Measles Molecular Epidemiology: Australia 2016

Victorian Infectious Diseases Reference Laboratory

Summary Report

VIDRL
Victorian Infectious Diseases Reference Laboratory

Doherty Institute
A joint venture between the University of Melbourne and the Royal Melbourne Hospital

Measles Molecular Epidemiology in Australia 2016

During the reporting period, a total of 796 samples from 716 individuals were tested for measles virus RNA by real-time RT-PCR. Of these individuals, 86 (12%) had measles virus RNA detected with genotyping possible from 79 cases. The remaining 7 cases had a virus load (ct>37) that was too low for genotyping (untypable).

An additional 2 genotyping results were submitted directly to the WHO Measles Nucleotide Surveillance database by Queensland Health Scientific Services.

Measles cases were detected in 29 of the 52 reporting weeks (Figure 1) with wild-type measles circulation identified in 6 Australian states and 1 territory (Figure 2). At least 20 imported measles cases from at least 6 countries were identified as possible sources. Three wild-type measles virus genotypes (D4, D8 and B3) were identified.

Genotype D8, the most common type detected (n=57), was imported from multiple countries (India, Indonesia, Nepal, New Zealand, Pakistan, Thailand and Vietnam) with at least 9 separate cases introduced from India alone (Figure 2). There were multiple phylogenetic lineages of D8 seen in Australia with the ‘Hulu’ lineage strain predominating (Figure 3).

There were only 3 cases of measles genotype B3. Phylogenetic analysis of these N-450 sequences revealed all belonging to the Harare lineage (Figure 3). Genotype B3 measles was imported from Pakistan (Figure 2).

A single case of genotype D4, imported from India, was also identified in week 48.

The remaining 20 vaccine-associated cases (genotype A) were differentiated using a specific measles-vaccine real-time PCR.

Figure 1. Distribution of measles genotypes identified at VIDRL by epi-week, Jan-Dec 2016.

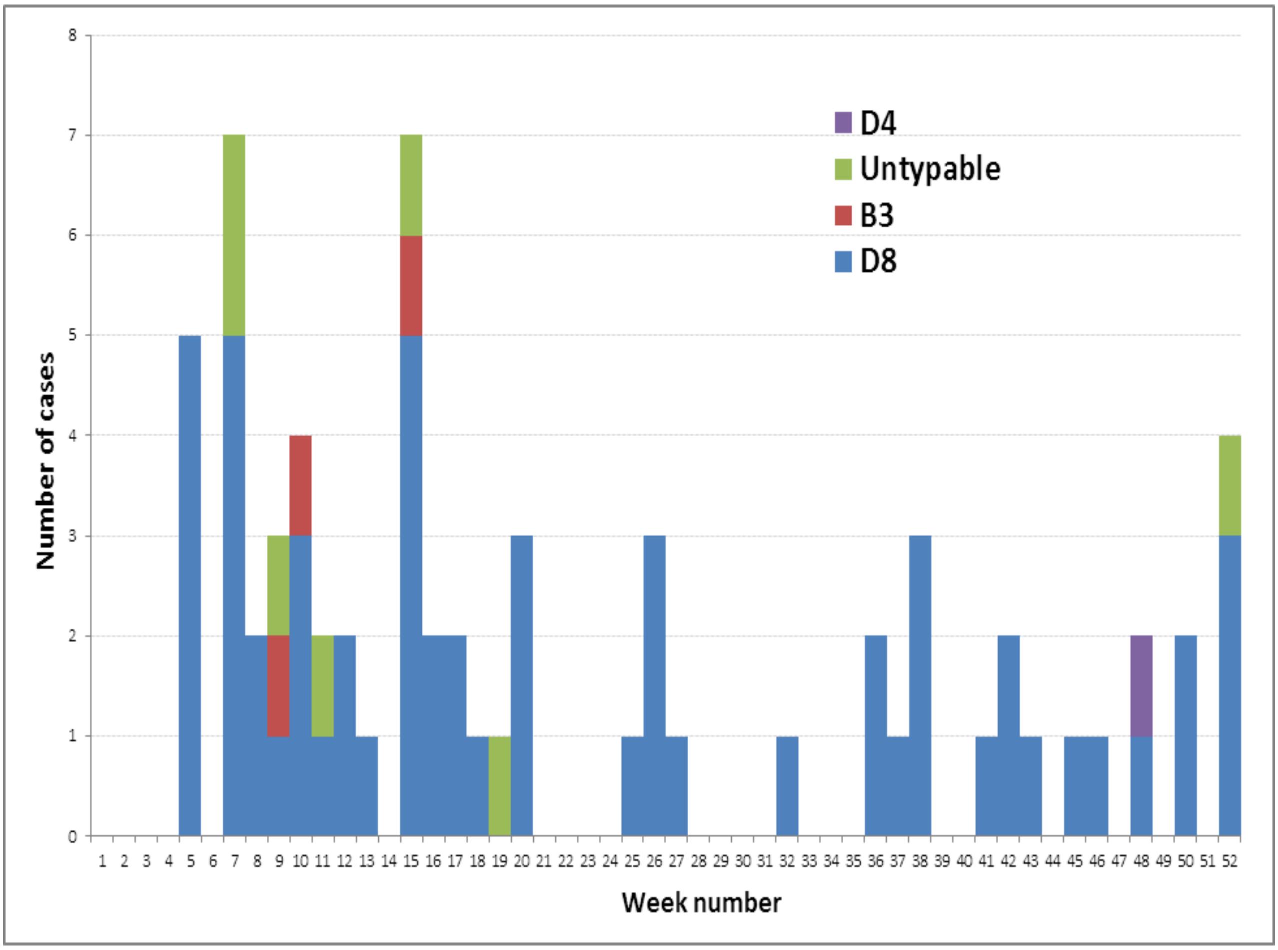

Figure 2. Measles virus genotypes imported into Australian states (January to December 2016 inclusive). The countries of importation are indicated (unknown = source of infection not determined). The source country of each confirmed measles case is based on the travel history provided to VIDRL and may not necessarily represent the 'true' country of origin for that genotype, since contact with the measles virus may have occurred in transit.

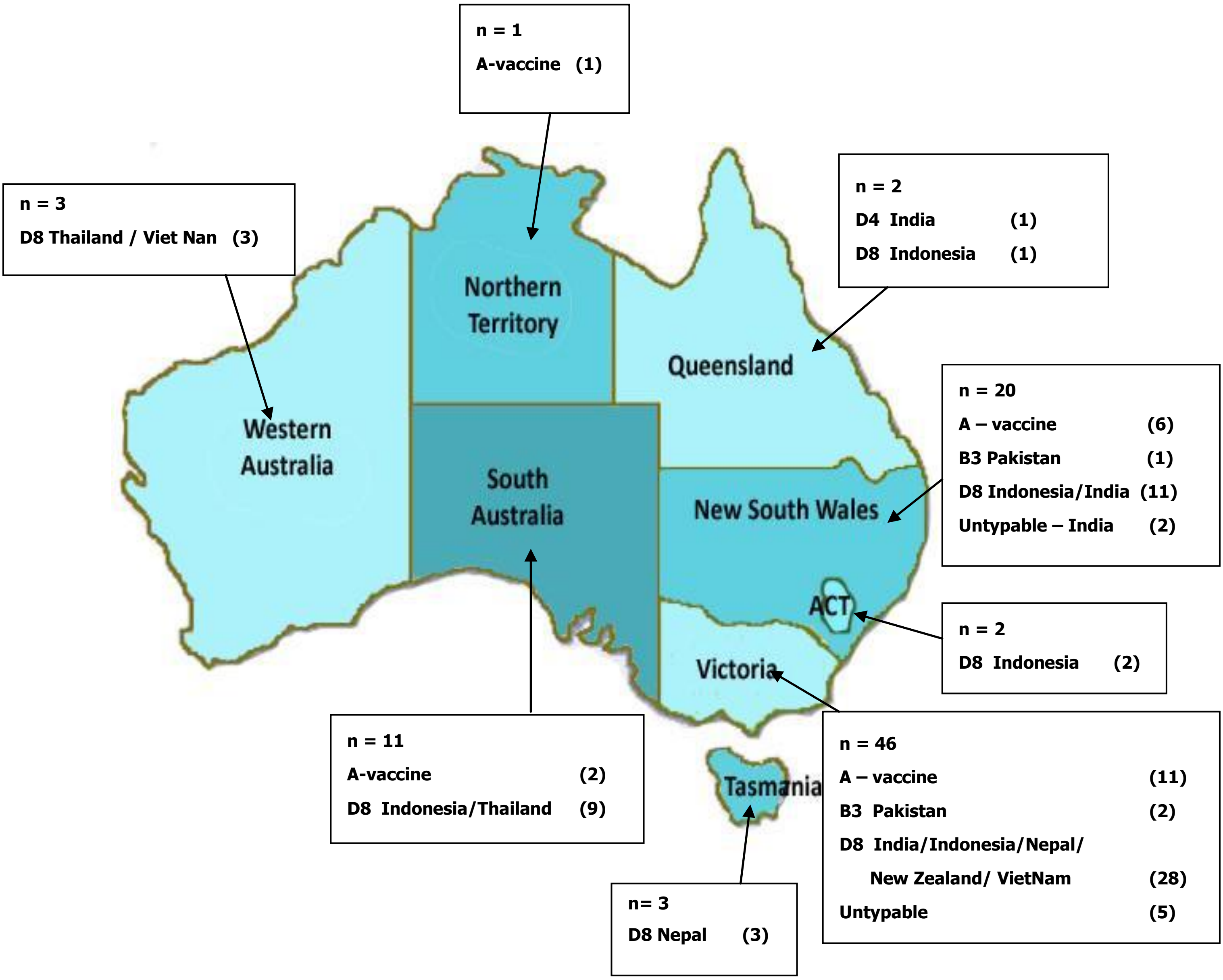

Figure 3. Phylogenetic tree comparing measles virus genotypes detected in Australia between January and December 2016. Reference strains are denoted by a solid red square. Named strains are denoted by a solid green circle.