Measles and Rubella Molecular Epidemiology: Australia 2020

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

1. Background

The measles and rubella laboratory at the Victorian Infectious Diseases Reference Laboratory (VIDRL) serves as the National Reference Laboratory for Australia and a WHO Regional Reference Laboratory for the Western Pacific Region. This laboratory provides a reference service for the detection and molecular genotyping of measles and rubella virus strains as part of its National Reference Laboratory function. Important aspects of laboratory molecular surveillance of measles and rubella at VIDRL during the post elimination phase include (i) genetic characterisation of circulating wild-type viruses to determine transmission events/pathways and support molecular epidemiological studies; (ii) differentiating vaccine strains from wild-type virus during outbreaks and (iii) monitoring the absence or persistence of endemic measles and rubella transmission.

Following a retrospective molecular epidemiological survey of Victorian measles strains from 1973-1998 (at the time the world's largest), VIDRL's measles molecular surveillance from 1999 indicates that measles transmission has been interrupted within Australia. Measles molecular epidemiological surveillance is widely accepted as a key criterion demonstrating the absence of an endemic genotype, and helping to demonstrate that a high proportion of cases and outbreaks are import-related. VIDRL's work has improved understanding of the global distribution of measles genotypes by defining those from source countries that were imported into Australia, and has identified three previously undescribed measles genotypes. Optimal periods for measles virus RNA recovery from specimens have been defined, together with validation of nucleic acid based measles detection direct on patient samples specifically for the measles vaccine strain and/or subsequent genotyping. The addition of an assay targeting a hypervariable region of the measles genome to complement standard genotyping methods will improve the genetic resolution when the genetic diversity of circulating measles strains diminishes.

More recently, genotyping evidence played an important role in verifying the interruption of endemic rubella virus in Australia for the years 2012 to 2017, one of the few countries in the region to have achieved this milestone. Australia was also successful in maintaining its measles elimination status for 2018 with genotyping evidence continuing to support the

absence of endemic measles transmission. Australia's measles and rubella elimination status for years 2019 and 2020 was not available at the time of submitting this report.

This annual report provides a comprehensive description on the molecular epidemiology of measles and rubella in Australia for year 2020 and provides virological evidence supporting the sustained interruption of endemic transmission, of both measles and rubella viruses, in 2020.

2. Measles Molecular Epidemiology Australia, 1 January to 31 December 2020

The number of samples tested for measles RNA by real-time PCR during the reporting period was 305, a decrease of 81.0% over the previous year. Of these, 45 (14.8%) samples had measles virus RNA detected from 32 cases. This compared to 283 measles cases in 2019. The significant decrease in both the number of measles PCR tests and number of laboratory confirmed measles cases can be attributed to the introduction of border restrictions in March 2020 due to the COVID-19 pandemic.

A measles genotype was obtained from all 32 cases of which 24 (73.3%) were identified as wild-type strains and 8 (26.7%) as a vaccine strain (Table 1).

From a minority of jurisdictions with local measles genotyping capabilities, an additional four N450 sequences were submitted to VIDRL or to the Measles Nucleotide Surveillance (MeaNS) database for inclusion in the national database and are included in this report (combined data n=28).

Wild-type measles cases were detected in only 7 of the 52 reporting weeks (Figure 1) with cases detected in four Australian states (Figure 2). At least 7 known importation events from 4 countries were identified as possible sources (Figure 3-4). As with previous years, only 2 wild-type measles genotypes, B3 and D8, were identified during this period.

Genotype D8, the most common type detected (n=23), circulated following at least 4 separate importation events from foreign countries including Nepal, Thailand and the Philippines (Figure 3). The genetic lineage for the majority of measles genotype D8 cases identified in Australia could be matched to a WHO named strain or to a genetic measles strain found circulating in other parts of the world (Figure 5). MVs/Gir Somnath.IND/42.16; MVs/Dagon

Seikkan.MMR/5.18 and MVs/Southern Finland.FIN/49.18/ were the named strains identified in 2020 for this genotype (Figure 5). For the single case (MVs/Victoria.AUS/04.20) with no exact N450 sequence match in MeaNS, epidemiologic data indicated a known country (Nepal) of acquisition.

Epi-week distribution of measles genotype D8 grouped by phylogenetic clusters provides strong evidence of no sustained transmission of any one genetic lineage of measles genotype D8 in Australia (Figure 3).

There were only 5 cases of measles genotype B3, with epidemiologic and genomic data consistent with imported or imported-related virus (Figure 6). Incursions of this genotype were from Italy and the Philippines (Figure 4). Two measles B3 cases in Australia were linked to the MVi/Gombak.MYS/40.15/ named strain and one to the MVi/Marikina City.PHL/10.18/ named strain (Figure 6). The 2 remaining unknown source cases (MVs/Queensland.AUS/5.20/ and MVs/Queensland.AUS/5.20/2) had measles N450 sequences matching strains from the United Kingdom. The extremely low numbers of this genotype in Australia is sufficient to suggest no endemic transmission of this genotype exists in Australia 2020.

3. Rubella Molecular Epidemiology Australia, 1 January to 31 December 2020

The prevalence of rubella virus infection in Australia remains extremely low. In 2020, 157 specimens were referred to VIDRL for rubella nucleic acid testing of which there were no RNA detections by the rubella real-time PCR.

Figure 1: Distribution of wild-type measles genotype identified at VIDRL epi-week, January to December 2020.

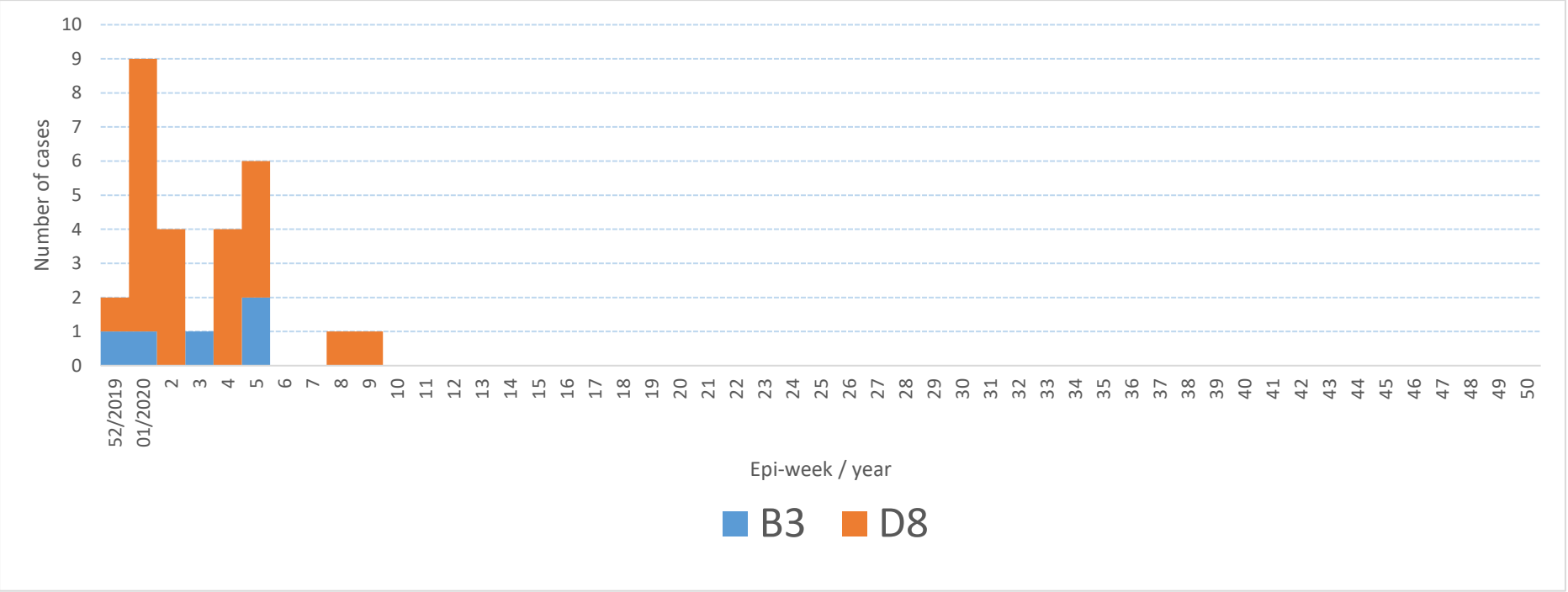
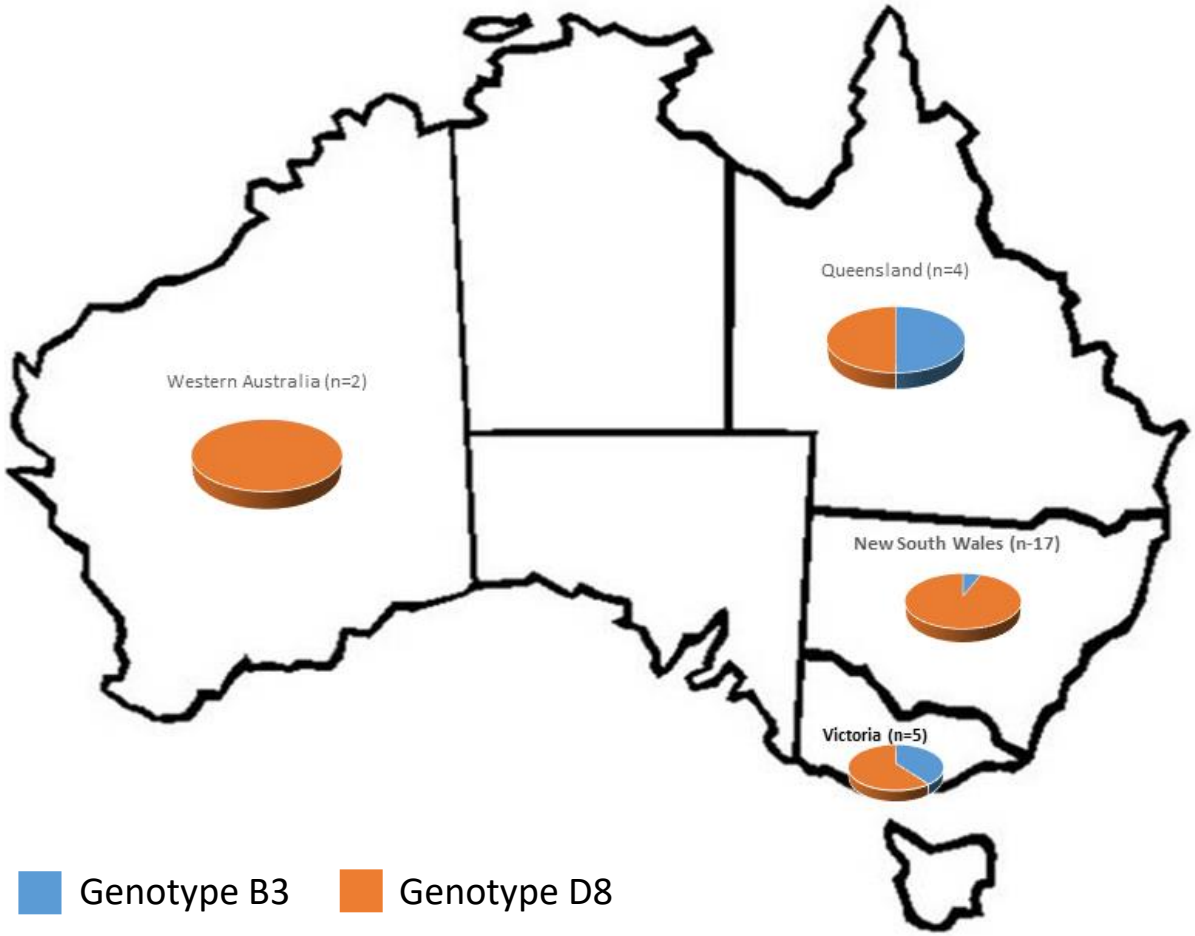
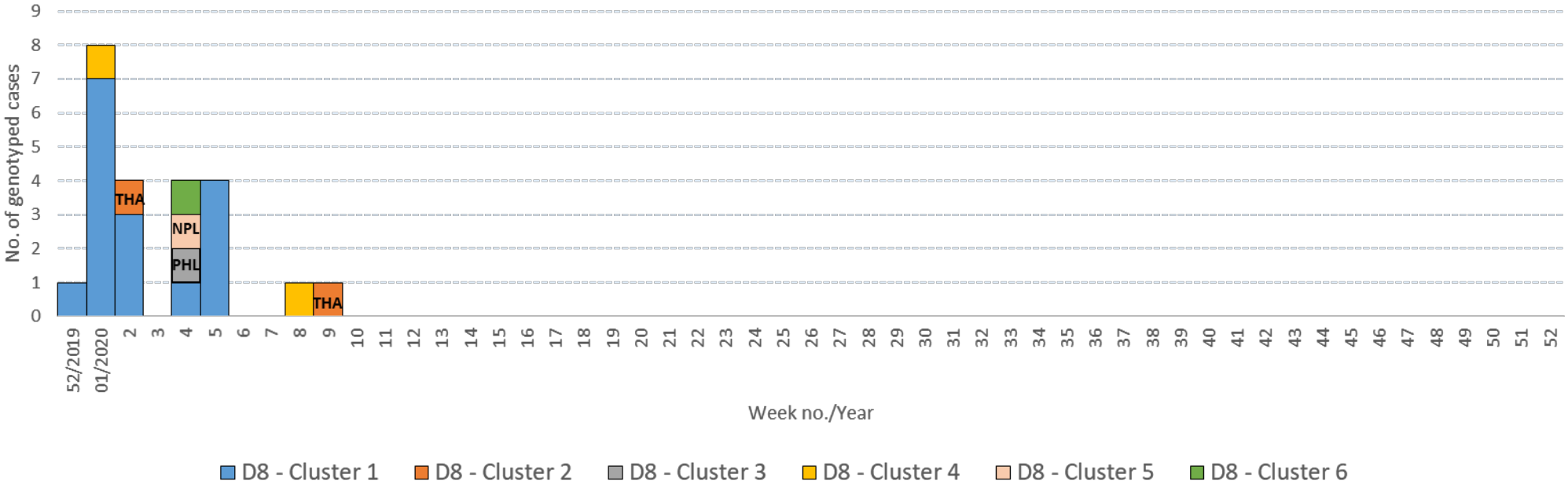


Figure 2: Geographical distribution of measles genotypes in Australia, 2020.



Note: size of pie charts not proportional to the number of cases genotypes.

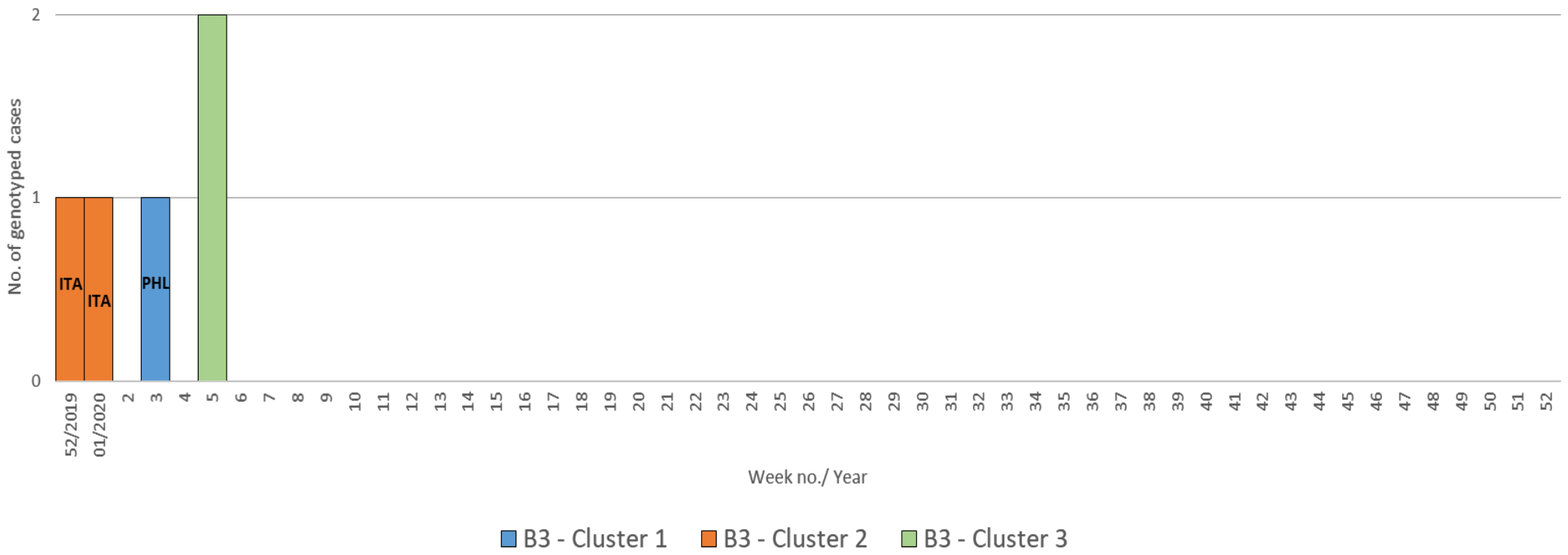
Figure 3: Distribution of measles genotype D8 genetic clusters by epi-week, January to December 2020.



Genetic clusters determined by Figure 5 phylogeny.

Country/region codes associated with imported measles cases are indicated (PHL = Philippines; NPL = Nepal; THA = Thailand))

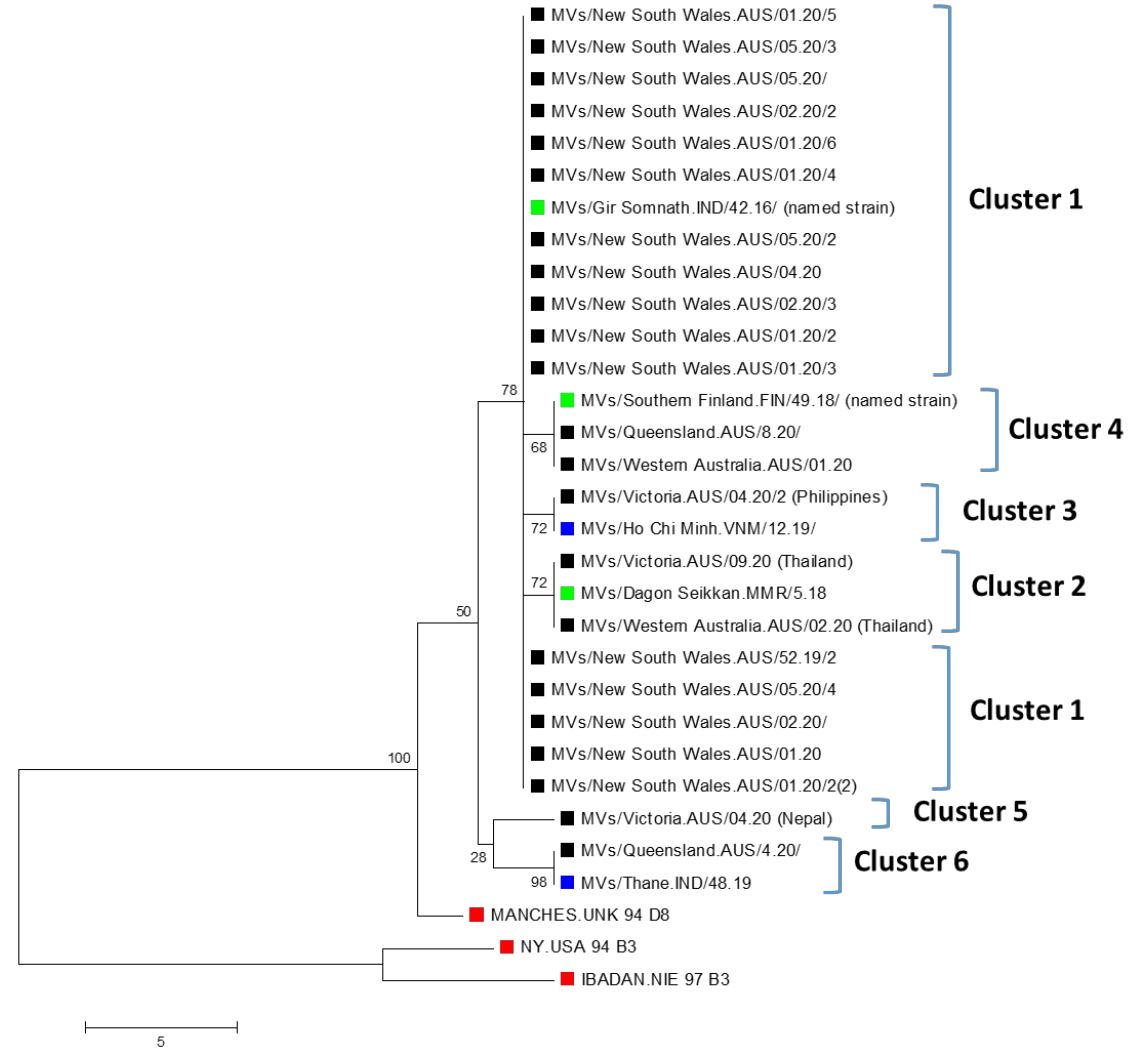
Figure 4: Distribution of measles genotype B3 genetic clusters by epi-week, January to December 2020.



Genetic clusters determined by Figure 6 phylogeny.

Country codes associated with imported measles cases are indicated (ITA – Italy; PHL=Philippines)

Figure 5: N450 phylogenetic relationships among measles genotype D8 strains identified in Australia, 2020.

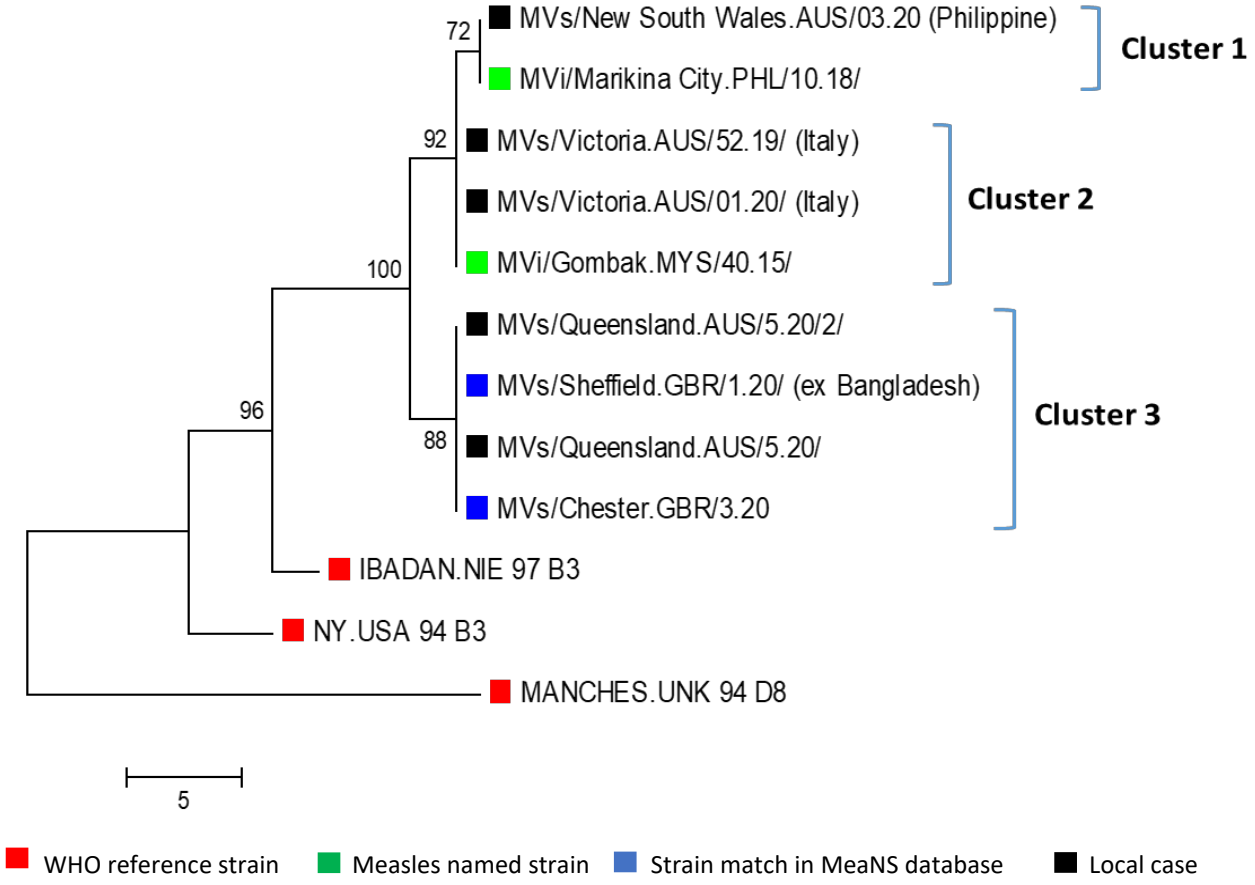


WHO reference strain | Strain match in MeaNS database | Measles named strain | Local case

Source country of measles virus provided in parenthesis.

The evolutionary history was inferred using the Maximum Parsimony method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. Evolutionary analyses were conducted in MEGA7.

Figure 6: N450 phylogenetic relationships among measles genotype B3 strains identified in Australia, 2020.



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