2021 survey of *Staphylococcus aureus* bacteraemia in New Zealand

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  - Labcare Pathology Ltd
  - MedLab Central Ltd
  - MedLab South Ltd Nelson
  - MedLab Timaru Ltd
  - Middlemore Hospital
  - North Shore Hospital
  - PathLab Bay of Plenty
  - Southern Community Labs Dunedin
  - Southern Community Labs Kew
  - Waikato Hospital
  - Wellington SCL (Wellington)
  - Wellington SCL (Wairarapa)
  - Whangarei Hospital

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1. EXECUTIVE SUMMARY

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 NZ than in many high-income countries, with the highest rates observed in Māori and Pacific Peoples.

The aims of the ESR *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 1,471 SAB episodes in New Zealand were reported to ESR, from 1 January to 31 December 2021. Of these, 69.4% were community-associated, and 9.7% were caused by methicillin-resistant *S. aureus* (MRSA).

Significantly more SAB cases were identified among males, with approximately two-thirds of cases in this survey reported in males. Incidence of SAB increased with age. The median age for SAB cases 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 15.9 and 4.5 times higher respectively. There were significantly more cases in people with higher socioeconomic deprivation.

The most common risk factors and comorbidities associated with SAB were tobacco smoking (40.2%), diabetes (29.6%), and obesity (13.5%).

The all-cause mortality for SAB at 30 days was 13.4%, although this was significantly lower amongst children (<18 years). There was no significant difference in mortality between community-associated and hospital-associated cases or isolates with differences in methicillin susceptibility.

The total incidence and incidence of MRSA SAB was highest in the Northern region of New Zealand, with incidence decreasing down the country. All isolates tested were susceptible to

linezolid and vancomycin. The highest percentage of resistance was found for fusidic acid (12.2%). Overall, 10.1% of isolates were erythromycin resistant, 8.5% were clindamycin resistant, 2.1% were co-trimoxazole resistant and 1.7% had resistance to tetracycline or doxycycline. The Panton-Valentine leukocidin (PVL) toxin gene was detected in 9.9% of SAB isolates and was more prevalent in MRSA.

Based on *spa* typing data, methicillin-susceptible *S. aureus* (MSSA) isolates from SAB were more diverse than MRSA. Using core genome multilocus sequence type (cgMLST), more than 100 complex types were identified. Similar MRSA clones were found in community-associated SAB and hospital-associated SAB cases.

The results of this report highlight the need for sustained epidemiological and molecular surveillance, infection prevention and control, antibiotic stewardship and continued focus on prevention initiatives. Of particular significance is the role of wound care, diabetes management, device management, dialysis and vascular line care, and targeted strategies to prevent SAB should be developed in these areas. Any strategies must be culturally safe and designed to meet the needs of Māori and Pacific peoples who are disproportionately impacted by SAB and its complications. Ideally the development and delivery of an effective vaccine to prevent *S. aureus* infections should also be investigated.

2. INTRODUCTION

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 (Hill, Birch, et al., 2001; Hill, Wong, et al., 2001; Williamson et al., 2013; Heffernan et al., 2015).

Methicillin-resistant *S. aureus* (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 methicillin-susceptible *S. aureus* (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 as a key indicator of healthcare quality and as an outcome measure for the Hand Hygiene New Zealand programme (Barratt et al., 2022). Despite positive progress in hand hygiene performance, the median quarterly healthcare-associated *S. aureus* bacteraemia rate rose steadily from 0.11 healthcare-associated *S. aureus* bacteraemia events per 1,000 bed-days in 2016 to 0.15 bed-days in 2019 (Barratt et al., 2022).

Molecular characterisation and antimicrobial resistance (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 community-associated *S. aureus* bacteraemia (CA-SAB) in NZ.

The aims of the ESR *S. aureus* bacteraemia (SAB) surveillance programme were to document rates of 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 patient age, ethnicity, socioeconomic deprivation and co-morbidities.

Earlier reports on *S. aureus* surveillance in New Zealand are available on the ESR website at https://www.esr.cri.nz/our-research/nga-kete/infectious-disease-intelligence/antimicrobial-resistance-amr/

3. SUMMARY OF METHODS

3.1 ISOLATES AND PATIENT INFORMATION

New Zealand diagnostic laboratories were requested to refer all *S. aureus* isolates from blood culture samples isolated from 1st January to 31st December 2021 to ESR. 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). These data were supplemented by patient information, including ethnicity and NZ deprivation index data, and hospitalisation event data from the Ministry of Health National Minimum Dataset (NMDS). Hospitalisation event data included admission and discharge dates, and diagnosis codes.

Cases 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, which is the same 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).

In May 2021, the former Waikato District Health Board (Waikato DHB, now part of the Health New Zealand Te Whatu Ora Te Manawa Taki region) was affected by a cyber-attack. In the months following the cyber-attack ESR received susceptibility data for 81 isolates from SAB cases; however, these isolates were not referred to ESR for further molecular testing.

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 et al,. 2004). For further information on all isolate characterisation methods refer to Appendix A.

All MRSA isolates underwent whole genome sequencing (WGS) using Illumina-based sequencing technology. Data were used to define the MRSA clone, as described in Appendix A.

3.3 DATA ANALYSIS

Data cleaning and statistical tests were performed in R version 4.1.0 (R Core Team, 2021) using tidyverse (Wickham et al., 2019) and AMR packages (Berends et al., 2022). For further details refer to Appendix A.

4. RESULTS

4.1 ISOLATES SELECTED

From 1 January to 31 December 2021, ESR received 1,592 *S. aureus* blood culture isolates. In total, 121 isolates were excluded from our analysis: 62 were duplicate isolates, 57 could not be matched to National Minimum Dataset (NMDS) hospitalisation data from a hospitalisation event within 48 hours of sample collection, and two were collected within 48 hours of birth.

Of the 1,471 isolates included in our analysis, 1,021 (69.4%) were classified as CA-SAB whilst 450 (30.6%) were HA-SAB (Table 1). Significantly more HA-SAB cases were MRSA than CA-SAB cases (12.2% vs. 8.5%, P = .035). All 132 MRSA isolates contained the *mecA* gene, with no *mecC*-mediated resistance detected (10 MRSA isolates from Waikato DHB were not tested for *mecA* or *mecC* genes). No *mecA* or *mecC* genes were found among MSSA isolates, although one isolate contained a truncated, non-functional *mecC* gene (Miller et al. 2024).

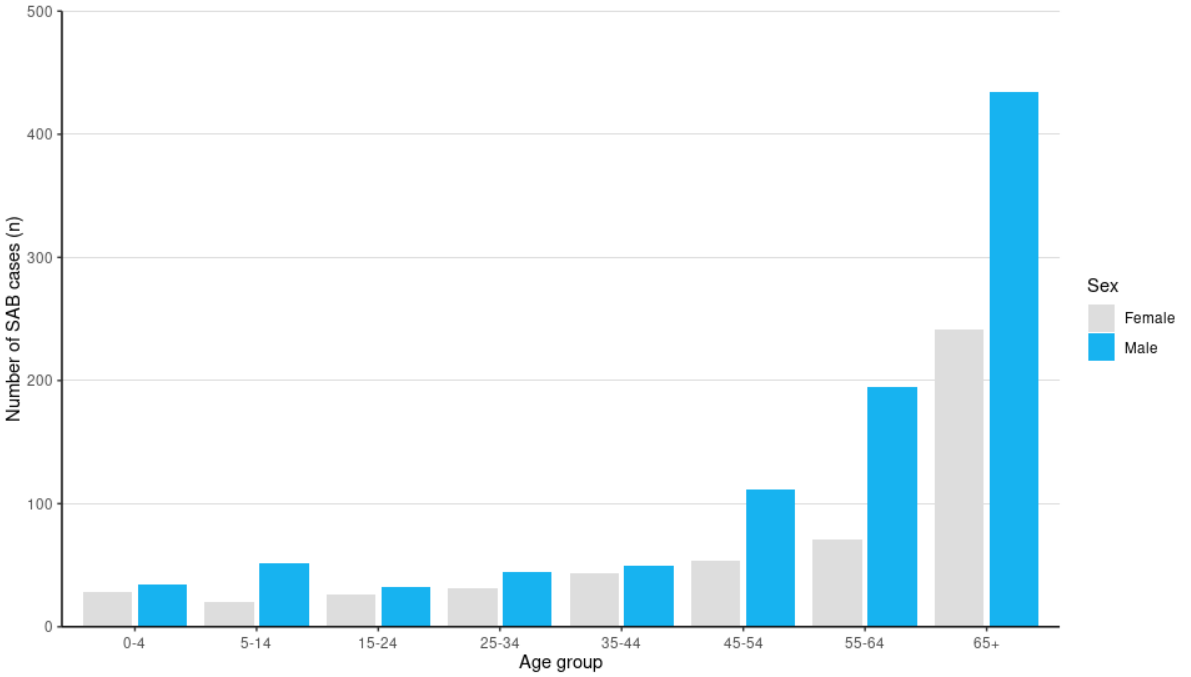
Table 1. *S. aureus* bacteraemia by methicillin susceptibility and place of onset, 2021

Methicillin susceptibility	Percent (No.) of place of onset			P-value
	Overall	Community-associated SAB	Hospital-associated SAB	
Total	1,471	1,021	450	
MRSA	9.7 (142)	8.5 (87)	12.2 (55)	.035
MSSA	90.3 (1,329)	91.5 (934)	87.8 (395)	

4.2 PATIENT DEMOGRAPHICS

Data for age and sex were available for all patients with SAB. The majority were male (all SAB, 65.0% (656/1471); CA-SAB, 65.7% (671/1021); and HA-SAB, 63.3% (285/450)). Nearly half of SAB cases were in those aged ≥ 65 years (all SAB, 45.9% (675/1471); CA-SAB, 44.9% (458/1021); and HA-SAB, 48.2 (217/450)).

Increasing age was a surrogate risk factor for SAB (Figure 1). The proportion of SAB episodes in patients under 45 years was only 24.5% (361/1471). The proportion of patients aged under 15 years was 9.1% (134/1471).



Sex	Percent (No.) of Age (years)									
	0-9	**10-19**	**20-29**	**30-39**	**40-49**	**50-59**	**60-69**	**70-79**	**80-89**	**90+**
Total no.	100	69	56	78	129	216	275	280	203	62
Female	40.0 (40)	31.9 (22)	42.9 (24)	39.7 (31)	44.2 (57)	29.6 (64)	28.4 (78)	35.4 (99)	36.9 (75)	38.7 (24)
Male	60.0 (60)	68.1 (47)	57.1 (32)	60.3 (47)	55.8 (72)	70.4 (152)	71.6 (197)	64.6 (181)	63.1 (128)	61.3 (38)

Figure 1. Number of episodes of SAB, by patient age group and sex, 2021

Table 2 shows the distribution of SAB cases by methicillin susceptibility and region. A total of 569 (38.7%) SAB cases were from the Northern region, 304 (20.7%) from Te Manawa Taki, 323 (22.0%) from Central, and 274 (18.6%) from Te Waipounamu.

Additionally, incidence rates for both MSSA and MRSA SAB were highest for the Health New Zealand, Northern region (Table 2). SAB isolates from the combined Auckland health districts (Waitematā, Te Toka Tumai Auckland, and Counties Manukau) made up the majority (80.0%) of isolates from the Northern Region and 32.3% of the total cohort. Data on the distribution of SAB cases by place of onset and region are shown in Appendix C Table C1.

Table 2. Rates of SAB by region and methicillin susceptibility, 2021

Methicillin susceptibility	Overall Rate[1] (No.)	Region			
		Northern Rate[1] (No.)	Te Manawa Taki Rate[1] (No.)	Central Rate[1] (No.)	Te Waipounamu Rate[1] (No.)
Total	28.8 (1471)	29.5 (569)	30.0 (304)	33.2 (323)	22.9 (274)
MRSA	2.8 (142)	4.0 (77)	3.2 (32)	2.3 (22)	0.9 (11)
MSSA	26.0 (1329)	25.5 (492)	26.8 (272)	30.9 (301)	22.0 (263)

1 Rate information per 100 000 population

The demographic characteristics gender, age, ethnicity, geographical region and socioeconomic deprivation and are shown in Figure 2 and detailed as counts in Table 3. By absolute numbers, most cases were in people of European or Other ethnicity (61.5%), followed by Māori (21.2%), Pacific Peoples (16.5%), and Asian (5.0%) ethnicities (Figure 2 and Table 3). The median age for SAB cases was considerably younger among all other ethnic groups compared with European and Other, with differences statistically significant.

The percentage of SAB cases increased with increasing socioeconomic deprivation (Table 3) which was measured by the NZDep18 index, with 28.3% of cases from quintile 5 (most deprivation) compared to 13.9% from quintile 1 (least deprivation), P < .001.

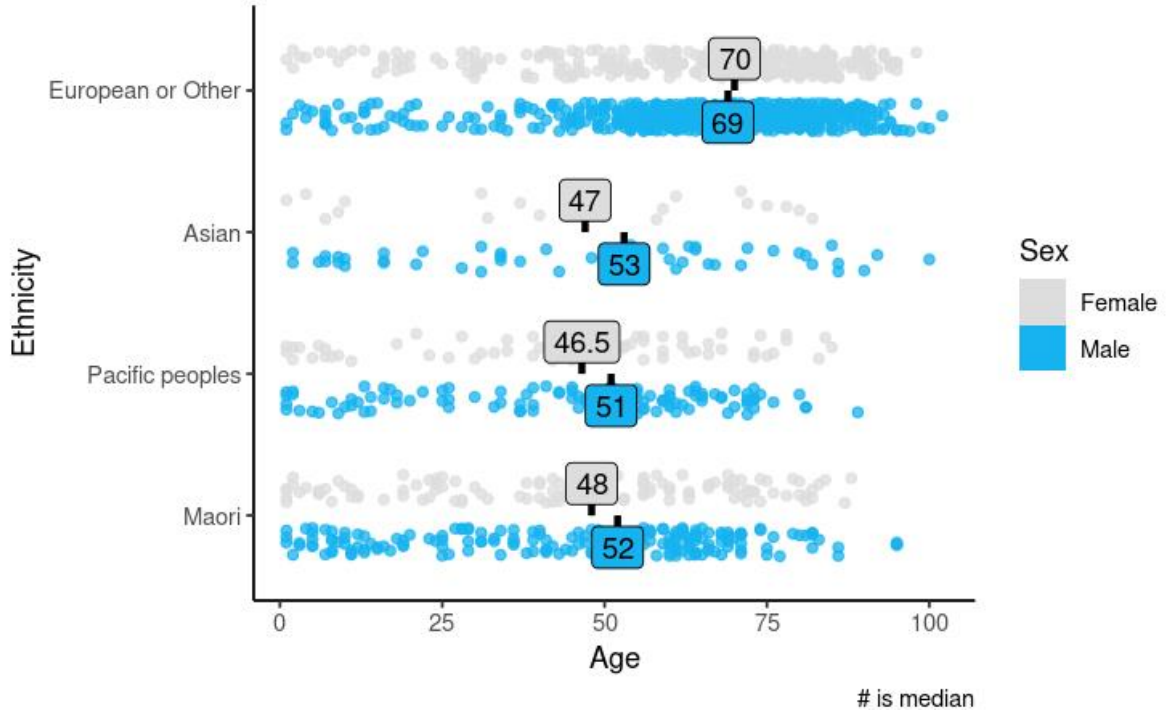


Figure 2. Age distribution and median age of patients with SAB, by ethnicity and sex, 2021

Table 3. Demographic characteristics of SAB cases stratified by place of onset, 2021

Demographic Characteristic	Overall % (No.)	Place of Onset: Community-associated SAB % (No.)	Place of Onset: Hospital-associated SAB % (No.)	P-value
Sex				
Female	35.0 (515)	34.3 (350)	36.7 (165)	.406
Male	65.0 (956)	65.7 (671)	63.3 (285)	
Age (years)[1]				
0-4	4.2 (62)	3.8 (39)	5.1 (23)	.331
5-14	4.9 (72)	5.9 (60)	2.7 (12)	
15-24	3.9 (58)	3.7 (38)	4.4 (20)	
25-34	5.2 (76)	5.0 (51)	5.6 (25)	
35-44	6.3 (93)	6.1 (62)	6.9 (31)	
45-54	11.3 (166)	11.5 (117)	10.9 (49)	
55-64	18.1 (266)	18.9 (193)	16.2 (73)	
≥65	45.9 (675)	44.9 (458)	48.2 (217)	
Ethnicity				
Māori	21.2 (312)	22.1 (226)	19.1 (86)	<.001
Pacific peoples	12.4 (182)	14.1 (144)	8.4 (38)	
Asian	5.0 (73)	4.3 (44)	6.4 (29)	
European or Other	61.5 (904)	59.5 (607)	66.0 (297)	
Region[2]				
Northern	38.7 (569)	39.2 (400)	37.6 (169)	.115
Te Manawa Taki	20.7 (304)	21.7 (222)	18.2 (82)	
Central	22.0 (323)	20.4 (208)	25.6 (115)	
Te Waipounamu	18.6 (274)	18.7 (191)	18.4 (83)	
NZDep18[3]				
Quintile 1	13.9 (204)	12.5 (128)	16.9 (76)	<.001
Quintile 2	16.7 (245)	15.7 (160)	18.9 (85)	
Quintile 3	16.6 (244)	16.9 (173)	15.8 (71)	
Quintile 4	24.5 (360)	23.9 (244)	25.8 (116)	
Quintile 5	28.3 (417)	31.0 (316)	22.4 (101)	

1 Eight CA-SAB cases did not have age data.
2 One HA-SAB case did not have region data.
3 Quintile of the 2018 New Zealand Deprivation Index (1 = least socioeconomically deprived and 5 = most socioeconomically deprived). One HA-SAB case did not have NZDep18 quintile data.

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 130.4 per 100,000 and 36.8 per 100,000, respectively, compared to 10.3 per 100,000 for Asian, and 8.2 per 100,000 for European and Other, respectively. This ethnic inequity was more prominent for community-associated SAB than for hospital-associated SAB.

4.3 ALL-CAUSE LENGTH OF HOSPITAL STAY

The total length of hospital admission was available for patients with SAB. Table 4 shows the length of hospital stay by methicillin susceptibility and place of onset. Overall, 14.8% of patients with SAB had a hospital stay of < 7 days, 37.6% had a hospital stay of 7 – 14 days, 27.3% had a hospital stay of 15-30 days, and 20.3% had a hospital stay of > 30 days.

Table 4. Length of hospital stay for SAB cases, by methicillin susceptibility and place of onset, 2021

Methicillin susceptibility	Length of hospital stay (Percent (No.))				
	Overall	< 7 days	7 - 14 days	15 - 30 days	> 30 days
Total	1,471	14.8 (217)	37.6 (553)	27.3 (402)	20.3 (299)
MRSA	142	11.3 (16)	31.0 (44)	28.9 (41)	28.9 (41)
CA-SAB	87	17.2 (15)	35.6 (31)	27.6 (24)	19.5 (17)
HA-SAB	55	1.8 (1)	23.6 (13)	30.9 (17)	43.6 (24)
MSSA	1,329	15.1 (201)	38.3 (509)	27.2 (361)	19.4 (258)
CA-SAB	934	20.8 (194)	42.1 (393)	24.5 (229)	12.6 (118)
HA-SAB	395	1.8 (7)	29.4 (116)	33.4 (132)	35.4 (140)

The median length of hospital stay for all SAB was 14 (Inter quartile range (IQR) 9-25) days, and was significantly longer for MRSA infections compared to MSSA infections (MRSA: 17.5, IQR 10-36, MSSA: 13, IQR 9-25, P < .01) although this was not the case for HA-SAB cases with MRSA (MRSA: 26, IQR 14.5-53.5, MSSA: 22, IQR 13-44, P =0.302).

Table 5. Median all-cause hospital length of stay (days) for cases with SAB, by place of onset and methicillin susceptibility, 2021

	Methicillin susceptibility[1]		
Place of onset	MRSA	MSSA	P-value
All SAB	17.5 (10-36)	13 (9-25)	< .01
CA- SAB	14 (8-24)	11 (7-19)	.032
HA-SAB	26 (14.5-53.5)	22 (13-44)	.302

1 Values are Median (IQR).

4.4 ALL-CAUSE MORTALITY

A total of 197 (13.4%) individuals with SAB died within 30 days of a positive *S. aureus* blood culture result. Among the isolates associated with patient deaths, 170 (86.3%) were MSSA and 27 (13.7%) 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 = .051; CA-SAB, P = .312; and HA-SAB, P = .070).

Refer to Appendix C Table C3 for age-standardised mortality rates. Age standardised mortality rates were higher for Pacific Peoples and Māori compared to European or Other and Asian ethnic groups.

Table 6. 30-day all-cause mortality from SAB, by methicillin susceptibility and place of onset, 2021

	Overall		Community-associated SAB		Hospital-associated SAB	
Methicillin susceptibility	Total	Died, % (No.)	Total	Died, % (No.)	Total	Died, % (No.)
Total	1,471	13.4 (197)	1,021	12.6 (129)	450	15.1 (68)
MRSA	142	19.0 (27)	87	16.1 (14)	55	23.6 (13)
MSSA	1,329	12.8 (170)	934	12.3 (115)	395	13.9 (55)

RISK FACTORS, COMBORBIDITIES AND COMPLICATIONS

4.5 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

4.6 RISK FACTORS, COMORBIDITIES AND COMPLICATIONS

Table 7 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).

A total of 60.0% (882/1471) of SAB cases had a diagnosis code related to at least one of the risk factors, comorbidities or complications assessed, including 59.1% (603/1021) of CA-SAB and 62.0% (279/450) of HA-SAB. Among the risk factors and comorbidities assessed, tobacco smoking (40.2%) was the most common followed by diabetes mellitus (29.6%) and obesity (13.5%). Among complications assessed, those associated with prosthetics/ implantable devices were the most common (16.2%). However, only the prevalence of complications associated with vascular catheters differed by place of onset, with greater prevalence among those with HA-SAB compared to CA-SAB (17.1% vs. 14.0%, $P < .01$).

Table 7. Number of all SAB cases with a diagnosis code relating to select risk factors, comorbidities and complications, by place of onset, 2021

	Place of onset			
Common risk factors, comorbidities and complications	Overall % (No.)	Community-associated SAB % (No.)	Hospital-associated SAB % (No.)	P-value
Total	1471	1021	450	
Tobacco smoking	40.2 (592)	39.0 (398)	43.1 (194)	.149
Diabetes mellitus	29.6 (435)	29.9 (305)	28.9 (130)	.757
Obesity	13.5 (199)	12.9 (132)	14.9 (67)	.321
Surgical site infection	4.4 (64)	3.9 (40)	5.3 (24)	.215
Complications associated with vascular catheters	14.8 (218)	7.6 (78)	31.1 (140)	<.001
Complications associated with prosthetics/ implantable devices	16.2 (238)	17.1 (175)	14.0 (63)	.144

5. ANTIMICROBIAL SUSCEPTIBILITY

The following section presents the results of antimicrobial susceptibility testing by methicillin susceptibility, and multidrug resistance for only those isolates resistant to methicillin (MRSA). Susceptibility testing methods are described in Appendix A.

5.1 ANTIMICROBIAL RESISTANCE

Table 8 shows the number of isolates tested against each antimicrobial and the susceptibility results. All MSSA isolates tested were susceptible to cefoxitin (flucloxacillin), linezolid, and vancomycin. All MRSA were susceptible to daptomycin, linezolid, rifampicin, teicoplanin and vancomycin. Resistance to non-beta lactam antimicrobials among MSSA was lower than for MRSA isolates but highest for erythromycin (9.2%) and fusidic acid (8.6%).

There were 783 MSSA isolates (58.8%) with both oxacillin and cefoxitin results available. Of these, 14 (1.8%) MSSA isolates were borderline oxacillin resistant *S. aureus* (BORSA) with oxacillin MIC values > 2 mg/L but susceptible (MIC values ≤4 mg/L) to cefoxitin (flucloxacillin). The same or higher levels of resistance were found for all antimicrobials in isolates from patients with HA-SAB.

Table 8. Antimicrobial susceptibility among 2021 SAB isolates by methicillin susceptibility

Antimicrobial	Methicillin susceptibility					
	Overall		MRSA		MSSA	
	No. isolates tested	Resistant (%)	No. isolates tested	Resistant (%)	No. isolates tested	Resistant (%)
Cefoxitin (flucloxacillin)	1,471	9.7	142	100.0	1,329	0.0
Ciprofloxacin	1,375	4.3	137	17.5	1,238	2.8
Clindamycin	1,358	8.5	130	13.1	1,228	8.0
Co-trimoxazole	1,458	2.1	140	4.3	1,318	1.9
Daptomycin	945	0.1	97	0.0	848	0.1
Doxycycline/tetracycline[1]	1,448	1.7	139	4.3	1,309	1.5
Erythromycin	1,460	10.1	141	19.1	1,319	9.2
Fusidic acid	1,272	12.2	132	43.2	1,140	8.6
Gentamicin	1,348	2.0	129	7.0	1,219	1.5
Linezolid	972	0.0	99	0.0	873	0.0
Mupirocin	861	0.9	72	1.4	789	0.9
Oxacillin	872	11.8	89	100.0	783	1.8
Rifampicin	1,211	0.3	112	0.0	1,099	0.4
Teicoplanin	955	0.2	98	0.0	857	0.2
Vancomycin	998	0.0	117	0.0	881	0.0

1 Isolates resistant to doxycycline and/or tetracycline

Figure 3 shows the variability in MRSA from SAB across the four New Zealand health regions. Nationally, 9.7% of SAB episodes were caused by MRSA. Methicillin resistance varied significantly across regions; ranging from 13.5% of isolates referred from Northern region to 4.0% of isolates referred from the Te Waipounamu region ($P < .01$). Please note geographic location data was not available for one isolate.

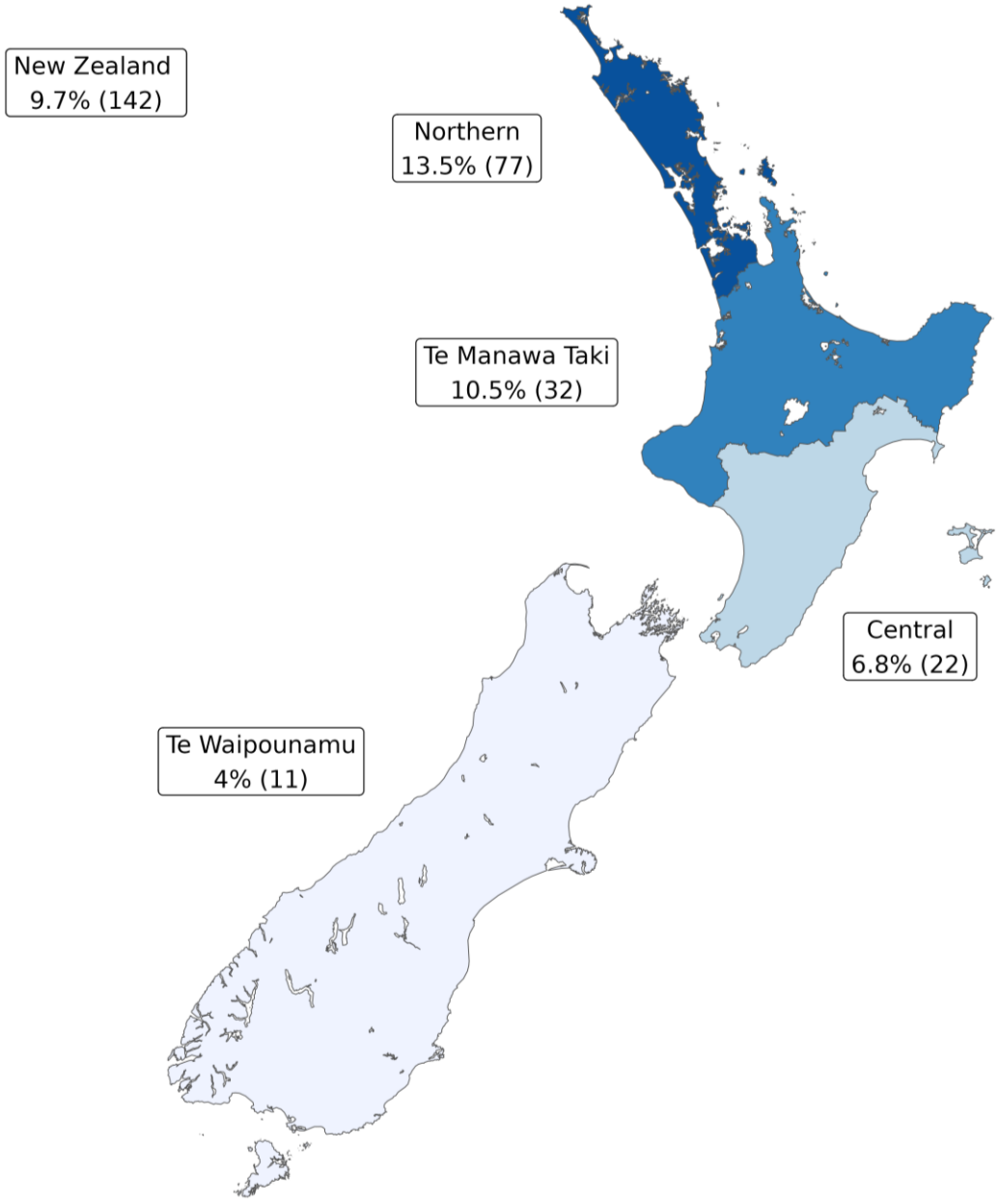


Figure 3. Percentage of MRSA from patients with SAB by region, 2021.

Table 9 shows the number of SAB isolates, by methicillin susceptibility, isolated from patients from each ethnic group. The percentage of MRSA found in each ethnic group was: 15.9% (29/182) in Pacific People, 12.8% (40/312) in Māori, 8.2% (6/73) in Asians, and 7.4% (67/904) in people belonging to the European or Other ethnic group. The differences in the percentage of MRSA found across ethnic groups was statistically significant (P < .001).

Table 9. Methicillin susceptibility among SAB isolates by ethnicity, 2021

Methicillin resistance	Percent (No.) of Ethnic Group					P-value
	Overall	Māori	Pacific peoples	Asian	European or Other	
Total	1,471	312	182	73	904	
MRSA	9.7 (142)	12.8 (40)	15.9 (29)	8.2 (6)	7.4 (67)	<.001
MSSA	90.3 (1,329)	87.2 (272)	84.1 (153)	91.8 (67)	92.6 (837)	

5.2 MULTIDRUG RESISTANCE

The definitions defined by 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.

Table 10 shows the percentage of isolates with acquired resistance to multiple antimicrobial groups. Only isolates tested against all six antimicrobial groups were included in the analysis (cefoxitin/oxacillin, clindamycin, co-trimoxazole, erythromycin, gentamicin and doxycycline/tetracycline). A total of 24.0% of MRSA were multidrug resistant.

Table 10. Multiple acquired resistance in MRSA from SAB isolates, 2021[1]

	Percent (No.) of classes (non-MDR)		Percent (No.) of classes (MDR)				
Overall	1	2	3	4	5	6	Total MDR (%)
100.0 (125)	64.0 (80)	12.0 (15)	19.2 (24)	2.4 (3)	1.6 (2)	0.8 (1)	24.0 (30)

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

Table 11 shows multidrug resistance by place of onset and 30-day all-cause mortality. All-cause mortality was greater for individuals with a multidrug resistant infection and in those with HA-SAB. There was no statistical significance in mortality by MDR status.

Table 11. Multidrug resistance in MRSA, by place of onset and 30-day all-cause mortality, 2021[1]

	Overall		Community-associated SAB		Hospital-associated SAB	
MDR status	Number	Deaths % (No.)	Number	Deaths % (No.)	Number	Deaths % (No.)
MDR	30	23.3 (7)	14	35.7 (5)	16	12.5 (2)
Non-MDR	95	20.0 (19)	63	12.7 (8)	32	34.4 (11)

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

6. MOLECULAR EPIDEMIOLOGY

6.1 *SPA* TYPES

A *spa* result was available for 1361 of the 1471 SAB isolates (see Table 12 footnotes), of which 394 unique *spa* types were identified: 44 in MRSA and 373 in MSSA.

Within MRSA SAB isolates, *spa* type t002 was the most common, accounting for 34.8% of all isolates, 34.6% of CA-SAB and 35.3% of HA-SAB. Other *spa* types found in more than 4% of MRSA SAB isolates were t3949 (9.8%) t359 (7.6%) and t008 (4.5%).

Table 12. Most prevalent *spa* types among isolates from SAB cases stratified by place of onset and methicillin susceptibility, 2021

MRSA[1,2]

Overall (n=132)			CA-SAB (n=81)			HA-SAB (n=51)		
spa	**No.**	**Percent**	***spa***	**No.**	**Percent**	***spa***	**No.**	**Percent**
t002	46	34.8	t002	28	34.6	t002	18	35.3
t3949	13	9.8	t3949	9	11.1	t359	6	11.8
t359	10	7.6	t008	4	4.9	t3949	4	7.8
t008	6	4.5	t359	4	4.9			

MSSA[1,3]

Overall (n=1244)			CA-SAB (n=870)			HA-SAB (n=374)		
spa	**No.**	**Percent**	***spa***	**No.**	**Percent**	***spa***	**No.**	**Percent**
t189	122	9.8	t189	84	9.7	t189	38	10.2
t002	74	5.9	t1265	52	6.0	t002	24	6.4
t1265	71	5.7	t002	50	5.7	t1265	19	5.1
t127	64	5.1	t127	47	5.4	t127	17	4.5

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

2 Ten MRSA isolates from the former Waikato DHB were not referred to ESR, six CA-SAB and four HA-SAB.

3 A total of 85 MSSA isolates (71 from Waikato, seven from Lakes, three from Bay of Plenty, two from Counties Manukau, one from Taranaki and one from Canterbury) were not referred to ESR, 64 were CA-SAB and 21 were HA-SAB. A further 14 MSSA isolates were referred to ESR but were untypeable. Of these 11 were CA-SAB and three were HA-SAB.

Within MSSA SAB isolates, *spa* type t189 was the most common, accounting for 9.8% of all isolates, 9.7% of CA-SAB and 10.2% of HA-CAB. Other *spa* types found in more than 4% of MSSA SAB isolates were t002 (5.9%), t1265 (5.7%) and t127 (5.1%).

6.2 MRSA STRAINS: WHOLE GENOME SEQUENCING

Whole genome sequencing (WGS) data was used to describe the molecular epidemiology of MRSA from blood. Of the 142 MRSA reported, 132 (93.0%) were sequenced. Ten isolates were not available due to the 2021 cyber-attack at the former Waikato DHB.

Table 13 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 sequence type and SCC*mec* types. 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. These strain classifications were initially defined based on antibiogram and phage type and were subsequently defined by PFGE type and *spa* type. The strain classifications have been included to facilitate comparison with earlier New Zealand surveillance reports.

There were 27 unique MRSA clones found within the 132 MRSA sequenced. Fourteen of these combinations were only found in a single isolate each. The most common MRSA clones were ST5-IV (AK3, n = 47, 35.6%), ST93-IV (Queensland clone, n = 16, 12.1%), ST97-IV (WR/AK1, n = 16, 12.1%), ST8-IV (USA300, n = 9, 6.8%), ST22-IV (n = 6, 4.5%) and ST30-IV (WSPP, n = 5, 3.8%). All other MRSA clones were found in less than five isolates each. There was only one ST398-V (CC398 clone), from a case with CA-SAB.

The dominant MRSA clone was ST5-IV (n=46, 34.8%) and it was dominant among various ethnic groups. The ST5-IV MRSA clone was more prevalent, although not significantly so, among CA-SAB (n = 32, 39.5%), those aged < 15 years of age (n = 5, 45.5%), Māori (n = 19, 51.4%), and those in NZDep18 Quintile 5 (n = 23, 51.1%) compared to MRSA overall. ST93-IV (Queensland clone) was significantly more prevalent among Pacific Peoples (n = 12, 41.4%) than all MRSA overall (n = 16, 12.1%, P < .01). ST97-IV (WR/AK1) was more prevalent, although not significantly so, among HA-SAB cases (n = 7, 13.7%); cases ≥ 65 years of age (n = 9, 16.1%); and European or Other cases (n = 10, 16.7%), compared to MRSA overall (n = 16, 12.1%).

Table 13. Association of MRSA clones with patient demographics, 2021

MRSA clone (ST-SCCmec[1])	MRSA Strain[2]	Percent (No.) within each demographic group[1]									
		Onset			Age group		Ethnicity				NZDep18
		All MRSA n = 132	CA-SAB n = 81	HA-SAB n = 51	< 15 years n = 11	≥ 65 years n = 56	Māori n = 37	Pacific peoples n = 29	Asian n = 6	European or Other n = 60	Quintile 5[3] n = 45
ST5-IV	AK3	34.8 (46)	39.5 (32)	27.5 (14)	45.5 (5)	48.2 (27)	51.4 (19)	34.5 (10)	33.3 (2)	25.0 (15)	51.1 (23)
ST93-IV	Queensland clone	12.1 (16)	13.6 (11)	9.8 (5)	9.1 (1)	8.9 (5)	5.4 (2)	41.4 (12)	0.0 (0)	3.3 (2)	13.3 (6)
ST97-IV	WR/AK1	12.1 (16)	11.1 (9)	13.7 (7)	27.3 (3)	16.1 (9)	8.1 (3)	10.3 (3)	0.0 (0)	16.7 (10)	8.9 (4)
ST8-IV	USA300	6.1 (8)	6.2 (5)	5.9 (3)	9.1 (1)	7.1 (4)	10.8 (4)	0.0 (0)	0.0 (0)	6.7 (4)	6.7 (3)
ST22-IV	-	4.5 (6)	3.7 (3)	5.9 (3)	0.0 (0)	7.1 (4)	5.4 (2)	0.0 (0)	0.0 (0)	6.7 (4)	0.0 (0)
ST30-IV	WSPP	3.8 (5)	3.7 (3)	3.9 (2)	0.0 (0)	0.0 (0)	5.4 (2)	3.4 (1)	33.3 (2)	0.0 (0)	4.4 (2)
ST6-IV	-	3.0 (4)	3.7 (3)	2.0 (1)	0.0 (0)	3.6 (2)	2.7 (1)	0.0 (0)	0.0 (0)	5.0 (3)	0.0 (0)
ST5662-IV	AK3	2.3 (3)	1.2 (1)	3.9 (2)	9.1 (1)	1.8 (1)	0.0 (0)	3.4 (1)	0.0 (0)	3.3 (2)	0.0 (0)
ST1-IV	-	2.3 (3)	2.5 (2)	2.0 (1)	0.0 (0)	5.4 (3)	0.0 (0)	3.4 (1)	0.0 (0)	3.3 (2)	4.4 (2)
ST5-V	-	2.3 (3)	1.2 (1)	3.9 (2)	0.0 (0)	3.6 (2)	0.0 (0)	0.0 (0)	0.0 (0)	5.0 (3)	0.0 (0)
ST398-V	CC398 clone	0.8 (1)	1.2 (1)	0.0 (0)	0.0 (0)	1.8 (1)	0.0 (0)	0.0 (0)	0.0 (0)	1.7 (1)	0.0 (0)

1 MRSA clone: ST-SCC*mec* types not shown if found in two or fewer isolates. There were an additional five isolates of AK3 MRSA strain type: ST149-IV (2), ST8326-IV (1), ST8330-IV (1), and ST8331-IV (1); one Queensland clone MRSA: ST8329-IV (1); three WR/AK1 MRSA: ST8327-IV (2) and ST1-I (1); and 12 isolates not recognised as an MRSA strain: ST59-IV (2), ST1649-IV (1), ST188-IV (1), ST45-IV (1), ST5-II (1), ST5-IV (1), ST59-V (1), ST779-IV (1), ST8-IV (1), ST8-V (1), ST8332-IV (1).

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

3 NZDep18 quintile 5 represents the most deprived group

Most MRSA clones identified were commonly associated with one *spa* type (Table 14). The ST5-IV MRSA clone (AK3) was most commonly associated with spa type t002; ST93-IV (Queensland clone) with t3949; ST97-IV (WR/AK1) with t359; ST8-IV (USA300) with t008; ST22-IV with t005; ST30-IV (WSPP) with t138; and ST398-V (CC398 clone) with t034 (Table 14). However, several other MRSA clones-*spa* type combinations were also identified among isolates and are listed in Table 14 and Table C4. There was only one ST398-V (CC398) with *spa* type t034, from a case with community-associated SAB.

There were 22 isolates with combinations of sequence type and SCC*mec* type that were not associated with a recognised MRSA strain. The most common MRSA clone-*spa* type combination among these isolates were ST6-IV and t1853, (3 isolates), ST1-IV and t1853 (3 isolates) and ST5-V and t311 (2 isolates). There were 14 other MRSA clone-*spa* type combinations that only had a single isolate, and none of these were associated with a known MRSA strain.

The genetic diversity of MRSA isolates was further investigated using core genome multilocus sequence typing (cgMLST). The cgMLST method characterises a larger portion of the genome compared to 7-gene MLST and is therefore more discriminatory. The Ridom SeqSphere+ software enabled the cgMLST type to be determined, as well as the cgMLST complex type (CT), which is a number that summarises the cgMLST results in a similar way to the seven gene multilocus sequence type (MLST) sequence types. Analysis of the cgMLST results showed that the MRSA clones circulating were diverse, with over 100 cgMLST complex types identified (Figure 4).

Table 14. MRSA clone and *spa* type combinations found in MRSA from SAB cases by place of onset, 2021

MRSA clone (ST-SCC*mec*)[1,2]	MRSA Strain[3]	*spa* type	Place of onset		
			Overall % (No.) n = 132	Community-associated SAB % (No.) n = 81	Hospital-associated SAB % (No.) n = 51
ST5-IV	AK3	t002	29.5 (39)	30.9 (25)	27.5 (14)
ST93-IV	Queensland clone	t3949	9.1 (12)	9.9 (8)	7.8 (4)
ST97-IV	WR/AK1	t359	7.6 (10)	4.9 (4)	11.8 (6)
ST8-IV	USA300	t008	3.8 (5)	3.7 (3)	3.9 (2)
ST5662-IV	AK3	t002	2.3 (3)	1.2 (1)	3.9 (2)
ST22-IV	-	t005	2.3 (3)	1.2 (1)	3.9 (2)
ST6-IV	-	t304	2.3 (3)	2.5 (2)	2 (1)
ST1-IV	-	t1853	2.3 (3)	2.5 (2)	2 (1)
ST93-IV	Queensland clone	t202	1.5 (2)	2.5 (2)	0 (0)
ST97-IV	WR/AK1	t521	1.5 (2)	2.5 (2)	0 (0)
ST8327-IV	WR/AK1	t267	1.5 (2)	0 (0)	3.9 (2)
ST8-IV	USA300	t024	1.5 (2)	2.5 (2)	0 (0)
ST30-IV	WSPP	t138	1.5 (2)	2.5 (2)	0 (0)
ST5-V	-	t311	1.5 (2)	1.2 (1)	2 (1)
ST398-V	CC398 clone	t034	0.8 (1)	1.2 (1)	0 (0)

1 Ten MRSA isolates from the former Waikato DHB were not referred to ESR for molecular testing and were excluded from this analysis.

2 MRSA clone and *spa* type combinations listed for combinations with two or more isolates only, except for the CC398 clone. See Table C4, in Appendix C, for details of MRSA clone-*spa* type combinations found in only one isolate.

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

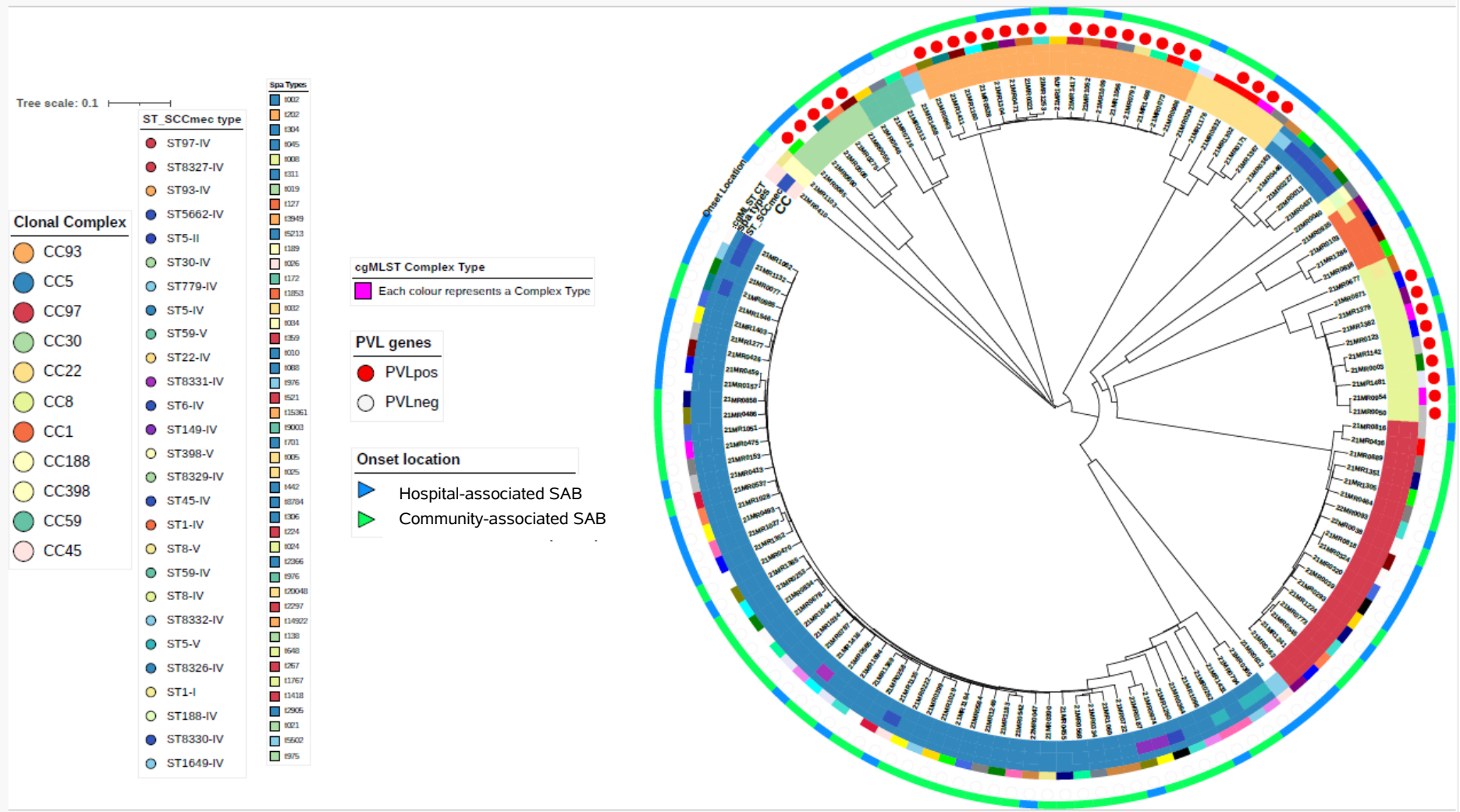


Figure 4. Phylogenetic analysis of 132 methicillin-resistant SAB isolates, 2021, by clonal complex, by MRSA clone, *spa* type, cgMLST type, PVL genes and place of onset.

6.3 PANTON-VALENTINE LEUKOCIDIN (PVL) RESULT

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 2021 SAB isolates, 9.9% were PVL-positive, including 25.8% (34/132) MRSA and 8.3% (10/1245) of MSSA (Table 15). CA-SAB were more likely to be PVL-positive ($P < .01$).

PVL was detected in five of the 27 MRSA clones (Table 16). The most frequently isolated PVL-positive clone was ST93-IV (Queensland clone). All isolates of ST8-IV (USA300) and ST30-IV (WSPP) were PVL-positive, whereas all isolates of ST5-IV (AK3), ST5662-IV (AK3) and ST149-IV (AK3) and ST97-IV and ST8327-IV (WR/AK1) were PVL-negative. In contrast, PVL was variable among ST22-IV.

Four of the six SAB 2021 ST22-IV isolates were PVL-positive: three in the Northern health region and one in the Central health region (Table 16). PVL-positive ST22-IV are frequently isolated in the South Asian subcontinent. The MRSA clone ST22-IV is genetically diverse, it has a PVL-negative hospital-associated clone and a PVL-positive community-associated clone known to cause hospital outbreaks, but it is generally considered to be community-associated.

Table 15. Panton-Valentine Leukocidin (PVL) status of SAB isolates 2021, stratified by methicillin susceptibility, place of onset, age and ethnicity

Characteristic	Overall[1,2]		MRSA[1]		MSSA[2]	
	Number	% PVL positive	Number	% PVL positive	Number	% PVL positive
Place of onset						
CA-SAB	951	11.7	81	28.4	870	10.1
HA-SAB	426	6.1	51	21.6	375	4.0
Age group (years)[3]						
0-4	57	12.3	6	0.0	51	13.7
5-14	68	14.7	5	40.0	63	12.7
15-24	55	12.7	7	28.6	48	10.4
25-34	75	18.7	8	25.0	67	17.9
35-44	87	18.4	12	66.7	75	10.7
45-54	156	11.5	15	53.3	141	7.1
55-64	252	9.9	23	13.0	229	9.6
≥65	624	6.3	56	16.1	568	5.3
Ethnicity						
Māori	280	15.0	37	27.0	243	13.2
Pacific peoples	181	19.3	29	44.8	152	14.5
Asian	71	9.9	6	33.3	65	7.7
European or Other	845	6.3	60	15.0	785	5.6

1 Ten MRSA isolates from the former Waikato DHB were not referred to ESR for spa typing, six were CA-SAB and four were HA-SAB.

2 A total of 85 MSSA isolates (71 from the former Waikato DHB, seven from Lakes, three from Bay of Plenty, two from Counties Manukau, one from Taranaki and one from Canterbury) were not referred to ESR for spa typing, 64 were CA-SAB and 21 were HA-SAB.

3 Three MSSA isolates did not have an associated age provided.

Table 16. Methicillin-resistant *S. aureus* (MRSA) clones by health region and Panton-Valentine Leukocidin (PVL) status, 2021

MRSA clone[1]	Clonal complex	PVL	MRSA Strain[2]	Region				
				Overall[1, 2]	Northern	Te Manawa Taki[3]	Central	Te Waipounamu
ST5-IV	CC5	-	AK3	47	30	9	6	2
ST97-IV	CC97	-	WR/AK1	16	10	3	2	1
ST93-IV	CC93	+	Queensland clone	15	12	0	2	1
ST8-IV	CC8	+	USA300	9	4	3	1	1
ST30-IV	CC30	+	WSPP MRSA	5	1	0	2	2
ST6-IV	CC5	-	-	4	0	1	2	1
ST22-IV	CC22	+	-	4	3	0	1	0
ST5662-IV	CC5	-	AK3	3	2	0	1	0
ST5-V	CC5	-	-	3	2	0	0	1
ST1-IV	CC1	-	-	3	2	0	1	0
ST149-IV	CC5	-	AK3	2	2	0	0	0
ST8327-IV	CC97	-	WR/AK1	2	2	0	0	0
ST22-IV	CC22	-	-	2	2	0	0	0
ST59-IV	CC59	-	-	2	1	0	1	0

1 The MRSA clones are only listed if there were ≥2 isolates of the type. There was one PVL-positive CC93 ST8329-IV isolate. Details of 13 PVL-negative isolates with clonal complex/SCC*mec* combinations found in one isolate each are: CC1 ST1-I; CC5 ST5-II, CC5 ST1649-IV, CC5 ST8326-IV, CC5 ST8330-IV and CC5 ST8331-IV; CC8 ST8-V; CC45 ST45-IV, CC59 ST59-V; CC398 ST398-V; CC188 ST188-IV; unassigned clones ST779-IV and ST8332-IV.

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

3 Ten MRSA isolates from the Te Manawa Taki region (former Waikato DHB) were not referred to ESR for molecular testing.

7. LIMITATIONS

Our data represent only patients for whom a *S. aureus* isolate was referred to ESR, and for which there was a public hospitalisation record available. This survey will likely underrepresent the true burden of SAB, given it relied on voluntary isolate referrals, 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. The length of hospital stay used in the report was independent of when SAB was diagnosed, which limited our ability to determine the impact of SAB diagnosis on length of hospital stay. Our survey analysis was further limited by our inability to accurately attribute clinical infection source or risk factors for every SAB case 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). An HQSC study of patient records from 2017-2021 identified 893 hospital-associated SAB cases, of which 65% related to medical device (central venous catheter or peripheral intravenous catheter) and 12% 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. We were also limited in our ability to generate insights from whole genome sequencing. Future work is planned to analyse a subset of isolates from this study, particularly for paediatric and HA-SAB cohorts to identify if any previously unrecognised clusters or trends e.g. dialysis cohorts and to identify virulence genes associated with SAB.

8. DISCUSSION

This is the first in a series of three annual surveys of *S. aureus* from people 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 from this study are not directly comparable with previous *S. aureus* (Heffernan *et al*. 2015) or previous MRSA surveillance in New Zealand (Heffernan and Bakker, 2018), but information on the molecular epidemiology can be compared.

The 2021 study on *S. aureus* bacteraemia has highlighted several findings. The most significant of these are the large diversity of *S. aureus* clones circulating in New Zealand, the geographical distribution of MRSA from SAB in New Zealand, and the substantial inequities in the incidence of SAB by socioeconomic deprivation and ethnicity.

This survey identified 1471 cases of SAB in New Zealand in 2021. The onset for the majority of SAB cases was in the community (69.4%) and the majority were MSSA (90.3%).

We observed that almost two-thirds of all SAB cases were male and more than 40% of all SAB cases were aged over 65 years. Most cases belonged to the European or Other ethnic group. However, age standardised rates of SAB cases in Pacific people were nearly 16 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.

The burden of SAB also increased with increasing socioeconomic deprivation index.

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). Despite the limitations with interpreting ICD-10-AM diagnostic codes, tobacco smoking was the most commonly identified risk factor or comorbidity associated with SAB, followed by diabetes and obesity. Use of vascular catheters and prosthetics/implantables was also common in 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 wound care, diabetes management, device management, dialysis lines care and IPC measures within hospitals. Ideally investigation of an effective vaccine to prevent *S. aureus* infections should also be investigated.

There were low levels of antimicrobial resistance in isolates from SAB cases. A total of 9.7% of isolates were MRSA, which is lower than the rate of MRSA reported in Australia (Coombs et al, 2023). When compared to European data New Zealand ranks 15th out of 29 countries contributing to the European Antimicrobial Resistance Surveillance network program (https://atlas.ecdc.europa.eu/public/index.aspx), with country 1 having the highest rates of MRSA. Multidrug resistance was more common in MRSA isolates and in cases with hospital-associated SAB.

Characterisation of MRSA using whole genome sequencing-based methods provided a comprehensive assessment of the genetic diversity of the MRSA strains causing SAB in New Zealand. It also facilitated identification of MRSA clones causing infection and easier comparison to international data, compared to the *spa* typing and DNA macrorestriction methods used previously in New Zealand surveillance activities (Heffernan and Bakker, 2018 and 2016, Heffernan *et al*. 2015)).

The ST5-IV clone (AK3) was the most common MRSA, and most commonly associated with *spa* type t002. The next most prevalent clones were the ST93-IV (Queensland clone) and the ST97-IV (WR/AK1), which were commonly associated with the t3949 and t359 *spa* types respectively. Together these three strains accounted for 59.1% of isolates. The AK3, Queensland clone and WR/AK1 MRSA were also the dominant MRSA strains found in New Zealand surveillance studies in 2017 and 2015 (Heffernan and Bakker, 2016 and 2018). However, in contrast to previous surveys the most common WR/AK1 MRSA in this study were ST97-IV, whereas in previous surveys ST1-IV were common (Heffernan and Bakker, 2016 and 2018). While all three of these clones are found in Australia (Coombs et al, 2023), the prevalence of each differs compared to that found in New Zealand.

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 the much higher genetic diversity of MSSA SAB compared to MRSA SAB.

All PVL positive isolates belonged to four MRSA clones (ST93-IV (Queensland clone), ST8-IV (USA300), ST30-IV (WSPP), ST22-IV). MRSA were more likely to be PVL-positive, as were isolates from CA-SAB. PVL status was strongly associated with MRSA clone ST93-IV, the Queensland clone. The percentage of MRSA that were PVL positive in 2021 (25.8%) was lower than what was found in both 2017 (34.1%) and 2015 (30.1%) (Heffernan and Bakker, 2018 and 2016)

Despite the source of the isolates being different in this study compared to previous studies, that included isolates from all clinical site (Heffernan and Bakker, 2018) or all sites, including

screening isolates (Heffernan and Bakker, 2016), there were a number of parallels in the data. High levels of community-associated *S. aureus* were reported in all studies, as well as higher numbers of cases in the northern regions of New Zealand. High age standardised rates continue to be found in people of Pasifika and Māori ethnicities as well as in people with high levels of deprivation. The most common strains found in this study is consistent with previous surveillance reports (Heffernan and Bakker, 2018 and 2016), despite the source of the isolates being different. As was found in previous studies MRSA clones associated with the AK3 strain were had high rates of fusidic acid resistance.

Ongoing surveillance of SAB is necessary to inform further refinement of prevention and treatment strategies, most notably in hospitals. 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 *S. aureus* in New Zealand is inequitable with the highest burden borne by the most vulnerable populations (i.e., Māori, Pacific Peoples, and those with the greatest material deprivation). We provide greater insight into the epidemiological and molecular characteristics of CA-SAB in New Zealand and compare these to HA-SAB. The data produced and analysed for this report form an invaluable resource for ongoing surveillance of SAB in NZ. Isolates collected in further surveys will be able to be compared to this 'baseline' data, with analyses helping to describe trends in SAB and refine public health strategies, targeted interventions, and research.

9. RECOMMENDATIONS

- There is a need for ongoing epidemiological and molecular surveillance of isolates from SAB in New Zealand.
- Targeted strategies to prevent SAB should be developed, including those related to wound care, diabetes management, device management, dialysis lines care and IPC measures within hospitals. These must be culturally safe and designed to meet the needs of Māori and Pacific peoples who are disproportionately impacted by SAB and its complications.

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11. GLOSSARY

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.

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*).

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.

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.

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. aureu*s 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.

MRSA strain

As described in section 12.5, 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. MRSA strains are referred to in this report so data in earlier New Zealand surveillance reports can be compared. However, if data is available to define the MRSA clone this is used preferentially. Common MRSA strains in New Zealand, and their relationship to MRSA clones is outlined in Table A1

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

12. APPENDIX A: METHODS

12.1 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.

12.2 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, 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 the European Committee on Antimicrobial Susceptibility Testing (EUCAST), except for Middlemore Hospital laboratory which utilised the Clinical & Laboratory Standards Institute (CLSI) guidelines.

12.3 *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 ESR had not yet correlated to an MRSA strain.

PFGE of *Sma*I-digested genomic DNA was performed as described by Goering et al. (Goering RV, 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.

12.4 WHOLE GENOME SEQUENCING

All 2021 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/bigsdb?db=pubmlst_saureus_seqdef). SCC*mec* elements were identified using KmerFinder v3.0.2 and the SCC*mec* 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). Ridom SeqSphere+ version 10.0 was used to determine the core genome MLST (cgMLST) Complex Type.

12.5 ASSIGNING MRSA STRAINS

In this report, MRSA strain designation of MRSA isolates was performed primarily using *spa* typing and antimicrobial susceptibility data, with PFGE used as a supplementary tool for situations described in section 12.3.

Historically, strain names for an isolate, which are still frequently referred to, were generated using phage typing data and an antibiogram as well as information on the geographical locations and order of outbreak. For example, AK3 MRSA was first found in Auckland (AK, index strain 2005) and was the third MRSA outbreak in the region, and was typically susceptible to ciprofloxacin and resistant to fusidic acid. As molecular methods were developed, PFGE typing and PCR base methods for *spa* typing and *SCCmec* typing replaced phage typing.

Whole genome sequencing-based methods are now mainstream, and the data generated provides a high level of discrimination, making the method the gold standard (Lakhundi 2018).

WGS data can provide the *spa* type, sequence type, cgMLST Complex Type and SCC*mec* type. Although still frequently used, and sometimes interchangeably, MRSA strain name has

been superseded by the development of international molecular-based nomenclature for tracking clones of *S. aureus* and in particular MRSA, which lists the sequence type (ST) and for MRSA, the Staphylococcal Cassette Chromosome *mec* (SCC*mec* type). There are 14 documented SCC*mec* 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 SCC*mec* 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	*spa* type(s)	Typical antimicrobial resistance pattern	PVL	Epidemiology
Hospital-associated MRSA clones:					
ST239-III	AKh4 Alternative names: EMRSA-1, AUS-2 EMRSA 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.
ST36-II	EMRSA-16	t018	Resistant to ciprofloxacin and erythromycin	Negative	Originated in the UK
Community-associated MRSA clones:					
ST5-IV	AK3	t002	Non-multiresistant, with variable susceptibility but often fusidic acid or erythromycin resistant or only resistant to β-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 β-lactams only	Positive	Dominant community-associated MRSA in Australia.
ST8-IV	USA300	t008	Resistant to ciprofloxacin and/or erythromycin	Positive	Widely disseminated in the USA. Isolated from community and hospital patients throughout NZ.

Table A1 continued

MRSA clone	MRSA strain	*spa* type(s)	Typical antimicrobial resistance pattern	PVL	Epidemiology
ST1-IV	WR/AK1 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) Alternative name Southwest Pacific clone and Oceania clone	t019	Resistant to β-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.
ST78-IV	WA MRSA-2	t186	Resistant to β-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
Livestock-associated MRSA clone:					
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

12.6 DATA ANALYSIS

Patient information and susceptibility testing results were entered into ESR's laboratory information management system. Data cleaning and statistical tests were performed in R version 4.1.0 (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. We compared variables using statistical methods. For categorical variables we used the Fisher's exact test or chi-square test.

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.tewhatuora.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 2021 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 2021 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).

13. APPENDIX B: ICD-10 CODES

13.1 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, 10th 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[1]	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

14. APPENDIX C: SUPPLEMENTARY TABLES

Table C1. Rates of SAB cases by region, stratified by place of onset, 2021

	Region														
	Overall			Northern			Te Manawa Taki			Central			Te Waipounamu		
Place of onset	No.	Rate	(95% CI)	No.	Rate	(95% CI)	No.	Rate	(95% CI)	No.	Rate	(95% CI)	No.	Rate	(95% CI)
Total	1471	28.8	(27.3 - 30.3)	569	29.5	(27.1 - 32.0)	304	30.0	(26.6 - 33.3)	323	33.2	(29.6 - 36.8)	274	22.9	(20.2 - 25.6)
CA-SAB	1021	20.0	(18.7 - 21.2)	400	20.8	(18.7 - 22.8)	222	21.9	(19.0 - 24.7)	208	21.4	(18.5 - 24.3)	191	16.0	(13.7 - 18.2)
HA-SAB	450	8.8	(8.0 - 9.6)	169	8.8	(7.4 - 10.1)	82	8.1	(6.3 - 9.8)	115	11.8	(9.7-14.0)	83	6.9	(5.4 - 8.4)

Table C2. Age and ethnicity of SAB cases stratified by place of onset, 2021

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	62	20.3	(15.3 - 25.4)	26	30.9	(19 - 42.8)	14	47.4	(22.5 - 72.2)	9	16.5	(5.7 - 27.3)	13	9.9	(4.5 - 15.3)
5-14	72	10.9	(8.4 - 13.4)	27	15.2	(9.5 – 21.0)	18	27.9	(15.0 - 40.8)	6	6.7	(1.3 - 12)	21	6.5	(3.7 - 9.3)
15-24	58	9.0	(6.7 - 11.3)	21	14.8	(8.5 - 21.1)	10	16.3	(6.2 - 26.3)	4	3.7	(0.1 - 7.4)	23	7.1	(4.2 – 10.0)
25-34	76	10.1	(7.8 - 12.4)	27	22.0	(13.7 - 30.3)	13	24.3	(11.1 - 37.5)	8	4.3	(1.3 - 7.3)	28	7.5	(4.8 - 10.3)
35-44	93	14.2	(11.3 - 17.1)	31	32.1	(20.8 - 43.4)	21	49.0	(28.0 – 70.0)	5	3.8	(0.5 - 7.1)	36	9.8	(6.6 – 13.0)
45-54	166	25.4	(21.5 - 29.2)	42	46.2	(32.2 - 60.2)	31	80.0	(51.8 - 108.2)	8	9.7	(3.0 - 16.4)	85	19.6	(15.4 - 23.7)
55-64	266	42.9	(37.7 – 48.0)	62	85.4	(64.2 - 106.7)	36	134.4	(90.5 - 178.3)	13	19.7	(9.0 - 30.3)	155	34.4	(29 - 39.8)
≥65	675	82.6	(76.3 - 88.8)	76	136.8	(106.0 - 167.5)	39	167.8	(115.1 - 220.5)	20	36.2	(20.3 - 52)	540	79.4	(72.7 - 86.1)
Total cases and crude rate [1]	1,471	28.8	(27.3 - 30.2)	312	36.6	(32.6 - 40.7)	182	52.8	(45.1 - 60.4)	73	9.4	(7.2 - 11.6)	904	29.5	(27.6 - 31.4)
Age-standardised rate [2]		4.8	(4.6 - .05)		36.6	(32.6 - 40.7)		130.4	(111.5 - 149.3)		10.3	(7.9 - 12.7)		8.2	(7.7 - 8.7)
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	39	12.8	(8.8 - 16.8)	17	20.2	(10.6 - 29.8)	11	37.2	(15.2 - 59.2)	4	7.3	(0.1 - 14.5)	7	5.3	(1.4 - 9.3)
5-14	60	9.1	(6.8 - 11.3)	21	11.9	(6.8 - 16.9)	18	27.9	(15.0 - 40.8)	6	6.7	(1.3 – 12.0)	15	4.7	(2.3 – 7.0)
15-24	38	5.9	(4.0 - 7.8)	15	10.6	(5.2 - 15.9)	8	13.0	(4.0 - 22.0)	3	2.8	(-0.4 – 6.0)	12	3.7	(1.6 - 5.8)
25-34	51	6.8	(4.9 - 8.6)	14	11.4	(5.4 - 17.4)	11	20.5	(8.4 - 32.7)	5	2.7	(0.3 – 5.0)	21	5.7	(3.2 - 8.1)
35-44	62	9.5	(7.1 - 11.9)	23	23.8	(14.1 - 33.6)	13	30.3	(13.8 - 46.8)	1	0.8	(-0.7 - 2.2)	25	6.8	(4.1 - 9.5)
45-54	117	17.9	(14.6 - 21.1)	29	31.9	(20.3 - 43.5)	24	61.9	(37.2 - 86.7)	5	6.1	(0.7 - 11.4)	59	13.6	(10.1 - 17.1)
55-64	193	31.1	(26.7 - 35.5)	53	73.0	(53.4 - 92.7)	30	112.0	(71.9 - 152.1)	6	9.1	(1.8 - 16.3)	104	23.1	(18.6 - 27.5)
≥65	458	56.0	(50.9 - 61.2)	54	97.2	(71.3 - 123.1)	29	124.8	(79.4 - 170.2)	14	25.3	(12.1 - 38.6)	361	53.1	(47.6 - 58.5)
Total cases and crude rate [1]	1,021	20.0	(18.7 - 21.2)	226	26.5	(23.1 – 30.0)	144	41.8	(34.9 - 48.6)	44	5.7	(4.0 - 7.3)	607	19.8	(18.2 - 21.4)
Age-standardised rate [2]		3.3	(3.1 - 3.5)		26.5	(23.1 – 30.0)		103.1	(86.3 - 119.9)		6.2	(4.4 - 8)		5.5	(5.1 - 5.9)

Table C2 continued

Hospital-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	23	7.5	(4.5 - 10.6)	9	10.7	(3.7 - 17.7)	3	10.1	(-1.3 - 21.6)	5	9.2	(1.1 - 17.2)	6	4.6	(0.9 - 8.2)
5-14	12	1.8	(0.8 - 2.8)	6	3.4	(0.7 - 6.1)							6	1.9	(0.4 - 3.4)
15-24	20	3.1	(1.7 - 4.5)	6	4.2	(0.8 - 7.6)	2	3.3	(-1.3 - 7.8)	1	0.9	(-0.9 - 2.8)	11	3.4	(1.4 - 5.4)
25-34	25	3.3	(2.0 - 4.6)	13	10.6	(4.8 - 16.4)	2	3.7	(-1.4 - 8.9)	3	1.6	(-0.2 - 3.4)	7	1.9	(0.5 - 3.3)
35-44	31	4.7	(3.1 - 6.4)	8	8.3	(2.5 - 14)	8	18.7	(5.7 - 31.6)	4	3.0	(0.1 - 6)	11	3.0	(1.2 - 4.8)
45-54	49	7.5	(5.4 - 9.6)	13	14.3	(6.5 - 22.1)	7	18.1	(4.7 - 31.4)	3	3.6	(-0.5 - 7.7)	26	6.0	(3.7 - 8.3)
55-64	73	11.8	(9.1 - 14.5)	9	12.4	(4.3 - 20.5)	6	22.4	(4.5 - 40.3)	7	10.6	(2.7 - 18.4)	51	11.3	(8.2 - 14.4)
≥65	217	26.5	(23 - 30.1)	22	39.6	(23.1 - 56.1)	10	43	(16.4 - 69.7)	6	10.9	(2.2 - 19.5)	179	26.3	(22.5 - 30.2)
Total cases and crude rate [1]	450	8.8	(8.0 - 9.6)	86	10.1	(8.0 - 12.2)	38	11	(7.5 - 14.5)	29	3.7	(2.4 - 5.1)	297	9.7	(8.6 - 10.8)
Age-standardised rate [2]		1.5	(1.4 - 1.6)		10.1	(8.0 - 12.2)		27.2	(18.6 - 35.8)		4.1	(2.6 - 5.6)		2.7	(2.4 - 3.0)

1 Age information is missing for one Māori CA-SAB case, two Pacific Peoples CA-SAB cases., and five European or Other CA-SAB cases.
2 Age-standardised rates are directly standardised to the Māori population

Table C3. Age-standardised 30-day mortality rates among SAB cases stratified by place of onset and ethnicity, 2021

	All SAB		Community-associated SAB		Hospital-associated SAB	
Ethnicity	**No.**	**Rate (95% CI)[1]**	**No.**	**Rate (95% CI)[1]**	**No.**	**Rate (95% CI)[1]**
Māori	34	4 (2.7 - 5.3)	20	2.3 (1.3 - 3.3)	14	1.6 (0.8 - 2.4)
Pacific peoples	16	11.5 (5.9 - 17.1)	12	8.6 (3.7 - 13.5)	4	2.9 (0.1 - 5.7)
Asian	2	0.3 (-0.1 - 0.7)	2	0.3 (-0.1 - 0.7)	-	-
European or Other	145	1.3 (1.1 - 1.5)	95	0.9 (0.7 - 1.1)	50	0.5 (0.4 - 0.6)
Total	197	0.6 (0.5 - 0.7)	129	0.4 (0.3 - 0.5)	68	0.2 (0.2 - 0.2)

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

Table C4: Summary of typing results for MRSA clone-*spa* type combinations found in one isolate[1]

MRSA clone-	MRSA strain	*spa* type
ST5-IV	AK3	t010, t045, t088, t2366, t306, t5213, t8784
ST5662-IV	AK3	t045
ST149-IV	AK3	t002, t045
ST8326-IV	AK3	t045
ST8330-IV	AK3	t002, t045
ST8331-IV	AK3	t2905
ST97-IV	WR/AK1	t1418, t224, t2297, t267
ST1-I	WR/AK1	t127
ST93-IV	ST8329-IV	t14922, t15361
ST8329-IV	ST8329-IV	t3949
ST8-IV	USA300	t1767
ST22-IV	EMRSA-15	t025, t032, t20048
ST30-IV	WSPP	t019, t021, t975
ST6-IV	unrecognised strain	t701
ST5-V	unrecognised strain	t442
ST59-IV	unrecognised strain	t172, t976
ST1649-IV	unrecognised strain	t701
ST188-IV	unrecognised strain	t189
ST45-IV	unrecognised strain	t026
ST5-II	unrecognised strain	t002
ST5-IV	unrecognised strain	t002
ST59-V	unrecognised strain	t9003
ST779-IV	unrecognised strain	t5502
ST8-IV	unrecognised strain	t008
ST8-V	unrecognised strain	t648
ST8332-IV	unrecognised strain	t976

1 See Table 14 for details of MRSA clone-*spa* type combinations found in two or more isolates.

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