
|----------|-------------|-----------|
| qacA     | Quaternary ammonium compound/multidrug efflux protein A | + |
| qacC     | Quaternary ammonium compound/multidrug efflux protein C | + |
| *sdrM*   | Multidrug efflux pump | + |

**Resistance genotype: glycopeptides**

| Gene     | Description | Result by |
|----------|-------------|-----------|
| *vanA*   | Vancomycin resistance gene | - |
| *vanB*   | Vancomycin resistance gene from enterococci and *Clostridium* | - |
| *vanZ*   | Teicoplanin resistance gene from enterococci | - |

†Description as provided by the manufacturer (S. aureus Genotyping Kit 2.0 manual, Alere Technologies GmbH, Jena, Germany), except for ND cases

### Technical Appendix Table 2: Virulence profile of *S. aureus* UKM4229 determined by microarray and whole genome sequencing

| Gene     | Description† | Microarray | WGS | PSUWWU4229-1 | PSUWWU4229-2 |
|----------|--------------|------------|-----|---------------|---------------|
| *sea*    | Enterotoxin A (= *entA*) | - | - | - | - |
| *sea* (320E) | Enterotoxin A, allele from strain 320E | - | - | - | - |
| *seb*    | Enterotoxin B (= *entB*) | - | - | - | - |
| *sec*    | Enterotoxin C (= *entC*) | - | - | - | - |
| *sed*    | Enterotoxin D (= *entD*) | - | - | - | - |
| *see*    | Enterotoxin E (= *entE*) | - | - | - | - |
| *seg*    | Enterotoxin G (= *entG*) | - | - | - | - |
| *seh*    | Enterotoxin H (= *entH*) | - | - | - | - |
| *sei*    | Enterotoxin I (= *entI*) | - | - | - | - |
| *seq*    | Enterotoxin J (= *entJ*) | - | - | - | - |
| *seq* / *selj* | Enterotoxin gene cluster, consisting of seg, sei, seq, selm, seln, selo, seleu | - | - | - | - |
| *selj*   | Enterotoxin K (= *entK*) | - | - | - | - |
| *selj* / *sell* | Enterotoxin-like gene/protein M (= *sem*, *entM*) | - | - | - | - |
| *selm*   | Enterotoxin-like gene/protein N (= *sen*, *entN*) | - | - | - | - |
| *selo*   | Enterotoxin-like gene/protein O (= *seo*, *entO*) | - | - | - | - |
| *selp* / *sea* (N315) | Enterotoxin A, allele from strain N315 (= *entP*, *entP*) | - | - | - | - |
| *egc*    | Enterotoxin gene cluster, consisting of seg, sei, seq, selm, selo, seleu | - | - | - | - |
| *ser*    | Enterotoxin R (= *entR*) | - | - | - | - |
| *seu*    | Enterotoxin-like gene/protein U (= *seu*, *entU*) | - | - | - | - |

**Virulence: hemolysin gamma and leucocidins**

| Gene     | Description† | Result by |
|----------|--------------|-----------|
| *hlgA*   | Hemolysin gamma, component A | - |
| *lukF/PV* | Panton Valentine leucocidin F component | - |
| *lukS-PV* | Panton Valentine leucocidin S component | - |
| *lukF-PV (P83)* | F component of leucocidin from ruminants | - |
| *lukM*   | S component of leucocidin from ruminants | - |
| *lukD*   | Leucocidin D component | - |
| *lukE*   | Leucocidin E component | - |
| *lukK*   | Leucocidin/leucocidin hemolysin toxin family protein (= *lukA* or *lukG*) | - |
| *lukY*   | Leucocidin/leucocidin hemolysin toxin family protein (= *lukB* or *lukH*) | - |
| Gene       | Description† | Result by Microarray | WGS                                      |
|------------|--------------|----------------------|------------------------------------------|
| hla / hly  | Hemolysin alpha | + + – – |                          |
| hib        | Hemolysin beta | + + – – |                          |
| undiscrupted hib | Hemolysin beta without phage insertion | – – – – |                          |
| hld        | Hemolysin delta | ND + – – |                          |
|            |              |                      | **Virulence: hib-converting phage**      |
| sak        | Staphylokinase | + + – – |                          |
| chp        | Chemotaxis-inhibiting protein (CHIPS) | – + – – |                          |
| scn        | Staphylococcal complement inhibitor | + + – – |                          |
|            |              |                      | **Virulence: exfoliative toxins**        |
| etA        | Exfoliative toxin serotype A | – – – – |                          |
| etB        | Exfoliative toxin serotype B | – – – – |                          |
| etD        | Exfoliative toxin D | – – – – |                          |
|            |              |                      | **Virulence: epidermal cell differentiation inhibitors** |
| edinA      | Epidermal cell differentiation inhibitor | – – – – |                          |
| edinB      | Epidermal cell differentiation inhibitor B | – – – – |                          |
| edinC      | Epidermal cell differentiation inhibitor C | – – – – |                          |
|            |              |                      | **Virulence: ACME locus**                |
|            |              |                      |                                          |
|            |              |                      | **Virulence: proteases**                 |
| aur (consensus) | Aureolysin   | + + – – |                          |
| aur (other than MRSA252) | + + – – |                          |
| aur (MRSA252) | + + – – |                          |
| splA       | Serinprotease A | + + – – |                          |
| splB       | Serinprotease B | + + – – |                          |
| splC       | Serinprotease C | ND + – – |                          |
| splE       | Serinprotease E | + + – – |                          |
| splF       | Serinprotease F | ND + – – |                          |
| sspA       | Glutamylendopeptidase | + + – – |                          |
| sspB       | Staphopain B, protease | + + – – |                          |
| sspP (consensus) | Staphopain A (staphylopain A), protease | + + – – |                          |
|            |              |                      | **Capsule- and biofilm-associated genes** |
| cap 1 (total) | Capsule type 1 | – – – – |                          |
| cap 5 (total) | Capsule type 5 | – – – – |                          |
| cap 8 (total) | Capsule type 8 | + + – – |                          |
| capH8      | Capsular polysaccharide synthesis enzyme | + + – – |                          |
| capI8      | Capsular polysaccharide biosynthesis protein | + + – – |                          |
| capJ8      | O-antigen polymerase | + + – – |                          |
| capK8      | Capsular polysaccharide biosynthesis protein | + + – – |                          |
| iczA       | Intercellular adhesion protein A | + + – – |                          |
| iczC       | Intercellular adhesion protein C | + + – – |                          |
| iczD       | Biofilm PIA synthesis protein D | + + – – |                          |
| bap        | Surface protein involved in biofilm formation | – – – – |                          |
|            |              |                      | **Adhesion factors/MSCRAMM genes**       |
| bbp (total) | Bone sialoprotein-binding protein | + + – – |                          |
| clfA (total) | Clumping factor A | + + – – |                          |
| clfB (total) | Clumping factor B | + + – – |                          |
| cna        | Collagen-binding adhesin | – – – – |                          |
| eth (consensus) | Cell wall associated fibronectin-binding protein | + + – – |                          |
| ebpS (total) | Cell surface elastin binding protein | + + – – |                          |
| eno        | Enolase | + + – – |                          |
| fnb (total) | Fibrinogen binding protein (19 kDa) | + + – – |                          |
| fnbA (total) | Fibrinectin-binding protein A | + + – – |                          |
| Gene      | Description†                                    | Result by Microarray | Result by WGS   |
|-----------|-------------------------------------------------|----------------------|-----------------|
| fnbB (total) | Fibronectin-binding protein B                    | +                    | +               |
| map (total)  | Major histocompatibility complex class II analog protein (= Extracellular adherence protein, eap) | +                    | –               |
| sasG (total) | Staphylococcus aureus surface protein G          | –                    | –               |
| sdrC (total) | Ser-Asp rich fibrinogen-/bone sialoprotein-binding protein C | –                    | –               |
| sdrD (total) | Ser-Asp rich fibrinogen-/bone sialoprotein-binding protein D | +                    | –               |
| sdrE         | Ser-Asp rich fibrinogen-/bone sialoprotein-binding protein E | ND                   | –               |
| sdrF         | Ser-Asp rich fibrinogen-/bone sialoprotein-binding protein F | ND                   | –               |
| vwb (total)  | Van Willebrand factor binding protein            | +                    | –               |

†Description as provided by the manufacturer (S. aureus Genotyping Kit 2.0 manual, Alere Technologies GmbH, Jena, Germany), except for ND cases.

Technical Appendix Figure 1. Phylogenetic relationships of mec genes conferring methicillin resistance and overview of characteristic features. Evolutionary history was inferred by using the maximum likelihood method based on the Tamura-Nei model (1) in MEGA7 (2). Nucleotide sequences were aligned using MUSCLE (3). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Nucleotide identity (nt ID) between the mecB gene in strain UKM4229 and other mec genes was determined by sequence alignment using Clustal OMEGA (http://www.ebi.ac.uk/Tools/msa/clustalo/).
Technical Appendix Figure 2. Structural comparison of pSAWWU4229_1 and pMCCL2 (M. caseolyticus JCSC5402; NC_011996.1) performed by Easyfig software (49). Gray areas represent regions with nucleotide sequence similarities ranging between 69% and 100%. The mec-complex is colored in green, antibiotic resistance genes in red, and transposase/integrase genes in orange.

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