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Australian Meningococcal Surveillance Programme Annual Report, 2022

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Annual report

Australian Meningococcal Surveillance Programme Annual Report, 2022

Monica M Lahra, CR Robert George, Sebastiaan J van Hal and Tiffany R Hogan for the National Neisseria Network

Abstract

In Australia, both probable and laboratory-confirmed cases of invasive meningococcal disease (IMD) are reported to the National Notifiable Diseases Surveillance System (NNDSS). Compared to 2021, the number of IMD notifications in 2022 increased by 81% to 127, alongside the easing of COVID-19 containment measures. Laboratory confirmation occurred in 95% of these cases, with 51% (62/121) diagnosed by bacterial culture and 49% (59/121) by nucleic acid amplification testing. The serogroup was determined for 97% of laboratory-confirmed cases (117/121): serogroup B (MenB) accounted for 83% of infections (100/121); MenW for 4% (5/121); MenY for 10% (12/121); no infections were attributed to MenC disease. Fine typing was available on 67% of the cases for which the serogroup was determined (78/117). In MenB isolates, 27 *porA* types were detected, the most prevalent of which were P1.7-2,4 (18%;11/62), P1.22,14 (15%; 9/62), P1.18-1,34 (10%; 6/62) and P1.7,16-26 (10%; 6/62). All five MenW infections identified as *porA* type P1.5,2 with different MLST sequence types (ST): 11, 574, 1287, 12351, 13135 all belonging to clonal complex 11, the hypervirulent strain reported in outbreaks in Australia and overseas. In MenY, the predominant *porA* type was P1.5-1,10-1 (73%; 8/11), ST 1655 and from clonal complex 23.

Children less than 5 years of age and people aged 15–19 years were overrepresented with IMD notifications, accounting for 22% (27/121) and 23% (28/121) of laboratory-confirmed cases respectively. Fifteen percent of laboratory-confirmed notifications (18/121) were in persons aged 45–64 years. MenB infections were detected in all age groups but predominated in persons aged 15–19 years (93% of IMD in this age group; 26/28) and comprised 89% (24/27) of infections in children aged less than 5 years. MenW infections were markedly reduced in 2022, accounting for two IMD detections in children 1–4 years (2/16) and sporadic detections in other older age groups. MenY infections were largely detected in adults aged 45–64 years, accounting for 28% of IMD in this age group (5/18).

All 62 cultured IMD isolates had antimicrobial susceptibility testing performed. Minimum inhibitory concentration (MIC) values were categorised using Clinical Laboratory Standards Institute (CLSI) interpretative criteria: 5% (3/62) were defined as penicillin resistant (MIC value \geq 0.5 mg/L); 71% (44/62) had intermediate susceptibility to penicillin (MIC values 0.125 and 0.25 mg/L) and 24% (15/62) were susceptible to penicillin. All isolates were susceptible to ceftriaxone, ciprofloxacin and rifampicin.

Keywords: antimicrobial resistance; disease surveillance; invasive meningococcal disease; *Neisseria meningitidis*

Introduction

Established in 1979, the National Neisseria Network (NNN) is a network of reference laboratories in each Australian state and territory that collaboratively undertake surveillance of the pathogenic Neisseria species: N. meningitidis and N. gonorrhoeae. Since 1994, the NNN has coordinated laboratory data from cases of invasive meningococcal disease (IMD) for the Australian Meningococcal Surveillance Programme (AMSP), supported by the Australian Government Department of Health and Aged Care and the jurisdictions.¹ The NNN laboratories supplement notification data from the National Notifiable Diseases Surveillance System (NNDSS), which includes cases of probable and laboratory confirmed IMD.

Notifications of IMD in Australia peaked in 2002 at 3.5 cases per 100,000 persons per year,² with the majority of disease caused by MenB and MenC. After the introduction of the conjugate serogroup C meningococcal vaccine to the National Immunisation Program (NIP) in 2003, there was a significant and sustained reduction in serogroup C IMD notifications, and a reduction in overall notifications to a nadir of 0.6 cases per 100,000 in 2013.^{3,4} The IMD notification rate increased to 1.5 cases per 100,000 in 2017,² when MenACWY immunisation programmes were implemented across jurisdictions in targeted age groups. Following the substitution of the monovalent MenC vaccine with the quadrivalent MenACWY vaccine in 2018, IMD notifications declined further from 1.1 per 100,000 in 2018 to 0.8 per 100,000 in 2019. In 2020, there were 0.4 cases per 100,000 recorded and a continued reduction was recorded in 2021, to 0.3 cases per 100,000. This reduction in disease rate was beyond the expected vaccine impact and was likely attributable to the impact of public health measures implemented in response to the SARS-CoV-2 pandemic. In 2022, with the gradual easing of infection control containment measures, IMD notifications rose to 0.5 cases per 100,000 persons per year.

IMD is a rare disease in Australia, but one of public health concern; continued monitoring of phenotypic and genotypic features of IMD strains is critical to plan and inform clinical management of cases, case clusters and outbreaks of IMD locally and nationally, and to inform and monitor public health interventions.

Methods

Case confirmation of invasive meningococcal disease

Case confirmation is based on culture of *N. meningitidis*, or molecular diagnoses from a normally sterile site, defined as laboratory-definitive evidence of IMD according to national case definitions.⁵ Information regarding the site of infection and the age and sex of the patients is collated by the NNN for the AMSP.

Invasive *N. meningitidis* infections are categorised according to the site of isolation, or the specimen type from which meningococcal DNA was detected (blood, joint fluid, and vitreous fluid). For a given patient, when *N. meningitidis* is detected from both blood and cerebrospinal fluid (CSF) it is classified as one of meningitis.

Serogroup and genotyping of *Neisseria meningitidis*

Serogroup determination is by detection of soluble polysaccharide antigens, with molecular testing playing an increasing role.⁶ Genotyping of both isolates and DNA extracts is performed by sequencing products derived from amplification of the *porA* gene. Multi-locus sequence typing (MLST) and clonal complex assignment is additionally reported by some jurisdictions.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) of invasive meningococcal isolates is undertaken to determine minimum inhibitory concentration (MIC) values for antibiotics used for treatment (ceftriaxone, penicillin), and for clearance of carriage (ciprofloxacin and rifampicin). In this report, antibiotic susceptibilities are reported according to the Clinical Laboratory Standards Institute's (CLSI) M100 guidelines;⁷ this differs from historical reporting. By CLSI guidelines, MIC breakpoints are categorised as follows, for penicillin: susceptible (MIC ≤ 0.06 mg/L); intermediate susceptibility (MIC 0.125-0.25mg/L); and resistant (MIC ≥ 0.5 mg/L); for ceftriaxone: susceptible (MIC ≤ 0.125 mg/L); for ciprofloxacin: susceptible (MIC ≤ 0.03 mg/L), intermediate susceptibility (MIC 0.06mg/L); and resistant (MIC ≥ 0.125 mg/L); and for rifampicin: susceptible (MIC ≤ 0.5 mg/L); intermediate susceptibility (MIC 1.0 mg/L) and resistant (MIC ≥ 2 mg/L).

Results

In 2022, there were 127 IMD cases notified to the NNDSS, of which 121 were laboratory confirmed.² Laboratory data were available to the AMSP for all 121 laboratory-confirmed IMD cases, as shown in Figure 1. In 2022, an increase in IMD notifications was seen across all jurisdictions, particularly in New South Wales, Queensland and Western Australia where notification numbers doubled from those reported in 2021.⁸ In 2022, the peak incidence of IMD occurred in winter through early spring (1 July to 30 September), as shown in Table 1.

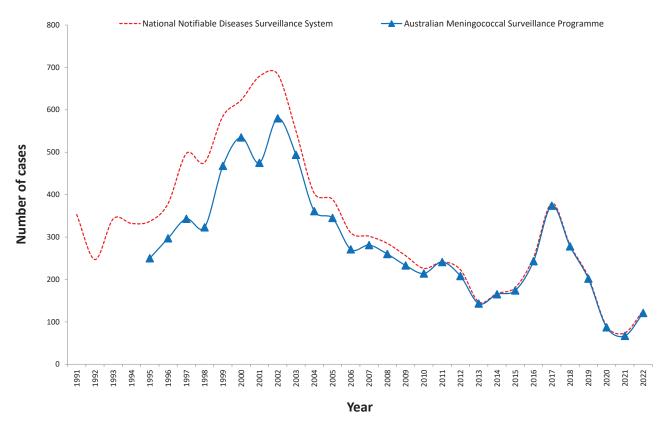
Laboratory diagnosis of IMD

In 2022, laboratory diagnosis of IMD was via culture in 51% of laboratory-confirmed cases (62/121) and by molecular testing (nucleic acid amplification testing) in 49% (59/121), as shown in Table 2. There were 52 diagnoses of meningitis, 66 diagnoses of bacteraemia, and three IMD diagnoses from joint fluid aspirates.

Notifications by jurisdiction

Across the jurisdictions in 2022, New South Wales reported the highest number of IMD notifications nationally (28%; 34/121), followed

Figure 1: Number of invasive meningococcal disease cases reported to the National Notifiable Diseases Surveillance System compared with laboratory-confirmed data from the Australian Meningococcal Surveillance Programme, Australia,^a 1991–2022



a Source: National Notifiable Diseases Surveillance System. Data extracted 10 May 2023.

| IMD serogroup | 1 January – 31 March | 1 April – 30 June | 1 July – 30 September | 1 October – 31 December | 2022 total |
|------------------|-------------------------|-------------------|--------------------------|----------------------------|------------|
| В | 13 | 22 | 35 | 30 | 100 |
| С | 0 | 0 | 0 | 0 | 0 |
| W | 0 | 4 | 1 | 0 | 5 |
| Y | 1 | 5 | 4 | 2 | 12 |
| NDª | 2 | 0 | 2 | 0 | 4 |
| Total | 16 | 31 | 42 | 32 | 121 |

Table 1: Laboratory-confirmed cases of invasive meningococcal disease, Australia, 2022

a ND: not determined.

Table 2: Number of laboratory-confirmed cases of invasive meningococcal disease, Australia,2022, by specimen type and method of confirmation

| Specimen | Bacterial culture | Nucleic acid amplification test | Total |
|-----------------|-------------------|---------------------------------|-------|
| Blood | 47 | 19 | 66 |
| $CSF \pm blood$ | 12 | 40 | 52 |
| Joint aspirate | 3 | 0 | 3 |
| Total | 62 | 59 | 121 |

Table 3: Number of laboratory-confirmed cases of invasive meningococcal disease, Australia, 2022, by jurisdiction and by serogroup

| Indiation | Serogroup | | | | | | | |
|------------------------------|-----------|---|---|----|-----|-------|--|--|
| Jurisdiction | В | c | w | Y | NDª | Total | | |
| Australian Capital Territory | 1 | 0 | 0 | 1 | 0 | 2 | | |
| New South Wales | 32 | 0 | 0 | 1 | 1 | 34 | | |
| Northern Territory | 1 | 0 | 0 | 0 | 0 | 1 | | |
| Queensland | 23 | 0 | 2 | 7 | 1 | 33 | | |
| South Australia | 12 | 0 | 0 | 1 | 1 | 14 | | |
| Tasmania | 3 | 0 | 0 | 0 | 0 | 3 | | |
| Victoria | 14 | 0 | 0 | 0 | 1 | 15 | | |
| Western Australia | 14 | 0 | 3 | 2 | 0 | 19 | | |
| Australia | 100 | 0 | 5 | 12 | 4 | 121 | | |
| % | 83 | 0 | 4 | 10 | 3 | | | |

a ND: not determined.

by Queensland (27%, 33/121). For New South Wales, the number of IMD notifications was higher than that reported in 2021 but the proportion similar (2021: 27% (18/67)), whereas for

Queensland, both the number and proportion were higher (2021: 21% (14/67)). In Western Australia, notification numbers increased in 2022 to 19/121 (16%) from 10/67 (15%) in 2021, but the proportion was similar. From Victoria, there were 15 notifications in 2022, an increase in number from 10 in 2021 but a decrease in proportion (2022: 15/121 (12%), 2021: 10/67 (15%)). In South Australia, IMD notifications decreased in both number and proportion in 2022 (12%, 14/121) after increasing sharply in 2021 (18%, 12/67) compared with 2020 (6%, 5/87). Jurisdictional case numbers are shown in Table 3.

In 2022, MenB accounted for 83% of IMD notifications (see Table 3), reaching a proportion not observed since 2008 – 2009 (see Figure 2). Of note, MenB proportionality was highest in New South Wales (94%, 32/34), Victoria (93%, 14/15) and South Australia (86%, 12/14). MenB IMD was reported across all age groups. Historically, from 2006 through 2014, the proportion of IMD attributable to MenB ranged from 74–84% nationwide, falling to 62% in 2015, and then 37% in 2016–2017. Subsequently, there has been an overall increase in the proportion of IMD attributable to MenB, rising to 44% in 2018, 50% in 2019, and 62% in 2020, with a temporally limited decrease to 52% observed in 2021. MenW and MenY respectively accounted for 4% and 10% of IMD nationally in 2022 (see Table 3). Since 2014, the rise in IMD notifications has generally coincided with increases in numbers of infections of both MenW and MenY (see Figure 1 and Figure 2). Regarding MenW, this serogroup was responsible for a relatively low proportion of IMD cases prior to 2015, ranging within 1-5% during 2000-2012. Increases to 8-10% were observed in 2013-2014, to 21% in 2015, and a peak proportion of 44% observed in 2016. Subsequently, rates have progressively declined, from 36-38% in 2017-2018, 18-26% in 2019-2021, and then falling sharply to 4% in 2022 (Figure 2). MenW disease was only reported in Western Australia (3) and Queensland (2). Regarding MenY, the proportion of IMD cases attributable to this serogroup ranged within 1-5% in the years 2000-2010 before increasing to 6-11% from 2011-2014, to 13% in 2015, 17% in 2016, and then 20% in 2017. The attributable proportion of MenY IMD ranged from 16% to 21% between 2018 and 2021, declining sharply to 10% in 2022 (see Figure 2). In 2022, MenY

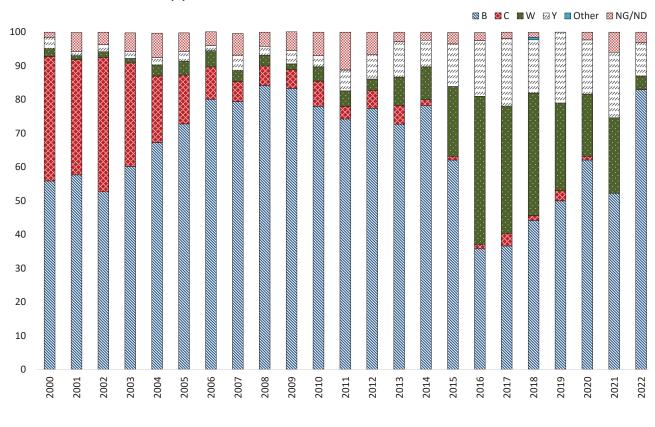


Figure 2: Proportion of serogroups of laboratory-confirmed invasive meningococcal disease, Australia, 2000 – 2022 by year

Commun Dis Intell (2018) 2023;47 (https://doi.org/10.33321/cdi.2023.47.44) Epub 24/8/2023

| Sorogroup | Age group (years) | | | | | | | | | |
|----------------------|-------------------|-------------|------|-------|-------------|-------|-------------|-------------|-------------|-------|
| Serogroup | < 1 | 1-4 | 5-9 | 10-14 | 15–19 | 20-24 | 25-44 | 45-64 | 65+ | Total |
| В | 11 | 13 | 6 | 6 | 26 | 15 | 9 | 12 | 2 | 100 |
| C | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| W | 0 | 2 | 0 | 1 | 0 | 0 | 1 | 1 | 0 | 5 |
| Υ | 0 | 0 | 0 | 0 | 1 | 0 | 3 | 5 | 3 | 12 |
| ND | 0 | 1 | 0 | 1 | 1 | 0 | 1 | 0 | 0 | 4 |
| Total | 11 | 16 | 6 | 8 | 28 | 15 | 14 | 18 | 5 | 121 |
| % B within age group | 100% | 81 % | 100% | 75% | 93 % | 100% | 64 % | 67 % | 40 % | 83% |

Table 4: Laboratory-confirmed cases of invasive meningococcal disease (IMD), Australia, 2022, by age and serogroup, and the proportion of IMD attributable to MenB

disease was largely reported from Queensland (7/33), accounting for 21% of jurisdictional notifications.

In 2022, no MenC IMD was reported from Australia. Additionally, very few cases of any serogroup were reported from the Australian Capital Territory (2 cases); the Northern Territory (1 case); and Tasmania (3 cases).

IMD age and serogroup distribution

In 2022, IMD notifications were reported in all age groups. Disease peaks occurred in children less than 5 years of age (27/121 cases; 22%) and in persons aged 15 to 19 years (28/121 cases; 23%). Fifteen percent of notifications (18/121) were in adults aged 45–64 years, as shown in Table 4. Serogrouping was determined for 117/121 cases of IMD (97%), with MenB accounting for 83%, MenY for 10% and MenW for 4%, as shown in Table 3. There were no notifications of MenC IMD nationwide in 2022. Serogroup distribution is also shown in Table 4 and Figure 3; MenB accounted for 83% of IMD, and was the majority serogroup in all age groups excepting in those aged 65 years and over.

IMD and genotyping

Finetyping was performed on 62 of 100 MenB IMD cases and this serogroup showed the greatest variability, with 27 *porA* types represented and with four *porA* types predominating:

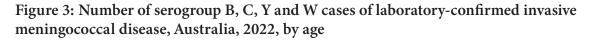
P1.7-2,4 (11/62; 18%), P1.22,14 (9/62; 15%), P1.18-1,34 (6/62, 10%) and P1.7,16-26 (6/62, 10%), as shown in Figure 4 and Table 5.

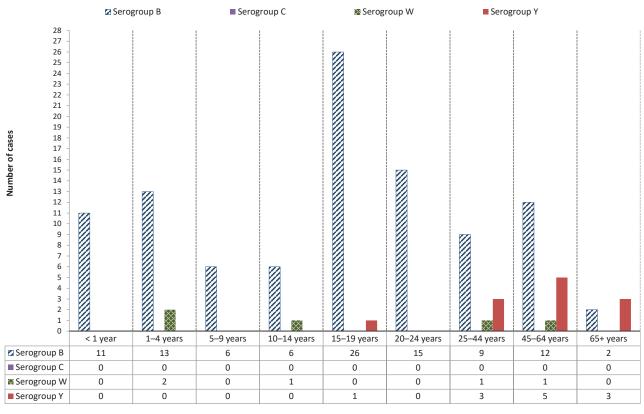
All of the five MenW IMD were determined to be from a single *por*A type, P1.5,2, as shown in Figure 4 and Table 5. Five different MLST sequence types were represented: 11; 574; 1287; 12351; and 13135, with all belonging to clonal complex 11. The *porA* type P1.5,2 has been the predominant genotype in recent years, from the clonal complex 11, which is the same strain type as the hypervirulent serogroup W strain reported in the United Kingdom and South America since 2009.^{9,10}

Of the 12 MenY cases, 11 had finetyping performed and were determined to be from four *porA* types, with P1.5-1,10-1 the most prevalent (8/11, 73%) (as shown in Figure 4 and Table 5), identifying as MLST sequence type 1655 and belonging to clonal complex 23. The *porA* type P1.5-1,10-1 has been the predominant MenY genotype circulating in Australia since 2014, when the increase in serogroup Y IMD was first noted in Australia.

Antimicrobial susceptibility testing

Neisseria meningitidis isolates are tested against currently recommended treatment (ceftriaxone and penicillin) and clearance antibiotics (rifampicin and ciprofloxacin). In 2022, national AST data are reported according to





Age group

CLSI interpretative guidelines, changed from historical reporting (1997 to 2020). Fifty-one percent of laboratory-confirmed IMD (62/121 isolates) had N. meningitidis cultures, permitting AST by NNN laboratories. Ceftriaxone AST was performed on all 62 isolates with each testing susceptible. The distribution of penicillin MIC values is shown in Table 6. Regarding penicillin, 24% of IMD isolates (15/62) tested susceptible (MIC \leq 0.06 mg/L); 71% (44/62) demonstrated intermediate susceptibility (MIC 0.125-0.25 mg/L); and 5% (3/62) were resistant (MIC ≥ 0.5 mg/L) (see Table 6). The proportion of penicillin-resistant isolates in 2022 was lower than reported in 2021 (13%, 6/46). Of the isolates that tested penicillin resistant, two were MenB and one was MenW. In recent years, MenW has demonstrated higher penicillin MIC values and higher proportions of resistance. Regarding the clearance antibiotics for IMD, all isolates tested in 2022 were susceptible to ciprofloxacin and rifampicin.

Discussion

In 2022, there were 127 IMD notifications nationally; an 81% increase from that reported in 2021, following the easing of COVID-19 containment measures. In recent years there has been an ongoing annual decrease in IMD notifications from 1.5 cases per 100,000 in 2017 to 1.1 per 100,000 in 2018; 0.8 cases per 100,000 in 2019; 0.4 cases per 100,000 in 2020; 0.3 cases per 100,000 in 2021. The notification rate in 2021 was the lowest recorded since records were kept and coincided with both widespread public health initiatives designed to reduce COVID-19 transmission and changes in the national immunisation programme (NIP) from a monovalent MenC to a quadrivalent MenACWY vaccine.^{11,12} In 2022, there were 0.5 IMD cases per 100 000 population reported, and 95% (121/127) of IMD notifications in Australia were laboratory confirmed.

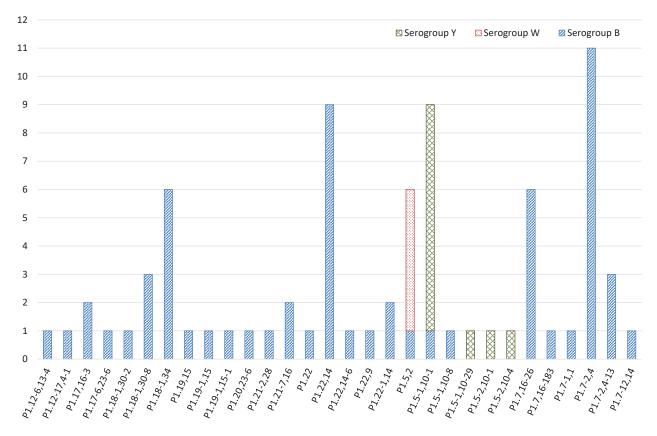


Figure 4: The number of *porA* types represented in serogroup B, W and Y invasive meningococcal disease notifications in Australia in 2022

In Australia in 2016-2017 the AMSP reported increased notifications of MenW and MenY IMD. In response, time-limited, jurisdictional MenACWY vaccination programs for target age groups were implemented; in July 2018, the MenC vaccine at 12 months of age was replaced with a quadrivalent ACWY vaccine on the NIP.¹² A decrease in both notifications and proportionality of MenW and MenY disease followed, accompanied by a gradual increase in the proportion of MenB disease (from 44% to 62% in 2018-2021 to 83% of IMD in 2022). Prior to the introduction of the MenC vaccine in 2003, the proportion of MenB IMD was 84-88% in the years 2006-2012. Notifications of IMD subsequently increased with the emergence of MenW and MenY disease since 2014 in Australia.^{4,13} In 2022, the number and proportion of IMD cases caused by MenB (100/121; 83%) was substantially greater than the MenB IMD reported in 2021 (35/67; 52%). New South Wales reported the largest number of MenB notifications. Fine typing of MenB notifications revealed the diversity of porA types (27 different porA types from

the 62 investigations). The predominant MenB *porA* genotype in Australia was P1.7-2,4 (18%, 11/62), followed by genotypes P1.22,14 (15%, 9/62), P1.18-1,34 (10%, 6/62) and P1.7,16-26 (10%, 6/62). Across the age groups, MenB was predominant in IMD in all age groups excepting in those over 65 years.

MenW accounted for 4% (5/121) of IMD. The proportion of IMD caused by MenW declined to 22% in 2021 from 38% in 2017. Of MenW notifications in 2022, two (2/5) occurred in children aged 1-4 years; in the previous year, MenW accounted for 50% (5/10) of IMD notifications in infants less than one year old. The predominant circulating strain of MenW continues to be porA genotype P1.5,2 with MLST types belonging to clonal complex 11. This same MenW strain previously emerged in the United Kingdom (UK) and South America in 2009,9,10 and spread to account for 25% of IMD in the UK in 2014-2015 and 59% of all cases in Chile in 2012. MenW ST11 is hypervirulent and associated with atypical clinical presentations,

Table 5: Distribution of *porA* genotypes in typed isolates of invasive meningococcal disease, Australia, 2022, by state or territory (n = 78/121)

| 2022 | Number per serogroup per state / territory ^a | | | | | | | | | |
|-----------|---|-----|-----|----|-----|----|------|------|----|-------|
| SEROGROUP | GENOTYPE_ PorA | АСТ | NSW | NT | Qld | SA | Tas. | Vic. | WA | TOTAL |
| В | P1.12-6,13-4 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| В | P1.12-17,4-1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.17,16-3 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 2 |
| В | P1.17-6,23-6 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| В | P1.18-1,30-2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.18-1,30-8 | 0 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 3 |
| В | P1.18-1,34 | 0 | 4 | 0 | 0 | 0 | 0 | 2 | 0 | 6 |
| В | P1.19,15 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| В | P1.19-1,15 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.19-1,15-1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| В | P1.20,23-6 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.21-2,28 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.21-7,16 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 2 |
| В | P1.22 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| В | P1.22,14 | 0 | 2 | 0 | 1 | 1 | 0 | 2 | 3 | 9 |
| В | P1.22,14-6 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| В | P1.22,9 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| В | P1.22-1,14 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 | 2 |
| В | P1.5-1,10-1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 1 |
| В | P1.5-1,10-8 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| В | P1.5,2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| В | P1.7,16-26 | 0 | 1 | 0 | 2 | 0 | 0 | 3 | 0 | 6 |
| В | P1.7,16-183 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.7-1,1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| В | P1.7-2,4 | 0 | 0 | 0 | 6 | 5 | 0 | 0 | 0 | 11 |
| В | P1.7-2,4-13 | 0 | 2 | 0 | 0 | 1 | 0 | 0 | 0 | 3 |
| В | P1.7-12,14 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| W | P1.5,2 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 3 | 5 |
| Y | P1.5-1,10-1 | 0 | 0 | 0 | 6 | 1 | 0 | 0 | 1 | 8 |
| Y | P1.5-1,10-29 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| Y | P1.5-2,10-1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| Y | P1.5-2,10-4 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| Total | | | | | | | | | | 78 |

a ACT: Australian Capital Territory; NSW: New South Wales; NT: Northern Territory; Qld: Queensland; SA: South Australia; Tas.: Tasmania; Vic.: Victoria; WA: Western Australia.

 Table 6: Penicillin MIC distribution of laboratory-confirmed invasive meningococcal disease isolates, Australia, 2022

| Penicillin MIC distribution | | | | | | | | | | |
|-----------------------------|---------|-------|-------|------|-----|----|----|----|-------|--|
| MIC mg/L | ≤ 0.032 | 0.064 | 0.125 | 0.25 | 0.5 | 1 | 2 | ≥4 | Total | |
| Number of isolates | 4 | 11 | 13 | 31 | 3 | 0 | 0 | 0 | 62 | |
| % | 6% | 18% | 21% | 50% | 5% | 0% | 0% | 0% | 100% | |

more severe disease, and a higher case fatality rate. ¹⁰ The initial increase in MenW overseas and in Australia was seen in older adults, but was subsequently reported in all age groups, particularly in adolescents and infants.¹⁴

In 2022, MenY accounted for 10% of IMD nationally (12/121), predominantly affecting older age groups. MenY accounted for 21% of notifications (3/14) in individuals aged 25–44 years, 28% of notifications (5/18) in individuals aged 45–64 years, and 60% of notifications (3/5) in individuals aged 65 years and greater. Since 2014, the predominant MenY genotype since 2014 continues to be P1.5-1,10-1, whereas previously MenY genotype distribution had been more heterogeneous.¹⁵

Antimicrobial susceptibility testing of IMD isolates in 2022 detected 5% (3/62) penicillin resistance (MIC values ≥ 0.5 mg/L) in clinical isolates. All IMD isolates tested in 2022 were susceptible to ceftriaxone, ciprofloxacin and rifampicin.

The NNN is continuing to lead further investigations with the Australian Government Department of Health and Aged Care and is closely monitoring the phenotypic and genotypic features of *N. meningitidis* causing IMD in Australia. Additional investigations by the NNN, including whole genome sequencing of IMD isolates, are in progress to enhance IMD surveillance in Australia. The AMSP data are used for informing treatment guidelines and disease prevention strategies; and to monitor the effect of interventions.

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