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2017 survey of methicillin-resistant *Staphylococcus aureus* (MRSA)

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Introduction

Each year between 2000 and 2015, ESR conducted annual surveys of methicillin-resistant *Staphylococcus aureus* (MRSA). For these surveys, hospital and community microbiology laboratories in New Zealand were asked to refer all MRSA isolated during a one-month period to ESR. MRSA isolated from both clinical specimens and surveillance/screening specimens were included in these surveys. The purpose of the annual surveys is to provide information on the epidemiology of MRSA in New Zealand and to monitor changes over time.

Commencing with this 2017 survey, several changes have been made to the national surveillance of MRSA. Surveys will no longer be conducted annually and consequently there was no survey in 2016. **Only isolates from clinical specimens will be collected and included in the surveys**. An extended range of analyses will be undertaken, including more analysis of the demographics of patients. The change to include only clinical isolates means that data in this report is not directly comparable with the data presented in reports for earlier MRSA surveys, which are available at https://surv.esr.cri.nz/antimicrobial/mrsa_annual.php.

Methods

MRSA isolates and data collection

Hospital and community diagnostic microbiology laboratories in New Zealand were asked to refer all MRSA isolated from clinical specimens during August 2017 to ESR. The Microbiology Laboratory, Middlemore Hospital, and Pathlab Bay of Plenty referred isolates during a 31-day period between mid-August and late-September 2017. All remaining laboratories referred MRSA during August 2017.

When referring isolates for the survey, laboratories were asked to supply selected epidemiological data, including the patient's date of birth, geographic location, hospitalisation status and history, and the body site from which the MRSA was isolated. Laboratories were also asked to provide, where available, information on the susceptibility of the MRSA isolate to the following non-β-lactam antibiotics: ciprofloxacin, co-trimoxazole, erythromycin, fusidic acid, gentamicin, mupirocin, rifampicin and tetracycline. Information on the patient's ethnicity and NZDep2013 deprivation index score was obtained from the Ministry of Health's national data collections. Additional DHB domicile information and hospitalisation history information was also obtained from the Ministry of Health's datasets. Patients from whom MRSA were isolated were categorised as hospital patients if they were inpatients in a healthcare facility (including a long-term care facility) when MRSA was isolated or had been in a healthcare facility in the previous three months. All other patients were categorised as community patients.

PCR for mecA, mecC, nuc *and* lukS-*PV genes*

A real-time PCR assay was used to detect *mecA; mecC;* the *S. aureus* species-specific thermostable nuclease gene, *nuc;* and one of the two genes encoding Panton-Valentine leukocidin (PVL), *lukS*-PV.[1] Only isolates that were confirmed as MRSA by the detection of *nuc* and either *mecA* or *mecC* were included in the survey.

While only the *lukS*-PV gene was targeted in the PCR assay, isolates in which *lukS*-PV was detected were assumed to have both PVL genes. For convenience, isolates positive for the *lukS*-PV gene are termed 'PVL positive' in this report and isolates in which the *lukS*-PV gene was not detected are termed 'PVL negative'.

spa *typing and based upon repeat pattern (BURP) analysis*

The polymorphic X region of the staphylococcal protein A gene (*spa*) was amplified as previously described.[2] PCR products were sequenced by the Sequencing Laboratory at ESR using an ABI 3130XL Sequencer. *spa* sequences were analysed using Ridom StaphType software version 2.2.1 (Ridom GmbH, Würzburg, Germany). Sequences were automatically assigned repeats and *spa* types using the software. Clustering of clonal complexes of related *spa* types (Spa-CCs) was performed using the based upon repeat pattern (BURP) algorithm of the Ridom StaphType software and the default settings of the software which exclude *spa* types with less than five repeats and allow a maximum four costs to cluster *spa* types into the same Spa-CC.[3]

Pulsed-field gel electrophoresis (PFGE) and profile analysis

PFGE of *Sma*I-digested genomic DNA was performed as previously described.[4] PFGE banding patterns were analysed using BioNumerics software version 7.6 (Applied Maths, St-Martens-Latem, Belgium), with the Dice coefficient and unweighted-pair group method with arithmetic averages, at settings of 0.5% optimisation and 1.5% position tolerance. PFGE banding patterns were interpreted using the criteria proposed by Tenover et al.[5]

Multilocus sequence typing (MLST) and sequence analysis

MLST was performed as previously described.[6] Sequences were analysed using BioNumerics software version 7.6 and sequence types (STs) were assigned using the *S. aureus* database accessible at http://saureus.mlst.net/.

Antibiotic susceptibility testing

Antibiotic 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).[7]

Assigning MRSA strains

Isolates were characterised primarily based upon *spa* types and antibiotic susceptibility patterns, with PFGE 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 antibiotic susceptibility pattern did not; (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.

Epidemiological analyses

Epidemiological data and test results were entered into ESR's laboratory information management system. Statistical analyses were performed with SAS software v.9.4 (SAS Institute Inc, Cary, NC, United States). Period-prevalence rates were calculated based on the number of MRSA isolated per 100 000 population during the period of the survey. Mid-year New Zealand population estimates were used to calculate these prevalence rates. The chi-square test was used to determine the significance of any observed differences and a *p* value of ≤ 0.05 was considered significant. Poisson distribution was used to estimate 95% confidence intervals. The statistical significance of time trends was calculated at a 95% confidence level using Poisson regression and the Mantel-Haenszel test for linear trend.

For surveys conducted before 2014, information was not specifically recorded on whether the MRSA was from a clinical specimen as opposed to a screening/surveillance specimen, but rather information was recorded on whether the MRSA was isolated from an infected site or a colonised site. In this report, any data for years before 2014 uses MRSA from infected sites as a proxy for MRSA from clinical specimens. Therefore, the data for these earlier years are not directly comparable with that for the years 2014-2017, and are likely to be underestimates of MRSA isolated from clinical specimens as some MRSA designated to be from colonised sites will have been isolated from clinical specimens.

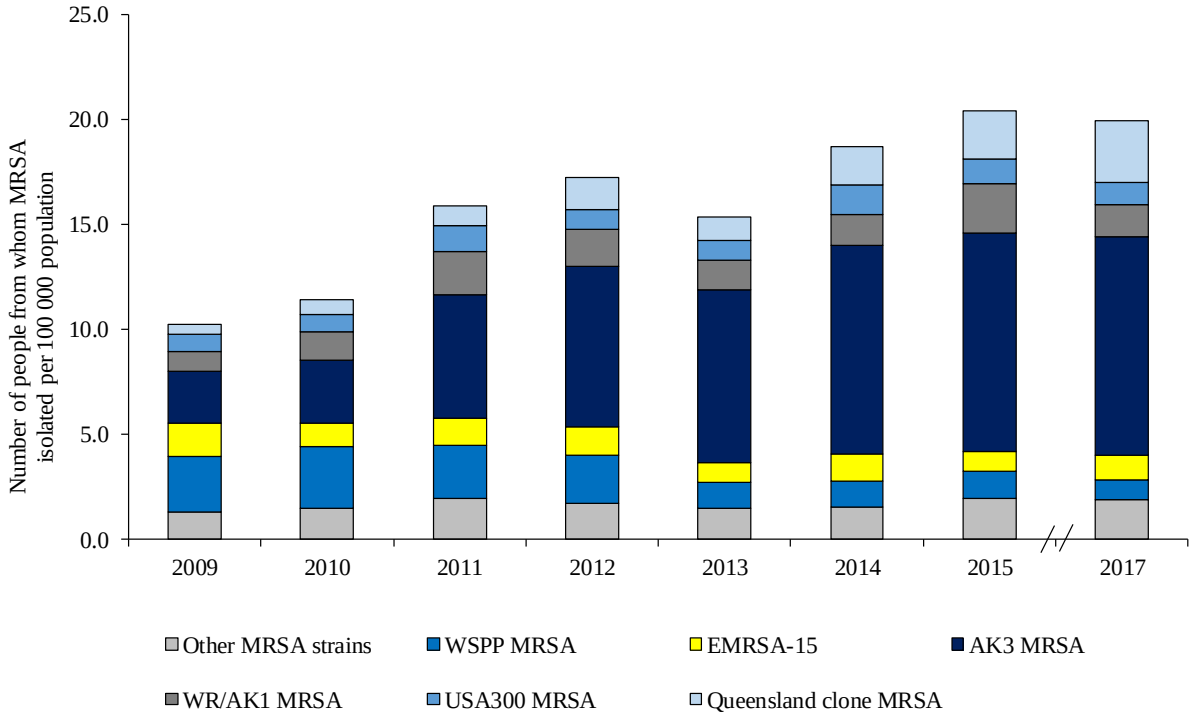
Results

During the 1-month period of the 2017 survey, MRSA were isolated from clinical specimens from 956 patients which equates to a national period-prevalence rate of 19.9 patients with MRSA per 100 000 population. All methicillin resistance was mediated by *mecA* with no *mecC* genes detected.

National period-prevalence rates of MRSA, 2009-2017

The 2017 period-prevalence rate (19.9 per 100 000) was similar to the rate of 20.4 recorded for the last survey in 2015. Over the years 2009 to 2017, the period-prevalence rate appears to have almost doubled from 10.2 to 19.9 per 100 000 (Figure 1), although the rate estimated for 2009 is likely to be an underestimate of MRSA isolated from clinical specimens as MRSA from infected sites were used as a proxy for MRSA from clinical specimens.

Figure 1. MRSA period-prevalence rates, 2009-2017



Rates presented in this graph are period-prevalence rates based on the number of isolates received during the 1-month duration of the surveys. Rates are based on MRSA isolated from clinical specimens only for the years 2014-2017. As data was not specifically collected on which MRSA were from clinical specimens as opposed to screening/surveillance specimens for the surveys conducted between 2009 and 2013 inclusive, MRSA isolates in these years that were specified as being from an infected site, rather than a colonised site, have been used as a proxy for MRSA from clinical specimens. There was no survey conducted in 2016.

Patient demographics

In 2017, of the 956 patients with MRSA, 89.2% were categorised as community patients and 10.8% as hospital patients. 90.8% (868) of the MRSA were isolated from skin and soft tissue infection (SSTI), 2.7% (26) from respiratory sources, 1.7% (16) from ears, 1.5% (14) from invasive sites, 1.5% (14) from urogenital specimens, 1.3% (12) from eyes, and the remaining 0.6% (6) from various diagnostic specimens.

The period-prevalence rate of MRSA was highest in the youngest age group (0-4 years) with the rate in this age group (54.6 per 100 000 population) almost twice that in any other age group (Table 1). The prevalence of MRSA by age was markedly different for the European and Other ethnic group, with the rate being highest in the oldest age group for this ethnic group whereas for other ethnic groups the rates were highest in the youngest age group.

The age-standardised rates were highest in the Pacific peoples and Māori ethnic groups, with the rates for these groups approximately 7 and 3 times, respectively, the rate for the European or Other ethnic group (Table 1). This difference in rates by ethnicity was particularly evident in the youngest age group, with rates for Pacific (179.1 per 100 000) and Māori (93.4 per 100 000) children under 5 years of age being 15 and 8 times, respectively, the rate for children of this age belonging to the European or Other ethnic group (11.8 per 100 000).

Table 1. Age and ethnicity of patients with MRSA isolated from a clinical specimen, 2017

Age group (years)	Māori		Pacific peoples		Asian		MELAA[1]		European or Other		Total[2]	
	No.	Rate[3]	No.	Rate	No.	Rate	No.	Rate	No.	Rate	No.	Rate
0-4	77	93.4	54	179.1	17	46.6	1	22.9	18	11.8	167	54.6
5-14	52	33.2	53	88.5	11	17.1	2	26.9	30	8.8	148	23.6
15-24	34	24.9	33	57.1	5	5.0	1	10.7	38	10.3	112	16.7
25-64	107	33.4	79	56.6	27	8.2	5	16.2	103	6.3	328	13.3
≥65	18	42.6	16	86.7	5	13.7	0	0.0	161	25.8	201	27.8
Total cases and crude rate	288	38.5	235	76.2	65	11.6	9	16.7	350	11.2	956	19.9
Age-standardised rate[4]		37.4		73.2		12.2		14.8		10.5		

1 Middle Eastern/Latin American/African.

2 Ethnicity not known for 9 (0.9%) patients: 1 patient in each of the 15-24 and ≥65 years age groups, and 7 patients in the 25-64 years age group. These 9 patients are included in the total numbers and rates for each age group.

3 1-month period-prevalence rate per 100 000 population. The denominator data used to determine disease rates for ethnic groups is based on the proportion of patients in each ethnic group from the usually resident 2013 census population applied to the 2017 mid-year population estimates from Statistics New Zealand. Ethnicity is prioritised in the following order: Māori, Pacific peoples, Asian, MELAA and European or Other ethnicity (including New Zealander). Caution should be used when considering rates based on small numbers of cases.

4 The age-standardised rates are direct standardised to the age distribution of the total New Zealand population.

Analysis by NZDep2013 deprivation index score showed that nearly one half of patients belonged to the most deprived quintile (ie, quintile 5). The distribution of patients in each quintile was: quintile 5, 47.2%; quintile 4, 17.7%; quintile 3, 14.7%; quintile 2, 11.7%; and quintile 1 (least deprived), 8.7%.

Patient demographics and association with MRSA strains

Six MRSA strains (AK3 MRSA, Queensland clone MRSA, WR/AK1 MRSA, EMRSA-15, USA300 MRSA and WSPP MRSA) were predominant in 2017 and collectively represented 90.6% of all MRSA (Table 2).

The dominance of the community-associated AK3 MRSA strain evident in recent years continued in 2017, but appears to have stabilised and has accounted for approximately 50% (range 51.0-53.4%) of the MRSA included in each survey since 2013 (Figure 1). The Queensland clone MRSA was the second most prevalent strain in 2017, and this strain has

increased in recent years from 9.7% of MRSA in 2014 to 14.7%. No other strain represented >10% of the MRSA in 2017 (Table 2).

There were some significant associations between some MRSA strains and particular patient groups. The AK3 strain was significantly (p <0.001) more prevalent among patients <5 years of age and among Māori, accounting for 69.5% and 70.8% of MRSA in this age group and ethnic group respectively, compared with 52.0% of MRSA overall. The Queensland clone MRSA was significantly (p <0.001) more prevalent among patients in the 15-64 years age groups and among Pacific peoples, accounting for 22.3% and 36.6% of MRSA in these age groups and ethnic group, respectively, compared with 14.7% of all MRSA. In addition, the EMRSA-15 (p <0.001) and USA300 MRSA (p 0.034) strains were both more prevalent in the oldest age group (≥65 years of age) accounting for 15.4% and 8.5% of MRSA in this age group compared with 6.0% and 5.4%, respectively, of all MRSA.

Table 2. MRSA strain prevalence and association with patient demographics, 2017

Strain[2]	Number (% of all MRSA isolations) n = 956	Proportion (%) of MRSA within each demographic group due to each strain							
			Age group		Ethnic group[1]				Deprivation score
		Community patients[3] n = 723	Patients <5 years of age n = 167	Patients ≥65 years of age n = 201	Māori n = 288	Pacific peoples n = 235	Asian n = 65	European or Other n = 350	NZDep13 quintile 5[4] n = 449
AK3 MRSA [ST5, SCC*mec* type IV[5]]	497 (52.0)	53.3	69.5	45.8	70.8	44.3	24.6	47.7	58.6
Queensland clone MRSA [ST93, SCC*mec* type IV]	141 (14.7)	15.6	9.0	4.0	9.7	36.6	4.6	5.4	17.1
WR/AK1 MRSA [ST1, SCC*mec* type IV]	73 (7.6)	7.2	6.0	11.0	4.9	6.4	7.7	10.6	5.3
EMRSA-15 [ST22, SCC*mec* type IV]	57 (6.0)	5.0	3.0	15.4	4.2	0.9	15.4	8.6	4.2
USA300 MRSA [ST8, SCC*mec* type IV]	52 (5.4)	5.0	2.4	8.5	2.8	5.1	3.1	8.3	4.7
WSPP MRSA [ST30, SCC*mec* type IV]	46 (4.8)	5.3	3.0	2.5	2.4	2.6	21.5	5.4	4.2
Other strains	90 (9.4)	8.4	7.2	12.9	5.2	4.3	23.1	14.0	5.8

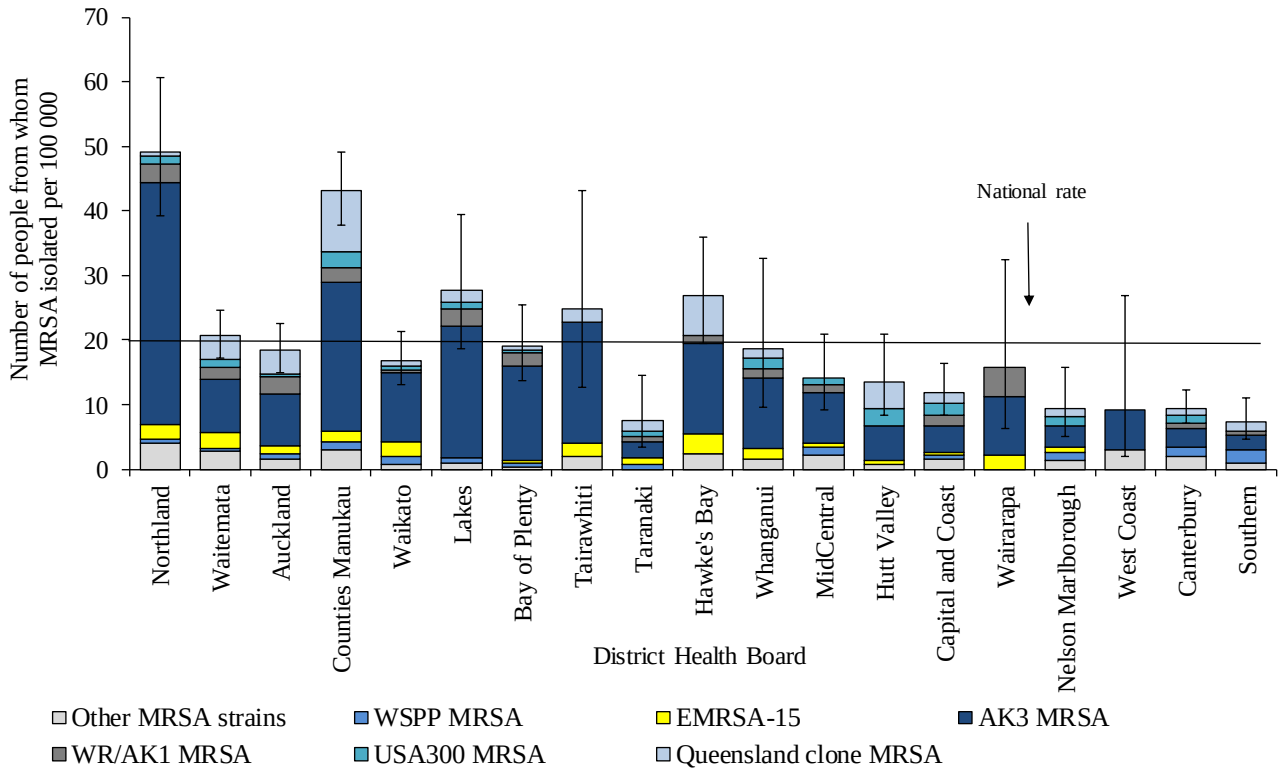
1 Data for the Middle Eastern/Latin American/African ethnic group not included as there were only 9 patients in this ethnic group.
2 Further information on each of these strains is available at: http://www.esr.cri.nz/assets/HEALTH-CONTENT/Images-and-PDFs/MRSAdescriptions.pdf.
3 Patients were categorised as community patients if they were not an inpatient in a healthcare facility (including a long-term care facility) when MRSA was isolated or had not been in a healthcare facility in the previous three months.
4 NZDep13 quintile 5 represents the most deprived group.
5 ST, multilocus sequence type; SCC*mec*, staphylococcal cassette chromosome *mec*.

Geographic distribution of MRSA

There were significant geographical differences in the period-prevalence rates of MRSA in 2017. Rates exceeded the national rate of 19.9 patients with MRSA from a clinical specimen per 100 000 population in six North Island district health boards (DHBs): Northland (49.0 per 100 000), Counties Manukau (43.2), Lakes (27.6), Hawke's Bay (26.8), Tairawhiti (24.7) and Waitemata (20.6) (Figure 2).

AK3 MRSA was the most prevalent MRSA strain in all DHBs except Southern where AK3 MRSA and WSPP MRSA were equally prevalent. Notably, AK3 MRSA accounted for around three-quarters of the MRSA in the Northland, Bay of Plenty and Lakes DHBs.

Figure 2. MRSA period-prevalence rates by district health board, 2017

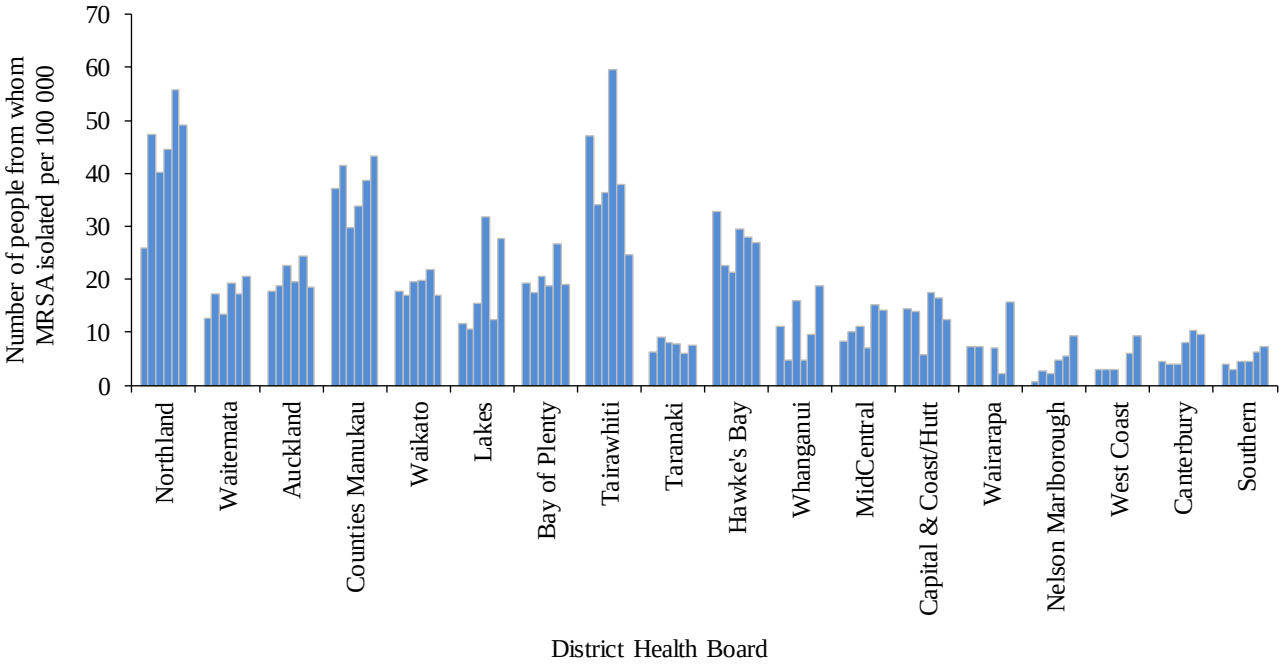


95% confidence intervals indicated by error bars. Data for the Canterbury and South Canterbury DHBs are combined as 'Canterbury'.

Period-prevalence rates of MRSA by district health board, 2011-2017

Over the 6-year period 2011 to 2017, there were significant increasing trends in MRSA in the Nelson Marlborough, Canterbury and Southern DHBs, and increasing trends of borderline statistical significance in the Northland, Waitemata and Lakes DHBs (Figure 3).

Figure 3. MRSA period-prevalence rates by district health board, 2011-2017



The series of bars for each DHB represent the individual years 2011, 2012, 2013, 2014, 2015 and 2017 from left to right. There was no survey conducted in 2016. Data for the Capital & Coast and Hutt DHBs are combined as 'Capital & Coast/Hutt', and data for the Canterbury and South Canterbury DHBs are combined as 'Canterbury'. The rates are based on MRSA isolated from clinical specimens only for the years 2014, 2015 and 2017. As data was not specifically collected on which MRSA were from clinical specimens as opposed to screening/surveillance specimens for the surveys conducted between 2011 and 2013 inclusive, MRSA isolates in these years that were specified as being from an infected site, rather than a colonised site, have been used as a proxy for MRSA from clinical specimens.

MRSA strain association with spa *types*

The AK3 MRSA strain was most commonly associated with *spa* type t002, the Queensland clone MRSA with t3949, the WR/AK1 MRSA with t127, EMRSA-15 with t032, USA300 MRSA with t008, and WSPP MRSA with t019 (Table 3). However, several other *spa* types were also identified among isolates of each of these MRSA strains. The *spa* types associated with any one strain usually belonged to the same *spa* clonal cluster, which indicates that they are closely related when analysed by the BURP algorithm.

Table 3. *spa* types of the six most prevalent MRSA strains in 2017

Strain	Number of isolates of the strain	*spa* clonal cluster	*spa* type[1]	Number of isolates of the *spa* type
AK3 MRSA [ST5, SCC*mec* type IV[2]]	497	Spa-CC002	t002	406
			t045	9
			t548	8
			t214	6
			t311	6
			t2069	6
			t062	5
			t010	4
			t105	4
			t688	4
			t5213	4
			t6787	4
			t088	3
			t179	2
			t242	2
			t5677	2
			t17246	2
		Excluded[3]	t535	2
Queensland clone MRSA [ST93, SCC*mec* type IV]	141	Spa-CC202	t3949	105
			t202	14
			t15361	6
			t4699	3
			t17089	3
			t16949	2
			t17272	2
WR/AK1 MRSA [ST1, SCC*mec* type IV]	73	Spa-CC127	t127	32
			t267	19
Alternative name: Western Australia (WA) MRSA-1			t359	8
			t2297	3
			t224	2
			t591	2

Strain	Number of isolates of the strain	*spa* clonal cluster	*spa* type[1]	Number of isolates of the *spa* type
EMRSA-15 [ST22, SCC*mec* type IV]	56[4]	Spa-CC032	t032	17
			t005	11
			t223	4
			t852	4
			t11331	4
			t4326	2
USA300 MRSA [ST8, SCC*mec* type IV]	51[5]	Spa-CC008	t008	40
			t024	4
			t1767	2
WSPP MRSA [ST30, SCC*mec* type IV] Alternative names: Southwest Pacific clone and Oceania clone	45[6]	Spa-CC019	t019	38
			t122	3

1 The *spa* types are only listed in the table if there were ≥2 isolates of the type. In addition to the *spa* types listed in the table:

among the AK3 MRSA isolates there was also 1 isolate of each of the following *spa* types: t306, t439, t458, t570, t1062, t1084, t1265, t2308, t4038, t4867, t6212, t7015, t7026, t7083, t16735, t17247, t17264 and t17533;

among the Queensland clone MRSA isolates there was also 1 isolate of each of the following *spa* types: t1819, t4178, t4675, t15545, t17263 and t17265;

among the WR/AK1 MRSA isolates there was also 1 isolate of each of the following *spa* types: t521, t693, t948, t1418, t4960, t7136 and t13147;

among the EMRSA-15 MRSA isolates there was also 1 isolate of each of the following *spa* types: t016, t020, t022, t192, t294, t309, t845, t1401, t1437, t2681, t3107, t5538, t12550 and t14895;

among the USA300 MRSA isolates there was also 1 isolate of each of the following *spa* types: t068, t121, t190, t211 and t1627; and

among the WSPP MRSA isolates there was also 1 isolate of each of the following *spa* types: t046, t975, t1752 and t13925.

2 ST, multilocus sequence type; SCC*mec*, staphylococcal cassette chromosome *mec*.

3 An excluded *spa* type does not have sufficient repeat sequences (ie, <5 repeats) to validly include it in the based upon repeat pattern (BURP) cluster analysis.

4 The total number of EMRSA-15 isolates was 57, but the *spa* type of 1 isolate remains unassigned. Therefore the strain of this isolate was identified by PFGE typing.

5 The total number of USA300 MRSA isolates was 52, but the *spa* type of 1 isolate could not be determined and therefore this isolate was identified solely by PFGE typing.

6 The total number of WSPP MRSA isolates was 46, but the *spa* type of 1 isolate could not be determined and therefore this isolate was identified solely by PFGE typing.

In addition to the six most prevalent MRSA strains listed in Table 3, isolates of two other recognised MRSA strains were identified. These included:

- 7 isolates of the CC398 MRSA clone (CC398, SCC*mec* type V); and
- 2 isolates of the WA MRSA-2 strain (ST78, SCC*mec* type IV).

CC398 MRSA is a livestock-associated MRSA which was originally identified in pigs in Northern European countries and first identified in New Zealand during the 2011 MRSA survey. Since then, CC398 MRSA has been isolated from several people involved in pig farming or the abattoir industry in the Canterbury region. All the isolates from these people have been *spa* type t011. The other common *spa* type among CC398 MRSA in New Zealand is t034, with isolates of this *spa* type mainly identified from people who appear to have acquired this MRSA strain overseas, especially in SE Asia. None of the seven CC398 MRSA isolates identified in the 2017 survey were from patients known to have direct contact with farm animals in New Zealand. Five of the seven isolates were *spa* type t034. Risk factor information was received for only two of the five patients with *spa* type t034 CC398 MRSA, both of whom had recently travelled to Vietnam. The other two CC398 MRSA were *spa* type t011. Risk factor information was not received for either patient with *spa* type t011 CC398 MRSA, one of whom resided in Canterbury DHB and the other in Auckland DHB.

WA MRSA-2 is a non-multiresistant, typically PVL-negative, community-associated MRSA (CA-MRSA) strain originally recognised in Western Australia.

There were 81 isolates not associated with a recognised MRSA strain, and the most common *spa* types among these isolates were t1853 (14 isolates) and t311 (11 isolates). There were ≤6 isolates of any other *spa* type not associated with a known MRSA strain.

PVL prevalence and association with MRSA strains and spa *types*

Overall, 34.1% of MRSA isolates were PVL positive (Table 4). Among the common MRSA strains, isolates of the Queensland clone, USA300 and WSPP MRSA strains were usually PVL positive, whereas isolates of AK3 MRSA were usually PVL negative. In contrast, PVL was very variable among isolates of the WR/AK1 MRSA and EMRSA-15 strains. Among the PVL-positive EMRSA-15 isolates, there was a diverse range of *spa* types (see footnote to Table 4), although 40.7% were t005.

The prevalence of PVL was significantly lower among MRSA from patients ≤14 years and ≥65 years of age compared with those 15-64 years old (25.2 vs 44.6%, p <0.001) (Table 4). This difference in large part reflects the different distribution of MRSA strains among the age groups. Similarly, the relatively low prevalence of PVL among MRSA from Māori (20.5%) reflects the high prevalence of the usually PVL-negative AK3 MRSA strain in this ethnic

group, while conversely the high prevalence of PVL in MRSA from Pacific peoples (47.7%) reflects the high prevalence of the usually PVL-positive Queensland clone MRSA in this group (Table 2 and Table 4).

Table 4. PVL prevalence by MRSA strain, patient demographics and site of isolation, 2017

	Percent (number) PVL positive	
All isolates (n=956)	34.1	(326)
MRSA strain		
AK3 MRSA (n=497)	2.4	(12)
Queensland clone MRSA (n=141)	99.3	(140)
WR/AK1 MRSA (n=73)	42.5	(31)
EMRSA-15 (n=57)	47.4	(27[1])
USA300 MRSA (n=52)	96.2	(50)
WSPP MRSA (n=46)	93.5	(43)
Patient age group (years)		
<5 (n=167)	22.8	(38)
5-14 (n=148)	29.1	(43)
15-24 (n=112)	53.6	(60)
25-64 (n=328)	41.5	(136)
≥65 (n=201)	24.4	(49)
Ethnic group[2]		
Māori (n = 288)	20.5	(59)
Pacific peoples (n = 235)	47.7	(112)
Asian (n = 65)	56.9	(37)
European or Other (n = 350)	30.9	(108)
Hospitalisation history of patients[3]		
Hospital patient (n=233)	29.2	(68)
Community patient (n=723)	35.7	(258)
Site of isolation		
SSTI (n=868)	34.8	(302)
Invasive sites (n=14)	35.7	(5)
Other sites (n=74)	25.7	(19)

1 The PVL positive EMRSA-15 isolates were the following *spa* types: t005 (11 isolates), t852 (4), t11331 (3), t223 (2), t016 (1), t192 (1), t309 (1), t845 (1), t2681 (1), t3107 (1) and t14895 (1).

2 Data for the Middle Eastern/Latin American/African ethnic group not included as there were only 9 patients in this ethnic group.

3 Patients were categorised as community patients if they were not an inpatient in a healthcare facility (including a long-term care facility) when MRSA was isolated or had not been in a healthcare facility in the previous three months.

Discussion

It is important to note that the MRSA included in this 2017 survey were confined to MRSA isolated from clinical specimens, whereas previous surveys have also included MRSA isolated from specimens taken for screening purposes. This change was made as surveillance based on MRSA isolated from clinical specimens is likely to provide a more accurate indication of trends in the prevalence and epidemiology of MRSA, as it will not be subject to changes in screening practices over time, in different settings, or in different parts of the country.

While the period-prevalence rate of MRSA isolated from clinical specimens appears to have almost doubled between 2009 and 2017, the rate has remained relatively stable over at least the last 4 years (ie, since 2014 and the period that directly comparable data on MRSA from clinical specimens is available): 18.7 patients with MRSA per 100 000 population in 2014 and 19.9 per 100 000 in 2017. However, as has been consistently recorded for many years, there are significant geographic variations in MRSA prevalence throughout New Zealand. Notably the three DHBs in which there has been a significant trend of increasing MRSA prevalence in recent years were all in the South Island (Nelson Marlborough, Canterbury and Southern), but these DHBs still have relatively low rates.

The overwhelming majority of MRSA were from community-associated SSTI, with 89% of the patients categorised as community patients and 91% of the MRSA isolated from SSTI. This finding is similar to the clinical picture for *S. aureus* infections in general in New Zealand.[8,9] All but one (EMRSA-15) of the six most common MRSA strains identified among the survey isolates are considered primarily CA-MRSA strains.

There were marked demographic differences in the rates of MRSA infections. The prevalence rate of MRSA was almost twice as high (55 per 100 000) in the youngest age group (<5 year olds) than in any other age grouping used in this study. Analysis of the prevalence of MRSA by ethnicity produced some striking contrasts, with the age-standardised rates for Pacific peoples and Māori being 7 and 3-4 times, respectively, those in the European and Other ethnic group. These ethnic differences were even more stark among young children <5 years of age, with the rate in Pacific children being 15 times, and the rate in Māori children being 8 times that in children of the same age belonging to the European

and Other ethnic group. Once again these age and ethnicity differences are in keeping with, but even more pronounced than, demographic differences found for *S. aureus* infections generally in New Zealand and in earlier studies of MRSA.[8-10]

The AK3 ST5-IV MRSA clone, which is characterised by a high rate of fusidic acid resistance,[9,11] has been the most prevalent MRSA clone in New Zealand since 2010 and has accounted for approximately 50% of the MRSA in each survey conducted since 2013. Interestingly, a national survey of antimicrobial susceptibility among clinical isolates of *S. aureus* undertaken by ESR in 2014 also reported a high rate of 95% fusidic acid resistance among the most common methicillin-susceptible *S. aureus* clone (MLST CC1, *spa* type t127) in New Zealand.[9] While the AK3 MRSA strain accounted for 52% of all MRSA in the 2017 survey, it was even more prevalent among children <5 years of age, accounting for 70% of MRSA in these children, and among Māori, accounting for 71% of MRSA from Māori patients.

While the AK3 MRSA strain continues to predominate in New Zealand, there have been some notable changes in the relative prevalence of other MRSA clones, in particular an increase in the Queensland ST93-IV clone. The Queensland clone has been the second most prevalent MRSA in surveys since 2014, and has increased over this time accounting for 9.7% of MRSA in the 2014 survey and 14.7% in the 2017 survey. Interestingly the strain was over-represented among Pacific peoples accounting for 37% of MRSA from this ethnic group. This MRSA clone was first described in the early 2000s in Queensland and is now the dominant CA-MRSA strain circulating in Australia. It is PVL positive but not multiresistant. A recent study analysed the genomes of an international collection, including New Zealand isolates, of ST93 MRSA. The results indicated this MRSA clone originated among indigenous populations in Northern Australia, with a clade harbouring SCC*mec* IVa expanding to Australia's east coast. While elsewhere in the world there have been sporadic but non-sustained introductions of ST93-IVa MRSA, in New Zealand this clade appears to have been sustainably transmitted with clonal expansion especially among the Pacific population in the Auckland region.[12]

None of the other MRSA strains accounted for more than 10% of the MRSA in the survey. The formerly prevalent CA-MRSA strain, WSPP MRSA, continues to now be relatively uncommon as does the healthcare-associated EMRSA-15 strain and USA300 MRSA strain.

Notably, no isolates of the multiresistant Bengal Bay MRSA or the AKh4 MRSA strain were identified in the 2017 survey.

MRSA with *mecC*-encoded, rather than the usual *mecA*-encoded, methicillin resistance have now been reported in several European countries and Australia.[13,14] We did not identify any MRSA isolates harbouring *mecC* in this year's survey, and, to the best of our knowledge, *mecC* has not been identified among *S. aureus* in New Zealand to date. Characteristically MRSA with *mecC* will test as oxacillin susceptible but cefoxitin resistant in standard antimicrobial susceptibility tests, and will be negative in tests for PBP2a.

The overall prevalence of PVL found in this survey (34%) is similar to that found in previous surveys.[15] The association between the presence of PVL genes and each of the common MRSA strains was as previously established, with the exception of EMRSA-15. This strain is considered first and foremost a PVL-negative strain, but 47% were PVL positive in this year's survey, a significantly higher proportion than has been found in previous surveys (average 12.2%). Another notable difference in 2017 was the diversity of *spa* types among the PVL-positive EMRSA-15 although 41% were t005 – a *spa* type that we have previously found, and has also been reported from other countries, to be associated with PVL.[16]

In conclusion, while the overall prevalence and molecular epidemiology of MRSA in New Zealand has been relatively stable in recent years, there are marked demographic and geographic differences in the burden of MRSA infections.

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