Measles Molecular Epidemiology: Australia 2017

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 2017

During the reporting period, a total of 714 samples from 649 individuals were tested for measles virus RNA by real-time RT-PCR. Of these individuals, 93 (14.3%) had measles virus RNA detected with genotyping possible from 86 cases (59 wild-type and 27 vaccine-strain). The remaining 7 cases had a virus load (ct>37) that was too low for genotyping (untypable).

Wild-type measles cases were detected in 30 of the 52 reporting weeks (Figure 1) with circulation identified in 4 Australian States and 2 Territories (Figure 2). At least 29 imported measles cases from at least 11 countries were identified as possible sources. Three wild-type measles virus genotypes (B3, D8 and D9) were identified.

Genotype D8, the most common type detected (n=54), was predominately imported from Indonesia. Importation of D8 from other source countries included Cambodia, India, Italy, Malaysia, Republic of Korea, Spain and Thailand. Sequence analysis of these measles D8 cases revealed multiple phylogenetic lineages of D8 seen in Australia with the 'Hulu Langat' lineage strain (n=21) and 'Osaka' lineage strain (n=12) predominating (Figure 3). The remaining cases did not cluster to any one highly prevalent circulating lineage. Further analysis of genotype D8 broken down by Australian States (Figure 4-6) revealed clustering of viral strains both genetically and epidemiologically. These clusters were often short in duration and were commonly associated with a known imported primary case. This genotypic picture, together with epidemiological data, is crucial in providing strong evidence that Australia has maintained the interruption of endemic measles transmission.

There were only 4 cases of measles genotype B3. Phylogenetic analysis of these N-450 sequences revealed 3 belonging to the 'Dublin' lineage and 1 being a variant of the 'Harare' lineage (Figure 3). The Dublin lineage was imported into Australia from Europe (Italy and Romania) and the Harare variant was imported from Pakistan (Figure 2).

A single case of genotype D9, imported from Vietnam, was also identified in week 42.

The remaining 27 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 2017.

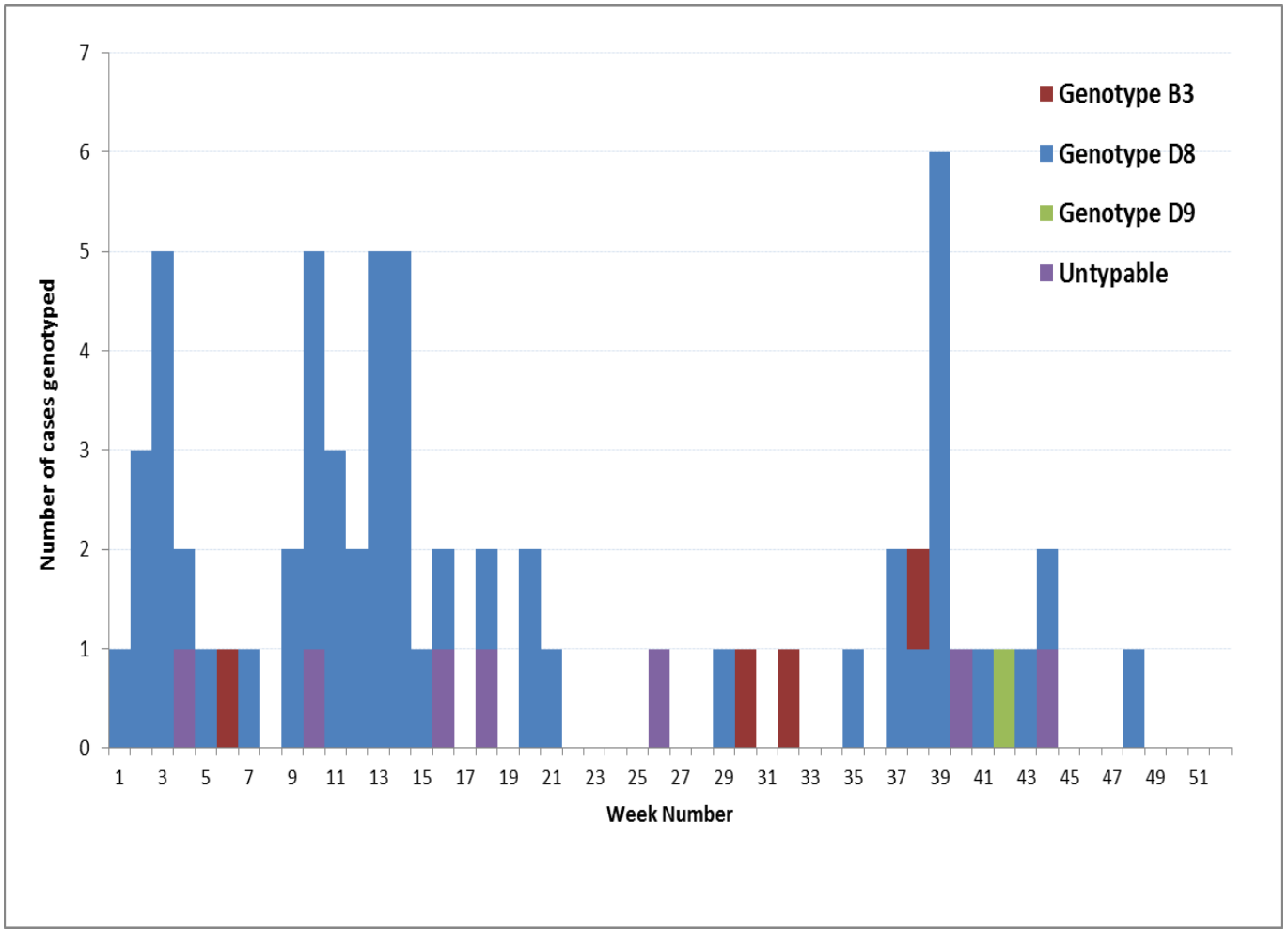


Figure 2. Measles virus genotypes imported into Australian states (January to December 2017 inclusive). The countries of importation are indicated (unknown = source of infection not determined). The source country of each confirmed measles case is based on the travel history provided to VIDRL and may not necessarily represent the 'true' country of origin for that genotype, since contact with the measles virus may have occurred in transit.

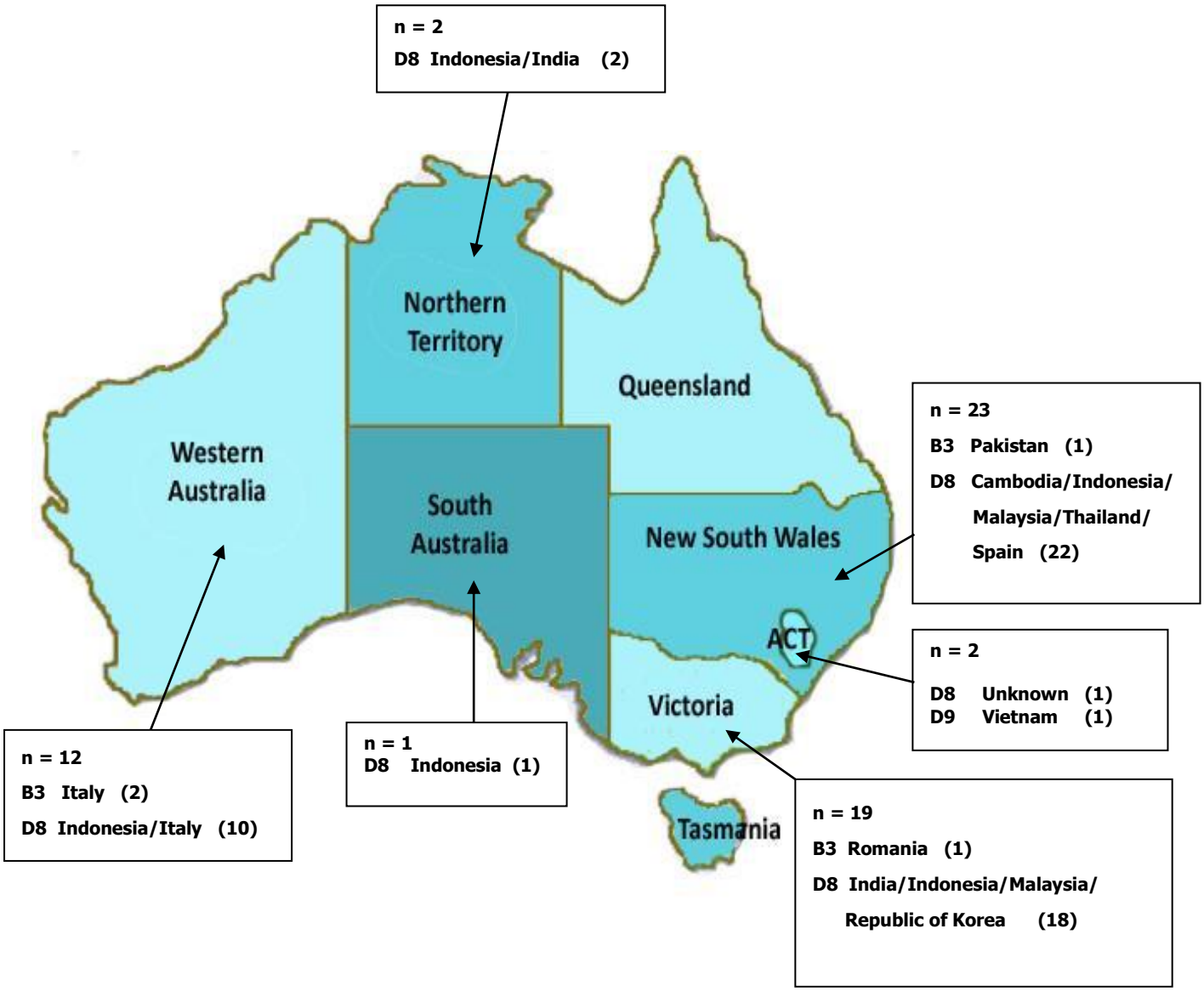


Figure 3. Phylogenetic tree comparing measles virus genotypes detected in Australia between January and December 2017. Reference strains are denoted by a solid red square. Named strains are denoted by a solid green circle.

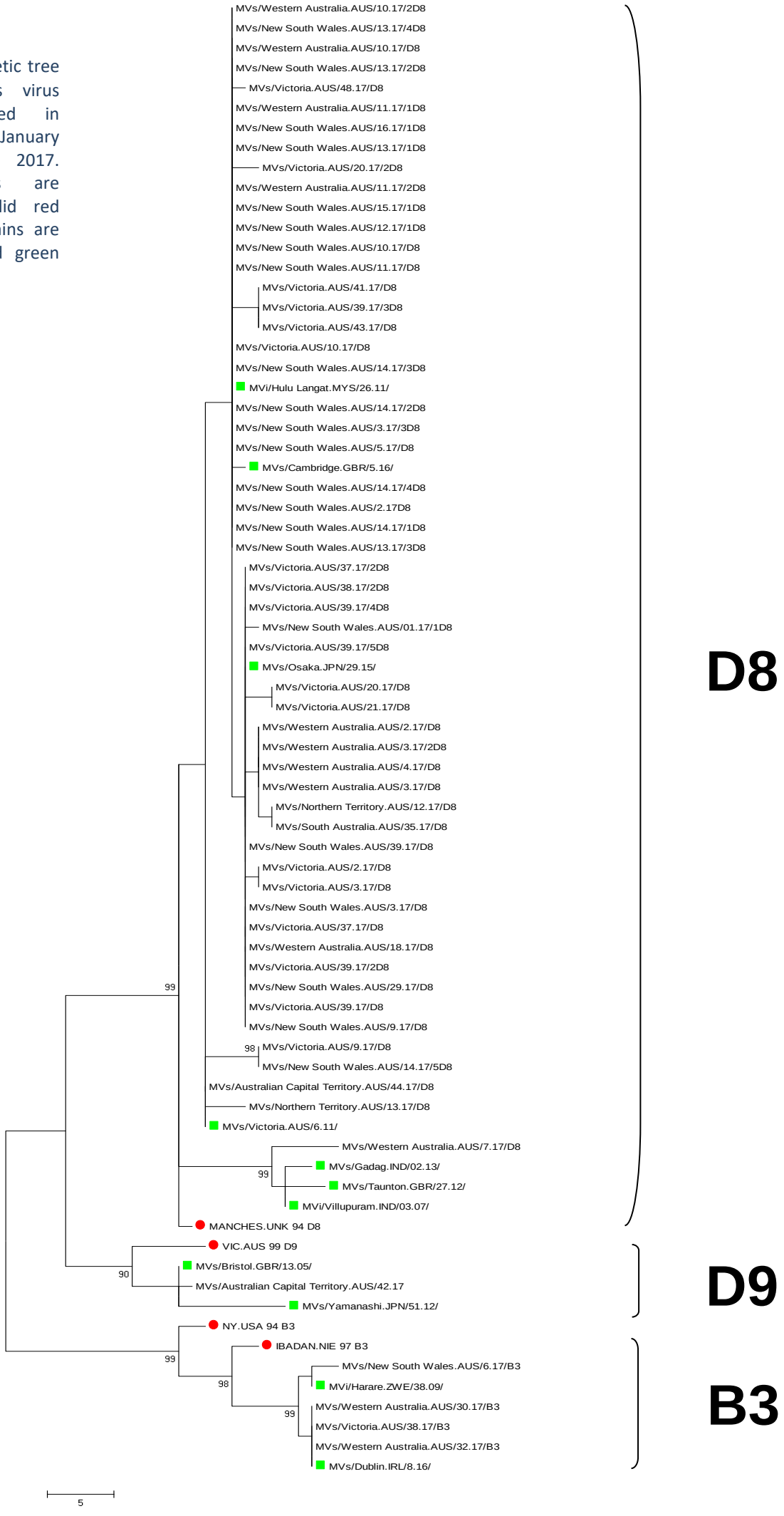


Figure 4a. Phylogeny clustering of measles D8 cases identified in Victoria in 2017.

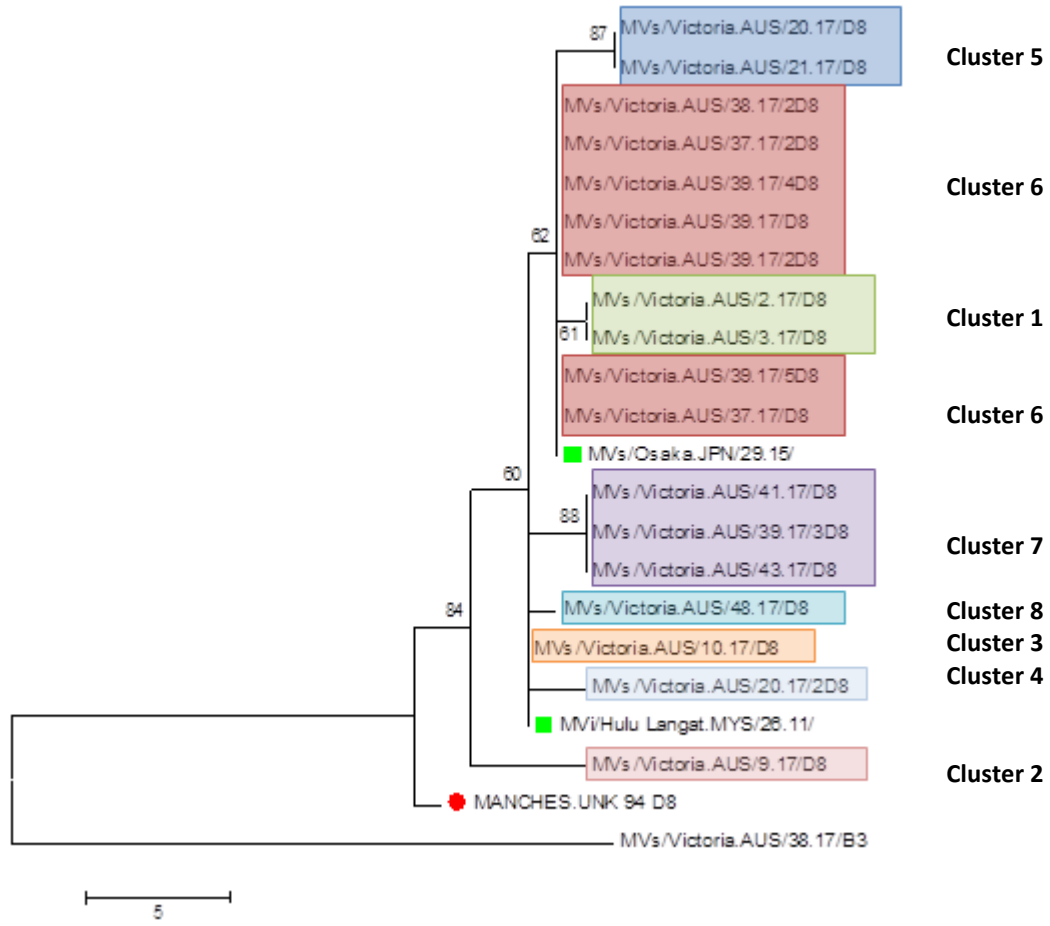
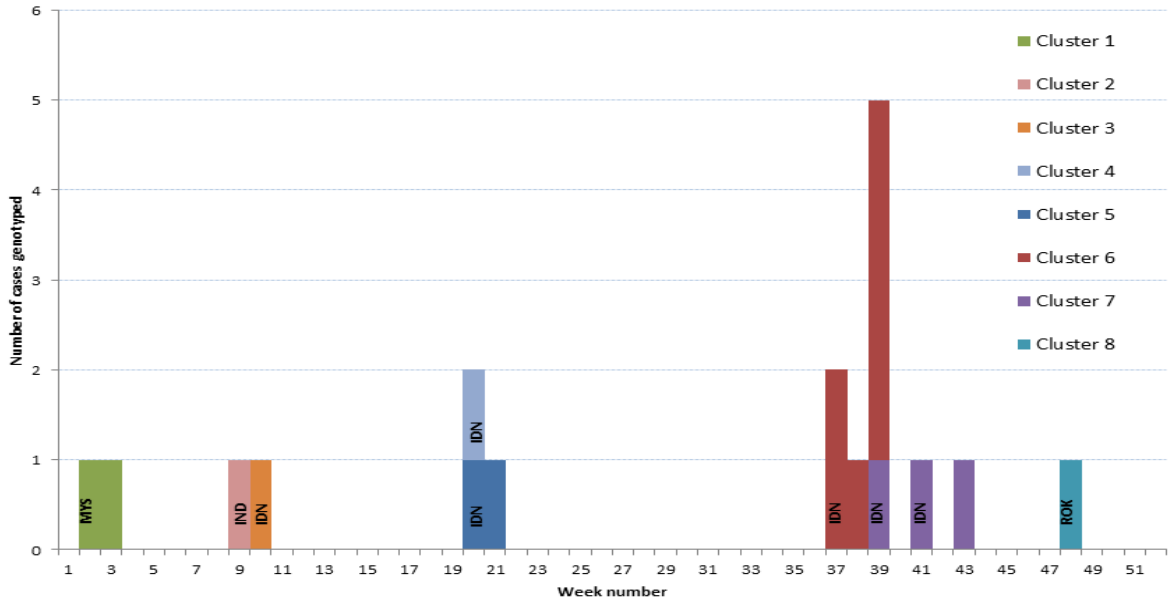


Figure 4b. Distribution of Victorian measles D8 cases by epi-week, Jan-Dec 2017.
Clusters determined by the above phylogeny.



Country codes of importation associated with measles cases are indicated (MYS=Malaysia; IND=India; IDN=Indonesia; ROK=Republic of Korea).

Figure 5a. Phylogeny clustering of measles D8 cases identified in New South Wales in 2017.

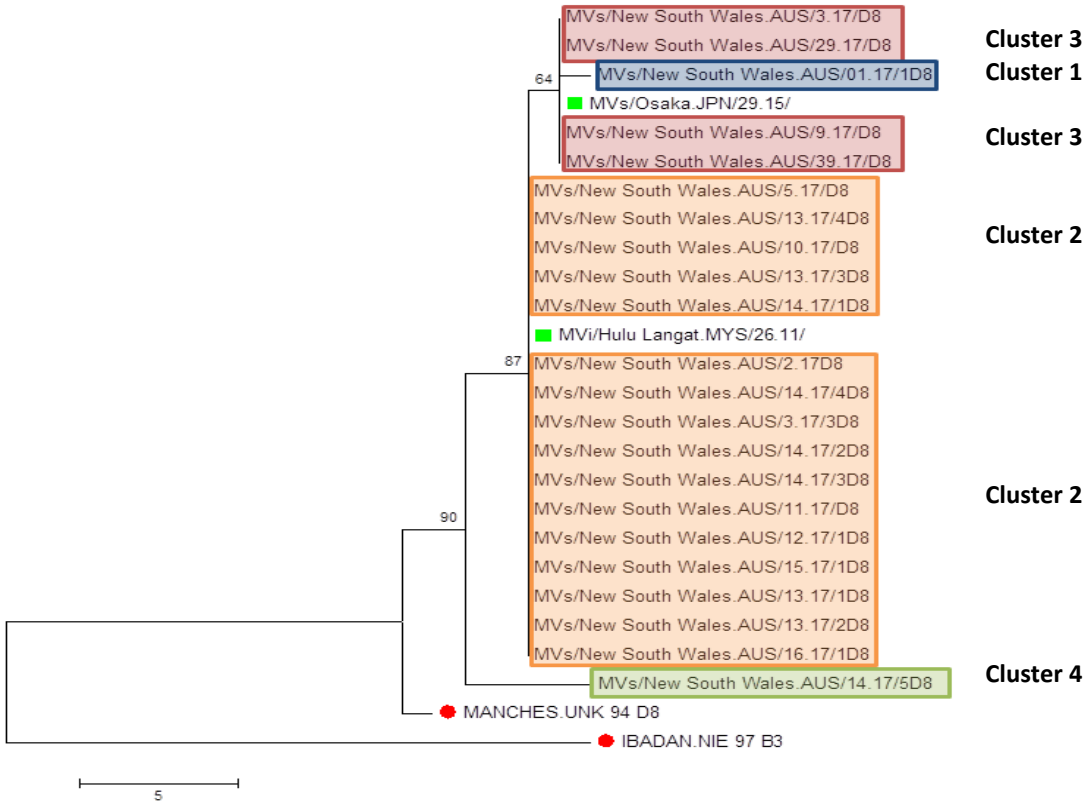
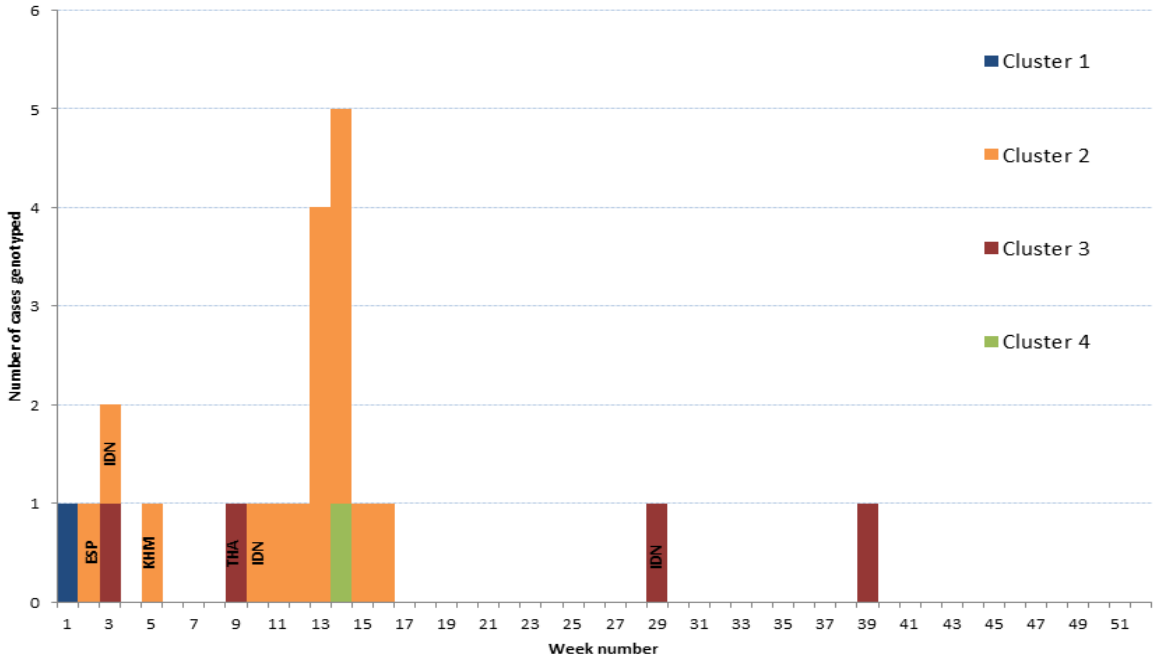


Figure 5b. Distribution of New South Wales measles D8 cases by epi-week, Jan-Dec 2017. Clusters determined by the above phylogeny.



Country codes of importation associated with measles cases are indicated (ESP=Spain; IDN=Indonesia; KHM=Cambodia; THA=Thailand)

Figure 6a. Phylogeny clustering of measles D8 cases identified in Western Australia in 2017.

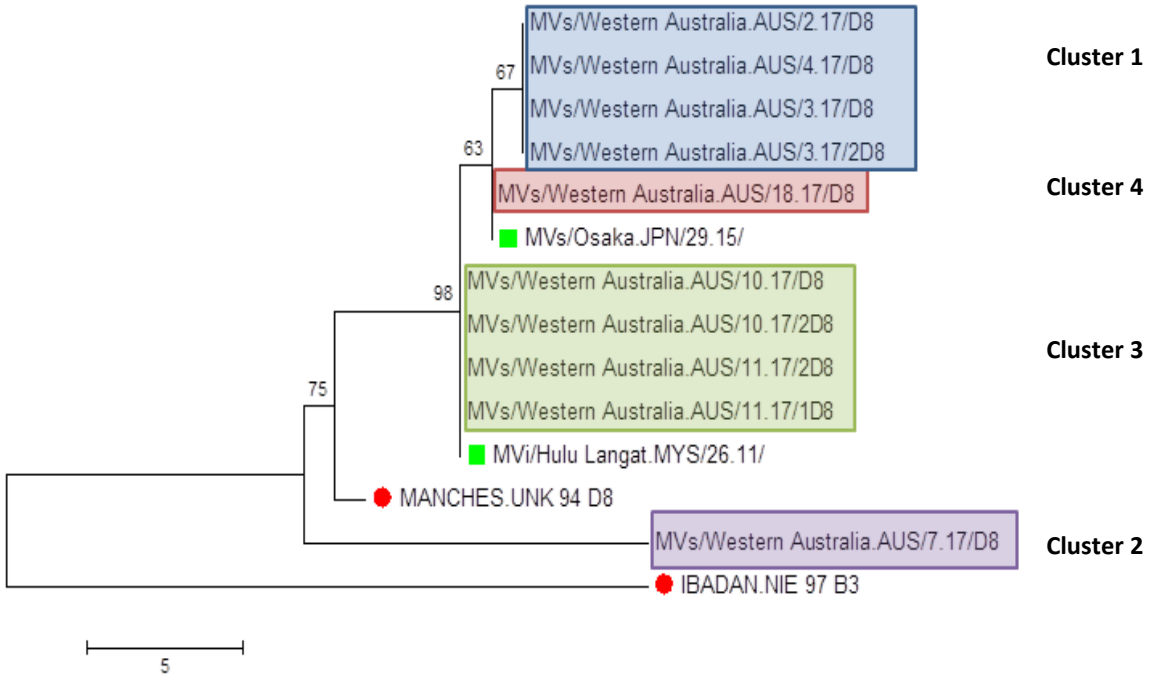
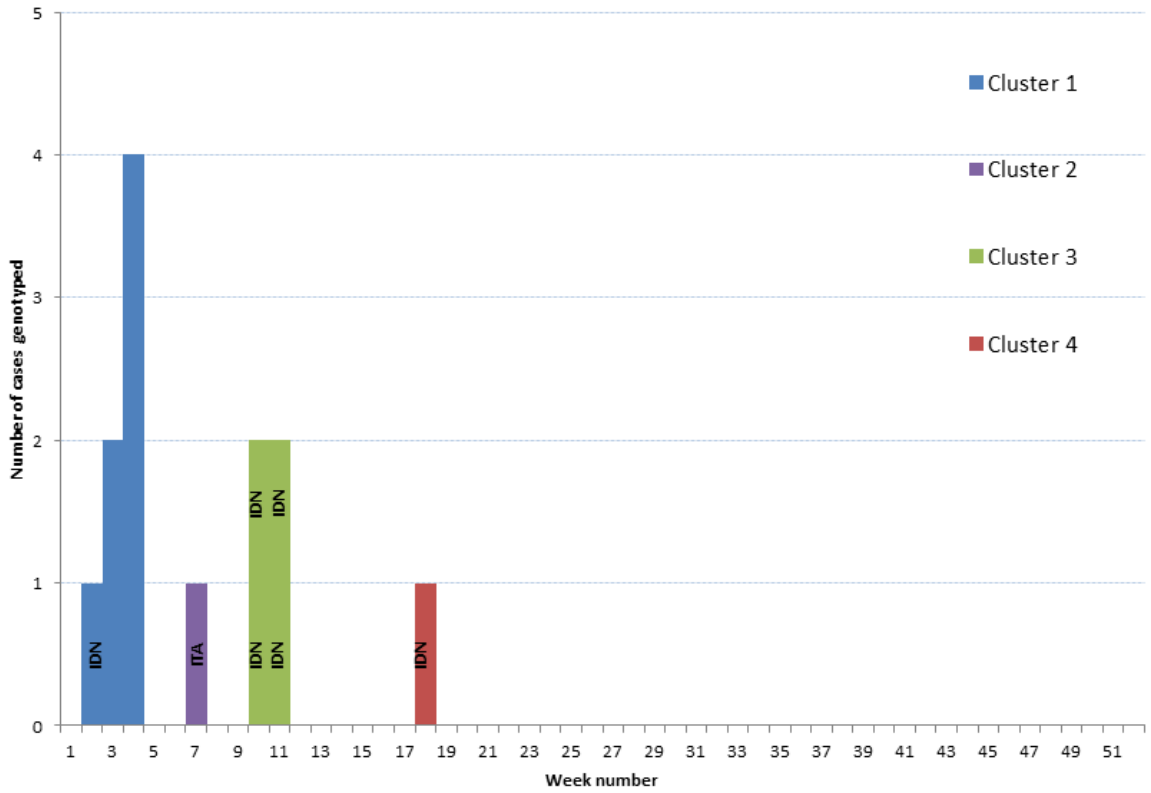


Figure 6b. Distribution of Western Australian measles D8 cases by epi-week, Jan-Dec 2017. Clusters determined by the above phylogeny.



Country codes of importation associated with measles cases are indicated (IDN=Indonesia; ITA=Italy).