

# 2022 survey of *Staphylococcus aureus* bacteraemia in New Zealand

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February 2026

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**CLIENT REPORT No:** FW 25052

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# ACKNOWLEDGEMENTS

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The authors thank:

- The Ministry of Health - Manatū Hauora for funding.
- Diagnostic laboratories for voluntarily referring SAB isolates and susceptibility testing data, without which this important work would not be possible.

Laboratories that contributed in 2022 were:

- |                                    |                         |
|------------------------------------|-------------------------|
| • Awanui Labs - Auckland           | • Kaitaia Hospital      |
| • Awanui Labs - Nelson Marlborough | • LabCare Taranaki      |
| • Awanui Labs - Otago              | • LabPLUS               |
| • Awanui Labs - Southland          | • MedLab Central Ltd    |
| • Awanui Labs - Timaru             | • Middlemore Hospital   |
| • Awanui Labs - Wairarapa          | • North Shore Hospital  |
| • Awanui Labs - Wellington         | • PathLab Bay of Plenty |
| • Canterbury Health Laboratories   | • Waikato Hospital      |
| • Te Nikau, Grey Hospital          | • Whangarei Hospital    |
| • Hawke's Bay Hospital             |                         |

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# 1. EXECUTIVE SUMMARY

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*Staphylococcus aureus* is a leading cause of both community-associated and hospital-associated bacteraemia in New Zealand and is a significant cause of morbidity and mortality in Aotearoa New Zealand. *S. aureus* is a common commensal but also a leading cause of skin and soft tissue infections, bone and joint infections, endocarditis, and sepsis. Previous research has shown the incidence of both invasive and non-invasive *S. aureus* infections is higher in New Zealand than in many high-income countries, with the highest rates observed in Māori and Pacific Peoples.

The aims of the PHF Science *S. aureus* bacteraemia (SAB) surveillance programme were to document rates of antimicrobial resistance (AMR), to better characterise the molecular epidemiology of isolates causing SAB, to examine variations in mortality rates and to examine variations in SAB rates according to place of onset, patient age, ethnicity, socioeconomic deprivation, risk factors and co-morbidities.

A total of 1,587 SAB episodes in New Zealand were reported to PHF Science, from 1 January to 31 December 2022, an increase of nearly 8% when compared to the number of SAB episodes reported in 2021. Of these, 71.8% were community-associated, and 11.3% were caused by methicillin-resistant *S. aureus* (MRSA).

Males accounted for approximately 65% of SAB episodes, representing a significantly higher proportion than females. Incidence of SAB increased with age. The median age for SAB was significantly lower among all ethnic groups compared to people of European or Other ethnicity.

The data show significant inequities for SAB by ethnicity and socioeconomic deprivation. Compared to the people of European or Other ethnicity, age-standardised rates in Pacific peoples and Māori were 16.9 and 4.5 times higher, respectively. There were significantly more cases in people with higher socioeconomic deprivation.

The all-cause mortality for SAB at 30 days was 15.1%, although this was significantly lower amongst children (<18 years). Age standardised mortality rates were 11.9 times higher for Pacific Peoples and 2.5 times higher for Māori compared to the European or Other ethnic group. There was no significant difference in mortality between

community-associated and hospital-associated cases or isolates with differences in methicillin susceptibility.

The most common risk factors and comorbidities associated with SAB were tobacco smoking (38.2%), diabetes (29.9%), and obesity (13.7%).

The total incidence of MRSA SAB was highest in the Northern region of New Zealand and within Pacific Peoples; over 20% of SAB episodes for Pacific Peoples were due to MRSA. MRSA SAB epidemiology should be taken into account when considering empiric sepsis antibiotic treatment.

Compared with methicillin-susceptible *S. aureus* (MSSA) isolates, MRSA isolates showed approximately double the resistance to erythromycin and clindamycin, and more than six-fold higher resistance to fusidic acid. This pattern was primarily driven by the dominance of the ST5-IV clone (colloquially referred to as the AK3 MRSA strain). All isolates tested remained susceptible to daptomycin, linezolid, and vancomycin.

Based on *spa* typing data, MSSA isolates from SAB were more diverse than MRSA. Using core genome multilocus sequence type (cgMLST), more than 140 complex types were identified compared to 102 cgMLST types in 2021. Similar MRSA clones were found in community-associated SAB and hospital-associated SAB cases.

The results of this report highlight the need for investment in sustained epidemiological and molecular surveillance, infection prevention and control, antimicrobial stewardship and continued focus on prevention initiatives. Of particular significance is the role of efforts to prevent skin infections, as well as smoking cessation, wound care, diabetes management, device management, dialysis and vascular line care, and ideally the development and equitable delivery of an effective vaccine against *S. aureus* infections.

## 2. INTRODUCTION

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*S. aureus* is a leading cause of both community-associated and hospital-associated bacteraemia in Aotearoa New Zealand (NZ). *S. aureus* is a common commensal but also a leading cause of skin and soft tissue infections, bone and joint infections, endocarditis, and sepsis (Tong et al., 2015). Previous research has shown the incidence of both invasive and non-invasive *S. aureus* infections is higher in NZ than in many high-income countries, with the highest rates observed in Māori and Pacific Peoples (Heffernan et al., 2015; Hill, Birch, et al., 2001; Hill, Wong, et al., 2001; Te Tāhū Hauora Health Quality Safety Commission, 2024; Williamson et al., 2013).

MRSA is of particular concern due to resistance to many antimicrobials commonly used to treat staphylococcal infections, and its association with higher morbidity and mortality compared with MSSA (World Health Organization, 2023). Consequently, since 2019, monitoring the incidence of MRSA bacteraemia as an indicator of antimicrobial resistance (AMR) has been a component of the World Health Organization's Sustainable Development Goals (World Health Organization, 2023).

Since the early 2000s, the Health Quality and Safety Commission (HQSC) has measured the incidence of healthcare-associated *S. aureus* bacteraemia (SAB) as a key indicator of healthcare quality and as an outcome measure for the Hand Hygiene New Zealand (HHNZ) programme (Barratt et al., 2022). Despite positive progress in hand hygiene performance, the median quarterly healthcare-associated SAB rate rose steadily from 0.11 healthcare-associated SAB events per 1,000 bed-days in 2016 to 0.15 healthcare-associated SAB events per 1,000 bed-days in 2019 (Barratt et al., 2022).

Molecular characterisation and AMR data are outside of the scope of the HQSC HHNZ programme, and there has previously been no systematic surveillance of the clinical and molecular epidemiology of isolates from *S. aureus* bacteraemia in the NZ community.

The aims of the PHF Science SAB surveillance programme were to assess AMR and molecular epidemiology of SAB isolates as well as examine variability in the rates of mortality and SAB according to patient demographics and co-morbidities. Earlier reports on *S. aureus* and SAB surveillance in New Zealand are available on the PHF Science website (<https://www.phfscience.nz/>).

## 3. SUMMARY OF METHODS

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### 3.1 ISOLATES AND PATIENT INFORMATION

New Zealand diagnostic laboratories were requested to refer to PHF Science all *S. aureus* isolates from blood culture samples isolated from 1<sup>st</sup> January to 31<sup>st</sup> December 2022. Duplicate isolates, cultured within 14-days of the initial sample, were not included, unless an isolate of a different *spa* type was identified. Any isolates collected less than 48 hours after birth were excluded as these infections were considered maternally acquired during delivery. Referring laboratories also supplied select patient information for each isolate, including the National Health Index number (NHI), sex, date of birth, and, if appropriate, healthcare facility as well as susceptibility testing data (see Appendix A). The relevant Health New Zealand region was determined by the recorded patient domicile address.

These data were supplemented by patient information and hospitalisation event data (admission and discharge dates, and diagnosis codes) from the Ministry of Health National Minimum Dataset (NMDS). The length of hospitalisation refers to the total time in hospital and will include days not directly due to SAB episodes. Where the domicile of the patient was overseas, the district of the referring laboratory was used.

Episodes were defined as community-associated SAB (CA-SAB), or hospital-associated SAB (HA-SAB) based on hospital admission and discharge dates. Isolates collected within 48-hours of hospital admission were classified as CA-SAB and those collected 48-hours or more after hospital admission or within 48-hours of hospital discharge were classified as HA-SAB. Data from multiple hospitalisation events, including interhospital transfers, with the same NHI were combined if the time between events was < 48 hours. This was consistent with the definition used in the Australian surveillance program (Coombs et al., 2023). Please note that the definition used in this report to define place of onset differs from that used by HQSC (Barratt et al., 2022).

The denominator data used to determine disease rates (except the data used to determine disease rates for ethnic groups) has been derived from the 2022 mid-year population estimates published by Statistics New Zealand.

Denominator data used to determine disease rates for ethnic groups is based on the proportion of people in each ethnic group from the 2018 'estimated resident population' applied to the 2022 mid-year population estimates from Statistics New Zealand. Ethnicity analysis is prioritised in the following order: Māori, Pacific peoples, Asian, European or Other (Middle Eastern/Latin American/African (MELAA) ethnic group.

For different ethnic groups, numbers and disease rates are based on a prioritised classification of ethnicity, with the Māori ethnic group prioritised first, followed by Pacific peoples, Asian, MELAA, and European or Other (including New Zealander) ethnic groups. A disadvantage of using prioritised ethnicity is that people who identify with more than one ethnic group can be placed into a group they may not self-identify with. Furthermore, prioritisation undercounts non-Māori ethnic groups. This has been found to be most significant for Pacific peoples. This undercount may generate an age-related bias, as the reporting of multiple ethnic groups is more common in younger age groups.

### **3.2 ISOLATE CHARACTERISATION**

Isolates were characterised using a real-time PCR that detected the methicillin resistance genes *mecA* and *mecC*, the *S. aureus* species-specific *nuc* gene and *lukS-PV* for detection of Panton-Valentine leukocidin (PVL) (Pichon et al., 2012). All isolates were also characterised using staphylococcal protein A gene (*spa*) typing (Strommenger et al., 2008) and, if needed, pulsed-field gel electrophoresis (PFGE, (Goering, 2004)). For further information on all isolate characterisation methods refer to Appendix A.

Antimicrobial susceptibility testing was performed, where necessary, to identify strains and to supplement the susceptibility data provided by referring laboratories. Disc susceptibility testing was performed and interpreted according to the methods of the European Committee on Antimicrobial Susceptibility Testing (EUCAST, (European Committee on Antimicrobial Susceptibility Testing, 2022)).

All MRSA underwent Illumina-based whole genome sequencing (WGS) (Appendix A), with data used to define the MRSA clone (Appendix A).

### **3.3 DATA ANALYSIS**

Data cleaning and statistical tests were performed in R version 4.4.3 (R Core Team, 2021) using tidyverse (Wickham et al., 2019) and AMR packages (Berends et al., 2022).

For further details refer to Appendix A. The definitions defined by Magiorakos et al. (Magiorakos et al., 2012) were applied in this survey, where multidrug resistance was defined as resistance to one or more agent in three or more antimicrobial groups.

## 4. RESULTS

### 4.1 SAB DATASET

PHF Science received 1,706 *S. aureus* blood culture isolates that were collected from 1 January to 31 December 2022. In total, 119 isolates were excluded from our analysis: 42 were duplicate isolates, 73 could not be matched to National Minimum Dataset (NMDS) hospitalisation data from a hospitalisation event within 48 hours of sample collection, and four were collected within 48 hours of birth.

Of the 1,587 isolates included in our analysis, 1,139 (71.8%) were classified as CA-SAB whilst 448 (28.2%) were HA- SAB (Table 1). Significantly more HA-SAB episodes were MRSA than CA-SAB episodes (14.7% vs. 10.0%,  $P = .01$ ). All 180 MRSA isolates contained the *mecA* gene, with no *mecC*-mediated resistance detected. No *mecA* genes were found among MSSA isolates, although one isolate contained a truncated, non-functional *mecC* gene (Miller et al., 2024).

There were 56 people with multiple episodes of SAB included in our analysis. Of these 51 people had two episodes, four people had three episodes and one person had four episodes.

**Table 1. SAB episodes by methicillin susceptibility and place of onset, 2022**

| Methicillin<br>susceptibility | Place of onset (% (No.)) |                              |                             | P-value |
|-------------------------------|--------------------------|------------------------------|-----------------------------|---------|
|                               | Overall                  | Community-<br>associated SAB | Hospital-<br>associated SAB |         |
| Total                         | 1,587                    | 1,139                        | 448                         |         |
| MRSA                          | 11.3 (180)               | 10.0 (114)                   | 14.7 (66)                   | .011    |
| MSSA                          | 88.7 (1,407)             | 90.0 (1,025)                 | 85.3 (382)                  |         |

## 4.2 PATIENT DEMOGRAPHICS

Data for age was available for 1585 patients with SAB and sex data was available for 1586 patients. The majority were male (all SAB, 65.8% 1044/1586; CA-SAB, 65.2% 743/1138; and HA-SAB, 67.2% 301/448). Just under half of all SAB and CA-SAB episodes, and over half of HA-SAB episodes were in those aged  $\geq 65$  years (all SAB, 49.9%; CA-SAB, 47.9%; and HA-SAB, 54.9%).

Increasing age was a surrogate risk factor for SAB (Table 2). The number of *S. aureus* bacteraemia episodes in patients aged less than 45 years was 23.8% ( $n = 377/1587$ ). The percentage of patients aged less than 15 years was 9.0% ( $n = 143/1585$ ).

**Table 2. Number of episodes of SAB, by patient age group and sex, 2022**

| Sex <sup>1</sup> | Age group (years, % (No.)) |              |              |              |                    |               |               |               |
|------------------|----------------------------|--------------|--------------|--------------|--------------------|---------------|---------------|---------------|
|                  | 0–4                        | 5–14         | 15–24        | 25–34        | 35–44 <sup>2</sup> | 45–54         | 55–64         | $\geq 65$     |
| Total            | 60                         | 83           | 56           | 77           | 101                | 161           | 255           | 792           |
| Female           | 41.7<br>(25)               | 37.3<br>(31) | 37.5<br>(21) | 46.8<br>(36) | 36.0<br>(36)       | 33.5<br>(54)  | 29.8<br>(76)  | 33.1<br>(262) |
| Male             | 58.3<br>(35)               | 62.7<br>(52) | 62.5<br>(35) | 53.2<br>(41) | 64.0<br>(64)       | 66.5<br>(107) | 70.2<br>(179) | 66.9<br>(530) |

1 Two episodes, one male and one female, did not have age data.

2 One episode, in age group 35–44 years did not have sex data.

The highest rate (per 100,000) of SAB episodes were in the Northern region (33.0, 634 episodes), followed by Te Manawa Taki (31.8, 326 episodes), Central (31.2, 304 episodes) and Te Waipounamu (26.9, 323 episodes). SAB isolates from the combined Auckland health districts (Waitematā, Te Toka Tumai Auckland, and Counties Manukau) made up the majority (86.0%, 545/634) of isolates from the Northern Region, and 34.3% of the total national cohort of isolates. Data on the distribution of SAB episodes by place of onset and region are shown in Appendix C Table C1.

Table 3 shows the distribution of SAB episodes by methicillin resistance and region of residence. Incidence rates for both MRSA and MSSA were highest in the Northern region and Te Manawa Taki, respectively.

**Table 3. Rates of patients with SAB by region and methicillin susceptibility, 2022**

| Methicillin<br>susceptibility | Region (Rate <sup>1</sup> (No.)) |            |                   |            |                  |
|-------------------------------|----------------------------------|------------|-------------------|------------|------------------|
|                               | Overall                          | Northern   | Te Manawa<br>Taki | Central    | Te<br>Waipounamu |
| Total                         | 31.0 (1587)                      | 33.0 (634) | 31.8 (326)        | 31.2 (304) | 26.9 (323)       |
| MRSA                          | 3.5 (180)                        | 5.4 (103)  | 2.5 (26)          | 3.7 (36)   | 1.2 (15)         |
| MSSA                          | 27.5 (1407)                      | 27.6 (531) | 29.3 (300)        | 27.5 (268) | 25.6 (308)       |

1 Rate per 100 000 population

The demographic characteristics gender, age, ethnicity, geographical region and socioeconomic deprivation are detailed as counts in Table 4. Most episodes were in people of European or Other ethnicity (60.7%, 964 episodes), followed by Māori (20.9%, 332 episodes), Pacific Peoples (12.7%, 202 episodes), and Asian (5.6%, 89 episodes) ethnicities. The Northern region accounted for a more marked proportion of the HA-SAB (47.3%, 212 episodes) than CA-SAB (37.1%, 422). The median age for SAB episodes was considerably younger among all other ethnic groups compared with European and Other, with differences statistically significant (Figure 1).

**Table 4. Demographic characteristics of SAB episodes by place of onset, 2022**

| Demographic/<br>Characteristic        | Place of Onset (% (No.)) |                          |                         |
|---------------------------------------|--------------------------|--------------------------|-------------------------|
|                                       | Overall                  | Community-associated SAB | Hospital-associated SAB |
| <b>Total</b>                          | 1587                     | 1139                     | 448                     |
| <b>Sex<sup>1</sup></b>                |                          |                          |                         |
| Female                                | 34.2 (542)               | 34.7 (395)               | 32.8 (147)              |
| Male                                  | 65.8 (1044)              | 65.2 (743)               | 67.2 (301)              |
| <b>Age group (years)<sup>1</sup></b>  |                          |                          |                         |
| 0–4                                   | 3.8 (60)                 | 3.0 (34)                 | 5.8 (26)                |
| 5–14                                  | 5.2 (83)                 | 6.3 (72)                 | 2.5 (11)                |
| 15–24                                 | 3.5 (56)                 | 4.0 (45)                 | 2.5 (11)                |
| 25–34                                 | 4.9 (77)                 | 5.0 (57)                 | 4.5 (20)                |
| 35–44                                 | 6.4 (101)                | 6.7 (76)                 | 5.6 (25)                |
| 45–54                                 | 10.1 (161)               | 10.6 (121)               | 8.9 (40)                |
| 55–64                                 | 16.1 (255)               | 16.3 (186)               | 15.4 (69)               |
| ≥65                                   | 49.9 (792)               | 47.9 (546)               | 54.9 (246)              |
| <b>Ethnicity (prioritised)</b>        |                          |                          |                         |
| Māori                                 | 20.9 (332)               | 21.5 (245)               | 19.4 (87)               |
| Pacific peoples                       | 12.7 (202)               | 12.4 (141)               | 13.6 (61)               |
| Asian                                 | 5.6 (89)                 | 4.9 (56)                 | 7.4 (33)                |
| European or Other                     | 60.7 (964)               | 61.2 (697)               | 59.6 (267)              |
| <b>Region</b>                         |                          |                          |                         |
| Northern                              | 39.9 (634)               | 37.1 (422)               | 47.3 (212)              |
| Te Manawa Taki                        | 20.5 (326)               | 22.1 (252)               | 16.5 (74)               |
| Central                               | 19.2 (304)               | 19.6 (223)               | 18.1 (81)               |
| Te Waipounamu                         | 20.4 (322)               | 21.2 (242)               | 18.1 (81)               |
| <b>NZDep18 quintile<sup>2,3</sup></b> |                          |                          |                         |
| Quintile 1                            | 13.1 (208)               | 13.6 (155)               | 11.8 (53)               |
| Quintile 2                            | 15.8 (251)               | 16.8 (191)               | 13.4 (60)               |
| Quintile 3                            | 19.7 (313)               | 18.3 (209)               | 23.2 (104)              |
| Quintile 4                            | 23.8 (377)               | 24.1 (274)               | 23.0 (103)              |
| Quintile 5                            | 27.3 (434)               | 27.0 (307)               | 28.3 (127)              |

1 One CA-SAB episode did not have sex data. Two CA-SAB episode did not have age data.

2 Three CA-SAB and one HA-SAB episodes did not have NZDep18 data.

3 Quintile of the 2018 NZ Deprivation Index (1 = least socioeconomically deprived and 5 = most socioeconomically deprived).

Annual age standardised rates for all, CA-SAB, and HA-SAB cases are shown in Appendix C, Table C2. For all SAB, the age standardised incidence rates were highest among Pacific Peoples and Māori with rates of 144.3 per 100,000 and 38.9 per 100,000, respectively, compared to 12.5 per 100,000 for Asian, and 8.7 per 100,000 for European and Other, respectively. This ethnic inequity was similar for HA-SAB and CA-SAB.

The percentage of SAB episodes increased with increasing socioeconomic deprivation as measured by the NZDep18 index, with 27.3% of episodes from quintile 5 (areas with most material deprivation) compared to 13.1% from quintile 1 (least deprivation),  $P = .110$ .

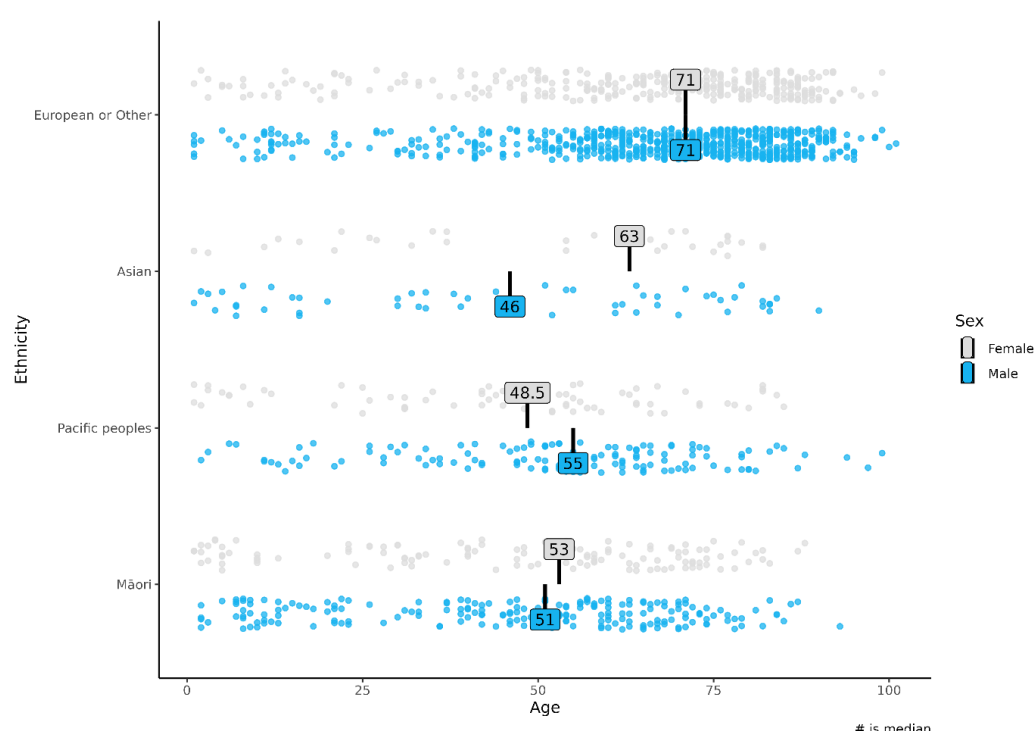


**Figure 1. Age distribution and median age of patients with SAB, by ethnicity and sex, 2022**

### 4.3 ALL-CAUSE LENGTH OF HOSPITAL STAY

Table 5 shows the length of hospital stay by methicillin susceptibility and place of onset for patients with SAB. Overall, 15.9% of patients with SAB had a hospital stay of <7 days, 34.4% had a hospital stay of 7–14 days, 28.2% had a hospital stay of 15–30 days, and 21.5% had a hospital stay of >30 days.

**Table 5. Length of hospital stay associated with SAB, by methicillin susceptibility and place of onset, 2022<sup>1</sup>**

| Methicillin susceptibility/<br>Place of onset | Episodes | Median length of stay (IQR) | Length of hospital stay (% (No.)) |            |            |            |
|-----------------------------------------------|----------|-----------------------------|-----------------------------------|------------|------------|------------|
|                                               |          |                             | <7 days                           | 7–14 days  | 15–30 days | >30 days   |
| Total                                         | 1,587    | 14 (8–27)                   | 15.9 (252)                        | 34.4 (546) | 28.2 (448) | 21.5 (341) |
| MRSA                                          | 180      | 18 (10–34)                  | 13.3 (24)                         | 27.8 (50)  | 30.0 (54)  | 28.9 (52)  |
| CA-SAB                                        | 114      | 12 (8–23)                   | 20.2 (23)                         | 34.2 (39)  | 26.3 (30)  | 19.3 (22)  |
| HA-SAB                                        | 66       | 29 (17–60)                  | 1.5 (1)                           | 16.7 (11)  | 36.4 (24)  | 45.5 (30)  |
| MSSA                                          | 1,407    | 14 (8–26)                   | 16.2 (228)                        | 35.3 (496) | 28.0 (394) | 20.5 (289) |
| CA-SAB                                        | 1,025    | 11 (7–20)                   | 20.6 (211)                        | 40.4 (414) | 25.6 (262) | 13.5 (138) |
| HA-SAB                                        | 382      | 23 (14–45)                  | 4.5 (17)                          | 21.5 (82)  | 34.6 (132) | 39.5 (151) |

<sup>1</sup> NMDS does not include onset dates for symptoms related to a SAB episode. Therefore, the length of hospitalisation refers to the total time in hospital and will include hospitalisation days that are unrelated to SAB for the HA-SAB episodes.

The median length of hospital stay for all SAB was 14 days (Inter quartile range (IQR) 8–27), and was significantly longer for MRSA infections compared to MSSA infections (MRSA: 18, IQR 10–34, MSSA: 14, IQR 8–26,  $P < .01$ ), although this was not the case when stratified into HA-SAB (MRSA: 29, IQR 17–60, MSSA: 23, IQR 14–45,  $P = .053$ ) and CA-SAB (MRSA: 12, IQR: 8–23, MSSA: 11, IQR 7–20,  $P = .182$ ).

#### 4.4 ALL-CAUSE MORTALITY

A total of 240 (15.1%) individuals with SAB died within 30 days of a positive *S. aureus* blood culture result. Among the isolates associated with patient deaths, 206 episodes (85.8%) were MSSA and 34 episodes (14.2%) were MRSA.

Table 6 shows the breakdown of 30-day all-cause mortality by methicillin susceptibility and place of onset. No statistically significant differences were observed in all-cause mortality between those with MSSA and MRSA infections (Overall,  $P = .150$ ; CA-SAB,  $P = .100$ ; and HA-SAB,  $P = .579$ ), and CA-SAB and HA-SAB (Overall  $P = .816$ ).

**Table 6. 30-day all-cause mortality from SAB, by methicillin susceptibility and place of onset, 2022**

| Methicillin<br>susceptibility | Overall |                 | Community-<br>associated SAB |                 | Hospital-<br>associated SAB |                 |
|-------------------------------|---------|-----------------|------------------------------|-----------------|-----------------------------|-----------------|
|                               | Total   | Died<br>% (No.) | Total                        | Died<br>% (No.) | Total                       | Died<br>% (No.) |
| Total                         | 1,587   | 15.1 (240)      | 1,139                        | 15.3 (174)      | 448                         | 14.7 (66)       |
| MRSA                          | 180     | 18.9 (34)       | 114                          | 20.2 (23)       | 66                          | 16.7 (11)       |
| MSSA                          | 1,407   | 14.6 (206)      | 1,025                        | 14.7 (151)      | 382                         | 14.4 (55)       |

Table 7 shows that 30-day all-cause mortality is highest among adults aged 65 years and over (23.1%, 183/792).

**Table 7. 30-day all-cause mortality from SAB, by age group, 2022**

| Age group (years) | Total SAB episodes<br>(No.) | Total deaths<br>(%, (No)) |
|-------------------|-----------------------------|---------------------------|
| 0–4               | 60                          | 5.0 (3)                   |
| 5–14              | 83                          | 0 (0)                     |
| 15–24             | 56                          | 0 (0)                     |
| 25–34             | 77                          | 5.2 (4)                   |
| 35–44             | 101                         | 5.9 (5)                   |
| 45–54             | 161                         | 6.2 (10)                  |
| 55–64             | 255                         | 13.3 (34)                 |
| 65+               | 792                         | 23.1 (183)                |

Table 8 shows age-standardised 30-day mortality rates. Age-standardised mortality rates were 11.9 times higher for Pacific Peoples and 2.5 times higher for Māori compared to the European or Other ethnic group. 30-day mortality rates were lower for HA-SAB than for CA-SAB across all ethnic groups.

**Table 8. Age-standardised 30-day mortality rates among SAB episodes stratified by place of onset, methicillin susceptibility and ethnicity, 2022**

| Ethnicity         | All SAB |                            | Community-associated SAB |                            | Hospital-associated SAB |                              | MRSA SAB |                              | MSSA SAB |                            |
|-------------------|---------|----------------------------|--------------------------|----------------------------|-------------------------|------------------------------|----------|------------------------------|----------|----------------------------|
|                   | No.     | Rate (95% CI) <sup>1</sup> | No.                      | Rate (95% CI) <sup>1</sup> | No.                     | Rate (95% CI) <sup>1,2</sup> | No.      | Rate (95% CI) <sup>1,2</sup> | No.      | Rate (95% CI) <sup>1</sup> |
| Māori             | 32      | 3.7 (2.4 - 5)              | 23                       | 2.7 (1.6 - 3.8)            | 9                       | 1.1 (0.4 - 1.8)              | 9        | 1.1 (0.4 - 1.8)              | 23       | 2.7 (1.6 - 3.8)            |
| Pacific peoples   | 25      | 17.9 (10.9 - 24.9)         | 18                       | 12.9 (6.9 - 18.9)          | 7                       | 5 (1.3 - 8.7)                | 7        | 5 (1.3 - 8.7)                | 18       | 12.9 (6.9 - 18.9)          |
| Asian             | 12      | 1.7 (0.7 - 2.7)            | 9                        | 1.3 (0.5 - 2.1)            | 3                       | -                            | 1        |                              | 11       | 1.5 (0.6 - 2.4)            |
| European or Other | 171     | 1.5 (1.3 - 1.7)            | 124                      | 1.1 (0.9 - 1.3)            | 47                      | 0.4 (0.3 - 0.5)              | 17       | 0.2 (0.1 - 0.3)              | 154      | 1.4 (1.2 - 1.6)            |
| Total             | 240     | 0.8 (0.7 - 0.9)            | 174                      | 0.6 (0.5 - 0.7)            | 66                      | 0.2 (0.2 - 0.2)              | 34       | 0.1 (0.1 - 0.1)              | 206      | 0.7 (0.6 - 0.8)            |

1 Rates (95% CI) are per 100,000 population.

2 Rates are not presented where there were fewer than five episodes.

Table 9 shows the number of SAB isolates, by methicillin susceptibility and ethnicity. The percentage of all MRSA SAB episodes by ethnicity was: 22.3% (45/202) in Pacific peoples, 13.9% (46/332) in Māori, 11.2% (10/89) in Asians, and 8.2% (79/964) for European or Other. The differences in the percentage of MRSA found across ethnic groups was statistically significant ( $P < .001$ ).

**Table 9. Methicillin susceptibility among SAB episodes by ethnicity, 2022**

| Methicillin susceptibility | Percent (No.) of Ethnic Group |               |                 |              |                   | P-value <sup>1</sup> |
|----------------------------|-------------------------------|---------------|-----------------|--------------|-------------------|----------------------|
|                            | Overall                       | Māori         | Pacific peoples | Asian        | European or Other |                      |
| Total                      | 1,587                         | 332           | 202             | 89           | 964               |                      |
| MRSA                       | 11.3<br>(180)                 | 13.9<br>(46)  | 22.3<br>(45)    | 11.2<br>(10) | 8.2<br>(79)       | <.001                |
| MSSA                       | 88.7<br>(1,407)               | 86.1<br>(286) | 77.7<br>(157)   | 88.8<br>(79) | 91.8<br>(885)     |                      |

Note: Ethnicity is prioritised. European or Other includes the MELAA category

## 4.5 RISK FACTORS, COMORBIDITIES AND COMPLICATIONS

### 4.5.1 ICD-10-AM DIAGNOSIS CODES

We investigated using ICD-10 diagnosis codes to attribute the clinical source of SAB, however no meaningful results were able to be generated with confidence, due to the complexities of hospital coding data.

### 4.5.2 RISK FACTORS, COMORBIDITIES AND COMPLICATIONS

Table 10 shows the number of SAB infections with a diagnosis code relating to certain risk factors, comorbidities or complications, by place of onset. Risk factors and comorbidities were identified through key word search of National Minimum Dataset hospitalisation records. Complications were identified using a list informed by previous work undertaken by the Australian Commission on Safety and Quality (Appendix B).

**Table 10. Number of all SAB episodes with a diagnosis code relating to select risk factors, comorbidities and complications, by place of onset, 2022**

| Common risk factors, comorbidities and complications           | Place of onset     |                                         |                                       | P-value |
|----------------------------------------------------------------|--------------------|-----------------------------------------|---------------------------------------|---------|
|                                                                | Overall<br>% (No.) | Community-<br>associated SAB<br>% (No.) | Hospital-associated<br>SAB<br>% (No.) |         |
| Total                                                          | 1587               | 1139                                    | 448                                   |         |
| Tobacco smoking                                                | 38.2 (607)         | 36.2 (412)                              | 43.5 (195)                            | .007    |
| Diabetes mellitus                                              | 29.9 (475)         | 29.8 (339)                              | 30.4 (136)                            | .855    |
| Obesity                                                        | 13.7 (218)         | 12.6 (143)                              | 16.8 (75)                             | .035    |
| Surgical site infection                                        | 3.5 (56)           | 3.3 (38)                                | 4.0 (18)                              | .546    |
| Complications associated with vascular catheters               | 14.6 (231)         | 8.0 (91)                                | 31.3 (140)                            | <.001   |
| Complications associated with prosthetics/ implantable devices | 17.0 (269)         | 17.6 (201)                              | 15.2 (68)                             | .265    |

A total of 71.3% (1131/1587) of SAB episodes had a diagnosis code related to at least one risk factor, comorbidities or complications assessed, including 67.5% (769/1139) of CA-SAB and 80.8% (362/448) of HA-SAB patients. Among the risk factors and comorbidities assessed, tobacco smoking (38.2%) was the most common followed by diabetes mellitus (29.9%) and obesity (13.7%). For context, the prevalence in the general population for adults over 15 years of age is as follows: current tobacco smoking 8.4%, diabetes<sup>1</sup> 5.9%, and obesity 32.5% (Ministry of Health, 2023).

Among complications assessed, those associated with prosthetics/implantable devices were the most common (17.0%). The prevalence of tobacco smoking and complications associated with vascular catheters differed by place of onset, with greater prevalence among with HA-SAB compared with CA-SAB (43.5% vs 36.2%,  $P < .01$  and 31.3% vs. 8.0%,  $P < .001$ , respectively).

## **4.6 ANTIMICROBIAL SUSCEPTIBILITY**

The following section presents the results of antimicrobial susceptibility testing by methicillin susceptibility, and multi-drug resistance for MRSA. Susceptibility testing methods are described in Appendix A.

### **4.6.1 ANTIMICROBIAL SUSCEPTIBILITY TESTING**

Table 11 shows the number of isolates tested against each antimicrobial and susceptibility results. All MSSA isolates tested were susceptible to cefoxitin (flucloxacillin), daptomycin, linezolid, and vancomycin. All MRSA were susceptible to daptomycin, linezolid, and vancomycin.

Resistance to non-beta lactam antimicrobials among MRSA was higher than for MSSA. Of note, fusidic acid resistance was over six times higher in MRSA (43.2% compared to 7.0% in MSSA). ST5-IV was the predominant MRSA clone (see section 4.7.2) associated with fusidic acid resistance, representing 40.9% of resistant MRSA isolates. Among MSSA resistance was highest against erythromycin (9.3%) and clindamycin (8.1%).

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<sup>1</sup> Adult respondents (aged 15+ years) are defined as having diabetes if they had ever been told by a doctor that they have diabetes. This does not include diabetes during pregnancy (gestational diabetes).

There were 950 MSSA isolates (67.5%) with both oxacillin and ceftazidime data. Of these, 12 (1.3%) MSSA isolates were borderline oxacillin resistant *S. aureus* (BORSA) with oxacillin MICs > 2 mg/L but susceptible (MIC ≤4 mg/L) to ceftazidime (ceftazidime).

Table 11 and Table 12 show susceptibility data for the 2022 SAB isolates and methicillin susceptibility by place of onset respectively. Isolates from HA-SAB had similar or higher levels of resistance compared to isolates from CA-SAB, however differences were not statistically significant.

In 2022 penicillin data were requested from diagnostic laboratories for the first time. Penicillin resistance was found in 78.4% of MSSA isolates. Within the penicillin susceptible *S. aureus* isolates (PSSA) 76.3% were CA-SAB and 23.7 % were HA-SAB.

**Table 11. Antimicrobial susceptibility among 2022 SAB isolates, by methicillin susceptibility**

| Antimicrobial                         | Methicillin susceptibility |               |              |               |              |               |
|---------------------------------------|----------------------------|---------------|--------------|---------------|--------------|---------------|
|                                       | Overall                    |               | MRSA         |               | MSSA         |               |
|                                       | No. isolates               | Resistant (%) | No. isolates | Resistant (%) | No. isolates | Resistant (%) |
| Benzylopenicillin                     | 1,157                      | 81.1          | 143          | 100.0         | 1,014        | 78.4          |
| Cefoxitin (flucloxacillin)            | 1,584                      | 11.4          | 180          | 100.0         | 1,404        | 0.0           |
| Ciprofloxacin                         | 1,495                      | 4.7           | 179          | 15.6          | 1,316        | 3.2           |
| Clindamycin                           | 1,516                      | 9.1           | 178          | 16.3          | 1,338        | 8.1           |
| Co-trimoxazole                        | 1,572                      | 0.8           | 180          | 1.1           | 1,392        | 0.8           |
| Daptomycin                            | 1,074                      | 0.0           | 138          | 0.0           | 936          | 0.0           |
| Doxycycline/tetracycline <sup>1</sup> | 1,557                      | 2.1           | 179          | 4.5           | 1,378        | 1.7           |
| Erythromycin                          | 1,578                      | 10.4          | 179          | 19.0          | 1,399        | 9.3           |
| Fusidic acid                          | 1,385                      | 11.6          | 176          | 43.2          | 1,209        | 7.0           |
| Gentamicin                            | 1,472                      | 3.1           | 176          | 8.5           | 1,296        | 2.3           |
| Linezolid                             | 1,097                      | 0.0           | 142          | 0.0           | 955          | 0.0           |
| Mupirocin                             | 976                        | 0.7           | 95           | 1.1           | 881          | 0.7           |
| Oxacillin                             | 1,094                      | 14.3          | 143          | 100.0         | 951          | 1.4           |
| Rifampicin                            | 1,266                      | 0.4           | 142          | 1.4           | 1,124        | 0.3           |
| Teicoplanin                           | 1,064                      | 0.2           | 141          | 0.7           | 923          | 0.1           |
| Vancomycin                            | 1,107                      | 0.0           | 160          | 0.0           | 947          | 0.0           |

1. Isolates resistant to doxycycline and/or tetracycline

**Table 12. Antimicrobial susceptibility among 2022 SAB isolates, by place of onset**

| MRSA <sup>1</sup>                     | Methicillin susceptibility |               |                         |               |                          |               |
|---------------------------------------|----------------------------|---------------|-------------------------|---------------|--------------------------|---------------|
|                                       | Overall                    |               | Hospital-associated-SAB |               | Community-associated-SAB |               |
|                                       | 180                        | 11.3%         | 66                      | 14.7%         | 114                      | 10%           |
| Antimicrobial                         | No. isolates               | Resistant (%) | No. isolates            | Resistant (%) | No. isolates             | Resistant (%) |
| Benzylpenicillin                      | 1,157                      | 81.1          | 340                     | 84.7          | 817                      | 79.6          |
| Cefoxitin (flucloxacillin)            | 1,584                      | 11.4          | 448                     | 14.7          | 1,136                    | 10.0          |
| Ciprofloxacin                         | 1,495                      | 4.7           | 422                     | 4.5           | 1,073                    | 4.8           |
| Clindamycin                           | 1,516                      | 9.1           | 434                     | 10.8          | 1,082                    | 8.4           |
| Co-trimoxazole                        | 1,572                      | 0.8           | 445                     | 0.2           | 1,127                    | 1.1           |
| Daptomycin                            | 1,074                      | 0.0           | 324                     | 0.0           | 750                      | 0.0           |
| Doxycycline/tetracycline <sup>2</sup> | 1,557                      | 2.1           | 444                     | 1.8           | 1,113                    | 2.2           |
| Erythromycin                          | 1,578                      | 10.4          | 448                     | 10.9          | 1,130                    | 10.2          |
| Fusidic acid                          | 1,385                      | 11.6          | 401                     | 16.0          | 984                      | 9.9           |
| Gentamicin                            | 1,472                      | 3.1           | 428                     | 3.7           | 1,044                    | 2.8           |
| Linezolid                             | 1,097                      | 0.0           | 332                     | 0.0           | 765                      | 0.0           |
| Mupirocin                             | 976                        | 0.7           | 278                     | 0.4           | 698                      | 0.9           |
| Oxacillin                             | 1,094                      | 14.3          | 333                     | 17.7          | 761                      | 12.7          |
| Rifampicin                            | 1,266                      | 0.4           | 332                     | 0.6           | 934                      | 0.3           |
| Teicoplanin                           | 1,064                      | 0.2           | 323                     | 0.0           | 741                      | 0.3           |
| Vancomycin                            | 1,107                      | 0.0           | 336                     | 0.0           | 771                      | 0.0           |

1. Total number of MRSA out of all SAB isolates, in each place of onset.

2. Isolates resistant to doxycycline and/or tetracycline.

Figure 2. shows the variability in the percentage of MRSA found in SAB across the four New Zealand health regions. Nationally, 11.3% of SAB episodes were caused by MRSA. Methicillin resistance varied significantly across regions; ranging from 16.2% (103/180) of isolates referred from Northern region to 4.7% (15/180) of isolates referred from the Te Waipounamu region ( $P < .01$ ). Please note that data on region was not available for two isolates.

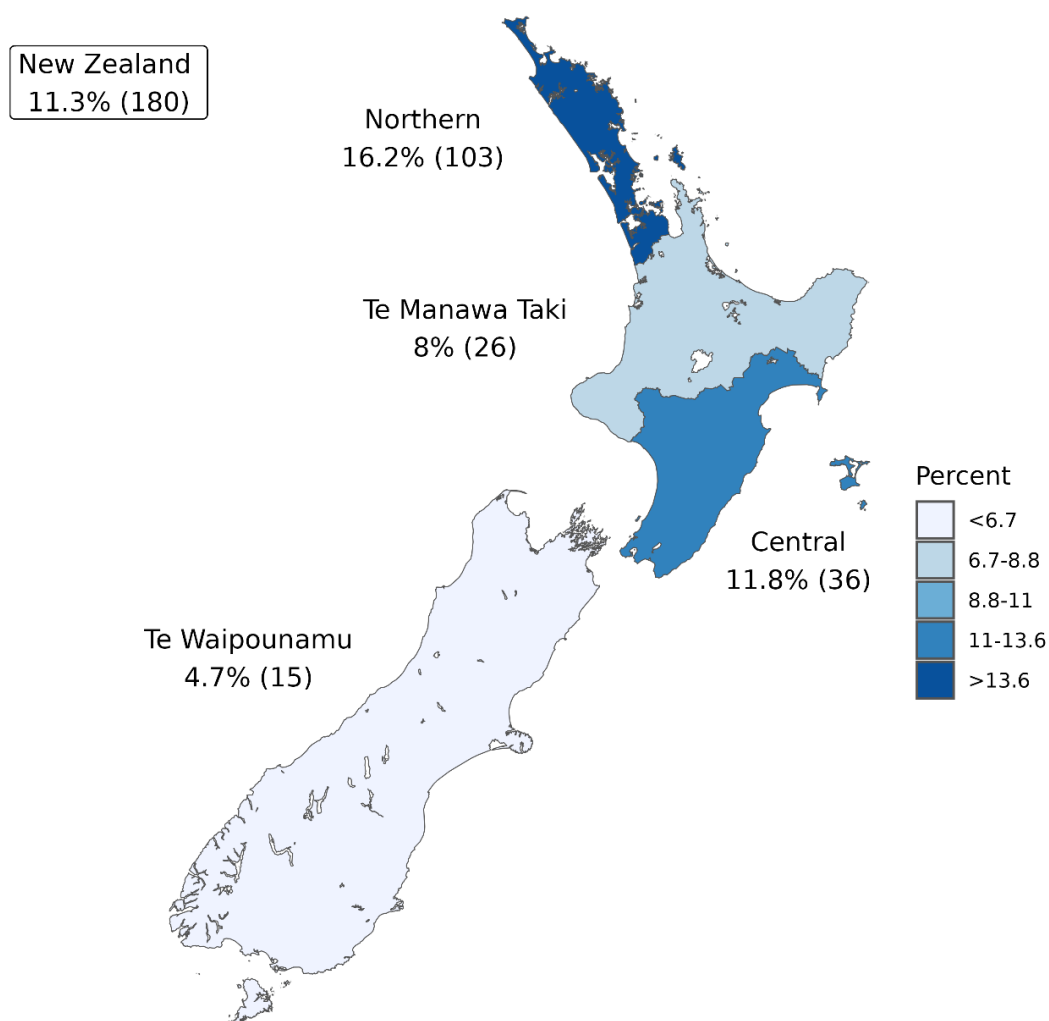


**Figure 2. Percentage (number) of SAB patients with MRSA by region, 2022.**

#### 4.6.2 MULTI-DRUG RESISTANCE

Table 13 shows the percentage of MRSA isolates with acquired resistance to multiple antimicrobial groups. Only the 173 isolates tested against all six antimicrobial groups (cefoxitin/oxacillin, clindamycin, co-trimoxazole, erythromycin, gentamicin and doxycycline/tetracycline) were included in the analysis. A total of 22.0% of MRSA were multi-drug resistant.

**Table 13. Multiple acquired resistance in MRSA from SAB isolates, 2022<sup>1</sup>**

| Overall        | Percent (No.) of classes (non-MDR) |             | Percent (No.) of classes (MDR) |             |            |            | Total MDR (% (No.)) |
|----------------|------------------------------------|-------------|--------------------------------|-------------|------------|------------|---------------------|
|                | 1                                  | 2           | 3                              | 4           | 5          | 6          |                     |
| 100.0<br>(173) | 69.4<br>(120)                      | 8.7<br>(15) | 13.3<br>(23)                   | 5.8<br>(10) | 1.7<br>(3) | 1.2<br>(2) | 22.0 (38)           |

<sup>1</sup> Resistance profiles for isolates tested for susceptibility to cefoxitin/oxacillin, clindamycin, co-trimoxazole, erythromycin, gentamicin and tetracycline/doxycycline.

Table 14 shows multidrug resistance by place of onset and 30-day all-cause mortality. There was no statistical significance in mortality by MDR status.

**Table 14. Number of MRSA SAB isolates and 30-day all-cause mortality, by place of onset and multidrug resistance status, 2022<sup>1</sup>**

| MDR status | Overall |                | Community-associated SAB |                | Hospital-associated SAB |                |
|------------|---------|----------------|--------------------------|----------------|-------------------------|----------------|
|            | Number  | Deaths % (No.) | Number                   | Deaths % (No.) | Number                  | Deaths % (No.) |
| MDR        | 38      | 18.4 (7)       | 22                       | 22.7 (5)       | 16                      | 12.5 (2)       |
| Non-MDR    | 135     | 19.3 (26)      | 87                       | 19.5 (17)      | 48                      | 18.8 (9)       |

<sup>1</sup> MDR was only assessed for isolates tested for susceptibility to cefoxitin/oxacillin, clindamycin, co-trimoxazole, erythromycin, gentamicin and tetracycline/doxycycline.

## 4.7 MOLECULAR EPIDEMIOLOGY

Whole genome sequencing (WGS) data were used to describe the molecular epidemiology of MRSA SAB; with all 180 MRSA sequenced. Data were used to characterise an isolates clonal complex, *spa* type, ST-SCC*mec* type (which determines the MRSA clone assignment), and cgMLST type. The clonal complex (CC) is the least discriminatory and the cgMLST the most discriminatory (see Glossary for more details).

### 4.7.1 SPA TYPES

A *spa* type was available for 1579 of the 1587 SAB isolates (see Table 15 footnotes), of which 418 unique *spa* types were identified: 47 in MRSA and 395 in MSSA.

**Table 15. Most prevalent *spa* types among isolates from SAB episodes stratified by place of onset and methicillin susceptibility, 2022**

| MRSA <sup>1,2</sup> |     |         |                                   |     |         |                                 |     |         |
|---------------------|-----|---------|-----------------------------------|-----|---------|---------------------------------|-----|---------|
| Overall (n=180)     |     |         | Community-associated SAB (n=114)  |     |         | Hospital-associated SAB (n=66)  |     |         |
| <i>spa</i> type     | No. | Percent | <i>spa</i> type                   | No. | Percent | <i>spa</i> type                 | No. | Percent |
| t002                | 67  | 37.2    | t002                              | 37  | 32.5    | t002                            | 30  | 45.5    |
| t3949               | 23  | 12.8    | t3949                             | 17  | 14.9    | t3949                           | 6   | 9.1     |
| -                   | -   | -       | t019                              | 6   | 5.3     | t267                            | 3   | 4.5     |
| -                   | -   | -       | t008                              | 5   | 4.4     | -                               | -   | -       |
| MSSA <sup>1,3</sup> |     |         |                                   |     |         |                                 |     |         |
| Overall (n=1407)    |     |         | Community-associated SAB (n=1025) |     |         | Hospital-associated SAB (n=382) |     |         |
| <i>spa</i> type     | No. | Percent | <i>spa</i> type                   | No. | Percent | <i>spa</i> type                 | No. | Percent |
| t189                | 149 | 10.6    | t189                              | 110 | 10.7    | t189                            | 39  | 10.2    |
| t1265               | 82  | 5.8     | t1265                             | 57  | 5.5     | t1265                           | 25  | 6.5     |
| t127                | 71  | 5.0     | t127                              | 49  | 4.8     | t127                            | 22  | 5.8     |
| t002                | 67  | 4.8     | t002                              | 48  | 4.7     | t002                            | 19  | 5.0     |
| -                   | -   | -       | -                                 | -   | -       | t1451                           | 16  | 4.2     |

1 Results for *spa* types found in more than 4% of isolates for Overall, CA-SAB, or HA-SAB categories.

2 One MRSA isolate was untypable (CA-SAB).

3 Seven MSSA isolates were untypable (3 CA-SAB and 4 HA-SAB).

Within MRSA SAB isolates, *spa* type t002 was the most common, accounting for 37.2% of all isolates, 32.5% of CA-SAB and 45.5% of HA-SAB. The only other *spa* type found in more than 4% of MRSA SAB isolates was t3949 (12.8%).

The most common MSSA *spa* types were similar for CA-SAB and HA-SAB, with *spa* type t189 the most common, accounting for 10.6% of all MSSA isolates, 10.7% of CA-SAB and 10.2% of HA-CAB. Other *spa* types found in more than 4% of overall MSSA SAB isolates were t1265 (5.8%), t127 (5.0%) and t002 (4.8%).

#### **4.7.2 GENOMIC DIVERSITY IN MRSA**

Table 16 shows the prevalence of MRSA clones, and their association with patient demographics. The clones were defined using international MRSA clone nomenclature according to differences in their 7-gene multilocus sequence type and SCCmec type. A description of the important MRSA clones identified in NZ can be found in Appendix A, Table A1. Table A1 also links the MRSA clone types to New Zealand's MRSA strain classifications referenced in historical reports.

There were 22 unique MRSA clones (defined by ST-SCCmec type), within the 180 MRSA sequenced, belonging to 13 different clonal complexes. The most common MRSA clones were ST5-IV (n = 78, 43.3%), ST93-IV (n = 40, 22.2%), ST97-IV (n = 11, 6.1%), ST22-IV (n = 8, 4.4%), ST30-IV (n = 8, 4.4%) and ST8-IV (n = 8, 4.4%), which were also the most common clones in 2021 (Carr et al., 2025). All other clones found in 2022 were present in less than 2% of MRSA. There were only two isolates of the ST398-V clone (CC398). Both isolates were from the same patient that had two SAB episodes 7 weeks apart: the first episode while the patient had HA-SAB and the second episode when the patient had CA-SAB. Eight of the MRSA clones were only found in a single isolate each. Compared to SAB 2021, there were no isolates of CC59 in SAB 2022 (3 isolates in 2021), and three clonal complexes absent in SAB 2021 but present in SAB 2022: CC88 (2 isolates), CC121 (1 isolate) and CC361 (2 isolates).

**Table 16. Association of MRSA clones with patient demographics, 2022**

| MRSA clone | Clonal complex | Percent (No.) within each demographic group by MRSA clone (ST-SCCmec <sup>1</sup> ) |                   |                   |               |               |                 |                           |                 |                             |                                   |
|------------|----------------|-------------------------------------------------------------------------------------|-------------------|-------------------|---------------|---------------|-----------------|---------------------------|-----------------|-----------------------------|-----------------------------------|
|            |                | Onset                                                                               |                   | Age group (years) |               |               | Ethnicity       |                           |                 | NZDep18                     |                                   |
|            |                | All MRSA<br>n = 180                                                                 | CA-SAB<br>n = 114 | HA-SAB<br>n = 66  | <15<br>n = 17 | ≥65<br>n = 81 | Māori<br>n = 46 | Pacific peoples<br>n = 45 | Asian<br>n = 10 | European or Other<br>n = 79 | Quintile 5 <sup>2</sup><br>n = 63 |
| ST5-IV     | CC5            | 43.3 (78)                                                                           | 36.8 (42)         | 54.5 (36)         | 38.9 (7)      | 51.9 (42)     | 54.3 (25)       | 20.0 (9)                  | 10.0 (1)        | 54.4 (43)                   | 38.1 (24)                         |
| ST93-IV    | CC93           | 22.2 (40)                                                                           | 25.4 (29)         | 16.7 (11)         | 33.3 (6)      | 11.1 (9)      | 21.7 (10)       | 53.3 (24)                 | 0.0 (0)         | 7.6 (6)                     | 28.6 (18)                         |
| ST97-IV    | CC97           | 6.1 (11)                                                                            | 5.3 (6)           | 7.6 (5)           | 0.0 (0)       | 7.4 (6)       | 2.2 (1)         | 11.1 (5)                  | 0.0 (0)         | 6.3 (5)                     | 7.9 (5)                           |
| ST22-IV    | CC22           | 4.4 (8)                                                                             | 4.4 (5)           | 4.5 (3)           | 5.6 (1)       | 3.7 (3)       | 8.7 (4)         | 0.0 (0)                   | 10.0 (1)        | 3.8 (3)                     | 3.2 (2)                           |
| ST30-IV    | CC30           | 4.4 (8)                                                                             | 7.0 (8)           | 0.0 (0)           | 5.6 (1)       | 2.5 (2)       | 2.2 (1)         | 6.7 (3)                   | 0.0 (0)         | 5.1 (4)                     | 3.2 (2)                           |
| ST8-IV     | CC8            | 4.4(8)                                                                              | 6.1 (7)           | 1.5 (1)           | 0.0 (0)       | 6.2 (5)       | 2.2 (1)         | 2.2 (1)                   | 10.0 (1)        | 6.3 (5)                     | 3.2 (2)                           |
| ST149-IV   | CC5            | 1.7 (3)                                                                             | 1.8 (2)           | 1.5 (1)           | 0.0 (0)       | 2.5 (2)       | 2.2 (1)         | 0.0 (0)                   | 0.0 (0)         | 2.5 (2)                     | 1.6 (1)                           |
| ST45-V     | CC45           | 1.7 (3)                                                                             | 2.6 (3)           | 0.0 (0)           | 5.6 (1)       | 2.5 (2)       | 2.2 (1)         | 0.0 (0)                   | 0.0 (0)         | 2.5 (2)                     | 3.2 (2)                           |
| ST6-IV     | CC5            | 1.7 (3)                                                                             | 1.8 (2)           | 1.5 (1)           | 0.0 (0)       | 2.5 (2)       | 0.0 (0)         | 0.0 (0)                   | 0.0 (0)         | 3.8 (3)                     | 1.6 (1)                           |

1 MRSA clone: ST-SCCmec types not shown if found in two or fewer isolates. There were two isolates of ST1-IV, ST398-V, ST5662-IV, ST78-IV. ST8743-V.

2 NZDep18 quintile 5 represents the most deprived group.

The prevalence of the two most common MRSA clones (ST5-IV and ST93-IV) in 2022 increased compared to 2021, with ST5-IV increasing by 8.5% and ST93-IV increasing by 10%. The ST5-IV MRSA clone was more prevalent, although not significantly so, among HA-SAB (n = 36, 54.5%), those aged  $\geq 65$  years of age (n = 42, 51.9%), Māori (n = 24, 52.3%) and European or Other (n=43, 54.4%) than all MRSA. As in 2021, ST93-IV was significantly more prevalent among Pacific Peoples (n = 24, 52.2%) where it was over twice as prevalent as all MRSA (n = 40, 22.2%,  $P < .01$ ), although less than in 2021 where this clone was over three times as prevalent as all MRSA for Pacific peoples. Other MRSA clones occurred in 6.1% or less of all MRSA SAB episodes with no significant indications.

Most MRSA clones identified were commonly associated with one *spa* type (Table 17). For *spa* types where more than five isolates were received, the ST5-IV MRSA clone was most commonly associated with *spa* type t002; ST93-IV with t3949; ST97-IV with t267; ST30-IV with t019; and ST8-IV with t008; However, several other MRSA clones-*spa* type combinations were also identified among isolates and are listed in Table 17 and in the Appendix Table C4.

The huge diversity among MRSA is highlighted by the observation that within the 142 complex types identified, 120 were found in a single isolate, 16 were found in two isolates, and three were found in three isolates. Three additional complex types contained 4, 5, and 10 isolates, respectively. Of the six complex types with more than two isolates, four represented repeat SAB episodes in the same patient. Only two complex types with more than two isolates contained isolates from different patients, involving the MRSA clones ST5-IV, *spa* t002, PVL-negative and ST22-IV, *spa* t016, PVL-positive.

**Table 17. MRSA clone and *spa* type combinations found in MRSA from SAB episodes by place of onset, 2022**

| MRSA clone<br>(ST-SCCmec) <sup>1,2</sup> | <i>spa</i> type | Place of onset (% (No.)) |                                         |                                       |
|------------------------------------------|-----------------|--------------------------|-----------------------------------------|---------------------------------------|
|                                          |                 | Overall<br>n = 180       | Community-<br>associated SAB<br>n = 114 | Hospital-<br>associated SAB<br>n = 66 |
| ST5-IV                                   | t002            | 33.9 (61)                | 28.1 (32)                               | 43.9 (29)                             |
| ST93-IV                                  | t3949           | 12.8 (23)                | 14.9 (17)                               | 9.1 (6)                               |
| ST97-IV                                  | t267            | 3.3 (6)                  | 2.6 (3)                                 | 4.5 (3)                               |
| ST30-IV                                  | t019            | 3.3 (6)                  | 5.3 (6)                                 | 0 (0)                                 |
| ST8-IV                                   | t008            | 3.3 (6)                  | 4.4 (5)                                 | 1.5 (1)                               |
| ST97-IV                                  | t267            | 3.3 (6)                  | 2.6 (3)                                 | 4.5 (3)                               |
| ST93-IV                                  | t202            | 2.8 (5)                  | 3.5 (4)                                 | 1.5 (1)                               |
| ST5-IV                                   | t105            | 1.7 (3)                  | 0.9 (1)                                 | 3 (2)                                 |
| ST149-IV                                 | t002            | 1.7 (3)                  | 1.8 (2)                                 | 1.5 (1)                               |
| ST93-IV                                  | t15361          | 1.7 (3)                  | 2.6 (3)                                 | 0 (0)                                 |
| ST45-V                                   | t1081           | 1.7 (3)                  | 2.6 (3)                                 | 0 (0)                                 |
| ST6-IV                                   | t701            | 1.7 (3)                  | 1.8 (2)                                 | 1.5 (1)                               |
| ST22-IV                                  | t016            | 1.7 (3)                  | 2.6 (3)                                 | 0 (0)                                 |
| ST5-IV                                   | t045            | 1.7 (3)                  | 2.6 (3)                                 | 0 (0)                                 |
| ST398-V                                  | t034            | 1.1 (2)                  | 0.9 (1)                                 | 1.5 (1)                               |

1 MRSA clone and *spa* type combinations listed for combinations with three or more isolates only, except for the CC398 clone (ST398-V). See Table C4, in Appendix C, for details of MRSA clone-*spa* type combinations found in less than three isolates.

2 For information on MRSA strain assignments, see Table A1, Appendix A.

The genetic diversity of MRSA is visualised in Figure 3, which shows the relationships between the 13 clonal complexes, 22 ST-SCCmec type, 47 *spa* types, and 142 cgMLST clonal complexes. This figure highlights the dominance of the CC5 (blue) and CC93 (orange) clonal complexes, the huge diversity found in the cgMLST complex types, and the correlation between presence of PVL gene and the CC/ST-SCCmec types.

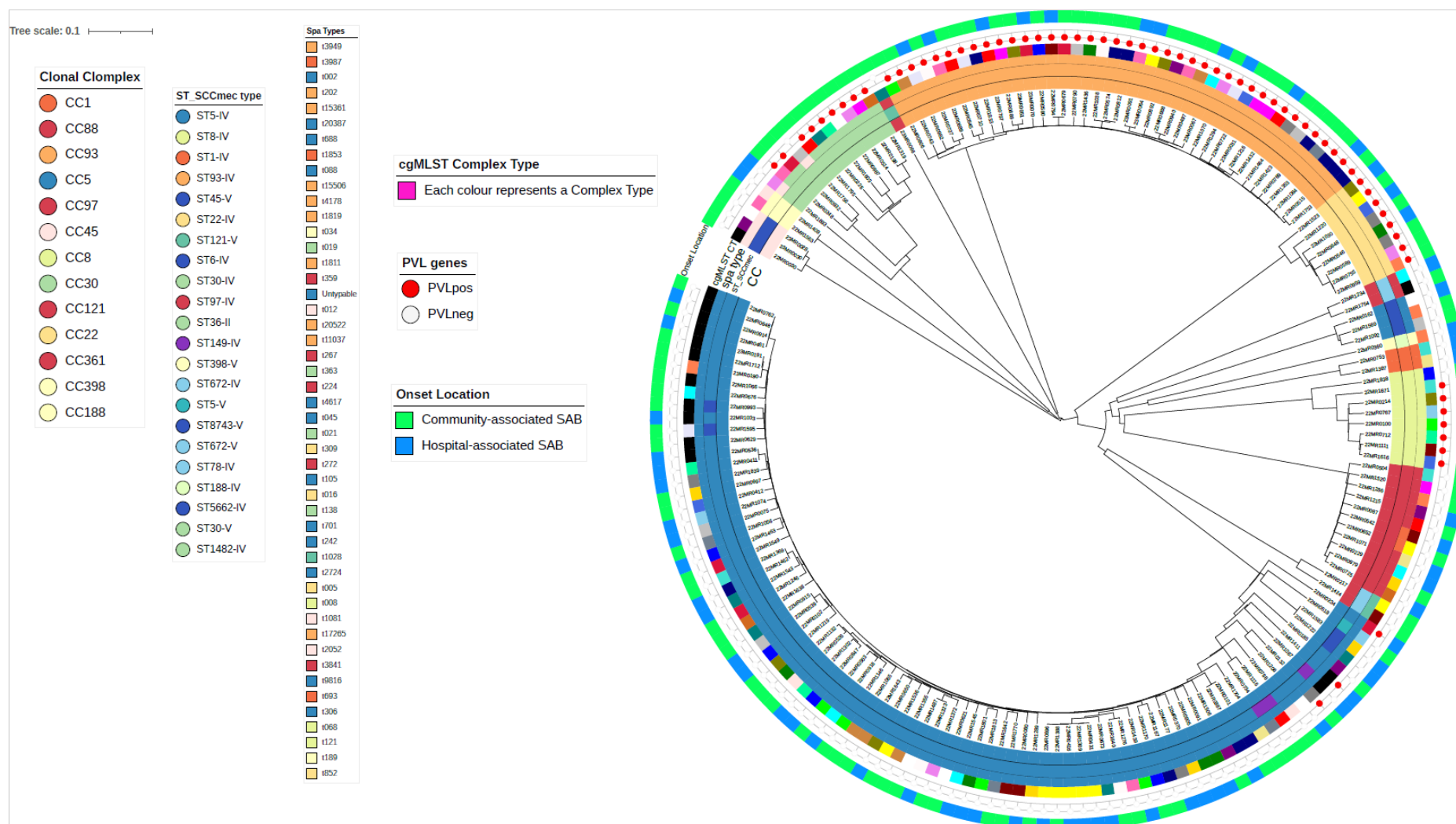


**Figure 3. Phylogenetic analysis of 180 methicillin-resistant SAB isolates, 2022, by clonal complex, MRSA clone, *spa* type, cgMLST type, PVL genes and place of onset.**

#### 4.7.3 PANTON-VALENTINE LEUKOCIDIN (PVL)

Panton-Valentine Leukocidin (PVL) is a pore-forming cytotoxin produced by some strains of *S. aureus* and presence of the toxin in isolates has been linked with necrotic lesions of the skin and mucosa. PVL-positive isolates are associated with outbreaks although the role in causing severe infection is less clear, and in New Zealand clinical management of a patient is not determined by the presence of the toxin in a *S. aureus* isolate. Both MSSA and MRSA isolates can carry the PVL toxin gene, and presence is more frequently found with community-associated infections compared to hospital-associated infections (Shallcross et al., 2013).

Among the 2022 SAB isolates, 12.1% were PVL-positive, including 37.2% (67/180) MRSA and 8.9% (125/1407) of MSSA. Community-associated SAB were more likely to be PVL-positive ( $P < .016$ ).

PVL was detected in six of the 22 MRSA clones (Table 18. ). All isolates of ST8-IV, ST30-IV and ST22-IV were PVL-positive, whereas all isolates of ST5662-IV, ST149-IV and ST97-IV were PVL-negative. By contrast, PVL was variable among ST5-IV (3 of 78 isolates were PVL positive): with one episode in the Northern health region, one in the Central health region and one Te Waipounamu (Table 18). The most frequently isolated PVL-positive clone was ST93-IV.

**Table 18. MRSA clones by health region and Panton-Valentine Leukocidin (PVL) status, 2022**

| MRSA clone <sup>1</sup> | Clonal complex | PVL | Region               |          |                |         |               |
|-------------------------|----------------|-----|----------------------|----------|----------------|---------|---------------|
|                         |                |     | Overall <sup>1</sup> | Northern | Te Manawa Taki | Central | Te Waipounamu |
| ST5-IV                  | CC5            | -   | 75                   | 39       | 12             | 20      | 4             |
| ST93-IV                 | CC93           | +   | 40                   | 28       | 2              | 7       | 3             |
| ST97-IV                 | CC97           | -   | 11                   | 7        | 0              | 4       | 0             |
| ST22-IV                 | CC22           | +   | 8                    | 6        | 1              | 0       | 1             |
| ST30-IV                 | CC30           | +   | 8                    | 5        | 2              | 1       | 0             |
| ST8-IV                  | CC8            | +   | 7                    | 1        | 2              | 3       | 1             |
| ST45-V                  | CC45           | -   | 3                    | 0        | 3              | 0       | 0             |
| ST149-IV                | CC5            | -   | 3                    | 2        | 0              | 0       | 1             |
| ST5-IV                  | CC5            | +   | 3                    | 1        | 0              | 1       | 1             |
| ST6-IV                  | CC5            | -   | 3                    | 1        | 2              | 0       | 0             |
| ST1-IV                  | CC1            | -   | 2                    | 2        | 0              | 0       | 0             |
| ST398-V                 | CC398          | -   | 2                    | 0        | 0              | 0       | 2             |
| ST5662-IV               | CC5            | -   | 2                    | 1        | 1              | 0       | 0             |
| ST8743-V                | CC5            | -   | 2                    | 2        | 0              | 0       | 0             |
| ST78-IV                 | CC88           | -   | 2                    | 1        | 0              | 0       | 1             |

<sup>1</sup> The MRSA clones are only listed if there were ≥2 isolates of the type. The PVL-positive isolate with clonal complex/*SCCmec* combinations found in one isolate each is: CC30 ST30-V. Details of 8 PVL-negative isolates with clonal complex/*SCCmec* combinations found in one isolate each are: CC121 ST121-V, CC188 ST188-IV, CC30 ST1482-IV, CC30 ST36-II, CC361 ST672-IV, CC361 ST672-V, CC5 ST5-V and CC8 ST8-IV.

## 5. LIMITATIONS

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Our data represent only patients for whom those a *S. aureus* isolate was referred to PHF Science, and for which there was a public hospitalisation record available. SAB is not a notifiable condition, so we likely had incomplete case ascertainment due to relying on voluntary isolate referrals, we also did not include those who sought care from a primary care physician, who sought care at a hospital but were not admitted, or who were treated in a private hospital. However, given the large number of isolates received from all regions, our study likely provides a good representation of SAB in NZ.

Our survey analysis was further limited by our inability to accurately attribute clinical infection source or risk factors for every episode of SAB using retrospective ICD coding data. For example, we could not identify different types of devices related to the site of entry nor could we reliably identify renal dialysis which previous studies have noted as an important risk factor for SAB (Laupland et al., 2008; Te Tāhū Hauora Health Quality Safety Commission, 2024). Similarly, obesity was under-represented in our data set which is likely an artefact due to inconsistent recording of obesity in clinical notes. Additionally, NMDS does not include onset or recovery dates for symptoms related to a SAB episode. Therefore, the length of hospitalisation refers to the total time in hospital for patients identified with a SAB episode. This means for all HA-SAB, and some CA-SAB, the total hospitalisation days will also include days due to non-SAB related causes.

An HQSC study of patient records from 1 July 2022 to 20 June 2023 identified 471 episodes of hospital-associated SAB, of which 71.1% related to medical device (central venous catheter or peripheral intravenous catheter) and 8.5% to surgical site infection (Barratt et al., 2022). We were unable to directly compare data from our survey with data collected by HQSC since the latter are collected by infection prevention and control staff and submitted without patient identifiers.

The ethnic-specific population estimates were based on the proportion of people in each ethnic group from the 2018 'estimated resident population' applied to the 2022 mid-year population estimates from Statistics New Zealand. Research indicates that census data consistently undercounts Pacific and Māori populations and that the same populations are undercounted in health user data (Boven et al., 2020; Sonder et al.,

2024). This limits the quality and reliability of the estimates of SAB rates by ethnicity. Additionally, reliable estimates of Pacific populations by level 2 ethnicity data are not available to calculate incidence for these population subgroups (Boven et al., 2020; Sonder et al., 2024).

For future studies, we could consider how better to capture risk factor information with the isolates in real-time. We did not attempt to investigate SAB attributable mortality due to the highly complex nature of this measure, but instead focused on 30-day all-cause mortality. We were also limited in our ability to generate insights from whole genome sequencing for MSSA. Future work is planned to analyse a subset of isolates from this study, particularly for the hospital-associated SAB cohorts, to identify further insights such as any previously unrecognised clusters within hospitals (e.g. dialysis cohorts) and specific virulence factors.

## 6. DISCUSSION

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This is the second in a series of three annual surveys of *S. aureus* from people in New Zealand with bacteraemia. These surveys will provide robust estimates of the trends in the prevalence and epidemiology of SAB, as sampling is not subject to changes in screening practices over time, in different settings, or in different parts of the country. Data in this report are directly comparable to the 2021 SAB report (Carr et al., 2025). Results are not directly comparable with previous *S. aureus* (Heffernan *et al.* 2015) or MRSA surveillance in New Zealand (Heffernan and Bakker, 2018) as these reports characterised very few isolates from blood (2.1% and 1.5% respectively from sterile sites). However, information on the molecular epidemiology from earlier surveillance work can be compared.

The 2022 study on *S. aureus* bacteraemia highlighted similar outcomes to those observed in the 2021 study (Carr et al., 2025). The most significant of these are the diversity of *S. aureus* causing bacteraemia in New Zealand, the higher numbers of SAB episodes in the northern regions of New Zealand, and the striking inequities in the incidence and 30-day mortality of SAB by socioeconomic deprivation and ethnicity.

This survey identified 1,587 episodes of SAB in New Zealand in 2022. The onset for the majority of SAB episodes was in the community (71.8%) and the majority were MSSA (88.7%). Multi-drug resistance was more common in community-associated SAB.

SAB was more common in males and in older people, with about 65.8% of SAB episodes in males and 50.0% of SAB were in people aged over 65 years. The burden of SAB also increased with increasing socioeconomic deprivation index. Overall, most episodes of SAB were among people in the European or Other ethnic group. However, age standardised rates of SAB in Pacific people were nearly 17 times the rates found in the European or Other population and rates in Māori were 4.5 times those found in the European or Other population. As noted in the limitations, it is well documented that both Pacific and Māori populations are undercounted in both census data and in health service user data (Harris et al., 2022; Sonder et al., 2024), which impacts our ability to provide reliable estimates by ethnicity. However, these data are based on best available evidence and align with the findings of the HQSC, and the wealth of evidence documenting stark inequities for both Māori and Pacific populations in New Zealand. The

higher incidence of diabetes, obesity, tobacco consumption and socioeconomic deprivation and poorer access and quality of healthcare services for Māori and Pacific populations (Talamaivao et al., 2020), likely contribute to these inequities in SAB incidence. However, there may also be other factors in these populations, their environments or specific pathogen virulence factors that we do not yet understand.

Risk factors for developing SAB are well described in the literature and include implanted devices, dependence on dialysis, organ transplantation, breach of natural barriers after surgery or trauma, and underlying conditions such as a human immunodeficiency virus (HIV) infection, cancer, rheumatoid arthritis and diabetes mellitus (Laupland et al., 2008; Wiese et al., 2013). We encountered significant difficulties using ICD-10-AM diagnostic codes for identification of risk factors and source attribution. However, despite these limitations we confirm tobacco smoking and diabetes were over-represented in their association with SAB. Notably, compared to the general population, patients with SAB episodes were less likely to have obesity. However, this is likely an artefact of the data collection and coding. Use of vascular catheters and prosthetics/implantable was also common patients with SAB, with the use of vascular catheters being significantly more common in patients with HA-SAB. We recommend additional attention be paid to the prevention of SAB through the development and implementation of targeted prevention strategies, including those related to measures to prevent skin and soft tissue infections, smoking cessation, wound care, diabetes management, device management, dialysis lines care and infection prevention measures within hospitals.

The 30-day age standardised mortality from SAB in New Zealand in 2022 was comparable to international studies. For all SAB episodes in New Zealand the 30-day all-cause mortality was 15.1%, which is comparable to data from Australia, where the 30-day all-cause mortality with all SAB was found to be 16.2% (Coombs et al., 2024). Our data is also comparable to data from a large systematic review and meta-analysis which found the pooled estimate of 30-day all-cause mortality for SAB cases (based on 46 studies from 2011 onwards) to be 18.1% (Bai et al., 2022). Of note however, were the inequities within the New Zealand 30-day age standardised all-cause mortality rates, with rates 11.9 times higher for Pacific Peoples and 2.5 times higher for Māori compared to European or Other ethnic group. We did not find a higher rate of all-cause mortality

with MRSA SAB compared with MSSA, which differs from some international reports (Adeiza & Aminul, 2024).

There were low levels of antimicrobial resistance in isolates from SAB episodes. A total of 11.3% of isolates were MRSA, which is lower than reported in Australia (15%) (Coombs et al., 2023). When compared to European data from 2022 New Zealand ranks 17<sup>th</sup> out of 29 countries contributing to the European Antimicrobial Resistance Surveillance network program (<https://atlas.ecdc.europa.eu/public/>), with country 1 having the highest percentage of invasive MRSA. However, Pacific Peoples with SAB were more likely to have MRSA than other ethnicities, with over 20% of episodes due to MRSA. This should be taken into account for empiric sepsis antibiotic treatment recommendations, since this may also be a contributing factor to the much higher overall SAB 30-day mortality rates for Pacific Peoples.

The proportion of penicillin susceptible *S. aureus* (PSSA) in New Zealand isolates was similar to the proportion of PSSA found in Australia (Coombs et al., 2023). This finding indicate that penicillin may remain a viable first-line agent for a meaningful subset of infections, provided that  $\beta$ -lactamase activity is excluded using appropriate phenotypic or molecular methods.

The most common strains found in this study is consistent with previous surveillance reports (SAB 2021, Heffernan and Bakker, 2018 and 2016). The ST5-IV clone remained the most common MRSA lineage, was most frequently associated with *spa* type t002 and was the predominant MRSA clone associated with fusidic acid resistance. The next most prevalent clone was ST93-IV, which was almost twice as common as reported in the 2021 SAB survey and was typically associated with *spa* type t3949. Together, these two clones accounted for 65.5% of isolates and were also the dominant MRSA clones identified in the 2021 survey. Notably, the MRSA clone ST97-IV, associated with *spa* type t359, which was the third most common clone in the 2021 SAB survey (Carr et al., 2025), was not a dominant clone in the current survey, comprising only ~1% of isolates. Ethnic variation in clone distribution was also observed, with isolates from Pacific peoples representing 53.3% of all ST93-IV MRSA. The distribution of MRSA clones in New Zealand differs from that reported in Australia, where the predominant CA-MRSA clone across all regions except Tasmania is ST93-IV (Coombs et al., 2023).

The *spa* typing data provided information on the genetic diversity in the MSSA causing SAB in New Zealand. This data did not provide the level of detail offered by whole genome sequencing although it did highlight that MSSA SAB have a much higher level of genetic diversity than MRSA SAB.

All PVL positive isolates belonged to six MRSA clones (ST93-IV, ST8-IV, ST30-IV, ST30-V, ST22-IV and ST5-IV). As shown in the SAB 2021 report (Carr et al., 2025), MRSA were more likely to be PVL-positive, as were isolates from CA-SAB. Due to the high prevalence of ST-93-IV MRSA, PVL status was strongly associated with this clone. The percentage of MRSA that were PVL positive in 2022 (37.2%) was higher than in 2021 (25.8%) and similar to what was found in both 2017 (34.1%) and 2015 (30.1%) (Heffernan & Bakker, 2016, 2018).

Continuous surveillance of SAB is necessary to inform further refinement of prevention and treatment strategies, most notably in hospitals. Ongoing monitoring of SAB must remain a public health priority given the high rates of infection and inequities. As with previous surveys in 2001 (Hill, Birch, et al., 2001) and 2013 (Williamson et al., 2013) our survey results reaffirm that the burden of *Staphylococcus aureus* in New Zealand is inequitable with the highest burden borne by Māori and Pacific populations and people living with material deprivation. These data build on previous work and once again highlights the need for targeted action to reduce the burden of staphylococcal infections in New Zealand and address persistent inequities. The data produced and analysed for this report form an invaluable “baseline” resource for ongoing surveillance of SAB in New Zealand, against which the success of any public health strategies and targeted interventions or research initiatives may be benchmarked and refined. This report highlights the need for health authorities, funders and policy makers to prioritise infection prevention interventions and support further research to address the underlying causes and develop novel prevention strategies and therapies.

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## 8. GLOSSARY

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### **Clonal Complex (CC)**

A clonal complex consists of a group of related sequence types that share alleles at the majority of MLST loci and are inferred to have descended from a recent common ancestor (Feil et al., 2004).

### **Core genome MLST (cgMLST)**

cgMLST is a standardised, high-resolution molecular typing method. A set of conserved genes are defined for each species, or group of closely related species. Genes are used instead of single nucleotide polymorphisms or concatenated sequences to mitigate the effects of recombination and to facilitate standardised nomenclature. The large number of genes defined for each species means that whole genome sequencing data is standardly used to generate the data. Alleles are used instead of single nucleotide polymorphisms (SNP) or concatenated sequences to mitigate the effects of recombination and to enable for a global and public nomenclature. For *S. aureus*, using cgMLST.org criteria, the schema used is based on 1,861 alleles. It is a more discriminatory method compared with MLST, as a larger portion of the genome is characterised.

### **Complex Type (CT)**

The cgMLST data is summarised using a single number, referred to as the complex type (CT), which facilitates easy communication of results. Isolates with similar cgMLST results will be assigned the same CT. The threshold for defining what cgMLST variability is found within a CT is species-specific. For *S. aureus* the CT threshold is 24 alleles (cgMLST.org). CT numbers are random, so CT numbers that are close may not contain isolates that are closely related.

## Multilocus sequence typing (MLST)

MLST is a method that characterises isolates using the DNA sequences of seven house-keeping genes, which are found in all strains of *S. aureus*, and whose sequences are known not to vary significantly over time. Internal fragments of approximately 450-500 base pairs are sequenced. Each unique gene sequence is called an 'allele', and the combination of the seven allelic sequences defines the allelic profile which is considered to be a distinct clone. The 7-gene sequence type is designated by a number, preceded by 'ST'.

For *S. aureus*, the seven genes are: carbamate kinase (*arcC*), shikimate dehydrogenase (*aroE*), glycerol kinase (*glp*), guanylate kinase (*gmk*), phosphate acetyltransferase (*pta*), triosephosphate isomerase (*tpi*), and acetyl coenzyme A acetyltransferase (*yqiL*).

Traditional 7-locus MLST is used to assign isolates to sequence types and clonal complexes. The discriminatory power of this method is much less compared to cgMLST which provides higher discriminatory resolution by analysing allelic variation across the core genome, that for *S. aureus*, equates to 1,861 alleles.

## MRSA clone

MRSA clone assignments are based on international nomenclature and are defined by a sequence type-SCC*mec* combinations that are derived from WGS data. The MRSA clone ST5-IV, has sequence type 5 and SCC*mec* type IV. Common MRSA clones in New Zealand, and their relationship to MRSA strains is outlined in Table A1.

## MRSA strain

As described in section 10.5, MRSA strains were originally defined using data from phage typing and antimicrobial susceptibility data, and more recently from *spa* typing and antimicrobial susceptibility data supplemented by DNA macrorestriction. Common MRSA strains in New Zealand, and their relationship to MRSA clones is outlined in Table A1, for comparison with earlier New Zealand surveillance reports

### **Staphylococcal Cassette Chromosome *mec* (SCC*mec*) type**

SCC*mec* is a large piece of mobile DNA (21-67 kb) that has been acquired and inserted into the staphylococcal chromosome (Uehara, 2022). The acquisition of SCC*mec* converts a MSSA clone of *S. aureus* to an MRSA clone, as by definition all SCC*mec* elements contain a *mec* gene, which confers methicillin resistance. There are at least 14 SCC*mec* variants, labelled type I to type XIV (Uehara, 2022), with each type defined by Roman numerals.

### ***spa* type**

*spa* typing is a sequence-based typing method for *S. aureus* that targets the polymorphic X region of the staphylococcal protein A gene (*spa*). This region of the gene consists of a variable number of 21 to 27 bp repeats with differing nucleotide sequences. The region is subject to spontaneous mutations, as well as loss and gain of repeats. The variation in the number and sequences of the repeats is the basis of *spa* typing. The repeats are assigned unique identifiers, and the combination of repeats results in a *spa* type.

## 9. APPENDIX A: METHODS

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### 9.1 NUCLEIC ACID AMPLIFICATION TESTING FOR SPECIES CONFIRMATION, METHICILLIN STATUS AND PVL GENE DETECTION

Isolates were characterised using an in-house real-time PCR testing for detection of methicillin resistance genes *mecA* and *mecC* gene, the *S. aureus* species-specific thermostable nuclease gene *nuc* (to confirm species identification), and *lukS-PV* (for detection of the virulence determinant PVL). The in-house PCR was developed from an assay previously described by Pichon and colleagues (Pichon et al., 2012). Isolates with *mecA* or *mecC* were classified as MRSA for all analyses in this report.

### 9.2 SUSCEPTIBILITY TESTING

If available, referring laboratories were asked to provide interpreted susceptibility testing results for the following agents: cefoxitin (flucloxacillin), ciprofloxacin, clindamycin, co-trimoxazole, daptomycin, doxycycline, erythromycin, fusidic acid, gentamicin, linezolid, mupirocin, penicillin, oxacillin, rifampicin, teicoplanin, tetracycline, and vancomycin. Interpreted results were from assays and clinical breakpoints used in each referring laboratory. Most laboratories utilised clinical breakpoint criteria set by EUCAST, except for Middlemore Hospital laboratory which utilised the Clinical & Laboratory Standards Institute (CLSI) guidelines. Penicillin data were collected for the first time in 2022, with referring laboratories confirming penicillin susceptibility as per the EUCAST or CLSI guidelines.

### 9.3 SPA TYPING AND PFGE TYPING

All unique isolates underwent *spa* typing (Strommenger et al., 2008). The polymorphic X region of the staphylococcal protein A gene (*spa*) was amplified as previously described (Strommenger et al., 2008). PCR products were sequenced using an ABI 3130XL Sequencer. Data were analysed using Ridom StaphType software version 2.2.1 (Ridom GmbH, Würzburg, Germany), which automatically assigned repeats and *spa* types.

Pulsed-field gel electrophoresis (PFGE) typing was used as a supplementary typing tool where *spa* typing was inconclusive.

There were three situations in which *spa* typing was considered inconclusive:

- i. when a *spa* type correlated to a known MRSA strain, but the antimicrobial susceptibility pattern did not; and
- ii. when an isolate had a novel *spa* type; and
- iii. when an isolate had a *spa* type PHF Science had not yet correlated to an MRSA strain PFGE of *Sma*I-digested genomic DNA was performed as described by Goering *et al.* (Goering, 2004). PFGE banding patterns were analysed using BioNumerics software version 8.1 (bioMérieux, Marcy-l'Étoile), with the Dice coefficient and unweighted-pair group method with arithmetic averages, at settings of 0.5% optimisation and 1.5% position tolerance.

#### 9.4 WHOLE GENOME SEQUENCING

All 2022 MRSA underwent whole genome sequencing (WGS) using Illumina-based sequencing technology. The 7-gene multilocus sequence type (MLST) was determined using the PubMLST database ([https://pubmlst.org/bigssdb?db=pubmlst\\_saureus\\_seqdef](https://pubmlst.org/bigssdb?db=pubmlst_saureus_seqdef)). *SCCmec* elements were identified using KmerFinder v3.0.2 and the *SCCmec* database curated from the Center for Genomic Epidemiology website (CGE). Genomic DNA was extracted using the Chemagic 360 (Perkin Elmer), the DNA library was created using the plexWell Library Preparation kit (SeqWell), and sequencing performed using Illumina technology. WGS data were analysed using an in-house developed pipeline linking together open-source established packages and in-house scripts. The open-source packages used included the nullarbor: 'Reads to report' for public health and clinical microbiology pipeline' (<https://github.com/tseemann/nullarbor>), SPAdes 3.10 (Bankevich *et al.*, 2012), and MLST (<https://github.com/tseemann/mlst>). Bruker MBioSEQ Ridom Typer+ version 11.1.0 was used to determine the cgMLST Complex Type.

#### 9.5 ASSIGNING MRSA STRAINS

Initial MRSA strain designation was performed primarily using *spa* typing and antimicrobial susceptibility data, with PFGE used as a supplementary tool for situations described in section 10.3.

WGS data was used to determine the isolates *spa* type, 7-gene multilocus sequence type, *SCCmec* type, and cgMLST complex type. The 7-gene multilocus sequence type and *SCCmec* type is used to define the MRSA clone based on international molecular-based nomenclature. It lists the sequence type (ST) and for MRSA, the Staphylococcal Cassette Chromosome *mec* (*SCCmec* type). There are 14 documented *SCCmec* type varieties with each type being designated by an upper-case roman numeral (Uehara 2022). The combination of both pieces of genetic information provides the full designation of a clone, for example an AK3 MRSA strain can be an ST5-MRSA-IV, meaning it is sequence type 5 and *SCCmec* type IV.

The use of WGS has enhanced the understanding of MRSA epidemiology, and MRSA can now be classified into three ‘types’: hospital-associated, community-associated and livestock-associated; each with a range of different clones. Table A1 describes the important MRSA clones that have been identified in New Zealand.

**Table A1. Key MRSA clones identified in New Zealand**

| MRSA clone                               | MRSA strain                                                           | <i>spa</i> type(s) | Typical antimicrobial resistance pattern                                                                                                | Typical PVL status | Epidemiology                                                                                                                                                  |
|------------------------------------------|-----------------------------------------------------------------------|--------------------|-----------------------------------------------------------------------------------------------------------------------------------------|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Hospital-associated MRSA clones:</b>  |                                                                       |                    |                                                                                                                                         |                    |                                                                                                                                                               |
| ST239-III                                | AKh4<br>Alternative names:<br>EMRSA-1, AUS-2 EMRSA<br>and AUS-3 EMRSA | t037               | Multiresistant to ciprofloxacin, co-trimoxazole, erythromycin, clindamycin, gentamicin and tetracycline                                 | Negative           | Originates from Australia and was first isolated in patients in Auckland hospitals. Sporadically isolated from patients throughout NZ                         |
| ST22-IV                                  | EMRSA-15                                                              | t032, t1401, t5501 | Resistant to ciprofloxacin with variable erythromycin susceptibility                                                                    | Negative           | Originated in the UK. Genetically distinct from community-associated ST22-IV clone (Australian Commission on Safety and Quality in Healthcare (ACSQH), 2020). |
| ST36-II                                  | EMRSA-16                                                              | t018               | Resistant to ciprofloxacin and erythromycin                                                                                             | Negative           | Originated in the UK                                                                                                                                          |
| <b>Community-associated MRSA clones:</b> |                                                                       |                    |                                                                                                                                         |                    |                                                                                                                                                               |
| ST5-IV                                   | AK3                                                                   | t002               | Non-multiresistant, with variable susceptibility but often fusidic acid or erythromycin resistant or only resistant to $\beta$ -lactams | Negative           | Prevalent MRSA clone in NZ. First recognised in annual MRSA survey in August 2005.                                                                            |
| ST93-IV                                  | Queensland clone                                                      | t202 and t3949     | Resistant to $\beta$ -lactams only                                                                                                      | Positive           | Dominant community-associated MRSA in Australia.                                                                                                              |
| ST8-IV                                   | USA300                                                                | t008               | Resistant to ciprofloxacin and/or erythromycin                                                                                          | Positive           | Widely disseminated in USA. Isolated from community and hospital patients in NZ.                                                                              |

**Table A1 continued**

| MRSA clone                              | MRSA strain                                                                                       | spa type(s)   | Typical antimicrobial resistance pattern                 | Typical PVL status                    | Epidemiology                                                                                                                           |
|-----------------------------------------|---------------------------------------------------------------------------------------------------|---------------|----------------------------------------------------------|---------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------|
| ST1-IV                                  | WR/AK1<br>Alternative name Western Australia-1: WA-1                                              | t127 and t359 | Resistant to fusidic acid and mupirocin                  | Positive                              | Originally isolated from patients in Whangarei/Auckland, now found throughout NZ.                                                      |
| ST30-IV                                 | WSPP (Western Samoan Phage Pattern)<br>Alternative name Southwest Pacific clone and Oceania clone | t019          | Resistant to $\beta$ -lactams only                       | Positive                              | First isolated from people with a Western Samoan connection. Once the most common MRSA strain isolated from community patients in NZ   |
| ST22-IV                                 | -                                                                                                 | t005          | Resistant to trimethoprim, gentamicin and ciprofloxacin  | Positive                              | Genetically distinct from hospital-associated ST22-IV clone (Australian Commission on Safety and Quality in Healthcare (ACSQH), 2020). |
| ST78-IV                                 | WA MRSA-2                                                                                         | t186          | Resistant to $\beta$ -lactams only                       | Negative                              | Originally recognised in Western Australia                                                                                             |
| ST772-V                                 | Bengal Bay clone                                                                                  | t657          | Resistant to ciprofloxacin, erythromycin and gentamicin. | Positive                              | First emerged in Bangladesh and India' associated with travel or ethnicity to the Bengal Bay area                                      |
| <b>Livestock-associated MRSA clone:</b> |                                                                                                   |               |                                                          |                                       |                                                                                                                                        |
| ST398-V                                 | Untypeable                                                                                        | t011, t034    | Resistant to tetracycline or doxycycline                 | t034 positive, t011 usually negative. | Emerged in Europe, first major problem there in 2003 with pigs and other livestock; First identified in NZ in 2011 MRSA survey         |

## 9.6 DATA ANALYSIS

Patient information and susceptibility testing results were entered into PHF Science's laboratory information management system. Data cleaning and statistical tests were performed in R version 4.1.1 (R Core Team, 2021) using tidyverse (Wickham et al., 2019) and AMR packages (Berends et al., 2022). Demographic information and clinical risk factors for disease were tabulated and analysed using descriptive statistics methods including counts, proportions, medians, and interquartile ranges. For categorical variables we used the Fisher's exact test or chi-square test. A P-value of < .05 was considered statistically significant.

Ethnicity was analysed using prioritised level 1 ethnicity data. Ethnicity data were prioritised as per Ministry of Health guidelines in the following order: 'Māori', 'Pacific Peoples', 'Asian', and 'European or Other' (Ministry of Health, 2017). When ethnicity was not available for a case, they were classified as Unknown. Geographic analyses were performed for each Health New Zealand – Te Whatu Ora region (<https://www.tewhatauora.govt.nz/corporate-information/our-health-system/health-sector-organisations/public-health-contacts/>). Socioeconomic status was assigned by use of the New Zealand deprivation index (NZDep18); the total NZ population is divided into five equal groups (quintiles) to form the denominators for these analyses. Quintile 1 represents the most affluent 20% of the population and quintile 5 represents the most socioeconomically disadvantaged 20% of the population.

Population data used to produce incidence rates were derived from the 2022 mid-year population estimates published by Statistics New Zealand. Both crude and age-standardised incidence rates and corresponding 95% confidence intervals (95% CI) were calculated. Direct age-standardisation was undertaken using the Census 2022 mid-year Māori population estimates as the reference to better describe the burden of disease for Māori given the difference in population structures between ethnic groups (Crengle et al., 2022).

## 10. APPENDIX B: ICD-10 CODES

### 10.1 DIAGNOSTIC CODES

This report uses data on hospitalisation events recorded by the NZ Ministry of Health in the National Minimum Dataset (NMDs). The NMDs records coded data on all publicly funded hospital admissions. Diagnoses are coded using the Australian Modification of the International Classification of Diseases, 10<sup>th</sup> Edition (ICD-10-AM). Further details on NMDs coding standards can be found in the *NMDs data dictionary v7.9.3* published by the Ministry of Health (<https://www.health.govt.nz/publication/national-minimum-dataset-hospital-events-data-dictionary>). Multiple hospitalisation ‘events’ where the gap between discharge and readmission was less than 48-hours were combined into a ‘continuous hospitalisation event’.

Risk factors and comorbidities were identified by searching for diagnosis keywords and creating a list of related ICD-10-AM codes (Table B1). We identified complications using a list of ICD-10-AM codes associated with surgical site infection, infections or inflammatory complications associated with peripheral/central venous catheters, or infection associated with prosthetics/implantable devices (Table B2). These codes were adapted from those used by the Australian Commission on Safety and Quality ([Australian Commission on Safety and Quality in Health Care \(ACSQHC\) Hospital-Acquired Complications List v3.1 \(12th ed.\)](#)).

**Table B1. ICD-10-AM codes for risk factors and comorbidities**

| Diagnosis       | Code <sup>1</sup>        | Description                                 |
|-----------------|--------------------------|---------------------------------------------|
| Diabetes        | E10.x – E14.x            | Various codes relating to diabetes mellitus |
| Obesity         | E66.x, U781              | Various codes relating to obesity           |
| Tobacco smoking | F17.x, T652, Z716, Z8643 | Various codes relating to tobacco smoking   |

1 The character “.x” in code listings represents any number (e.g., E10.01, E10.02, E10.11, ..., E10.21, ..., E10.9)

**Table B2. ICD-10-AM codes for complications**

| Diagnosis                                                         | Code  | Description                                                                                                            |
|-------------------------------------------------------------------|-------|------------------------------------------------------------------------------------------------------------------------|
| Surgical site infection                                           | T814  | Wound infection following a procedure, not elsewhere classified                                                        |
|                                                                   | T874  | Infection of amputation stump                                                                                          |
|                                                                   | O860  | Infection of obstetric surgical wound                                                                                  |
| Complications associated with peripheral/central venous catheters | T8274 | Infection and inflammatory reaction due to central vascular catheter                                                   |
|                                                                   | T8275 | Infection and inflammatory reaction due to peripheral vascular catheter                                                |
| Complications associated with prosthetics/implantable devices     | T826  | Infection and inflammatory reaction due to cardiac valve prosthesis                                                    |
|                                                                   | T8271 | Infection and inflammatory reaction due to electronic cardiac device                                                   |
|                                                                   | T8272 | Infection and inflammatory reaction due to coronary artery bypass and valve grafts                                     |
|                                                                   | T8273 | Infection and inflammatory reaction due to other vascular grafts                                                       |
|                                                                   | T8276 | Infection and inflammatory reaction due to surgically created arteriovenous fistula and shunt                          |
|                                                                   | T8277 | Infection and inflammatory reaction due to vascular dialysis catheter                                                  |
|                                                                   | T8279 | Infection and inflammatory reaction due to cardiac and vascular devices, implants and grafts, not elsewhere classified |
|                                                                   | T835  | Infection and inflammatory reaction due to prosthetic device, implant and graft in urinary system                      |
|                                                                   | T836  | Infection and inflammatory reaction due to prosthetic device, implant and graft in genital tract                       |
|                                                                   | T845  | Infection and inflammatory reaction due to internal joint prosthesis                                                   |
|                                                                   | T846  | Infection and inflammatory reaction due to internal fixation device [any site]                                         |
|                                                                   | T847  | Infection and inflammatory reaction due to other internal orthopaedic prosthetic devices, implants and grafts          |
|                                                                   | T8571 | Infection and inflammatory reaction due to peritoneal dialysis catheter                                                |
|                                                                   | T8572 | Infection and inflammatory reaction due to nervous system prosthetic devices, implants and grafts                      |
|                                                                   | T8573 | Infection and inflammatory reaction due to respiratory prosthetic devices, implants and grafts                         |
|                                                                   | T8574 | Infection and inflammatory reaction due to breast prostheses and implants                                              |
|                                                                   | T8575 | Infection and inflammatory reaction due to ocular prosthetic devices, implants, and grafts                             |
|                                                                   | T8576 | Infection and inflammatory reaction due to internal hearing devices, implants, and grafts                              |
|                                                                   | T8577 | Infection and inflammatory reaction due to other internal prosthetic devices, implants, and grafts                     |

## 11. APPENDIX C: SUPPLEMENTARY TABLES

**Table C1. Rates of SAB episodes by region, stratified by place of onset, 2022**

| Place of onset | Region  |      |              |          |      |             |                |      |             |         |      |             |               |      |             |
|----------------|---------|------|--------------|----------|------|-------------|----------------|------|-------------|---------|------|-------------|---------------|------|-------------|
|                | Overall |      |              | Northern |      |             | Te Manawa Taki |      |             | Central |      |             | Te Waipounamu |      |             |
|                | No.     | Rate | 95% CI)      | No.      | Rate | 95% CI      | No.            | Rate | 95% CI      | No.     | Rate | 95% CI      | No.           | Rate | 95% CI      |
| Total          | 1,587   | 31   | 29.4 - 32.5) | 634      | 33   | 30.4 - 35.6 | 326            | 31.8 | 28.4 - 35.3 | 304     | 31.2 | 27.6 - 34.7 | 323           | 26.9 | 23.9 - 29.8 |
| CA-SAB         | 1,139   | 22.2 | 20.9 - 23.5) | 422      | 22   | 19.9 - 24.1 | 252            | 24.6 | 21.6 - 27.6 | 223     | 22.9 | 19.9 - 25.8 | 242           | 20.1 | 17.6 - 22.7 |
| HA-SAB         | 448     | 8.7  | 7.9 - 9.6)   | 212      | 11   | 9.5 - 12.5  | 74             | 7.2  | 5.6 - 8.9   | 81      | 8.3  | 6.5 - 10.1  | 81            | 6.7  | 5.3 - 8.2   |

**Table C2. Age and ethnicity of SAB episodes stratified by place of onset, 2022**

| Age group (years)                       | All SAB                  |      |              |       |       |               |                 |       |                |       |      |             |                   |      |             |
|-----------------------------------------|--------------------------|------|--------------|-------|-------|---------------|-----------------|-------|----------------|-------|------|-------------|-------------------|------|-------------|
|                                         | Overall                  |      |              | Māori |       |               | Pacific peoples |       |                | Asian |      |             | European or Other |      |             |
|                                         | No.                      | Rate | 95% CI       | No.   | Rate  | 95% CI        | No.             | Rate  | 95% CI         | No.   | Rate | 95% CI      | No.               | Rate | 95% CI      |
| 0–4                                     | 60                       | 19.8 | 14.8 - 24.8  | 26    | 31.1  | 19.1 - 43     | 9               | 30.6  | 10.6 - 50.6    | 9     | 16.6 | 5.8 - 27.5  | 16                | 12.3 | 6.2 - 18.3  |
| 5–14                                    | 83                       | 12.6 | 9.9 - 15.3   | 33    | 18.7  | 12.3 - 25.1   | 13              | 20.2  | 9.2 - 31.2     | 6     | 6.7  | 1.3 - 12.1  | 31                | 9.7  | 6.3 - 13.1  |
| 15–24                                   | 56                       | 8.7  | 6.4 - 11     | 17    | 12    | 6.3 - 17.8    | 8               | 13.1  | 4 - 22.2       | 8     | 7.5  | 2.3 - 12.7  | 23                | 7.1  | 4.2 - 10    |
| 25–34                                   | 77                       | 10.4 | 8.1 - 12.7   | 23    | 19.1  | 11.3 - 26.9   | 20              | 37.9  | 21.3 - 54.6    | 9     | 4.9  | 1.7 - 8.1   | 25                | 6.8  | 4.2 - 9.5   |
| 35–44                                   | 101                      | 15.2 | 12.3 - 18.2  | 32    | 32.7  | 21.4 - 44     | 19              | 43.7  | 24 - 63.3      | 7     | 5.2  | 1.4 - 9.1   | 43                | 11.5 | 8.1 - 15    |
| 45–54                                   | 161                      | 24.8 | 21 - 28.6    | 52    | 57.6  | 42 - 73.3     | 37              | 96.2  | 65.2 - 127.2   | 7     | 8.5  | 2.2 - 14.9  | 65                | 15.1 | 11.4 - 18.7 |
| 55–64                                   | 255                      | 40.9 | 35.9 - 45.9  | 55    | 75.5  | 55.6 - 95.5   | 41              | 152.5 | 105.8 - 199.2  | 9     | 13.5 | 4.7 - 22.4  | 150               | 33.1 | 27.8 - 38.4 |
| ≥65                                     | 792                      | 94.3 | 87.7 - 100.8 | 93    | 163.2 | 130 - 196.3   | 55              | 230.6 | 169.6 - 291.5  | 33    | 58.1 | 38.3 - 78   | 611               | 87.4 | 80.4 - 94.3 |
| Total cases and crude rate <sup>1</sup> | 1,587                    | 31   | 29.4 - 32.5  | 332   | 38.9  | 34.7 - 43.1   | 202             | 58.4  | 50.4 - 66.5    | 89    | 11.4 | 9.1 - 13.8  | 964               | 31.4 | 29.4 - 33.4 |
| Age-standardised rate <sup>2</sup>      | 1,587                    | 5.2  | 4.9 - 5.5    | 332   | 38.9  | 34.7 - 43.1   | 202             | 144.3 | 124.4 - 164.2  | 89    | 12.5 | 9.9 - 15.1  | 964               | 8.7  | 8.2 - 9.2   |
| Age group (years)                       | Community-associated SAB |      |              |       |       |               |                 |       |                |       |      |             |                   |      |             |
|                                         | Overall                  |      |              | Māori |       |               | Pacific peoples |       |                | Asian |      |             | European or Other |      |             |
|                                         | No.                      | Rate | 95% CI       | No.   | Rate  | 95% CI        | No.             | Rate  | 95% CI         | No.   | Rate | 95% CI      | No.               | Rate | 95% CI      |
| 0–4                                     | 34                       | 11.2 | 7.4 - 15     | 15    | 17.9  | 8.9 - 27      | 3               | -     | -              | 6     | 11.1 | 2.2 - 19.9  | 10                | 7.7  | 2.9 - 12.4  |
| 5–14                                    | 72                       | 10.9 | 8.4 - 13.4   | 26    | 14.7  | 9.1 - 20.4    | 13              | 20.2  | 9.2 - 31.2     | 6     | 6.7  | 1.3 - 12.1  | 27                | 8.4  | 5.2 - 11.6  |
| 15–24                                   | 45                       | 7    | 5 - 9.1      | 14    | 9.9   | 4.7 - 15.1    | 7               | 11.4  | 3 - 19.9       | 5     | 4.7  | 0.6 - 8.8   | 19                | 5.9  | 3.2 - 8.5   |
| 25–34                                   | 57                       | 7.7  | 5.7 - 9.7    | 17    | 14.1  | 7.4 - 20.8    | 14              | 26.6  | 12.6 - 40.5    | 4     | -    | -           | 22                | 6    | 3.5 - 8.5   |
| 35–44                                   | 76                       | 11.5 | 8.9 - 14     | 22    | 22.5  | 13.1 - 31.9   | 14              | 32.2  | 15.3 - 49.1    | 5     | 3.7  | 0.5 - 7     | 35                | 9.4  | 6.3 - 12.5  |
| 45–54                                   | 121                      | 18.6 | 15.3 - 22    | 40    | 44.3  | 30.6 - 58.1   | 25              | 65    | 39.5 - 90.5    | 5     | 6.1  | 0.8 - 11.5  | 51                | 11.8 | 8.6 - 15.1  |
| 55–64                                   | 186                      | 29.8 | 25.5 - 34.1  | 43    | 59.1  | 41.4 - 76.7   | 27              | 100.4 | 62.5 - 138.3   | 6     | 9    | 1.8 - 16.2  | 110               | 24.3 | 19.7 - 28.8 |
| ≥65                                     | 546                      | 65   | 59.5 - 70.4  | 67    | 117.6 | 89.4 - 145.7  | 38              | 159.3 | 108.7 - 210    | 18    | 31.7 | 17.1 - 46.4 | 423               | 60.5 | 54.7 - 66.3 |
| Total cases and crude rate <sup>1</sup> | 1,139                    | 22.2 | 20.9 - 23.5  | 245   | 28.7  | 25.1 - 32.3   | 141             | 40.8  | 34.1 - 47.5    | 56    | 7.2  | 5.3 - 9.1   | 697               | 22.7 | 21 - 24.4   |
| Age-standardised rate <sup>2</sup>      | 1,139                    | 3.7  | (3.5 - 3.9)  | 245   | 28.7  | (25.1 - 32.3) | 141             | 100.7 | (84.1 - 117.3) | 56    | 7.9  | (5.8 - 10)  | 697               | 6.3  | (5.8 - 6.8) |

Table C2. continued

|                                         | Hospital-associated SAB |      |             |       |      |             |                 |      |              |       |      |             |                   |      |            |
|-----------------------------------------|-------------------------|------|-------------|-------|------|-------------|-----------------|------|--------------|-------|------|-------------|-------------------|------|------------|
|                                         | Overall                 |      |             | Māori |      |             | Pacific peoples |      |              | Asian |      |             | European or Other |      |            |
| Age group (years)                       | No.                     | Rate | 95% CI      | No.   | Rate | 95% CI      | No.             | Rate | 95% CI       | No.   | Rate | 95% CI      | No.               | Rate | 95% CI     |
| 0–4                                     | 26                      | 8.6  | 5.3 - 11.9  | 11    | 13.1 | 5.4 - 20.9  | 6               | 20.4 | 4.1 - 36.7   | 3     | -    | -0.7 - 11.8 | 6                 | 4.6  | 0.9 - 8.3  |
| 5–14                                    | 11                      | 1.7  | 0.7 - 2.6   | 7     | 4    | 1 - 6.9     | 0               | -    | -            | 0     | -    | -           | 4                 | -    | -          |
| 15–24                                   | 11                      | 1.7  | 0.7 - 2.7   | 3     | -    | -           | 1               | -    | -            | 3     | -    | -           | 4                 | -    | -          |
| 25–34                                   | 20                      | 2.7  | 1.5 - 3.9   | 6     | 5    | 1 - 9       | 6               | 11.4 | 2.3 - 20.5   | 5     | 2.7  | 0.3 - 5.1   | 3                 | -    | -          |
| 35–44                                   | 25                      | 3.8  | 2.3 - 5.3   | 10    | 10.2 | 3.9 - 16.5  | 5               | 11.5 | 1.4 - 21.6   | 2     | -    | -           | 8                 | 2.1  | 0.7 - 3.6  |
| 45–54                                   | 40                      | 6.2  | 4.3 - 8.1   | 12    | 13.3 | 5.8 - 20.8  | 12              | 31.2 | 13.6 - 48.9  | 2     | -    | -           | 14                | 3.2  | 1.5 - 4.9  |
| 55–64                                   | 69                      | 11.1 | 8.4 - 13.7  | 12    | 16.5 | 7.2 - 25.8  | 14              | 52.1 | 24.8 - 79.3  | 3     | -    | -           | 40                | 8.8  | 6.1 - 11.6 |
| ≥65                                     | 246                     | 29.3 | 25.6 - 32.9 | 26    | 45.6 | 28.1 - 63.2 | 17              | 71.3 | 37.4 - 105.1 | 15    | 26.4 | 13.1 - 39.8 | 188               | 26.9 | 23 - 30.7  |
| Total cases and crude rate <sup>1</sup> | 448                     | 8.7  | 7.9 - 9.6   | 87    | 10.2 | 8 - 12.3    | 61              | 17.6 | 13.2 - 22.1  | 33    | 4.2  | 2.8 - 5.7   | 267               | 8.7  | 7.6 - 9.7  |
| Age-standardised rate <sup>2</sup>      | 448                     | 1.5  | 1.4 - 1.6   | 87    | 10.2 | 8.1 - 12.3  | 61              | 43.6 | 32.7 - 54.5  | 33    | 4.6  | 3 - 6.2     | 267               | 2.4  | 2.1 - 2.7  |

1 Age information is missing for one Māori CA-SAB episode and one Asian CA-SAB episode.

2 Age-standardised rates are directly standardised to the Māori population

3 Rates are not presented where there were fewer than five episodes.

**Table C3. Summary of typing results for MRSA clone-*spa* type combinations found in one isolate**

| MRSA clone- | <i>spa</i> type                                     |
|-------------|-----------------------------------------------------|
| ST5-IV      | t088, t242, t306, t20387, t4617, t688, t9816        |
| ST93-IV     | t11037, t4178, t15506, t17265, t1811, t1819, t20522 |
| ST97-IV     | t359, t224, t3987, t693                             |
| ST22-IV     | t005, t309, t852                                    |
| ST30-IV     | t138, t363                                          |
| ST8-IV      | t068, t121                                          |
| ST1-IV      | t1853                                               |
| ST30-V      | t021                                                |
| ST36-II     | t012                                                |
| ST398-V     | t034                                                |
| ST5662-IV   | t002                                                |
| ST1482-IV   | t2052                                               |
| ST78-IV     | t1028                                               |
| ST121-V     | t272                                                |
| ST188-IV    | t189                                                |
| ST5-V       | t002                                                |
| ST672-IV    | t3841                                               |
| ST672-V     | t3841                                               |
| ST78-IV     | t1028                                               |
| ST8743-V    | t2724                                               |

1 See Table 17 for details of MRSA clone-*spa* type combinations found in two or more isolates.



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