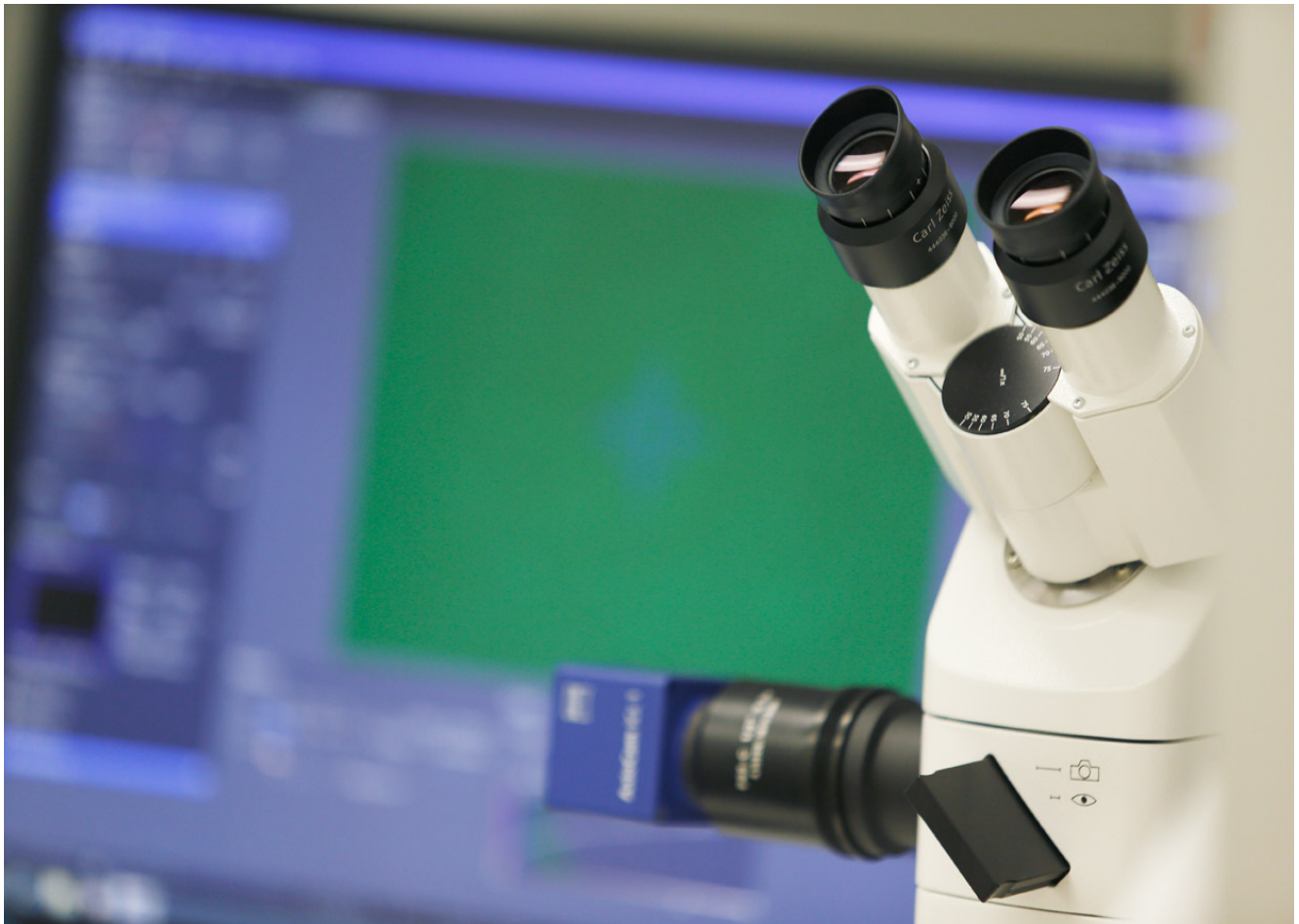# Measles Molecular Epidemiology:

Australia 2013

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 2013

Between January and December 2013 measles genotyping was attempted on 74 samples with genotyping possible on 62 cases. The remaining 12 cases had a virus load that was too low for genotyping (ct ≥ 36). The breakdown of genotyped samples by state and territory was: Victoria 32, New South Wales 14, Western Australia 15 and South Australia 1. An additional 20 genotyping results were submitted directly to the WHO Measles Nucleotide Surveillance database by Queensland Health Scientific Services.
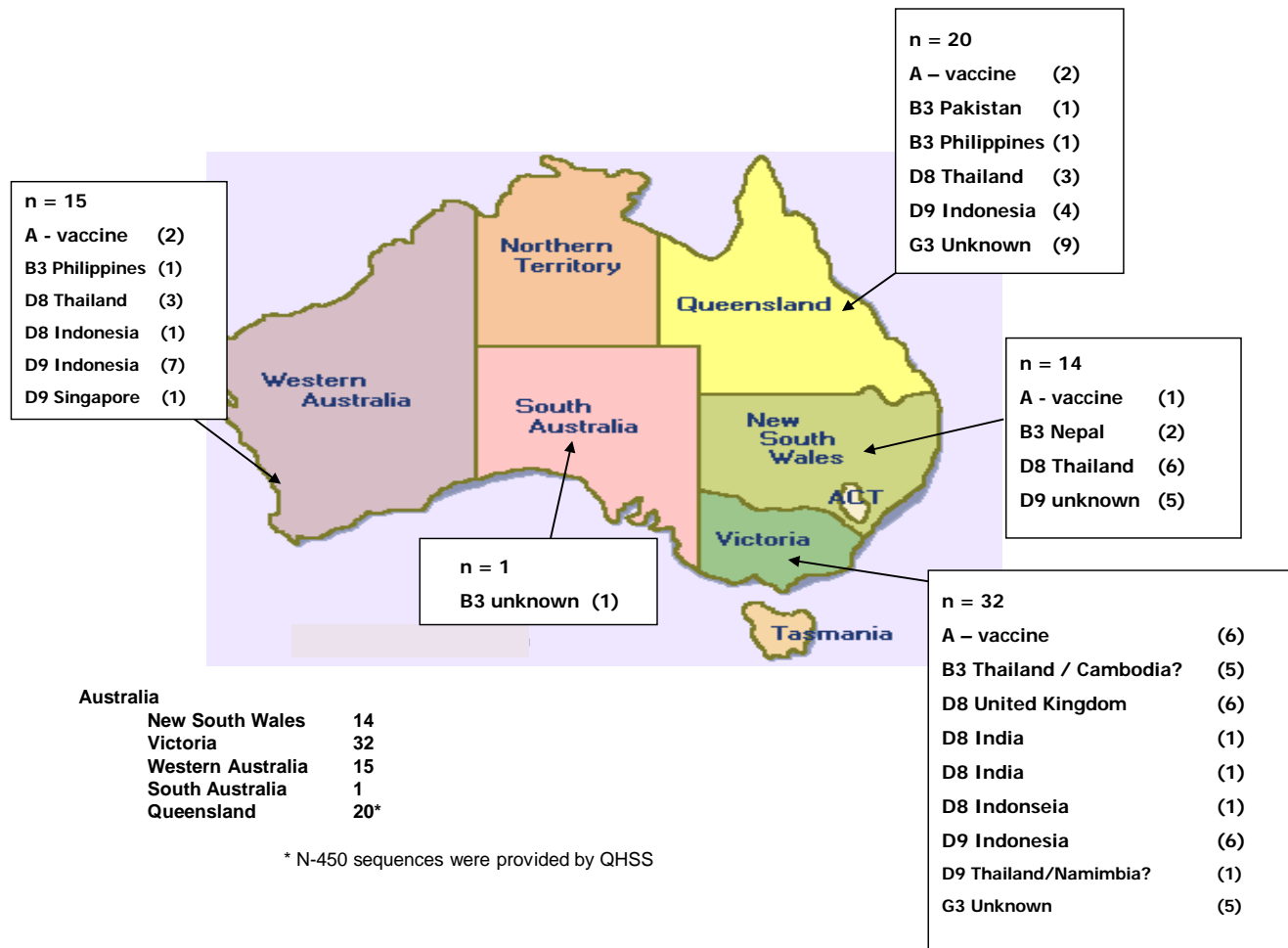
Four distinct genotypes (B3, D8, D9 and G3) were imported from at least 9 different countries (Figure 1). Genotype D9, the most common type detected (n=24), circulated after at least 5 separate cases were introduced from Indonesia. Variants of this genotype were also imported from Singapore and Thailand (Figure 2).

Twenty two cases of genotype D8, associated with importation (United Kingdom, Thailand and India), were found circulating in New South Wales, Western Australia, Queensland and Victoria. There were 4 phylogenetic lineages of genotype D8 identified (Figure 2) with each lineage having a unique source of importation.

Genotype B3 (n=11) was imported from a number of countries including Saudi Arabia, Thailand, Pakistan, Nepal and the Philippines. There were 7 unknown source cases of genotype G3. As there were no reported cases of this genotype from any other country in 2013 it was not possible to link Australian cases to possible geographical sources.

Measles vaccine-associated cases were detected in 11 cases all of which shared an identical N450 sequence to the vaccine strain (1 nucleotide different to wild-type Edmonston strain).

Figure 1. Measles virus genotypes imported into Australian states in 2013. 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.

n = 20
A – vaccine   (2)
B3 Pakistan   (1)
B3 Philippines (1)
D8 Thailand   (3)
D9 Indonesia   (4)
G3 Unknown   (9)

n = 15
A - vaccine   (2)
B3 Philippines (1)
D8 Thailand   (3)
D8 Indonesia   (1)
D9 Indonesia   (7)
D9 Singapore   (1)

n = 14
A - vaccine   (1)
B3 Nepal   (2)
D8 Thailand   (6)
D9 unknown   (5)

n = 1
B3 unknown (1)

n = 32
A – vaccine   (6)
B3 Thailand / Cambodia?   (5)
D8 United Kingdom   (6)
D8 India   (1)
D8 India   (1)
D8 Indonseia   (1)
D9 Indonesia   (6)
D9 Thailand/Namimbia?   (1)
G3 Unknown   (5)

Australia
New South Wales   14
Victoria   32
Western Australia   15
South Australia   1
Queensland   20*

* N-450 sequences were provided by QHSS

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Figure 2. Phylogenetic tree comparing 82 measles viruses and reference strains detected in Australia in 2013.
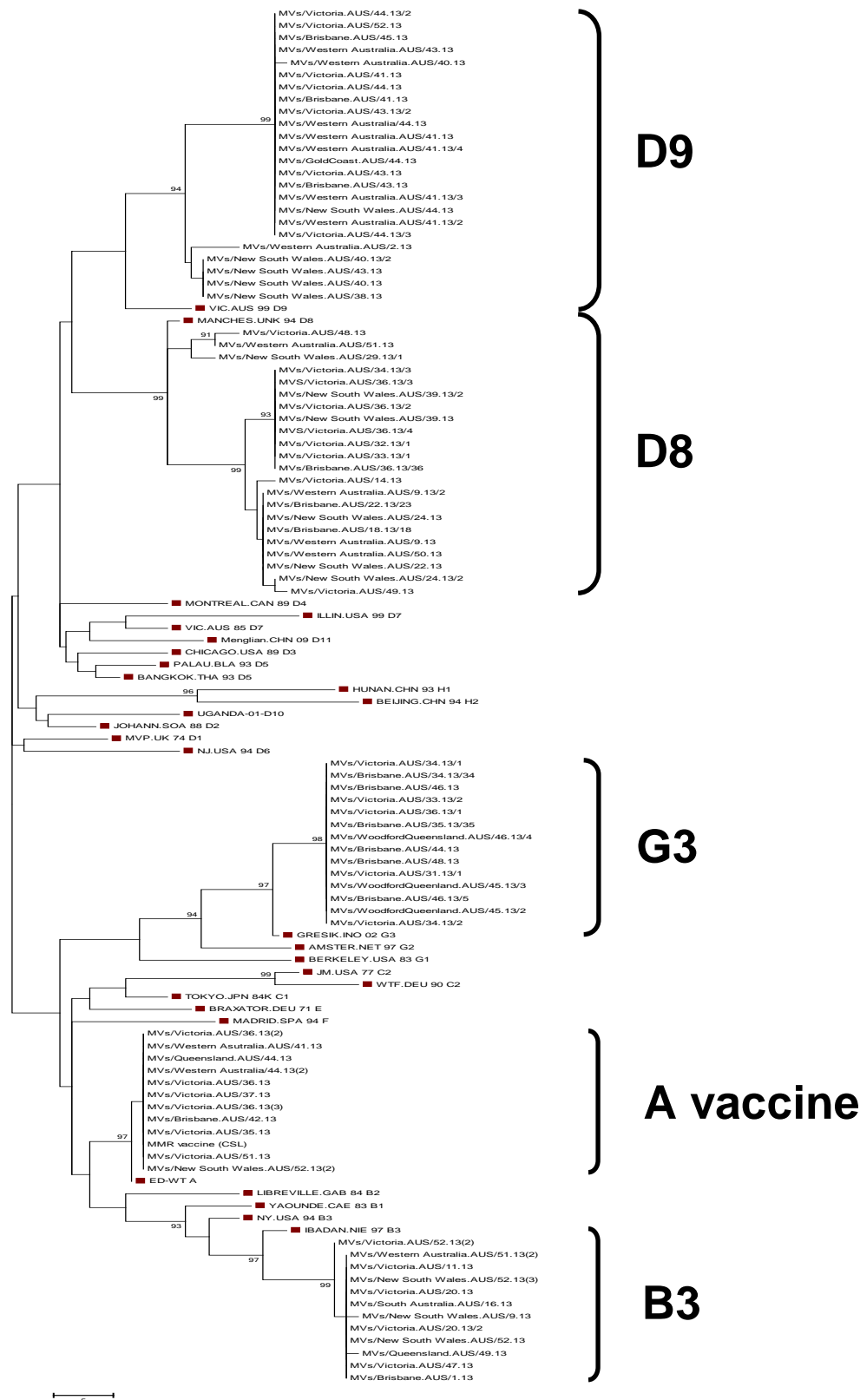
The distance-based phylogenetic tree was constructed by neighbour-joining methods using the Kimura 2-parameter model of evolution with optimised parameters based on 450nt nucleoprotein sequences. Bootstrap values greater than 90% are indicated. Measles virus reference strains are indicated by a solid red square.