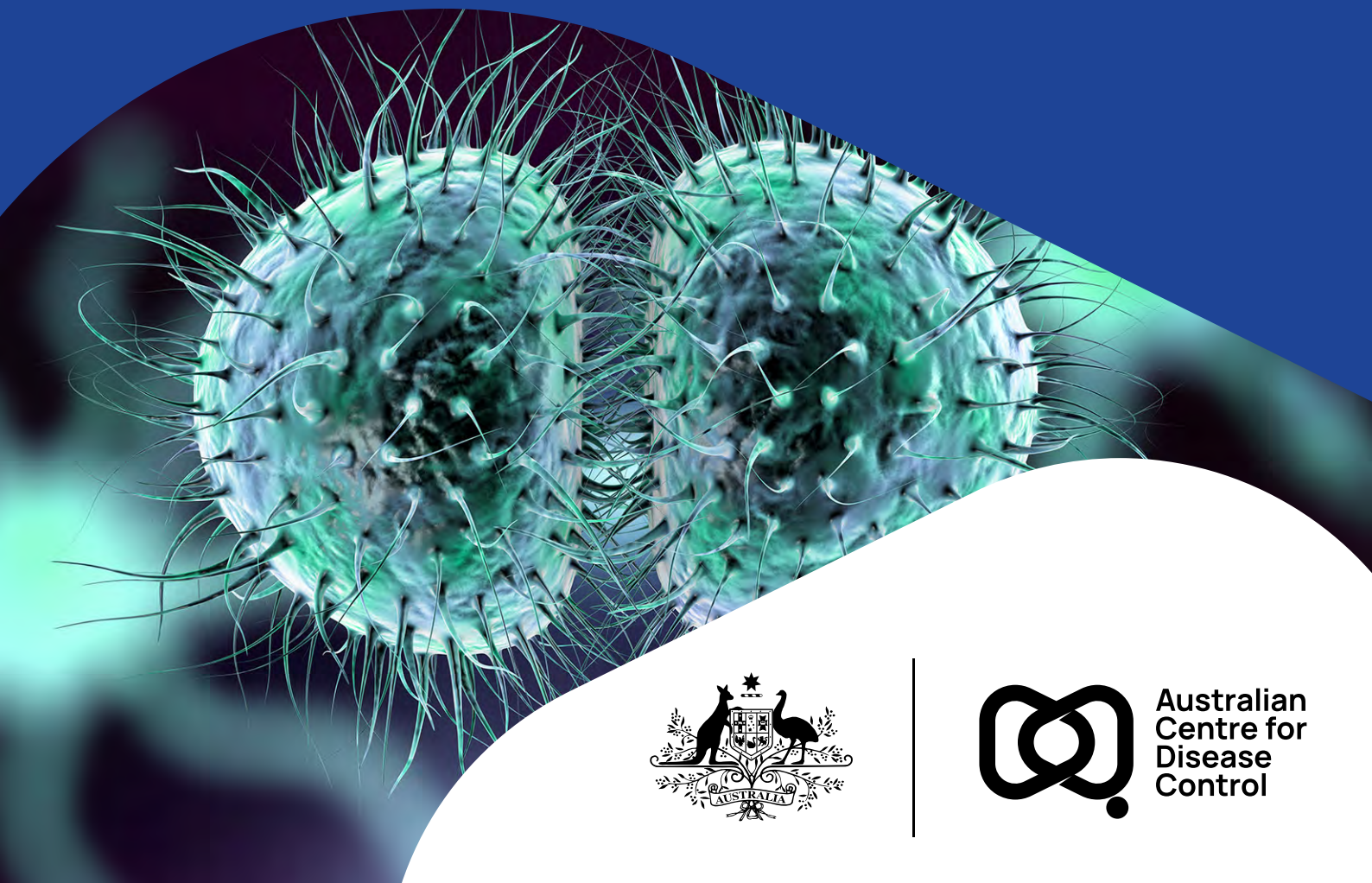
Communicable Diseases Intelligence

2026 • Volume 50 • cdc.gov.au/cdi • Epub date: 16.11.2026 • doi.org/10.33321/cdi.2026.50.063

Australian Meningococcal Surveillance Programme Annual Report, 2025

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Australian Centre for Disease Control

Communicable Diseases Intelligence

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ISSN: 2209-6051 Online

This journal is indexed by Index Medicus and Medline.

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Abstract

In Australia, both probable and laboratory-confirmed cases of invasive meningococcal disease (IMD) are reported to the National Notifiable Diseases Surveillance System (NNDSS). When compared to 2024, the number of IMD notifications in 2025 decreased by 13% to 118. IMD was confirmed by laboratory testing in 115/118 (97%) of 2025 IMD cases, with 66% (76/115) diagnosed by bacterial culture and 34% (39/115) by nucleic acid amplification testing. The genogroup was determined for 93% of laboratory-confirmed cases (107/115): genogroup B (MenB) accounted for 82.2% of infections (88/107); MenW and MenY for 7.5% of disease (8/107) each; MenC for 1.9% (2/107); and MenA for 0.9% (1/107). Finetyping was available for 67% of the cases for which the genogroup was determined (72/107). In MenB isolates, 28 *porA* types were detected: the most prevalent from amongst these were P1.7-2,4 (21%; 12/58) and P1.7,16-26 (14%; 8/58). Of the eight MenW isolates in 2025, six were finetyped and identified as *porA* type P1.5,2, MLST (ST) 11 and belonging to the clonal complex 11, the hypervirulent strain reported in outbreaks in Australia and overseas. In MenY infections, four *porA* types were detected from the five isolates finetyped: P1.21,16; P1.5,10-1; P1.5-1,10-1; and P1.5-2,10-1, with no dominant *porA* type detected. One of the two MenC isolates was typed, identifying as P1.5-2,10-1 and the single MenA isolate identified as P1.5-2,10.

Peaks of IMD occurred in children aged less than 5 years, in those aged 15–24 years, and in adults aged 25–44 years, accounting for 18% (21/115), 23% (26/115) and 22% (25/115) of laboratory-confirmed cases, respectively. In children aged under 5 years, 100% of IMD (21/21) was MenB; in those aged 15–24 years, 100% of IMD (25/25) was MenB; and in those aged 25–44 years, 82% of IMD (18/22) was MenB, with three MenW cases and one MenC case reported in this age group. IMD was reported in all age groups: < 5 years (18%; 21/115); 5–9 years (5%; 6/115); 10–14 years (2.6%; 3/115); 15–24 years (23%; 26/115); 25–44 years (22%; 25/115); 45–64 years (12%; 14/115); and in those aged 65 years and older (17%; 20/115). Whilst MenB predominated in all age groups, the majority of MenY IMD cases (6/8) were reported in adults aged 65 years and older, among whom it accounted for 6/18 cases (33%).

All cultured IMD isolates available for antimicrobial susceptibility testing (n = 76) were tested for ceftriaxone and penicillin. Minimum inhibitory concentration (MIC) values were reported using Clinical Laboratory Standards Institute (CLSI) interpretative criteria: 8% (6/76) were defined as penicillin resistant (MIC value ≥ 0.5mg/L); 64% (49/76) had intermediate susceptibility to penicillin (MIC values 0.125 and 0.25 mg/L); and 28% (21/76) were susceptible to penicillin (MIC values ≤ 0.064 mg/L). All isolates tested 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 undertakes laboratory 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 Centre for Disease Control (Australian CDC) 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.

IMD notifications in Australia peaked in 2002 at 3.5 cases per 100,000 persons per year,[2] with the majority of disease caused by genogroups B and C (MenB and MenC).[3] The introduction of the conjugate genogroup C meningococcal vaccine to the National Immunisation Program (NIP) in 2003 led to a significant and sustained reduction in genogroup C IMD notifications, and a reduction in overall notifications to a nadir of 0.6 cases per 100,000 persons in 2013.[4,5] However, from 2013 an increase in both MenW and MenY IMD in Australia was reported, and the IMD notification rate increased to 1.5 cases per 100,000 persons in 2017,[2] when MenACWY immunisation programmes were implemented across jurisdictions in targeted age groups. In 2018, the change from monovalent genogroup C to MenACWY vaccination expanded coverage on the national immunisation programme for infants and then adolescents.[3] Following the introduction nationally of the quadrivalent MenACWY vaccine in 2018, IMD notifications declined further from 1.1 per 100,000 persons in 2018 to 0.8 per 100,000 persons in 2019. In 2020, there were 0.4 cases per 100,000 persons recorded and a continued reduction was recorded in 2021, to 0.3 cases per 100,000 persons. 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 easing of infection control containment measures, IMD notifications rose to 0.5 cases per 100,000 persons per year and was unchanged through 2023 and 2024. In 2025, IMD notifications declined to 0.4 cases per 100,000 persons per year, coincident with the implementation of the MenB vaccine in three jurisdictions of Australia in addition to South Australia, which implemented in 2018 to targeted age groups.[6]

IMD is a rare disease in Australia but remains of public health concern. Continued monitoring of phenotypic and genotypic features of IMD strains is critical to planning and informing 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 the culture of *N. meningitidis*, or molecular diagnoses from a normally sterile site, defined as laboratory-definitive evidence of IMD according to national case definitions.[7] Australian CDC information regarding the site of infection and the age and sex of the patients is collated by the NNN for the AMSP. Patient outcome data was not available for the report.

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

Genogrouping and typing of *Neisseria meningitidis*

Genogrouping and genotyping are performed within the jurisdictions.

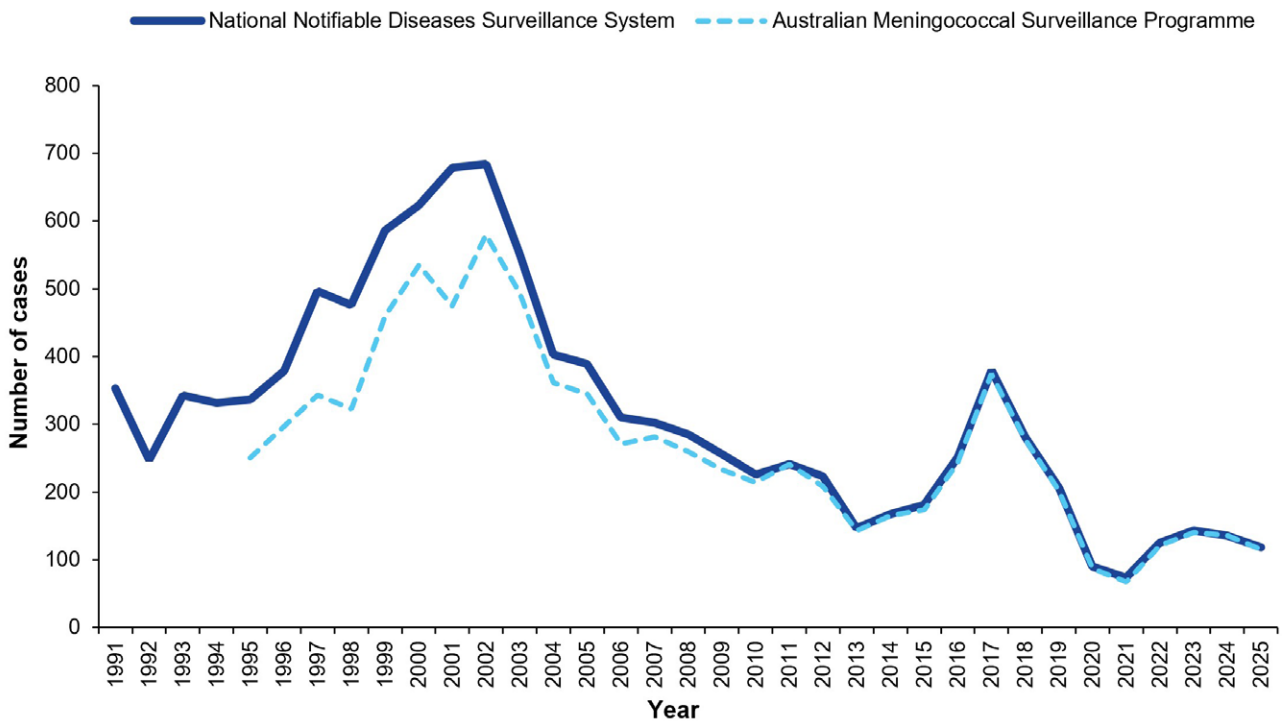
Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) of IMD isolates is routinely conducted to support patient care. Surveillance data of antibiotics used for treatment (ceftriaxone and penicillin) and for clearance of carriage (ciprofloxacin and rifampicin) are reported by the NNN. For the AMSP, antibiotic susceptibilities are reported according to the Clinical Laboratory Standards Institute's (CLSI) M100 guidelines.[8] Antimicrobial resistance to ciprofloxacin in *N. meningitidis* has been reportable to the national alert system for critical antimicrobial resistances (CARAlert) since January 2023.[9]

Results

In 2025, there were 118 IMD cases notified to the NNDSS, of which 115 (97%) were laboratory confirmed.[2] Laboratory data were available to the AMSP for all 115 laboratory-confirmed IMD cases, as shown in Figure 1. In 2025, an increase in the number of IMD notifications was observed in New South Wales, while in Queensland and South Australia IMD was reduced to almost half the number reported in 2024. IMD notifications for Victoria (n = 19) and Western Australia (n = 17) were the same number as in 2024, with few notifications reported from Tasmania (3), the Australian Capital Territory (1) and the Northern Territory (1). In 2025, the peak incidence of IMD occurred in autumn through winter to early spring (1 April to September), as shown in Table 1.

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] 1991–2025



a Source: National Communicable Diseases Surveillance Dashboard. Data extracted on 13 January 2026. https://nindss.health.gov.au/pbi-dashboard/.

Table 1: Laboratory-confirmed cases of invasive meningococcal disease, Australia, 2025 by quarter

IMD genogroup	1 January – 31 March	1 April – 30 June	1 July – 30 September	1 October – 31 December	2025 total
A	1	0	0	0	1
B	19	27	26	16	88
C	1	0	0	1	2
W	2	2	2	2	8
Y	3	1	4	0	8
ND[a]	2	2	1	3	8
Total	**28**	**32**	**33**	**22**	**115**

a ND: not determined.

Laboratory diagnosis of IMD

In 2025, a total of 76/115 (66%) of laboratory-confirmed cases were by bacterial culture and 39/115 (34%) by molecular testing (Table 2), of blood (81/115), CSF (29/115), joint fluid (2/115), post-mortem tissue (2/115) and pericardial fluid (1/115).

Table 2: Number of laboratory-confirmed cases of invasive meningococcal disease, Australia, 2025, by specimen type and method of confirmation

Specimen	Bacterial culture	Nucleic acid amplification test	Total
Blood	69	12	81
CSF ± blood	4	25	29
Other sterile sites (joint fluid, pericardial fluid and post-mortem tissue)	3	2	5
Total	**76**	**39**	**115**

Notifications by jurisdiction

In 2025, New South Wales reported the highest number and proportion of IMD notifications nationally (31%; 36/115), followed by Queensland (23%; 26/115) and Victoria (17%; 19/115). An increase in IMD notifications, both in number and proportionality, was reported in New South Wales from 2024 (18%; 24/136) to 2025 (31%; 36/115). In 2025, IMD notifications were lower in number and proportion than in 2024 in Queensland (2025: 23%; 26/115 cf. 2024: 35%; 47/136) and South Australia (2025: 13%; 15/115 cf. 2024: 21%; 29/136). The number of notifications and proportions of IMD from Victoria (2025: 17%; 19/115 cf. 2024: 14%;19/136) and Western Australia (2025: 12%; 14/115 cf. 2024: 10%;14/136) were similar to 2024, with notifications from Tasmania, the Australian Capital Territory and the Northern Territory remaining low in 2025. Jurisdictional case numbers are shown in Table 3.

Table 3: Number of laboratory-confirmed cases of invasive meningococcal disease, Australia, 2025, by jurisdiction and genogroup

	Genogroup						
Jurisdiction	**A**	**B**	**C**	**W**	**Y**	**ND[a]**	**Total**
Australian Capital Territory	0	0	0	1	0	0	1
New South Wales	0	22	1	4	5	4	36
Northern Territory	0	1	0	0	0	0	1
Queensland	0	22	1	2	0	1	26
South Australia	0	13	0	0	1	1	15
Tasmania	0	3	0	0	0	0	3
Victoria	1	15	0	0	1	2	19
Western Australia	0	12	0	1	1	0	14
Australia	**1**	**88**	**2**	**8**	**8**	**8**	**115**
% genogroup, where determined (n = 107)	0.9	82.2	1.9	7.5	7.5	—	—

a ND: genogroup not determined.

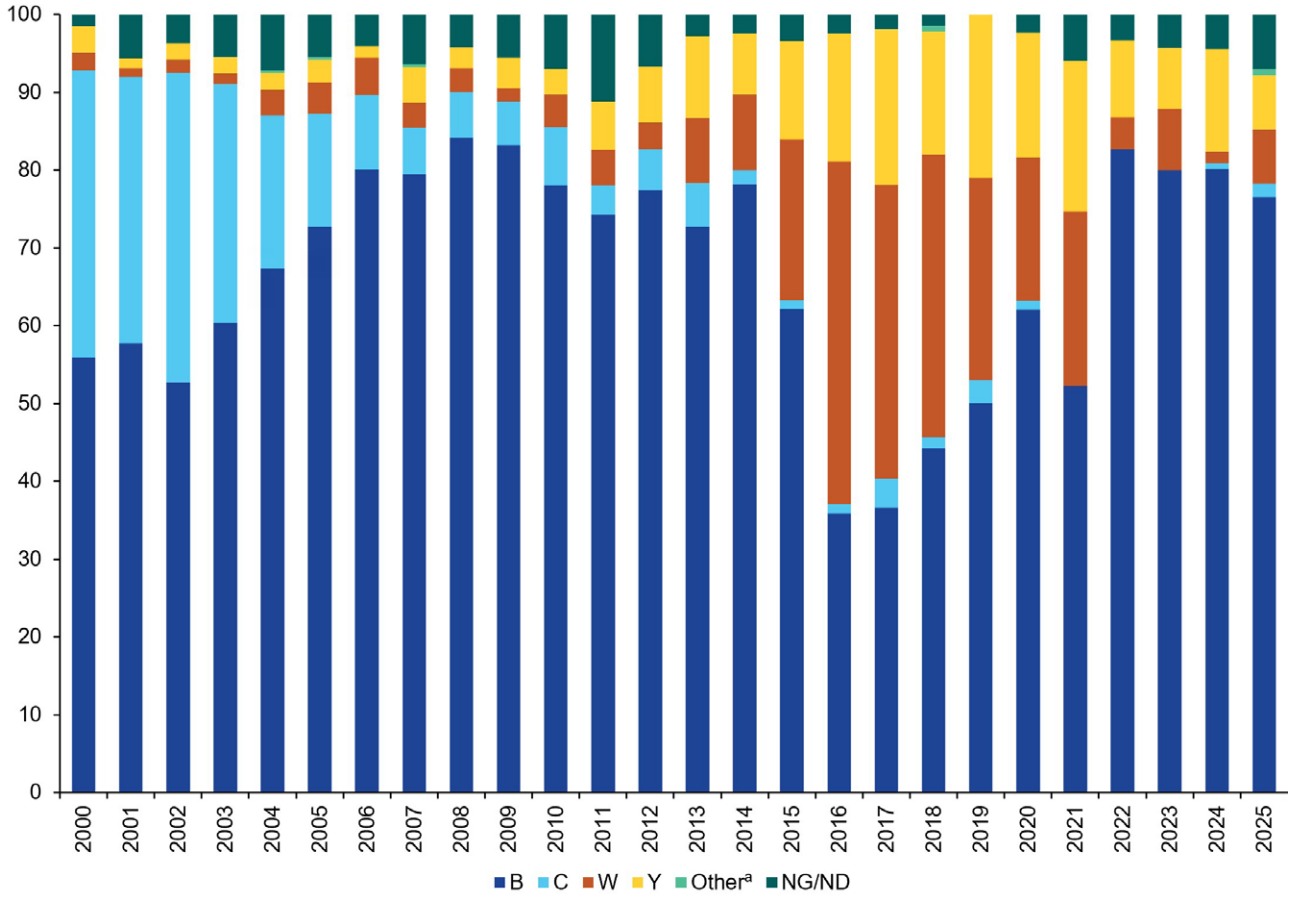
From 2006 through 2014, the proportion of IMD attributable to MenB ranged from 73 to 84% nationwide, falling to 62% in 2015, and then to 37% in 2016–2017. Subsequently, there has been an overall increase in the proportion of IMD attributable to MenB, rising to 44% in 2018; to 50% in 2019; and to 62% in 2020, with a temporally limited decrease to 52% observed in 2021. From 2022 to 2024, MenB accounted for more than 84% of IMD in Australia and then decreased in 2025 to 82%. MenB IMD was reported across all age groups in 2025.

MenW was responsible for a relatively low proportion of IMD prior to 2015 (1–5% in 2000–2012, 8-10% in 2013–2014). Increases to 21% were observed in 2015, to 44% in 2016. The proportion progressively declined, coincident with vaccination changes, from 36–38% in 2017–2018, 18–26% in 2019–2021, 4–8% in 2022–2023, to 1% in 2024 and increasing again to 7% in 2025 (Figure 2).

MenY accounted for 1–5% IMD in 2000–2010 before increasing to 6–13% in 2011–2015, rising to 16–21% in the years 2016–2021, then decreasing to 8–10% in 2022–2023. An increase in MenY IMD was observed in 2024 to 14%, before waning again to 7% in 2025 (see Figure 2). In 2025, MenW and MenY each attributed to 7% of IMD in Australia.

In 2025, there were two MenC IMD cases reported from New South Wales and Queensland and there was a rare notification of MenA IMD in Victoria involving a traveller from Eastern Europe. This MenA IMD is the first reported nationally since 2005. For IMD where a genogroup could not be determined as B,C,W or Y (8/115, 7%), further examination showed two isolates lacked functional genes for capsule synthesis (termed capsule null locus, *cnl*), and a genogroup E backbone was detected in another isolate (Table 3).[10]

Figure 2: Proportion of genogroups of laboratory-confirmed invasive meningococcal disease, Australia, 2000 – 2025 by year



a Cases grouped as 'Other' in the above graph are single instances of genogroup A, reported in 2004, 2005, and 2025; a single instance of genogroup X in 2007; and two instances of genogroup E reported in 2018.

IMD age and genogroup distribution

In 2025, IMD notifications were reported across all age groups. Disease peaks occurred in children less than 5 years of age (21/115 cases; 18%), with 38% of these children (8/21) aged less than one year. IMD was also observed to peak in those aged 15–24 years (26/115 cases; 23%) and 25–44 years (25/115 cases; 22%).

The genogroup was determined for 107/115 cases of IMD (93%). In children aged under 5 years and in those aged 15–24 years, all IMD was attributable to MenB, (21/21) and (25/25) respectively. In those aged 25–44 years, where genogroup was determined, 82% of IMD was MenB (18/22), 14% (3/22) was MenW and one case (1/22) of MenC was IMD reported. MenB accounted for 82% (88/107) of IMD overall, and was the most numerous genogroup in all age groups.

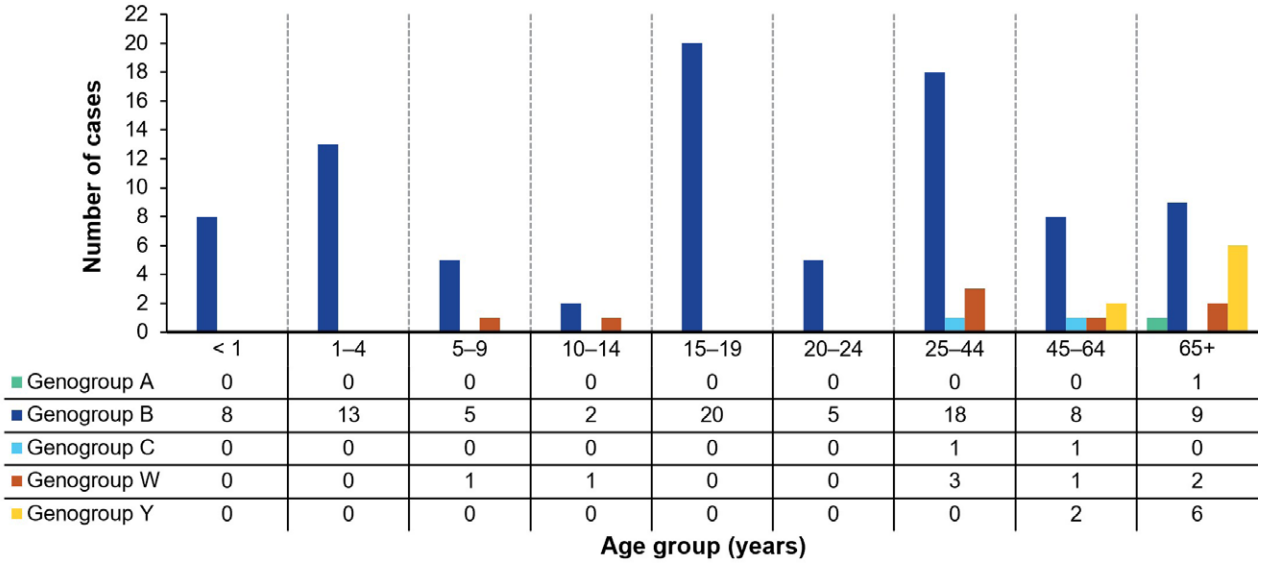
IMD attributed to MenW and MenY accounted for eight notifications each in 2025. MenW was responsible for infections across a range of ages (see Table 4 and Figure 3), whereas 75% of MenY infections (6/8) were in adults aged 65 years and older. The genogroup distribution for IMD nationally in 2025 is shown in Table 4 and Figure 3.

Table 4: Laboratory-confirmed cases of invasive meningococcal disease (IMB), Australia, 2025, by age and genogroup, and the proportion of IMD attributable to MenB

	Age group (years)									
Genogroup	**< 1**	**1–4**	**5–9**	**10–14**	**15–19**	**20–24**	**25–44**	**45–64**	**65+**	**Total**
A	0	0	0	0	0	0	0	0	1	1
B	8	13	5	2	20	5	18	8	9	88
C	0	0	0	0	0	0	1	1	0	2
W	0	0	1	1	0	0	3	1	2	8
Y	0	0	0	0	0	0	0	2	6	8
ND[a]	0	0	0	0	0	1	3	2	2	8
Total	**8**	**13**	**6**	**3**	**20**	**6**	**25**	**14**	**20**	**115**
% MenB IMD within age group (where a genogroup was determined)	100%	100%	83%	67%	100%	100%	82%	67%	50%	82%

a ND: genogroup not determined.

Figure 3: Number of genogroup A, B, C, W and Y cases of laboratory-confirmed invasive meningococcal disease, Australia, 2025, by age



IMD and genotyping

Finetyping was performed on 58/88 MenB isolates (66%); this genogroup showed the greatest variability. There were 28 *porA* types reported nationally, with one dominant *porA* type identified: P1.7-2,4 (12/58; 21%), as shown in Figure 4 and Table 5; nonetheless, the proportion and number of isolates of this *porA* type were both less than reported in 2024, when it contributed to 38% (29/76) of MenB IMD. The next most abundant MenB *porA* type in both 2024 and 2025 was P1.7,16-26, accounting for 14% of finetyped MenB isolates (8/58), an increase in proportion from 2024 (8/76;11%). In 2025, the *porA* type B:P1.7-2,4 was predominately detected in South Australia (7/12, 58%).

Of the eight MenW isolates reported in 2025, six were finetyped and one *porA* type was identified, P1.5,2, MLST (ST)-11 belonging to clonal complex 11 (see Figure 4 and Table 5). This *porA* type P1.5,2 has been in circulation in recent years and is the same as the hypervirulent genogroup W strain reported in the United Kingdom and South America since 2009.[11,12]

Of the eight MenY isolates in 2025, six were finetyped and four *porA* types were identified: P1.21,16, P1.5,10-1, P1.5-1,10-1 and P1.5-2,10-1 (see Figure 4 and Table 5). The *porA* type P1.5-1,10-1 has been the predominant MenY genotype circulating in Australia since 2015 (which marked the year when the increase in genogroup Y IMD was first observed); however, in 2025 there were only two notifications of this *porA* type. The *porA* type distribution for IMD nationally in 2025 is shown in Table 5 and Figure 4.

Figure 4: The number of *porA* types represented in genogroup A, B, C, W and Y invasive meningococcal disease notifications in Australia in 2025

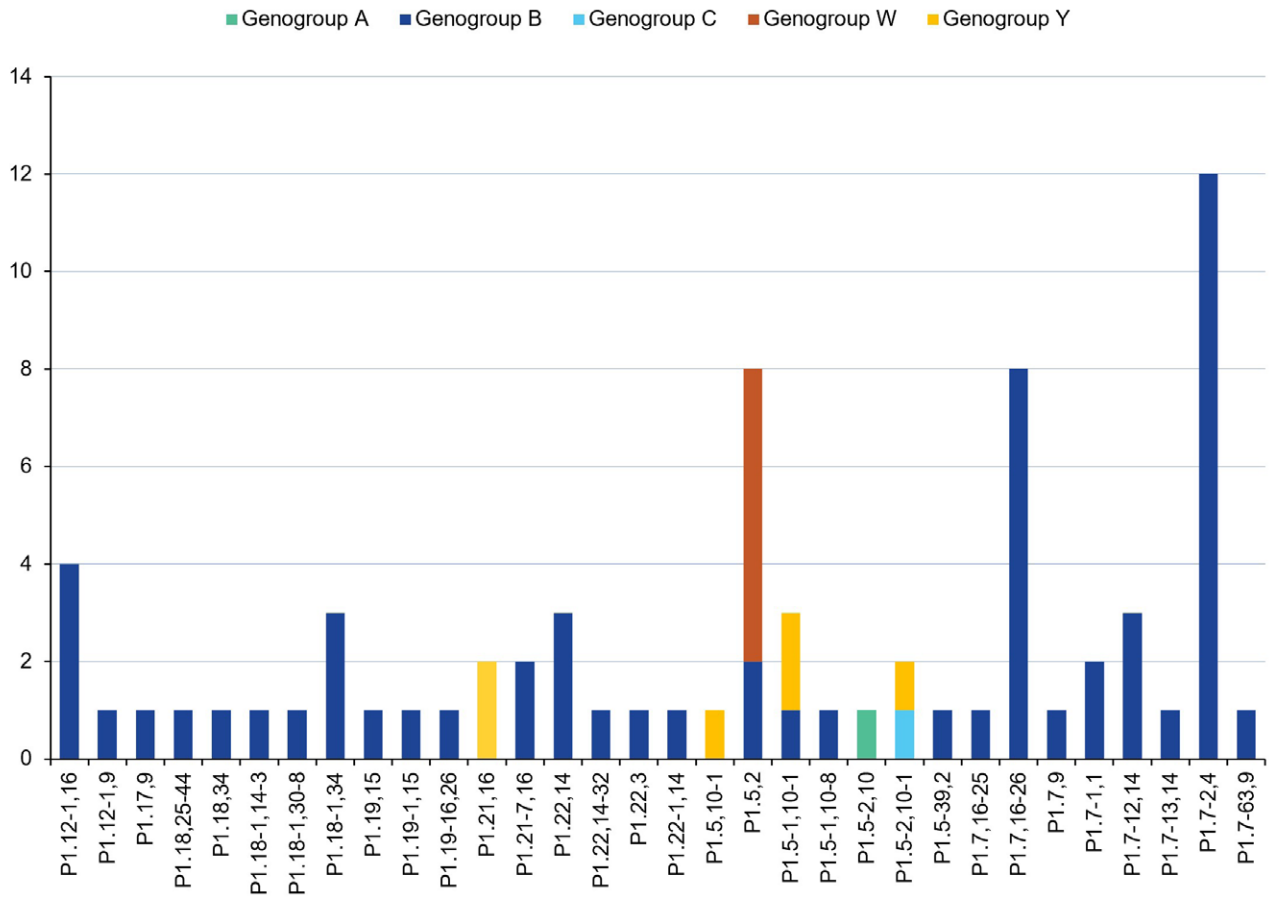


Table 5: Distribution of *porA* types in isolates of invasive meningococcal disease, Australia, 2025, by state or territory (n = 71/107)

2025 AMSP		Number per genogroup per state / territory[a]								
Genogroup	Genotype_ *PorA*	ACT	NSW	NT	Qld	SA	Tas.	Vic.	WA	Total
A	P1.5-2,10	0	0	0	0	0	0	1	0	1
B	P1.12-1,16	0	2	0	1	0	0	1	0	4
B	P1.12-1,9	0	0	0	0	0	0	0	1	1
B	P1.17,9	0	1	0	0	0	0	0	0	1
B	P1.18,25-44	0	0	0	0	1	0	0	0	1
B	P1.18,34	0	0	0	0	0	0	0	1	1
B	P1.18-1,14-3	0	0	0	0	0	0	0	1	1
B	P1.18-1,30-8	0	0	0	1	0	0	0	0	1
B	P1.18-1,34	0	1	0	2	0	0	0	0	3
B	P1.19,15	0	0	0	1	0	0	0	0	1
B	P1.19-1,15	0	0	1	0	0	0	0	0	1
B	P1.19-16,26	0	1	0	0	0	0	0	0	1
B	P1.21-7,16	0	0	0	2	0	0	0	0	2
B	P1.22,14	0	2	0	1	0	0	0	0	3
B	P1.22,14-32	0	0	0	0	0	0	1	0	1
B	P1.22,3	0	0	0	0	0	0	1	0	1
B	P1.22-1,14	0	0	0	1	0	0	0	0	1
B	P1.5,2	0	1	0	1	0	0	0	0	2
B	P1.5-1,10-1	0	1	0	0	0	0	0	0	1
B	P1.5-1,10-8	0	0	0	1	0	0	0	0	1
B	P1.5-39,2	0	0	0	1	0	0	0	0	1
B	P1.7,16-25	0	0	0	0	0	1	0	0	1
B	P1.7,16-26	0	1	0	3	0	0	3	1	8
B	P1.7,9	0	0	0	0	0	0	0	1	1
B	P1.7-1,1	0	1	0	1	0	0	0	0	2
B	P1.7-12,14	0	0	0	2	0	1	0	0	3
B	P1.7-13,14	0	0	0	1	0	0	0	0	1
B	P1.7-2,4	0	2	0	2	7	0	1	0	12
B	P1.7-63,9	0	0	0	1	0	0	0	0	1
C	P1.5-2,10-1	0	0	0	1	0	0	0	0	1
W	P1.5,2	1	3	0	2	0	0	0	0	6
Y	P1.21,16	0	1	0	0	1	0	0	0	2
Y	P1.5,10-1	0	2	0	0	0	0	0	0	1
Y	P1.5-1,10-1	0	1	0	0	0	0	0	0	2
Y	P1.5-2,10-1	0	0	0	0	0	0	1	0	1
Total with typing results		**1**	**20**	**1**	**25**	**9**	**2**	**9**	**5**	**72**

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

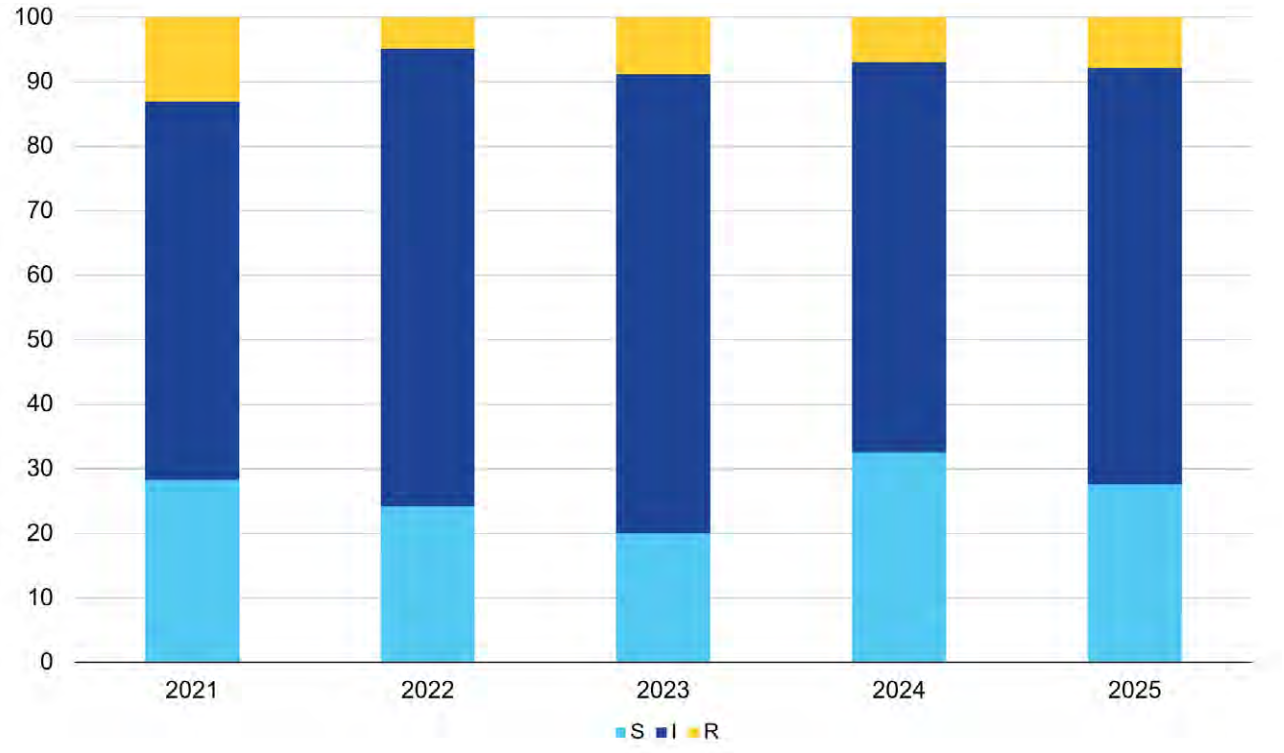
Antimicrobial susceptibility testing

Sixty-six percent of laboratory-confirmed IMD (76/115) had *N. meningitidis* cultures permitting AST by NNN laboratories. The distribution of penicillin MIC values is shown in Table 6, with 28% (21/76) susceptible; 64% (49/76) with intermediate susceptibility; and 8% (6/76) resistant (Figure 5, Table 6). Penicillin-resistant isolates in 2025 were proportionally similar to 2024 (7%; 6/86), and identified as four MenB of different *porA* types and two MenW belonging to the ST-11 complex.[11,12] In recent years, MenW of the ST-11 complex have demonstrated higher penicillin MIC values and higher proportions of resistance.[13] All isolates tested in 2025 were susceptible to ceftriaxone, ciprofloxacin and rifampicin.

Table 6: Penicillin MIC distribution of laboratory-confirmed invasive meningococcal disease isolates, Australia, 2025

	Penicillin MIC distribution								
MIC mg/L	≤ 0.032	0.064	0.125	0.25	0.5	1	2	≥ 4	Total
Number of isolates	9	12	27	22	6	0	0	0	76
%	12%	16%	36%	29%	8%	0%	0%	0%	100%

Figure 5: Proportion of invasive meningococcal disease isolates with susceptibility (S), intermediate susceptibility (I) and resistance (R) to penicillin, Australia in 2021 to 2025[8]



Discussion

In 2025, there were 118 IMD notifications nationally, a 13% decrease from 2024, coincident with changes in the National Immunisation Programme (NIP) to quadrivalent MenACWY vaccine and jurisdictional initiatives for the MenB vaccine.[6,14,15] In the United Kingdom (UK), following easing of pandemic restrictions it was observed that IMD genogroup versus age distributions provide evidence that vaccination programmes are maintaining low rates of MenC, MenW and MenY disease.[16] The surveillance reports of the AMSP show the impact of the NIP on the prevailing genogroup over time,[3] with MenB now predominating. In March 2024, MenB vaccination programmes were initiated in Queensland, followed by the Northern Territory and Tasmania in 2025.[6]

In 2025, ninety-seven percent of IMD notifications in Australia (115/118) were laboratory-confirmed. The distribution of IMD notifications across jurisdictions was proportionally higher than in 2024 for New South Wales (18% to 31%), but lower for Queensland (35% to 23%), and South Australia (21% to 13%). IMD notifications for Victoria (14% to 17%) and Western Australia (10% to 12%) were similar to 2024. The number of reported cases of IMD in Tasmania, the Northern Territory and the Australian Capital Territory are small.

Overall, MenB accounted for 82% IMD nationally in 2025 and caused the largest proportion of IMD in all age groups. In children less than 5 years of age, and in adolescents and young adults (15–24 years), all IMD was attributable to MenB. In those aged 65 years and over, where a genogroup was determined, MenB predominated (50%); however, 33% of IMD in this age group was attributable to MenY.

IMD was reported in all age groups in 2025, with predominance in children less than 5 years of age (21/115 cases; 18%); in those aged 15–24 years (26/115 cases; 23%); and those aged 25-44 years (25/115 cases; 22%). Notably, 30% IMD (34/115) occurred in those aged 45 years and over. The increase in IMD observed in older adults in Australia is consistent with observations in multiple locations internationally, with MenY the dominant or increasingly prevalent serogroup, warranting close observation.[17]

Finetyping revealed the continued diversity of MenB *porA* types in Australia, with 28 different *porA* types identified in 58 typed MenB isolates. There was a decrease in the predominant MenB *porA* genotype (P1.7-2,4) in Australia from 38% (29/76) in 2024 to 21% (12/58) in 2025. Most instances of this *porA* type were detected in South Australia (7/12, 58%). The next most prevalent MenB *porA* type, P1.7,16-26 (reported across several jurisdictions in 2025) has gradually declined from 16% (13/82) in 2023 to 11% (8/76) in 2024 and then increased in proportion, to 14% (8/58), in 2025.

MenW IMD increased in 2025 to 7% (8/107), after declining from 38% of IMD in 2017 to 1.5% (2/130) in 2024. These eight cases were mostly detected in adults aged 25 years and older (6/8), with only single instances in children aged 5 to 9 years and 10 to 14 years. Six MenW IMD in 2025 had genotyping data available: all were *porA* type P1.5,2, MLST (ST) 11, clonal complex 11. This strain emerged in the UK and South America in 2009, is hypervirulent and associated with atypical clinical presentations, more severe disease, and a higher case fatality rate.[11,12] The initial increase in MenW both overseas and in Australia was reported in older adults but subsequently was reported across all ages, particularly in adolescents and infants.[13]

In 2025, seven percent of IMD (8/107) was attributable to MenY, decreasing from 14% (8/107) in 2024, and mostly affecting adults aged 65 years and above (33%; 6/18). Four different *porA* types were identified in the six MenY IMD isolates finetyped in 2025. Since 2014 the predominant MenY genotype was P1.5-1,10-1, but in 2024 and 2025 the MenY genotype distribution displayed more heterogeneity than in 2023.[18]

Additionally, there was one case of MenA IMD reported in Australia, from a returned traveller; two cases of MenC IMD; and two isolates causing IMD in New South Wales and South Australia that were found to have a capsule null locus, lacking the genes to produce a capsule.[10] Another *N. meningitidis* isolate with an undetermined genogroup (not genogroup B,C,W or Y) in 2025, had on further examination a partial genogroup E backbone identified. These rare and sporadic cases, of IMD caused by *N. meningitidis* lacking intact capsules or capsular synthesis genes, have been detected in immunocompromised individuals.[10,19]

In 2023, a multijurisdictional outbreak of MenY ST-1466 urogenital infections was reported by the NNN.[20] Concurrently an outbreak of MenY ST-1466 IMD was reported in the United States of America (USA).[21] The MenY ST1466 *N. meningitidis* isolates circulating in Australia and the USA are capable of causing both urethritis and IMD.[22] In 2025, there were two IMD in Australian identified as ST-1466; P1.21,16; F3-7, one from South Australia and one from New South Wales. On analysis, the New South Wales isolate did not cluster genomically with the urogenital clone.

Whole genome sequencing (WGS) continues to be a useful tool in both surveillance and outbreak settings. Although tools have been developed to predict vaccine escape from genomic data, these should not be seen as definitive, due to several limitations including the inability to take into account synergistic effects of multiple antigens.

Testing of IMD isolates in 2025 detected 8% (6/76) penicillin resistance (MIC values ≥ 0.5 mg/L); all IMD isolates were susceptible to ceftriaxone, ciprofloxacin and rifampicin.

In 2025, the key findings of the AMSP Annual Report were a 13% decrease in IMD notifications from 2024 nationally and a continued predominance of MenB disease. IMD was reported in all age groups with predominance in children under 5 years of age and in the 15–24 and 25–44, year age groups. Notably, 30% of IMD (34/115) occurred those aged 45 years and over, with MenY IMD overrepresented in those aged 65 years and over. The NNN is continuing to lead further investigations in collaboration with the Australian CDC, closely monitoring the phenotypic and genotypic features of *N. meningitidis* causing IMD in Australia, including AMR. Additional investigations by the NNN, including whole genome sequencing of IMD isolates, are underway to enhance IMD surveillance in Australia. The AMSP data are utilized for informing treatment guidelines and disease prevention strategies, and to monitor the effects of interventions.

Acknowledgments

Meningococcal isolates were received in the reference centres from many laboratories throughout Australia. The considerable time and effort involved in forwarding these isolates is recognised and these efforts are greatly appreciated. These data could not have been provided without this assistance and the help of clinical colleagues and public health personnel. The Australian Centre for Disease Control provided funding for the National Neisseria Network.

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