

Characterization of Staphylococcal Cassette Chromosome *mec* Elements from Methicillin-Resistant *Staphylococcus pseudintermedius* Infections in Australian Animals

✉ Kate A. Worthing,^{a,b} Sybille Schwendener,^c ✉ Vincent Perreten,^c Sugiyono Saputra,^{d,e} Geoffrey W. Coombs,^{f,g} Stanley Pang,^{f,g} ✉ Mark R. Davies,^b Sam Abraham,^f Darren J. Trott,^d ✉ Jacqueline M. Norris^a

^aSydney School of Veterinary Science, University of Sydney, NSW, Australia

^bDepartment of Microbiology and Immunology, The University of Melbourne at the Peter Doherty Institute for Infection and Immunity, VIC, Australia

^cInstitute of Veterinary Bacteriology, University of Bern, Bern, Switzerland

^dAustralian Centre for Antimicrobial Resistance Ecology, School of Animal and Veterinary Sciences, University of Adelaide, Roseworthy, SA, Australia

^eResearch Center for Biology, Indonesian Institute of Sciences, Bogor, Indonesia

^fAustralia Antimicrobial Resistance and Infectious Diseases Laboratory, School of Veterinary Life Sciences, Murdoch University, Murdoch, WA, Australia

^gPathWest Laboratory Medicine—WA, Fiona Stanley Hospital, Murdoch, WA, Australia

ABSTRACT We examined the oxacillin resistance phenotype and genomic structure of staphylococcal cassette chromosome *mec* (SCC*mec*) elements from 77 veterinary methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) isolates. Isolates were characterized by oxacillin broth microdilution, whole-genome sequencing, and bioinformatics analysis. Five previously described SCC*mec* elements, and a sixth novel element, were identified: SCC*mec* III (also known as II-III), Ψ SCC*mec*₅₇₃₉₅, and SCC*mec*_{NA45} (a SCC*mec* VII variant), all previously described in MRSP, and SCC*mec* IVg and SCC*mec* V_T, previously described in both methicillin-resistant *Staphylococcus aureus* (MRSA) and MRSP. The sixth element was novel and found among nine geographically clustered isolates. This novel pseudostaphylococcal cassette chromosome (Ψ SCC*mec*_{KW21}) contained a class A *mec* gene complex but lacked *ccr* genes. It also harbored heavy metal (cadmium) resistance determinants. The median oxacillin MIC values among Ψ SCC*mec*_{KW21}, SCC*mec* III, and SCC*mec* V_T isolates were significantly higher than those determined for the SCC*mec*_{NA45} VII variant isolates and Ψ SCC*mec*₅₇₃₉₅ and SCC*mec* IVg isolates. Ψ SCC*mec*_{KW21} was found exclusively in sequence type 497 (ST497), an MRSP clone that is locally successful in Victoria, Australia. Future studies are necessary to determine if this clone has disseminated further afield and if Ψ SCC*mec*_{KW21} has moved into other MRSP lineages or staphylococcal species.

IMPORTANCE *Staphylococcus pseudintermedius* is a significant veterinary pathogen and occasional cause of infections in humans. β -Lactams are an important group of antimicrobials used to treat staphylococcal infections in humans and animals. However, when staphylococci become methicillin resistant via the acquisition of a mobile genetic element called staphylococcal cassette chromosome *mec* (SCC*mec*), they become resistant to all β -lactams. This study detected a novel SCC*mec* element among a cluster of methicillin-resistant *S. pseudintermedius* isolates from animals in Australia. It also detected SCC*mec* elements in *S. pseudintermedius* that had high similarity to those identified in methicillin-resistant *Staphylococcus aureus*, demonstrating how human and animal pathogens can share the same resistance determinants.


Received 4 September 2018 Accepted 17 October 2018 Published 7 November 2018

Citation Worthing KA, Schwendener S, Perreten V, Saputra S, Coombs GW, Pang S, Davies MR, Abraham S, Trott DJ, Norris JM. 2018. Characterization of staphylococcal cassette chromosome *mec* elements from methicillin-resistant *Staphylococcus pseudintermedius* infections in Australian animals. mSphere 3:e00491-18. <https://doi.org/10.1128/mSphere.00491-18>.

Editor Paul D. Fey, University of Nebraska Medical Center

Copyright © 2018 Worthing et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Jacqueline M. Norris, jacqui.norris@sydney.edu.au.

 Bacteria from dogs can harbor the same resistance genes as bacteria from humans. This study reports a new way that dog bacteria can harbor antimicrobial resistance.

KEYWORDS SCCmec, *Staphylococcus pseudintermedius*, antimicrobial resistance, methicillin resistance, veterinary, zoonotic infections

Methicillin-resistant *Staphylococcus pseudintermedius* (MRSP) has become an important opportunistic pathogen in veterinary small-animal practice (1) and is an occasional zoonotic pathogen (2). *S. pseudintermedius* is part of the canine skin microbiota but can cause a wide range of opportunistic clinical infections across many body systems. MRSP infections are more complicated than methicillin-susceptible *S. pseudintermedius* (MSSP) infections due to the lack of potential treatment options. In staphylococci, methicillin resistance is determined by the *mecA* gene and its homologues, *mecB* and *mecC* (3–5). *mecA* and *mecC* are harbored within a mobile genetic element called the staphylococcal cassette chromosome *mec* (SCCmec) element (4, 6), whereas *mecB*, typically found in *Macrococcus caseolyticus* (7), has recently been detected on a multidrug resistance plasmid in methicillin-resistant *Staphylococcus aureus* (MRSA) (5). SCCmec elements are composed of a methicillin resistance determinant (*mecA*, *mecB*, or *mecC*) contained within a *mec* gene complex and include site-specific recombinase genes (*ccr*), which are responsible for insertion of the SCCmec cassette into the core genome (6). SCCmec types were initially defined by their combination of the *mec* gene class complex and the *ccr* gene complex (8). However, assignment of nomenclature and classification of SCCmec elements have been hampered by the existence of composite cassettes (9, 10) and pseudo-SCCmec elements that do not harbor *ccr* genes (11). Eleven SCCmec cassettes are formally recognized in the database of the International Working Group on the Staphylococcal Cassette Chromosome (IWG-SCC) and were named I to XI according to the chronological order in when they were first reported. Several SCCmec elements are reported in MRSP, including SCCmec III (previously described as II-III [12]), which is found in the globally dominant sequence type 71 (ST71) lineage (13); SCCmec V₊ variants (14); and a newly reported cassette, SCCmec_{NA45}, which harbors a class C1 *mec* gene complex and *ccrC* recombinase gene (15). Other SCCmec elements have been identified in *S. pseudintermedius* that are not recorded in the IWG-SCC database, including Ψ SCCmec₅₇₃₉₅ (11), which lacks *ccr* genes, and SCCmec_{KM241} (12) and SCCmec_{A116} (10) (Table 1). Despite the difficulties associated with characterizing some SCCmec elements, SCCmec typing can provide useful information about the phylogenetic and epidemiological origin of isolates. Echoing the epidemiological division of human-derived MRSA into health care-associated (HA) and community-associated (CA) lineages (16, 17), Kasai et al. found that veterinary MRSP isolates with SCCmec III tended to be HA-MRSP lineages whereas isolates with SCCmec V tended to be CA-MRSP (18). Recently, we described the molecular epidemiology of 77 MRSP isolates collected from clinical infections in animals in Australia during a national surveillance study and found that the population was phylogenetically diverse (19). The current study characterized the SCCmec elements in these isolates.

Characterization of SCCmec elements. Isolates originated from a larger collection of 669 *S. pseudintermedius* isolates collected during the first Australian survey into antimicrobial resistance in veterinary pathogens (20, 21). All isolates were identified using a BD Bruker MALDI Biotyper and were screened for methicillin resistance using manual oxacillin broth microdilution according to CLSI guidelines (22). The end dilution for MIC testing was 64 mg/liter oxacillin. Oxacillin resistance was confirmed by detection of an oxacillin MIC of ≥ 0.5 mg/liter using Vitek 2, in accordance with the manufacturer's instructions, and detection of the *mecA* gene by whole-genome sequencing as previously described (19). DNA extraction, library preparation, and initial *de novo* assembly were undertaken as previously described (19). SCCmec typing was undertaken by downloading the sequences of the *mec* gene complex and *ccr* elements of the SCCmec elements described by the IWG-SCC (8) from the NCBI online database (<https://www.ncbi.nlm.nih.gov/>). SCCmec elements previously identified in *S. pseudintermedius* but not included in the SCCmec working group website were also downloaded (Table 1). Downloaded SCCmec element sequences underwent BLASTn searches

TABLE 1 SCCmec elements previously identified in methicillin-resistant *S. pseudintermedius* isolates that are not described in the SCCmec database of the IWG-SCC

SCCmec name	Reference isolate	Accession number	mec complex	ccr complex
Ψ SCCmec ₅₇₃₉₅	MRSP 57395	HE984157.2	C1	No ccr
SCCmec _{KM241}	MRSP KM241	AM904731.1	A	A5B3
SCCmec _{AI16}	MRSP AI16	LN864705.1	A	A1B3
SCCmec _{NA45}	MRSP NA45	CP016072.1	C1	C6

against *de novo* contigs using CLC Genomics Workbench. BLASTn results required more than 85% sequence homology to be assigned a particular *ccr* gene. *mec* gene complexes were assigned based on the gene structure of *mecA*, its regulators, and associated insertion sequences (ISs). If a SCCmec type could not be assigned, contigs were mapped against a scaffold of reference SCCmec types (8) and the reference methicillin-susceptible *S. pseudintermedius* genome, ED99 (accession no. [CP002478.1](#)). The Kruskal-Wallis test was used to determine whether the median oxacillin MICs differed across SCCmec types. The Mann-Whitney U test was used to assess differences between SCCmec types in the median oxacillin MIC. SCCmec types with more than eight isolates were compared as separate entities in analyses; other isolates were grouped together.

Diversity of SCCmec types. Six SCCmec types were identified among 74 of the 77 MRSP from Australia (Table 2). The SCCmec type of the remaining three isolates (two ST497 isolates and one ST71 isolate) could not be determined because of poor sequencing quality (low read coverage and contig breaks) in the region around the *mecA* gene. Isolates from the same multilocus sequence type (MLST) tended to harbor the same SCCmec type. Four of the SCCmec types have previously been characterized in MRSP or MRSA as follows: SCCmec III ($n = 34$) and Ψ SCCmec₅₇₃₉₅ ($n = 7$), previously described in MRSP; and SCCmec V_T ($n = 10$) and SCCmec IVg ($n = 5$), previously described in MRSP and MRSA (11, 12, 23, 24). The 34 SCCmec III isolates, which were mostly ST71 and ST316, demonstrated 98% to 100% sequence homology to the *mec* and *ccr* gene complexes of the III element from MRSP KM1381 (12). Ψ SCCmec₅₇₃₉₅ isolates had no *ccr* genes but had 99 to 100% sequence homology to the region spanning from *orfx* to IS256 from MRSP 57395 (11). The V_T isolates displayed 96% to 100% homology to the *ccrC1* gene from MRSP 06-3228 (23) and 100% homology to its *mecA* and IS431 genes, but the *mecR1* gene was variably truncated from 23 bp to 93 bp. SCCmec IVg isolates had 97% to 100% sequence homology to the entire cassette from MRSA isolated from bovine milk described previously by Kwon et al. (24).

The fifth SCCmec element has 99% sequence homology to the novel element recently reported in MRSP NA45 (15). In our study, this element was identified in nine geographically dispersed isolates from eight different STs (Table 2). These isolates harbored a class C1 *mec* complex with 99% sequence homology to SCCmec X from MRSA JCSC6945 but did not harbor the same *ccr* genes as this element. Instead, the isolates harbored a recombinase gene with 99% homology to *ccrC6*, recently identified in a 43,922-bp SCCmec element in ST84 MRSP (15) and methicillin-resistant *S. schleiferi*

TABLE 2 SCCmec types and multilocus sequence types (MLST) of methicillin-resistant *Staphylococcus pseudintermedius* isolates from clinical infections in animals in Australia, 2013 to 2014

Element	MLST ^a
SCCmec III ($n = 34$)	ST71 ($n = 25$), ST316 ($n = 8$), ST25 ($n = 1$)
Ψ SCCmec ₅₇₃₉₅ ($n = 7$)	ST45 ($n = 6$), ST544 ($n = 1$)
SCCmec V _T ($n = 10$)	ST496 ($n = 8$), ST64 ($n = 1$), ST751 ($n = 1$)
SCCmec IVg ($n = 5$)	ST498 ($n = 3$), ST258 ($n = 1$), ST539 ($n = 1$)
SCCmec _{NA45} (VII variant ^b) ($n = 9$)	ST64 ($n = 2$), ST84 ($n = 1$), ST283 ($n = 1$), ST499 ($n = 1$), ST500 ($n = 1$), ST501 ($n = 1$), ST525 ($n = 1$), ST547 ($n = 1$)
Ψ SCCmec _{KW21} ($n = 9$)	ST497 ($n = 9$)
Not determined ^c ($n = 3$)	ST497 ($n = 2$), ST71 ($n = 1$)

^aMLST, multilocus sequence types.

^bThe SCCmec_{NA45} VII variant element harbors a C1 *mec* complex and a *ccrC6* element (15). Ψ SCCmec_{KW21} is a novel element that is described in this paper.

^cThe SCCmec elements of three isolates could not be determined due to poor sequence and assembly quality (contig breaks around the *mecA* gene).

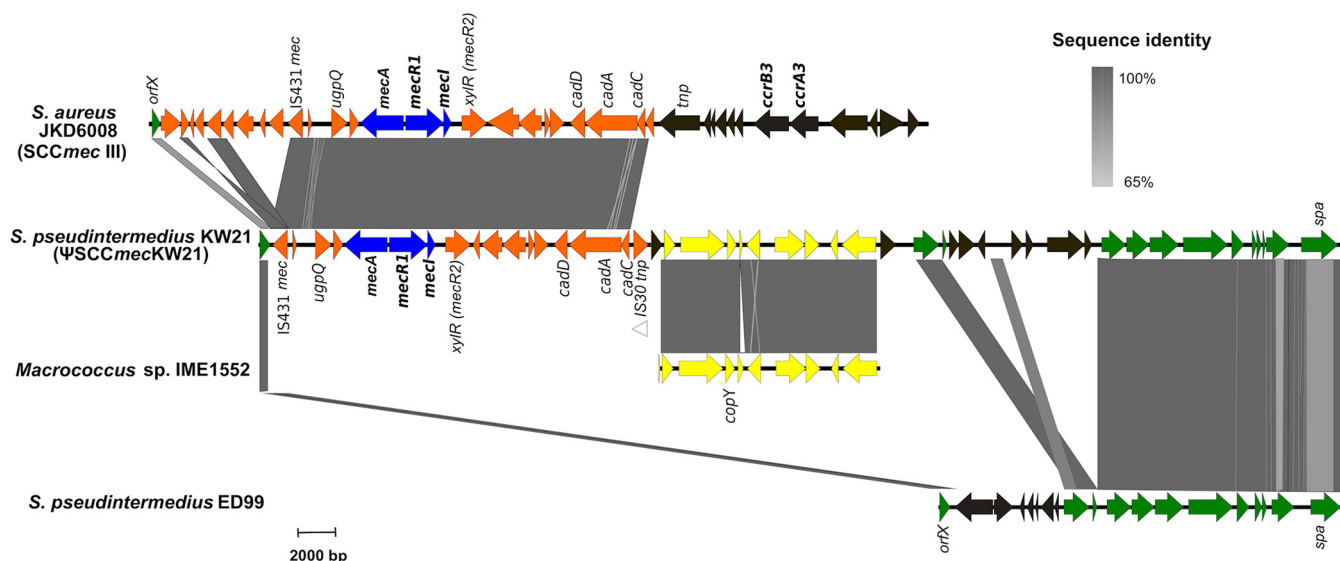


FIG 1 Alignment of the novel *SCCmec* element Ψ *SCCmec*_{KW21}, its flanking regions, and related sequences. The 16,711-bp Ψ *SCCmec*_{KW21} element, delineated by *orfX* and a truncated *IS30* transposase, is a truncated version of *SCCmec* III. The *mecA* gene complex and cadmium resistance genes (*cadCAD*) of Ψ *SCCmec*_{KW21} have high homology to the same region in ST239 MRSA (*S. aureus* JKD6008). Ψ *SCCmec*_{KW21} inserts into the genome of KW21 at the 3' end of the *orfX* gene and is bordered by an ~10,000-bp region with 99% homology to *Macrocooccus* sp. IME1552. This region, which includes a putative copper transport repressor (*copY*), is then bordered by sequence with 99% homology to the region harboring the *spa* gene in methicillin-susceptible *S. pseudintermedius* ED99. Areas of sequence homology, determined by BLASTn, are indicated with gray shading. Green arrows, coding DNA sequences (CDS) shared with MSSP ED99; orange arrows, CDS shared with *S. aureus* JKD6008; blue arrows, class A *mec* gene complex; yellow arrows, CDS shared with *Macrocooccus* IME1552; black arrows, unique CDS. The alignment was created in EasyFig V.5 (34).

(MRSS) (25). This element is also present in ST398 MRSA RIVM3897 (26), but the RIVM3987 element lacks the final 8,164 bp at the 3' end of the *SCCmec* cassette in ST84 MRSP and MRSS. The nine isolates in this study showed 99% homology to the entire *SCCmec* cassette from MRSP NA45, which contained heavy metal resistance genes *arsB*, *arsC*, *arsR* (arsenic resistance) and *copA* (copper resistance) but no antimicrobial resistance genes. On the basis of typing recommendations of the IWG-SCC (8), the element in these nine isolates and in MRSP NA45 could be described as *SCCmec* VII because it harbors a class C1 *mec* gene complex and *ccrC* recombinase gene (Fig. S1). However, as the *mec* gene complex is positioned in reverse orientation in comparison to *SCCmec* VII, we feel that it is more appropriate to refer to this cassette as “*SCCmec*_{NA45},” a *SCCmec* VII variant. Most of the isolates harboring the *SCCmec* VII variant *SCCmec*_{NA45} did not harbor the variable repeat region of the *spa* gene and therefore could not be assigned a *spa* type (19).

The final nine MRSP isolates, all ST497, could not be mapped to previously described *SCCmec* elements. All ST497 isolates were from a geographic cluster in Melbourne, Victoria (19). To characterize the novel element found in the remaining nine isolates, a representative ST497 isolate (KW21) underwent further sequencing by Illumina HiSeq and Nanopore long-read technology using Minlon. Minlon long reads were used to verify the structure of the *de novo* assembly. *De novo* assembly of Illumina HiSeq reads using Geneious yielded a 319,216-bp contig that contained the entire putative *SCCmec* element. This contig was subjected to a blast search against the NCBI database to determine putative components of the element. The element was annotated using PROKKA (27) and manually verified using the BLASTn algorithm in CLC Genomics Workbench.

Ψ *SCCmec*_{KW21} element. The novel *SCCmec* element, designated “ Ψ *SCCmec*_{KW21},” was integrated at the 3' end of the *orfX* gene (*rmlH*) (Fig. 1). The characteristic direct repeat and insertion sequences (ISs) that typically flank *SCCmec* elements were absent at the right side (10, 28). The element contained a class A *mec* gene complex that had 99% BLASTn similarity to the class A *mec* gene complex *SCCmec* cassettes from MRSA JKD6008 (29), MRSP KM241 (12) and MRSP A116 (10) (accession numbers CP002120.1,

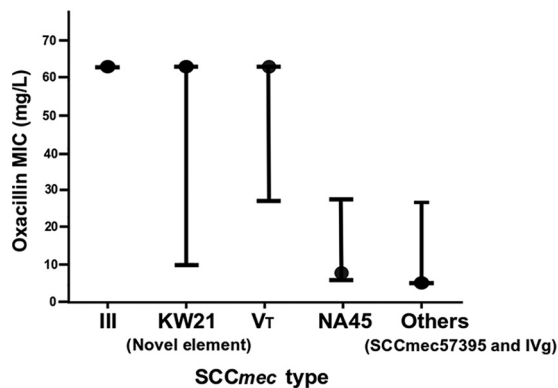


FIG 2 Oxacillin MIC for SCCmec types of MRSP isolates from Australia collected in 2013 to 2014. Black dots indicate the median MIC value; error bars indicate the interquartile range.

AM904731.1, and LN864705 respectively). The element did not contain any *ccr* genes. The 16,711-bp region of Ψ SCCmec_{KW21} that spanned from *orfX* to the cadmium resistance operon, *cadCAD*, had 99% sequence homology to the same region of SCCmec III from ST239 MRSA isolate JKD6008 (Fig. 1). We therefore propose that Ψ SCCmec_{KW21} is a truncated version of SCCmec III that lost the segment containing *ccr* genes after the cassette was inserted into the genome. Unlike SCCmec III from ST239 MRSA, Ψ SCCmec_{KW21} does not harbor *ccr* genes; instead, *cadA* and *cadC* are bordered by a truncated IS30 family transposase. To the right of this transposase is a 10,116-bp region that had 97% BLASTn similarity to a chromosomal region of *Macrocooccus* sp. IME1152 (accession number CP017156.1) that includes the *copY* gene, encoding a putative copper transport repressor. BLASTn analysis of the *de novo* contigs of ST497 isolates against the SCCmec element from KW21 revealed that all nine isolates had the same *mec* gene complex, the genomic region with *Macrocooccus* sequence homology, and no *ccr* genes. Consequently, they were considered to have the same pseudoelement as KW21. ST239 is an important health care-associated MRSA lineage in humans, so screening of healthy and diseased animals across Australia is now indicated to determine if ST497 and/or other lineages harboring Ψ SCCmec_{KW21} continue to exist within a geographic cluster or whether this lineage has disseminated across Australia or overseas, as has occurred with ST239 MRSA in humans (30).

Variation in oxacillin MICs amongst different SCCmec types. Fig. 2 shows the oxacillin MIC range for the major SCCmec types. The median oxacillin MICs differed significantly depending on SCCmec type (Fig. 2; $P < 0.001$). The median oxacillin MICs of Ψ SCCmec₅₇₃₉₅ and SCCmec IVg isolates (1 mg/liter) and of SCCmec_{NA45-VII} variant isolates (4 mg/liter) were significantly lower than the median oxacillin MIC of SCCmec III, SCCmec V_T and Ψ SCCmec_{KW21} isolates (64 mg/liter; $P < 0.01$). Recently, Kasai and colleagues (18) similarly reported differences in oxacillin MIC on the basis of MRSP SCCmec types. Specifically, they found that isolates with SCCmec III generally had higher oxacillin MICs and were more often associated with suspected hospital-acquired infections than isolates with SCCmec V. Analogous to analyses of MRSA in human medicine, they concluded that oxacillin MIC may give clues as to an isolate's epidemiological origin, where a high oxacillin MIC may indicate that an MRSP isolate is from a successful "health care-associated" clone whereas isolates with lower MICs may represent "community-associated" clones (18). There were insufficient epidemiological data available in our study to draw similar conclusions, but our results do support the notion that the oxacillin MIC is significantly affected by the SCCmec type and that isolates of the same multilocus sequence type generally harbor the same SCCmec type. Thus, it follows that different MRSP lineages would demonstrate different oxacillin MICs. The *mecA* gene can be repressed by either *mecl* or *blal*, but MRSA and MRSP isolates with *bla* regulators typically demonstrate more rapid induction and higher expression of *mecA* than isolates with *mec* regulators alone (31–33). To determine whether the

oxacillin MIC was influenced by the presence of the *blaI* and *mecl* genes rather than simply by the SCCmec type, we screened all isolates for these repressor genes using a BLAST-based command line script (screen_assembly3.py: https://github.com/shimbalama/screen_assembly). Most (45/77) isolates harbored *blaI*, but only SCCmec III and Ψ SCCmec_{KW21} harbored both *blaI* and *mecl*. The high median oxacillin MIC (64 mg/liter) of III and Ψ SCCmec_{KW21} isolates could have been due to the fact that *blaI* attenuates the strong *mecA* repression expected from the cognate *mec* regulators (32).

In summary, we found six SCCmec types among 77 MRSP isolates collected from clinical infections in Australian animals. The oxacillin MIC varied according to SCCmec type. We also described Ψ SCCmec_{KW21}, a novel pseudo-SCCmec element that was found only in a geographic cluster of clinical isolates. This report highlights the utility of nation-wide surveillance studies in unearthing novel and emerging resistance determinants and demonstrates how genomic resistance elements found in significant human pathogens such as *S. aureus* can also be found in veterinary pathogens such as *S. pseudintermedius*.

Accession number(s). The genomic sequence of Ψ SCCmec_{KW21} has been deposited in the National Center for Biotechnology Information (NCBI) database under GenBank accession number [MH713898](https://ncbi.nlm.nih.gov/nucl/MH713898). The contig sequences of the MRSP isolates described in this study were also deposited under BioProject number [PRJNA439160](https://ncbi.nlm.nih.gov/bioproject/PRJNA439160) and BioSample accession numbers [SAMN08741522](https://ncbi.nlm.nih.gov/biosample/SAMN08741522) to [SAMN08741590](https://ncbi.nlm.nih.gov/biosample/SAMN08741590).

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <https://doi.org/10.1128/mSphere.00491-18>.

FIG S1, TIF file, 2.7 MB.

ACKNOWLEDGMENTS

We acknowledge the assistance and support of all private, governmental, and university veterinary diagnostic laboratories within Australia for the provision of isolates. We gratefully thank Thomas Gottlieb, Charlotte Webster, and John Huynh and the team at the Department of Microbiology and Infectious Diseases at Concord Hospital (NSW, Australia) for their assistance in using matrix-assisted laser desorption ionization–time of flight (MALDI-TOF). We acknowledge the Sydney Informatics Hub and University of Sydney Core Research Facilities for providing subsidized access to CLC Genomics Workbench and associated support. We thank Emily Hudson for her assistance in processing the isolates and Seamus O'Reilly and Harvey Norman for their ongoing support in reviewing the manuscript.

The collection of the 77 MRSP isolates was supported by Zoetis Pty Ltd. and the Australian Research Council-Linkage Grant (grant number LP130100736). Sequencing of Ψ SCCmec_{KW21} was supported by internal funds of the Institute of Veterinary Bacteriology of the University of Bern, Bern, Switzerland.

REFERENCES

- dos Santos TP, Damborg P, Moodley A, Guardabassi L. 2016. Systematic review on global epidemiology of methicillin-resistant *Staphylococcus pseudintermedius*: inference of population structure from multilocus sequence typing data. *Front Microbiol* 7:1599. <https://doi.org/10.3389/fmicb.2016.01599>.
- Somayaji R, Priyantha M, Rubin J, Church D. 2016. Human infections due to *Staphylococcus pseudintermedius*, an emerging zoonosis of canine origin: report of 24 cases. *Diagn Microbiol Infect Dis* 85:471–476. <https://doi.org/10.1016/j.diagmicrobio.2016.05.008>.
- Utsui Y, Yokota T. 1985. Role of an altered penicillin-binding protein in methicillin- and cephem-resistant *Staphylococcus aureus*. *Antimicrob Agents Chemother* 28:397–403. <https://doi.org/10.1128/AAC.28.3.397>.
- García-Álvarez L, Holden MTG, Lindsay H, Webb CR, Brown DFJ, Curran MD, Walpole E, Brooks K, Pickard DJ, Teale C, Parkhill J, Bentley SD, Edwards GF, Girvan EK, Kearns AM, Pichon B, Hill RLR, Larsen AR, Skov RL, Peacock SJ, Maskell DJ, Holmes MA. 2011. Methicillin-resistant *Staphylococcus aureus* with a novel *mecA* homologue in human and bovine populations in the UK and Denmark: a descriptive study. *Lancet Infect Dis* 11:595–603. [https://doi.org/10.1016/S1473-3099\(11\)70126-8](https://doi.org/10.1016/S1473-3099(11)70126-8).
- Becker K, van Alen S, Idelevich EA, Schleimer N, Seggewiß J, Mellmann A, Kaspar U, Peters G. 2018. Plasmid-encoded transferable *mecB*-mediated methicillin resistance in *Staphylococcus aureus*. *Emerg Infect Dis* 24:242–248. <https://doi.org/10.3201/eid2402.171074>.
- Katayama Y, Ito T, Hiramatsu K. 2000. A new class of genetic element, *Staphylococcus* cassette chromosome *mec*, encodes methicillin resistance in *Staphylococcus aureus*. *Antimicrob Agents Chemother* 44:1549–1555. <https://doi.org/10.1128/AAC.44.6.1549-1555.2000>.
- Tsubakishita S, Kuwahara-Arai K, Baba T, Hiramatsu K. 2010. *Staphylococcal* cassette chromosome *mec*-like element in *Macrococcus caseolyticus*. *Antimicrob Agents Chemother* 54:1469–1475. <https://doi.org/10.1128/AAC.00575-09>.

8. International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements (IWG-SCC). 2009. Classification of staphylococcal cassette chromosome mec (SCCmec): guidelines for reporting novel SCCmec elements. *Antimicrob Agents Chemother* 53:4961–4967. <https://doi.org/10.1128/AAC.00579-09>.
9. Wilson LK, Coombs GW, Christiansen K, Grubb WB, O'Brien FG. 2016. Characterization of a novel staphylococcal cassette chromosome composite island from community-associated MRSA isolated in aged care facilities in Western Australia. *J Antimicrob Chemother* 71:3372–3375. <https://doi.org/10.1093/jac/dkw317>.
10. Chanchaithong P, Prapasarakul N, Perreten V, Schwendener S. 2016. Characterization of a novel composite staphylococcal cassette chromosome mec in methicillin-resistant *Staphylococcus pseudintermedius* from Thailand. *Antimicrob Agents Chemother* 60:1153–1157. <https://doi.org/10.1128/AAC.02268-15>.
11. Perreten V, Chanchaithong P, Prapasarakul N, Rossano A, Blum SE, Elad D, Schwendener S. 2013. Novel pseudo-staphylococcal cassette chromosome mec element (Ψ SCCmec₅₇₃₉₅) in methicillin-resistant *Staphylococcus pseudintermedius* CC45. *Antimicrob Agents Chemother* 57:5509–5515. <https://doi.org/10.1128/AAC.00738-13>.
12. Descloux S, Rossano A, Perreten V. 2008. Characterization of new staphylococcal cassette chromosome mec (SCC mec) and topoisomerase genes in fluoroquinolone- and methicillin-resistant *Staphylococcus pseudintermedius*. *J Clin Microbiol* 46:1818–1823. <https://doi.org/10.1128/JCM.02255-07>.
13. Perreten V, Kadlec K, Schwarz S, Andersson UG, Finn M, Greko C, Moodley A, Kania SA, Frank LA, Bemis DA, Franco A, Iurescia M, Battisti A, Duim B, Wagenaar JA, Duijkeren E, Weese JS, Fitzgerald JR, Rossano A, Guardabassi L. 2010. Clonal spread of methicillin-resistant *Staphylococcus pseudintermedius* in Europe and North America: an international multicentre study. *J Antimicrob Chemother* 65:1145–1154. <https://doi.org/10.1093/jac/dkq078>.
14. Duim B, Verstappen K, Kalupahana RS, Ranathunga L, Fluit AC, Wagenaar JA. 2018. Methicillin-resistant *Staphylococcus pseudintermedius* among dogs in the description of novel SCCmec variants. *Vet Microbiol* 213:136–141. <https://doi.org/10.1016/j.vetmic.2017.11.022>.
15. Riley MC, Perreten V, Bemis DA, Kania SA. 2016. Complete genome sequences of three important methicillin-resistant clinical isolates of *Staphylococcus pseudintermedius*. *Genome Announc* 4:e01194-16. <https://doi.org/10.1128/genomeA.01194-16>.
16. Okuma K, Iwakawa K, Turnidge JD, Grubb WB, Bell JM, O'Brien FG, Coombs GW, Pearman JW, Tenover FC, Kapi M, Tiensasitorn C, Ito T, Hiramatsu K. 2002. Dissemination of new methicillin-resistant *Staphylococcus aureus* clones in the community. *J Clin Microbiol* 40:4289–4294. <https://doi.org/10.1128/JCM.40.11.4289-4294.2002>.
17. Lindsay JA. 2013. Hospital-associated MRSA and antibiotic resistance—what have we learned from genomics?. *Int J Med Microbiol* 303:318–323. <https://doi.org/10.1016/j.ijmm.2013.02.005>.
18. Kasai T, Saegusa S, Shirai M, Murakami M, Kato Y. 2016. New categories designated as healthcare-associated and community-associated methicillin-resistant *Staphylococcus pseudintermedius* in dogs. *Microbiol Immunol* 60:540–551. <https://doi.org/10.1111/1348-0421.12401>.
19. Worthing KA, Abraham S, Coombs GW, Pang S, Saputra S, Jordan D, Trott DJ, Norris JM. 2018. Clonal diversity and geographic distribution of methicillin-resistant *Staphylococcus pseudintermedius* from Australian animals: discovery of novel sequence types. *Vet Microbiol* 213:58–65. <https://doi.org/10.1016/j.vetmic.2017.11.018>.
20. Saputra S, Jordan D, Worthing KA, Norris JM, Wong HS, Abraham R, Trott DJ, Abraham S. 2017. Antimicrobial resistance in coagulase-positive staphylococci isolated from companion animals in Australia: a one year study. *PLoS One* 12:e0176379. <https://doi.org/10.1371/journal.pone.0176379>.
21. Abraham S, Jordan D, Wong HS, Johnson JR, Toleman MA, Wakeham DL, Gordon DM, Turnidge JD, Mollinger JL, Gibson JS, Trott DJ. 2015. First detection of extended-spectrum cephalosporin- and fluoroquinolone-resistant *Escherichia coli* in Australian food-producing animals. *J Glob Antimicrob Resist* 3:273–277. <https://doi.org/10.1016/j.jgar.2015.08.002>.
22. CLSI. 2013. Performance standards for antimicrobial disk and dilution susceptibility tests for bacteria isolated from animals; approved standard—4th ed. CLSI, Wayne, PA, USA.
23. Black CC, Solyman SM, Eberlein LC, Bemis DA, Woron AM, Kania SA. 2009. Identification of a predominant multilocus sequence type, pulsed-field gel electrophoresis cluster, and novel staphylococcal chromosomal cassette in clinical isolates of *meaA*-containing, methicillin-resistant *Staphylococcus pseudintermedius*. *Vet Microbiol* 139:333–338. <https://doi.org/10.1016/j.vetmic.2009.06.029>.
24. Kwon N, Park KT, Moon J, Jung W, Kim S, Kim J, Hong S, Koo H, Joo Y, Park Y. 2005. Staphylococcal cassette chromosome mec (SCC mec) characterization and molecular analysis for methicillin-resistant *Staphylococcus aureus* and novel SCC mec subtype IVg isolated from bovine milk in Korea. *J Antimicrob Chemother* 56:624–632. <https://doi.org/10.1093/jac/dki306>.
25. Misic AM, Cain CL, Morris DO, Rankin SC, Beiting DP. 2015. Complete genome sequence and methylome of *Staphylococcus schleiferi*, an important cause of skin and ear infections in veterinary medicine. *Genome Announc* 3:e01011-15. <https://doi.org/10.1128/genomeA.01011-15>.
26. Bosch T, Witteveen S, Haenen A, Landman F, Schouls LM. 2016. Next-generation sequencing confirms presumed nosocomial transmission of livestock-associated methicillin-resistant *Staphylococcus aureus* in the Netherlands. *Appl Environ Microbiol* 82:4081–4089. <https://doi.org/10.1128/AEM.00773-16>.
27. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
28. Ito T, Ma XX, Takeuchi F, Okuma K, Yuzawa H, Hiramatsu K. 2004. Novel type V staphylococcal cassette chromosome mec driven by a novel cassette chromosome recombinase, *ccrC*. *Antimicrob Agents Chemother* 48:2637–2651. <https://doi.org/10.1128/AAC.48.7.2637-2651.2004>.
29. Howden BP, Seemann T, Harrison PF, McEvoy CR, Stanton J-AL, Rand CJ, Mason CW, Jensen SO, Firth N, Davies JK, Johnson PDR, Stinear TP. 2010. Complete genome sequence of *Staphylococcus aureus* strain JKD6008, an ST239 clone of methicillin-resistant *Staphylococcus aureus* with intermediate-level vancomycin resistance. *J Bacteriol* 192:5848–5849. <https://doi.org/10.1128/JB.00951-10>.
30. Monecke S, Slickers P, Gawlik D, Müller E, Reissig A, Ruppelt-Lorz A, Akpaka PE, Bandt D, Bes M, Boswihi SS. 6 July 2018. Molecular typing of ST239-MRSA-III from diverse geographic locations and the evolution of the SCCmec III element during its intercontinental spread. *Front Microbiol* <https://doi.org/10.3389/fmicb.2018.01436>.
31. McKinney TK, Sharma VK, Craig WA, Archer GL. 2001. Transcription of the gene mediating methicillin resistance in *Staphylococcus aureus* (*meaA*) is corepressed but not coinduced by cognate *meaA* and β -lactamase regulators. *J Bacteriol* 183:6862–6868. <https://doi.org/10.1128/JB.183.23.6862-6868.2001>.
32. Arède P, Ministro J, Oliveira DC. 2013. Redefining the role of the β -lactamase locus in methicillin-resistant *Staphylococcus aureus*: β -lactamase regulators disrupt the Mecl-mediated strong repression on *meaA* and optimize the phenotypic expression of resistance in strains with constitutive *meaA* expression. *Antimicrob Agents Chemother* 57:3037–3045. <https://doi.org/10.1128/AAC.02621-12>.
33. Black C, Eberlein L, Solyman S, Wilkes RP, Hartmann F, Rohrbach BW, Bemis DA, Kania SA. 2011. The role of *meaA* and *blaZ* regulatory elements in *meaA* expression by regional clones of methicillin-resistant *Staphylococcus pseudintermedius*. *Vet Microbiol* 151:345–353. <https://doi.org/10.1016/j.vetmic.2011.03.026>.
34. Sullivan MJ, Petty NK, Beatson SA. 2011. Easyfig: a genome comparison visualizer. *Bioinformatics* 27:1009–1010. <https://doi.org/10.1093/bioinformatics/btr039>.