Australian Meningococcal Surveillance Programme, 1 July to 30 September 2016

Monica M Lahra, Rodney P Enriquez for the Australian Meningococcal Surveillance Programme

Introduction

The reference laboratories of the National Neisseria Network, Australia report laboratory data on invasive meningococcal disease (IMD) cases confirmed by laboratory testing using culture and non-culture based techniques for the Australian Meningococcal Surveillance Programme (AMSP). Culture positive cases, where Neisseria meningitidis is grown from a normally sterile site or skin lesions, and non-culture based diagnoses, derived from results of nucleic acid amplification testing (NAAT) and serological techniques, are defined as IMD according to Public Health Laboratory Network definitions. Data contained in quarterly reports are usually restricted to a description of the numbers of cases by jurisdiction and serogroup, where known. Some minor corrections to data in the Table may be made in subsequent reports if additional data are received. A full analysis of laboratory confirmed cases of IMD in each calendar year is contained in the AMSP annual reports published in Communicable Diseases Intelligence. For more information see Commun Dis Intell 2016;40(1):E179.

Results

Of note in this quarter of 2016 is the number and proportion of IMD caused by serogroup W.

This is particularly evident in New South Wales and Victoria, which have both shown substantial increases in both the number and proportion of serogroup W cases compared with previous years. In the years 2007–2011 the proportion of IMD caused by serogroup W in Australia ranged from 1.8% to 4.5%, and increased to 8.6% to 9.9% in 2013-2014. In 2015 this increased markedly to 31/81 (21.4%) IMD cases in Australia. In 2015 25 serogroup W IMD strains were genotyped, and 81% were sequence type (ST)-11, and had the porA antigen encoding gene type P1.5,2, the same genotype as the hypervirulent strain reported in the United Kingdom and South America since 2009. Nationally, enhanced surveillance strategies including whole genome sequencing and phylogenetic inference has been applied to the recent emergence of *N. meningitidis* serogroup W in Australia.

Author details

Monica M Lahra^{1,2} Rodney P Enriquez¹

- Neisseria Reference Laboratory and World Health Organisation Collaborating Centre for STD, Sydney. Department of Microbiology, South Eastern Area Laboratory Services, The Prince of Wales Hospital, Randwick, New South Wales.
- School of Medical Sciences, Faculty of Medicine, The University of New South Wales, for the National Neisseria Network, New South Wales

Table: Number of laboratory confirmed cases of invasive meningococcal disease, Australia, 1 July to 30 September 2016, by serogroup and state or territory

		Serogroup													
State or		Α		В		С		Υ		W135		ND		All	
territory	Year	Q3	YTD	Q3	YTD	Q3	YTD	Q3	YTD	Q3	YTD	Q3	YTD	Q3	YTD
Australian Capital Territory	2016	0	0	1	1	0	0	0	0	1	1	0	0	2	2
	2015	0	0	0	1	0	0	1	1	0	0	0	0	1	2
New South Wales	2016	0	0	8	18	0	1	6	9	13	22	1	3	28	53
	2015	0	0	4	16	0	1	5	7	4	6	0	1	13	31
Northern Territory	2016	0	0	0	2	0	0	0	0	0	0	0	0	0	2
	2015	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Queensland	2016	0	0	6	11	0	0	2	8	5	10	1	3	14	32
	2015	0	0	7	16	0	0	1	2	3	3	0	1	11	22
South Australia	2016	0	0	6	17	0	0	0	0	2	2	0	0	8	19
	2015	0	0	15	24	0	0	0	0	0	0	0	0	15	24
Tasmania	2016	0	0	0	0	0	0	0	0	2	4	0	0	2	4
	2015	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Victoria	2016	0	0	2	9	0	1	2	4	8	23	1	1	13	38
	2015	0	0	7	23	0	0	4	6	6	12	0	0	17	41
Western Australia	2016	0	0	1	3	0	0	0	0	6	9	0	0	7	12
	2015	0	0	3	7	0	0	1	2	3	3	0	0	7	12
Total	2016	0	0	24	61	0	2	10	21	37	71	3	7	74	162
	2015	0	0	36	88	0	1	12	18	16	24	0	2	64	133