Annual survey of methicillin-resistant *Staphylococcus aureus* (MRSA), 2009

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Introduction

ESR has undertaken national surveillance of methicillin-resistant *Staphylococcus aureus* (MRSA) since MRSA was first identified in New Zealand in 1975.[1] For the next decade, MRSA remained uncommon in New Zealand, with a maximum of 13 people identified with MRSA in any one year. In a 1982 national survey of antimicrobial resistance among *S. aureus*, just one (0.05%) of 2077 isolates included in the survey was methicillin resistant.[2]

In 1985 the numbers of MRSA being isolated began to increase and, during the three years 1985 to 1987, two major hospital-based MRSA outbreaks occurred.[3-5] These outbreaks were successfully controlled and MRSA isolations decreased again.[6]

While MRSA was originally considered first and foremost a nosocomial pathogen, over approximately the last 15 years, many countries have reported a growing problem with MRSA in the community.[7] New Zealand was one of the first countries to experience community-associated MRSA (CA-MRSA).[8] The MRSA strains causing community-associated infections often belong to lineages distinct from MRSA associated with hospital-acquired infections,[7] although this distinction is blurring with some CA-MRSA strains now also causing hospital-acquired infections.[9,10] In New Zealand, there was a rapid increase in MRSA in the 1990s, which was largely due to the emergence in 1992 and increasing dominance throughout the decade of the community-associated, non-multiresistant Western Samoan phage pattern (WSPP) MRSA strain.[11-14] As a consequence, by the late 1990s almost two-thirds of MRSA were isolated from people categorised as community patients.

The epidemiology of MRSA in New Zealand changed at the beginning of the 2000s with the introduction (mainly via patients and staff from British hospitals) and spread of the British healthcare facility-associated EMRSA-15 strain. As a result, MRSA became more common in New Zealand healthcare facilities, including residential-care facilities for the elderly.[15] By 2002 EMRSA-15 was as common as the WSPP MRSA strain,[16] and between the years 2001 and 2007 MRSA were isolated in almost equal numbers from hospital patients or staff, and people in the community. However since 2007, concomitant with the spread of several new CA-MRSA strains such as AK3 MRSA and USA300 MRSA, the proportion of MRSA isolated from people in the community has begun to increase again.

Originally the national surveillance of MRSA was continuous, and diagnostic laboratories were requested to refer all MRSA isolates to ESR for the laboratory-based surveillance of these organisms. A standard set of epidemiological data was collected for each isolate. This continuous surveillance ceased in 1998 due to the increasing prevalence of MRSA. Annual one-month 'snap-shot' surveys were instituted as a means of providing ongoing information on the epidemiology of MRSA. Reports on these annual surveys are routinely published at http://www.surv.esr.cri.nz/antimicrobial/mrsa_annual.php.

The results of the 2009 survey are presented in this report, along with data on trends in MRSA prevalence since 2000.

Methods

MRSA isolates and data collection

Hospital and community microbiology laboratories in New Zealand were asked to refer all MRSA isolated during a one-month period in 2009 to ESR. All but two laboratories referred MRSA during August 2009. Because of changes in the provision of community laboratory services in the Auckland area during August and September 2009, the two community laboratories in the area (Labtests and Diagnostic Medlab) referred MRSA during October 2009. Laboratories supplied epidemiological data including patient age, geographic location, hospitalisation status, MRSA isolation site, infection or colonisation status, and if MRSA was obtained from a screen or a diagnostic specimen. Laboratories also provided information on the susceptibility of the MRSA isolates to non-β-lactam antibiotics. As Labtests and Diagnostic Medlab receive specimens from multiple district health boards (Waitemata, Auckland and Counties Manukau), these laboratories provided patient or staff addresses that were geocoded at ESR to assign people to a district health board (DHB).

People were classified as hospital patients or hospital staff if (i) they were hospital inpatients or outpatients when MRSA was isolated, or had been in the previous three months; (ii) they were occupying a residential-care facility when MRSA was isolated, or had been in the previous three months; or (iii) they were employed by a healthcare facility (including residential-care facility) when MRSA was isolated. Patients or staff were classified as people in the community if (i) MRSA was isolated from patients while in the community and the patients had no history of occupying a healthcare facility in the previous three months; (ii) MRSA was isolated on hospital admission screening of patients who had no history of occupying a healthcare facility in the previous three months; or (iii) MRSA was isolated from pre-employment swabs of healthcare staff with no employment history supplied. All MRSA isolates received at ESR were assumed to be pure cultures of MRSA and methicillin/oxacillin resistance was not routinely confirmed.

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.[17] PCR products were sequenced by the Sequencing Laboratory at ESR using an ABI 3130XL Sequencer. *spa* sequences were analysed using Ridom StaphType software version 1.5 (Ridom GmbH, Würzburg, Germany). Sequences were automatically assigned repeats and *spa* types using the software. *spa* types were compared using the BURP algorithm, and by excluding *spa* types with less than five repeats and setting a maximum cost of four between members of a *spa* group cluster.[18]

Pulsed-field gel electrophoresis (PFGE) and profile analysis

Where necessary to identify strains, PFGE of *Sma*I-digested genomic DNA was performed as previously described.[19] PFGE banding patterns were analysed using BioNumerics software version 5.1 (Applied Maths, St-Martens-Latern, 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.[20]

Multilocus sequence typing (MLST) and sequence analysis

Where necessary to characterise strains, MLST was performed as previously described.[21] Sequences were analysed using BioNumerics software version 5.1 and sequence types (STs) were assigned using the *S. aureus* database accessible at http://www.mlst.net.

Antibiotic susceptibility testing

Antibiotic susceptibility testing was performed where necessary to identify strains and to supplement the susceptibility information provided by laboratories. Disc susceptibility testing was performed according to the methods of the Clinical and Laboratory Standards Institute (CLSI).[22] Except for fusidic acid, zones of inhibition were interpreted according to CLSI criteria.[23] Fusidic acid zones of inhibition were determined with a 10 μg disc and interpreted as ≥21 mm susceptible, 20 mm intermediate and ≤19 mm resistant.[24]

PCR triplex for nuc, mecA *and staphylococcal-specific 16S rRNA*

Isolates that were not able to be *spa* typed were tested for the genes encoding staphylococcal-specific 16S rRNA, *S. aureus*-specific thermostable nuclease (*nuc*) and methicillin resistance (*mecA*) by triplex PCR as previously described.[25]

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 results were entered into ESR's laboratory information management system. Data and results were extracted and analysed using customised Microsoft Access 2003 queries. Point-prevalence rates were calculated based on the number of MRSA isolated per 100 000 population during the period of the survey. The 2001 and 2006 census population data was used to calculate prevalence rates for 2001 and 2006, respectively. For the other years, the mid-year New Zealand population estimates for the relevant year were used. 95% confidence intervals were calculated based on Poisson distribution. Linear regression was used to calculate the significance and direction of time trends.

Results

During the survey, MRSA were referred from 693 people (683 patients and 10 staff) equating to an estimated point-prevalence rate of 16.1 MRSA per 100 000 population; a 15.6% decrease on the 2008 rate of 19.0 (Figure 1). There was a significant (P=0.0035) increase in the rate of MRSA over the 10 years, 2000 to 2009.

Among the 683 patients with MRSA, 42.8% were categorised as hospital patients and 57.2% as community patients. MRSA was reported as causing infection in 74.3% of the 595 patients for whom this information was provided.

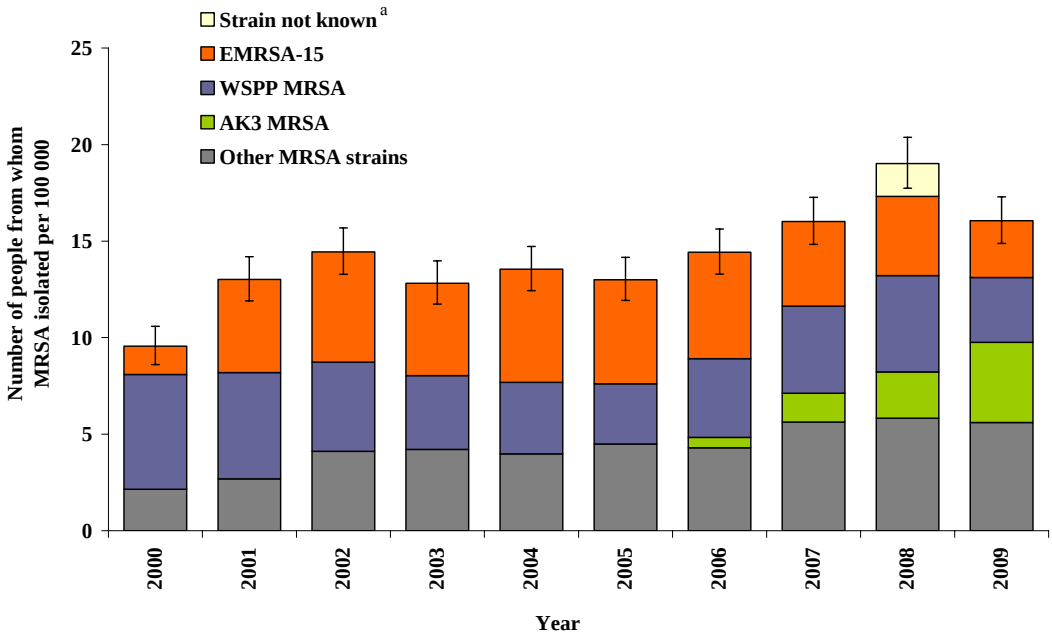

Figure 1. MRSA point-prevalence rates, 2000-2009, showing 95% confidence intervals.
[a] The category 'Strain not known' for 2008 represents the number of people identified with MRSA by Middlemore Hospital laboratory which did not refer the isolates to ESR for strain identification.

Six MRSA strains (AK3 MRSA, WSPP MRSA, EMRSA-15, USA300 MRSA, WR/AK1 MRSA and Queensland clone MRSA) were predominant in 2009 and collectively represented 85.7% of all MRSA isolations (Table 1). AK3 MRSA, WSPP MRSA and WR/AK1 MRSA were more commonly associated with people in the community, whereas EMRSA-15 was more commonly associated with hospital patients or staff (Table 1).

AK3 MRSA was most commonly associated with *spa* type t002 (Table 2). Similarly, WSPP MRSA was most commonly associated with *spa* type t019, EMRSA-15 with *spa* type t032, USA300 MRSA with *spa* type t008, WR/AK1 MRSA with *spa* type t127 and Queensland clone MRSA with *spa* type t3949 (Table 2).

Two *spa* types identified in the survey, t976 and t1853, are likely to be associated with emerging MRSA strains (Table 3). The majority (8 out of 10) of MRSA with *spa* type t976 were resistant to erythromycin with variable resistance to fusidic acid, rifampicin and tetracycline (Table 3). In contrast, all the MRSA with *spa* type t1853, and the single-repeat variant, *spa* type t5720, were resistant only to β-lactams.

As in previous years, there were geographical differences in the point-prevalence rates of MRSA isolations in 2009, with rates above the national rate of 16.1 MRSA per 100 000 population occurring in the Northland, Auckland, Counties Manukau, Waikato, Bay of Plenty and Hawke's Bay DHBs (Figures 2 and 3). Similar geographical differences were evident in the point-prevalence rates of MRSA isolated only from infection, with the exception of Waikato DHB which fell below the national point-prevalence rate of 10.2 MRSA causing infection per 100 000 population (Figure 4).

Table 1. MRSA strain prevalence, association with healthcare facilities versus the community, and association with patient age, 2009

Strain	Proportion (%) of all MRSA isolations[a]	Proportion (%) of each strain isolated from:		
		hospital patients or staff	people in the community	patients ≥60 years of age[b]
AK3 MRSA	25.8	31.8	68.2	18.9
WSPP MRSA	20.9	33.1	66.9	11.0
EMRSA-15 MRSA	18.3	62.2	37.8	73.6
USA300 MRSA	8.4	48.3	51.7	32.7
WR/AK1 MRSA	7.9	36.4	63.6	21.8
Queensland clone MRSA	4.3	46.7	53.3	3.3
AKh4 MRSA	0.9	100	0	100

[a] Other strains accounted for the remaining MRSA. Except for one isolate of the EMRSA-16 strain, none of the other isolates belonged to a recognised strain. [b] Age distribution for patients only, staff not included.

Table 2. Frequency of MRSA strains and *spa* types, 2009

Strain	Number of isolates	*spa* type (number)[a]	*spa* repeat succession (Ridom)
AK3 MRSA [ST5, SCC*mec* type IV]	179	t002 (159)	26-23-17-34-17-20-17-12-17-16
		t045 (5)	26-17-20-17-12-17-16
		t010 (3)	26-17-34-17-20-17-12-17-16
		t088 (2)	26-23-17-34-17-20-17-12-12-17-16
		t306 (2)	26-23-17-34-17-20-17-12-17-17-16
		t548 (2)	26-23-17-34-17-20-17-12-16
		t062 (1)	26-23-17-12-17-16
		t105 (1)	26-23-17-34-17-20-17-17-16
		t214 (1)	26-23-17-34-17-20-17-12-17-16-16
		t586 (1)	26-16
		t5213 (1)	26-23-17-34-17-20-17-12-12-12-12-16
		t5677 (1)	26-17-20-17-12-12-12-12-12-16
WSPP MRSA [ST30, SCC*mec* type IV] Alternative names: Southwest Pacific clone and Oceania clone	145	t019 (134)	08-16-02-16-02-25-17-24
		t122 (2)	08-16-02-16-02-25-17-24-24
		t138 (2)	08-16-02-25-17-24
		t975 (2)	08-16-02-16-02-25-17
		t021 (1)	15-12-16-02-16-02-25-17-24
		t779 (1)	08
		t1752 (1)	08-16-06-16-02-25-17-24
		t1836 (1)	08-16-02-16-02-25-17-17-24
		t5783 (1)	08-16-34-16-02-25-17-24
EMRSA-15 [ST22, SCC*mec* type IV]	127	t032 (82)	26-23-23-13-23-31-29-17-31-29-17-25-17-25-16-28
		t1401 (13)	26-23-23-13-23-31-29-17-31-29-17-25-17-25-16-28-17-25-16-28
		t5501 (5)	26-23-23-13-23-31-29-22-13-23-31-29-17-25-16-28
		t022 (4)	26-23-13-23-31-29-17-31-29-17-25-17-25-16-28
		t852 (4)	07-23-13-23-31-05-17-25-17-25-16-28
		t5538 (3)	26-23-23-20-13-23-31-29-17-31-29-17-25-17-25-16-28-17-25-16-28
		t379 (2)	26-23-23-13-23-31-29-17-25-17-25-16-28
		t790 (2)	26-23-13-23-31-29-17-25-17-25-16-28
		t1214 (2)	26-23-23-13-23-31-29-17-31-29-17-25-16-28
		t5785 (2)	26-23-13-23-31-29-17-31-29-17-25-17-25-16-28-17-25-16-28
		t005 (1)	26-23-13-23-31-05-17-25-17-25-16-28
		t578 (1)	26-23-23-13-23-31-29-17-31-29-17-25-17-25-28
		t646 (1)	26-23-23-13-23-31-29-17-31-29-25-17-25-16-28
		t749 (1)	26-23-23-13-23-31-29-17-31-29-17-25-17-25-17-25-16-28
		t906 (1)	07-23-31-29-17-31-29-17-25-17-25-16-28
		t1279 (1)	26-23-23-13-28
		t3612 (1)	26-23-23-13-23-31-29-31-29-17-25-17-25-16-28
		t5836 (1)	26-23-23-13-23-31-29-22-13-23-31-29-17-16-28

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Table 2. Frequency of MRSA strains and *spa* types, 2009 (continued)

Strain	Number of isolates	*spa* type (number)	*spa* repeat succession (Ridom)
USA300 MRSA [ST8, SCC*mec* type IV]	58	t008 (55)	11-19-12-21-17-34-24-34-22-25
		t024 (2)	11-12-21-17-34-24-34-22-25
		t2849 (1)	11-19-17-34-24-34-22-25
WR/AK1 MRSA [ST1, SCC*mec* type IV] Alternative name: Western Australia (WA) MRSA-1	55	t127 (44)	07-23-21-16-34-33-13
		t591 (3)	07-23-21-21-16-34-33-13
		t701 (2)	11-10-21-17-34-24-34-22-25-25
		t114 (1)	07-16-34-33-13
		t359 (1)	07-23-12-21-17-34-34-33-34
		t521 (1)	07-23-12-21-17-34-34-34-34-33-34
		t559 (1)	07-23-21-13
		t5736 (1)	07-23-21-22-13
		t5837 (1)	07-23-12-34-33-13
Queensland clone MRSA [ST93, SCC*mec* type IV]	30	t3949 (21)	11-17-23-17-17-17-16-16-25
		t202 (8)	11-17-23-17-17-16-16-25
		t1819 (1)	11-17-23-17-16-16-25
AKh4 MRSA [ST239, SCC*mec* type III] Alternative names: EMRSA-1, AUS-2 EMRSA and AUS-3 EMRSA	6	t037 (2)	15-12-16-02-25-17-24
		t631 (2)	15-12-16-17
		t4150 (2)	15-12-16-17-24

[a] *spa* types t002, t045, t088, t127 and t359 were not exclusively identified in isolates belonging to an MRSA strain. There were three isolates with *spa* type t002, three with *spa* type t045 and one with *spa* type t088 that were not the AK3 MRSA strain. There was one isolate with *spa* type t127 and one with *spa* type t359 that were not the WR/AK1 MRSA strain.

Table 3. Frequency of *spa* types t976, t1853 and t5720 and their associated multilocus sequence types (MLSTs) and district health boards

spa type (number)	*spa* repeat succession (Ridom)	Antibiogram (number)[a]	Associated MLST[b]	DHB (number)[c]
t976 (10)	04-20-17-20-31-16-34	EmR (5) EmR RfR (2) EmR TeR (1) FaR (1)	ST-59	Counties Manukau (6) Auckland (2) Canterbury (1) Nelson Marlborough (1)
t1853 (12)	07-23-21-17-13-34-16-13-33-13		ST-1	Counties Manukau (6)
t5720 (2)	07-23-21-17-13-16-13-33-13		ND	Auckland (6) Canterbury (1) Waitemata (1)

[a] EmR, erythromycin resistant; RfR, rifampicin resistant; TeR, tetracycline resistant; FaR, fusidic acid resistant. [b] Associated MLSTs identified at ESR prior to the 2009 MRSA survey. ND, not done.
[c] DHB, district health board. Data for the Canterbury and South Canterbury DHBs is combined as 'Canterbury'.

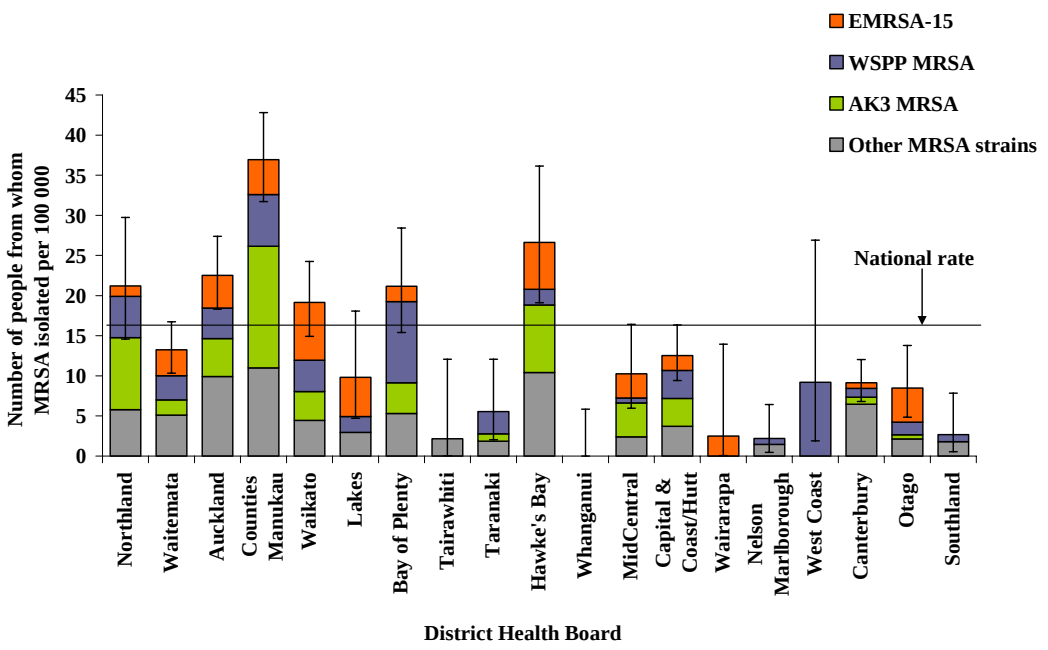

Figure 2. Point-prevalence rates of MRSA by district health board, 2009, showing 95% confidence intervals. Data for the Capital & Coast and Hutt District Health Boards (DHBs) is combined as 'Capital & Coast/Hutt', and data for the Canterbury and South Canterbury DHBs is combined as 'Canterbury'.

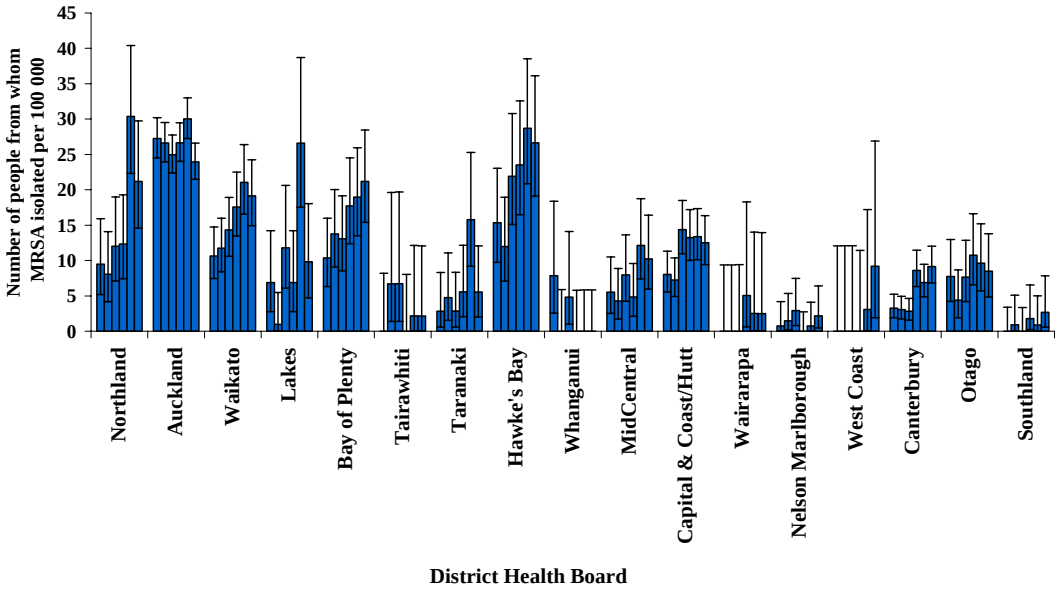

Figure 3. Point-prevalence rates of MRSA by district health board, 2004-2009, showing 95% confidence intervals**.** The series of bars for each district health board (DHB) represent the individual years 2004 to 2009 from left to right. Data for the Waitemata, Auckland and Counties Manukau DHBs is combined as 'Auckland', data for the Capital & Coast and Hutt DHBs is combined as 'Capital & Coast/Hutt', and data for the Canterbury and South Canterbury DHBs is combined as 'Canterbury'.

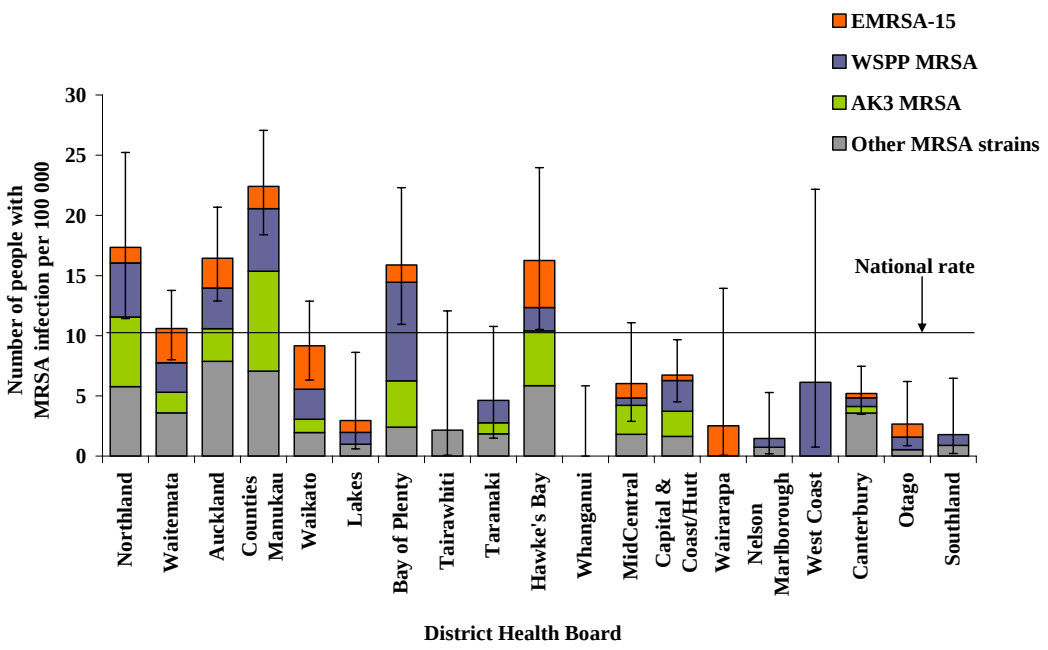

Figure 4. Point-prevalence rates of MRSA infections by district health board, 2009, showing 95% confidence intervals. Data for the Capital & Coast and Hutt District Health Boards (DHBs) is combined as 'Capital & Coast/Hutt', and data for the Canterbury and South Canterbury DHBs is combined as 'Canterbury'.

There were also differences in the geographical distribution of MRSA strains. In particular, rates of the AK3 MRSA strain were highest in the Northland, Counties Manukau and Hawke's Bay DHBs, and this strain was not identified in the Lakes, Tairawhiti, Whanganui, Wairarapa, Nelson Marlborough, West Coast or Southland DHBs (Figure 2). USA300 MRSA was particularly prevalent in the Canterbury/South Canterbury DHBs and accounted for 45.1% of all MRSA isolated in these DHBs.

Discussion

Until 1999, national surveillance of MRSA was continuous, with hospital and community microbiology laboratories asked to refer all MRSA isolated throughout the year to ESR. Since 2000 annual surveys have been conducted, with laboratories asked to refer all MRSA isolated during a one-month period only. Data from the one-month surveys was initially annualised so that it could be compared with data from earlier years when surveillance was continuous. As there is now 10 years (2000-2009) of data from one-month surveys that can be directly compared, the data is no longer being annualised. Beginning with this report, the rates presented are point-prevalence rates and are based on the number of MRSA isolated per 100 000 population during the one-month period of the survey. This change means that data in this report is not directly comparable with that presented in reports on earlier surveys.

Although there was a drop in the national rate of MRSA between 2008 and 2009, over the last 10 years there has been a significant trend of increasing rates. While rates of MRSA are generally increasing in many parts of the world, there have been some notable successes in reducing MRSA rates especially among bloodstream infections in some settings in some countries, including the United Kingdom, the United States of America (USA) and parts of Europe.[26-28]

Consistent with earlier years, in 2009 there were large geographical differences in the prevalence of MRSA within New Zealand, with rates generally highest in DHBs in the upper half of the North Island and Hawke's Bay. As MRSA from both diagnostic specimens and screening specimens were included in the survey, any apparent differences in MRSA rates between DHBs could be partly due to differences in screening policies. However, the relative rates of MRSA infections between DHBs were very similar to the rates of all MRSA isolations. Rates of MRSA infections may also be influenced by different policies for obtaining and processing diagnostic specimens.

Eight MRSA strains are currently recognised in New Zealand: AK3 MRSA [ST5, SCC*mec* type IV], AKh4 MRSA [ST239, SCC*mec* type III], EMRSA-15 [ST22, SCC*mec* type IV], EMRSA-16 [ST36, SCC*mec* type II], Queensland clone MRSA [ST93, SCC*mec* type IV], USA300 MRSA [ST8, SCC*mec* type IV], WR/AK1 MRSA [ST1, SCC*mec* type IV] and WSPP MRSA [ST30, SCC*mec* type IV]. More detailed descriptions of these strains along with typical antibiotic susceptibility patterns are available at http://www.esr.cri.nz/competencies/communicabledisease/Pages/MRSA%20strains.aspx.

During the 2008 MRSA survey, the WSPP MRSA and EMRSA-15 strains represented 31.5% and 25.8% of all MRSA isolations, respectively.[29] In the 2009 MRSA survey there was a decrease in the proportion of WSPP MRSA and EMRSA-15, and these strains represented 20.9% and 18.3% of all MRSA isolations, respectively (Table 1). The AK3 MRSA strain was first recognised in New Zealand among MRSA referred during the 2005 MRSA survey. Since this time, its prevalence in New Zealand has increased, and during the 2009 MRSA survey, AK3 MRSA represented the highest proportion (25.8%) of all MRSA isolations. AK3 MRSA has therefore taken the place of WSPP MRSA as the predominant CA-MRSA strain in New Zealand. EMRSA-15 continues to be the predominant healthcare-associated

MRSA (HA-MRSA) strain. The two other recognised HA-MRSA strains, AKh4 MRSA and EMRSA-16, accounted for only a small proportion of all MRSA isolations during the 2009 MRSA survey.

Despite USA300 and Queensland clone MRSA strains being considered to be primarily community associated, 48.3% of USA300 MRSA isolates and 46.7% of Queensland clone MRSA isolates were from hospital patients or staff. There have been several recent reports of USA300 MRSA being the cause of healthcare-associated infection in the USA.[30,31] While 46.7% of Queensland clone isolates were from patients categorised as hospital patients, the age profile of these patients was more typical of community- than hospital-associated MRSA infections (Table 1).

The Queensland clone MRSA strain was first recognised in Queensland, Australia, in 2000 and has since spread to become the predominant CA-MRSA strain, representing 44.1% of MRSA in a 2008 CA-MRSA survey in Australia.[32,33] In New Zealand, the Queensland clone MRSA strain was first reported in the 2008 MRSA survey where it accounted for 2.1% of MRSA isolations.[29] In 2009, this proportion increased to 4.3%. WA MRSA-1 is the second most prevalent CA-MRSA in Australia, and in 2008 represented 18.5% of MRSA in a survey of CA-MRSA.[33] In New Zealand this strain is known as WR/AK1 MRSA and, like Queensland clone MRSA, represented a relatively low proportion (7.9%) of the total MRSA isolations in the 2009 MRSA survey, when compared to other CA-MRSA strains, AK3 MRSA and WSPP MRSA.

During the 2009 MRSA survey, *spa* types t976, t1853 and t5720 were identified in multiple MRSA isolates. These *spa* types are not associated with any of the MRSA strains currently recognised in New Zealand. *spa* type t5720 is a single-repeat variant of t1853 and was also related by PFGE to isolates with *spa* type t1853, indicating that these *spa* types are associated with the same strain. *spa* type t1853 is associated with ST1. In 2008, ST1 MRSA isolates with *spa* type t1853, and another single-repeat variant, *spa* type t6080, were identified among MRSA from Samoa referred to ESR. *spa* type t976 is associated with ST59. CA-MRSA isolates with *spa* type t976 were recently characterised in Australia and were designated WA MRSA-15 [ST59, SCC*mec* type IVa].[34] In a 2008 survey of CA-MRSA in Australia, the WA MRSA-15 strain represented just 0.6% of CA-MRSA.[33] ESR will be carrying out further work to characterise New Zealand isolates with the *spa* types t976, t1853 and t5720.

Besides the limitations in comparing DHBs' rates due to potential differences in screening and diagnostic specimen processing procedures, the data available from these surveys had some other limitations. First, just as differences in screening and diagnostic specimen processing procedures could affect the relative rates between DHBs, so any changes over time in these procedures could affect any time-trend analyses. Second, the limited duration of the survey (a one-month period) means that rates could be skewed by short-term outbreaks occurring during the survey collection period. Third, we cannot collect the information that would be required to designate whether a person acquired their MRSA in a healthcare facility or the community. We therefore, as a proxy, categorised people as either hospital patients or staff, or people in the community, according to where they were when their MRSA was isolated and their recent (previous three months) hospitalisation history. However, it is difficult to obtain accurate hospitalisation histories especially for patients whose MRSA isolates were referred from community laboratories. Therefore, it is highly likely that some people who had been in a healthcare facility within the previous three months were

categorised as community patients. Conversely, our categorisation of patients as hospital patients if they were in hospital when their MRSA was isolated would overcall healthcare-associated MRSA, especially when the patient had a known CA-MRSA strain, as in many of these cases the patient was probably admitted with their MRSA.

In addition to the information on the prevalence and epidemiology of MRSA provided by these surveys, information on MRSA in New Zealand is available from two other surveillance systems that ESR operates. First, the proportion of *S. aureus* isolates that are methicillin/oxacillin resistant is estimated each year based on the results of routine susceptibility testing performed in diagnostic laboratories throughout the country. This data indicates that during the nine years, 2000-2008, methicillin/oxacillin resistance among *S. aureus* ranged from a low of 6.8% in 2002 to a high of 8.7% in 2008.[35]

Second, the web-based *Health care facility antibiotic resistance surveillance system* provides information on the current prevalence and outbreaks of antibiotic-resistant organisms, including MRSA, in participating public and private healthcare facilities. The purpose of the system is to provide information to assist healthcare facilities to operate appropriate screening and isolation protocols for patients being transferred between facilities, and thereby minimise the transmission and spread of resistant organisms. The system relies on participating healthcare facilities regularly reporting data from their facility. The data entered by each facility links through to a report table that presents the data reported by each participating healthcare facility. This report can be accessed by all facilities registered to use the system.[36]

References

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