

Measles Molecular Epidemiology: Australia 2015



Victorian Infectious Diseases Reference Laboratory Summary Report

Measles Molecular Epidemiology in Australia 2015

Between January and December 2015 measles genotyping was attempted on 63 samples with genotyping possible from 60 cases. The remaining 3 cases had a virus load (ct>37) that was too low for genotyping (untypable). The breakdown of genotyped samples by state and territory was: Victoria 34, New South Wales 17, Australian Capital Territory 1, South Australia 1, Western Australia 6, and Northern Territory 1. An additional 7 genotyping results were submitted directly to the WHO Measles Nucleotide Surveillance database by Queensland Health Scientific Services.

Measles cases were detected in 36 of the 52 reporting weeks (Figure 1) with measles circulation identified in 5 states and 2 Territories (Figure 2). At least 13 countries were identified as possible sources with the majority of measles cases determined to be from importation or were import-related. A small number of unknown source cases were also detected. Four wild-type measles virus genotypes (B3, D4, D8 and H1) were identified.

Genotype D8, the most common type detected (n=38), was imported from multiple countries (Azerbaijan, Indonesia, Malaysia and Vietnam) with at least 8 separate cases introduced from India alone (Figure 2). There were multiple phylogenetic lineages of D8 seen in Australia with the Hulu, Villupuram and Frankfurt strains identified (Figure 3).

There were 5 cases of measles genotype H1. Phylogenetic analysis of N-450 sequences revealed 2 distinct lineages, one belonging to the Hong Kong H1 lineage and the other to the Hebei lineage (Figure 3). Genotype H1 measles was imported from China and Switzerland.

The 8 cases of Harare lineage genotype B3 were imported from Afghanistan, India, Somalia, Papua New Guinea, Vanuatu and Norway.

The remaining 13 cases were genotype A (vaccine strain), differentiated using a specific measles-vaccine real-time PCR. All these cases presented with an adverse reaction to the first dose of MMR vaccine at 12 months of age.

Figure 1. Distribution of measles genotypes identified at VIDRL by epi-week, Jan-Dec 2015.

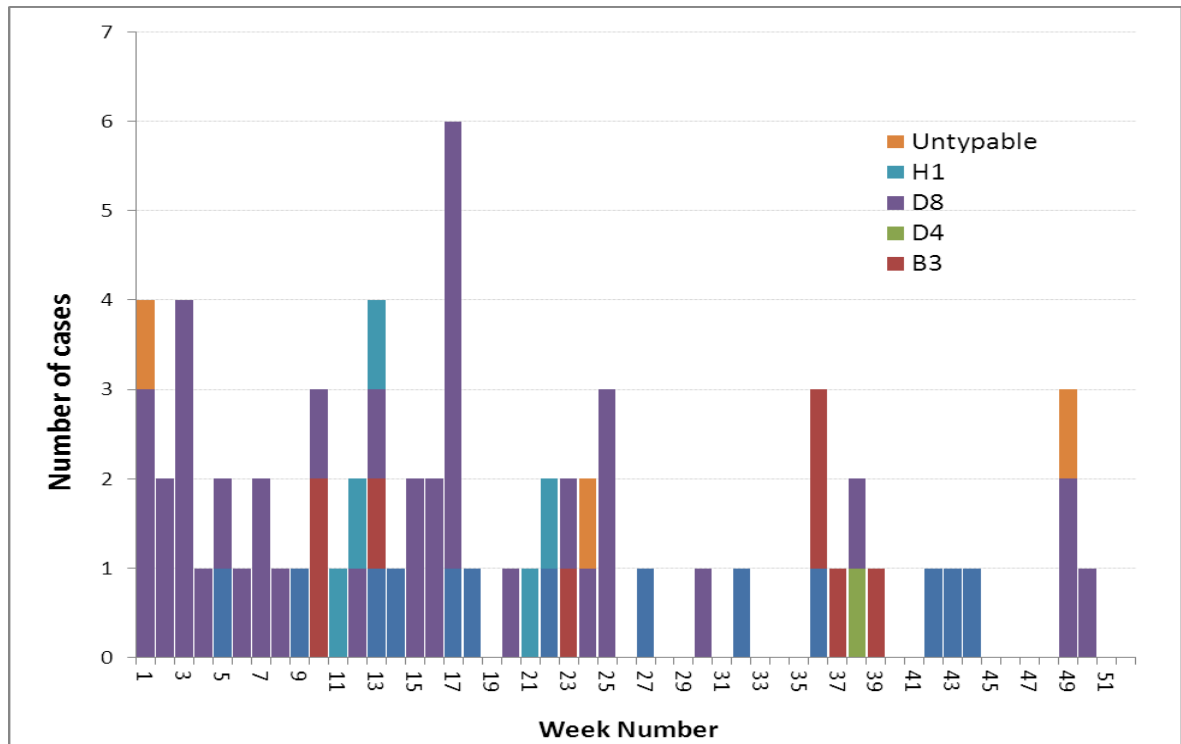


Figure 2. Measles virus genotypes imported into Australian states (January to December 2015 inclusive). The countries of importation are indicated (unknown = source of infection not determined). The source country of each confirmed measles case is based on the travel history provided to VIDRL and may not necessarily represent the ‘true’ country of origin for that genotype, since contact with the measles virus may have occurred in transit.

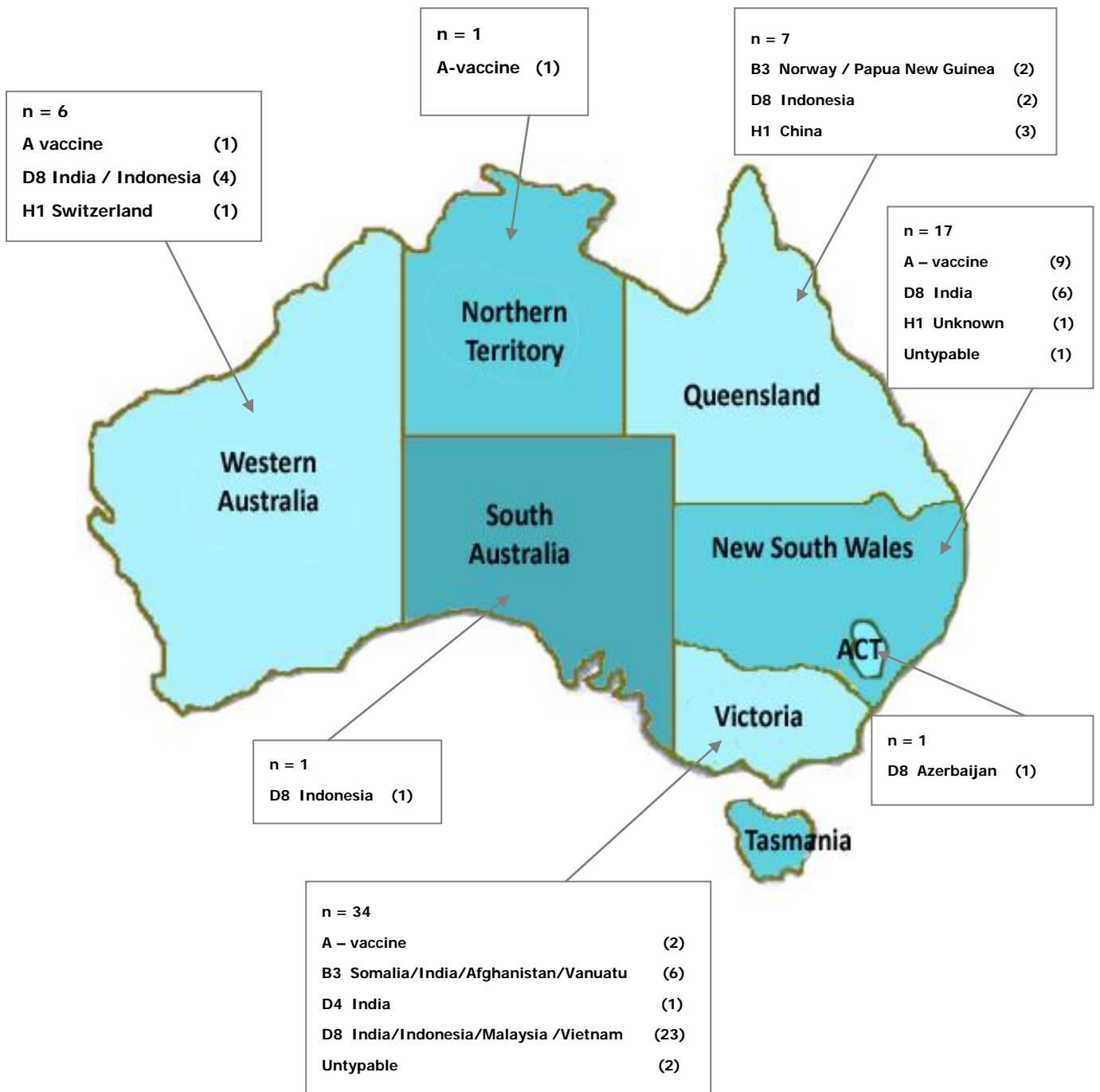


Figure 3. Phylogenetic tree comparing measles virus genotypes detected in Australia between January and December 2015. Reference strains are denoted by a solid red square. Named strains are denoted by a solid green circle. The source country of measles importation for a measles case is noted.

