

Canterbury

District Health Board

Te Poari Hauora o Waitaha

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8 October 2019

9(2)(a)

RE Official Information Act request CDHB 10186

I refer to your email dated 25 September 2019 requesting the following information under the Official Information Act from Canterbury DHB.

A copy of any documentation/presentations 9(2)(a) gave at the World Health Organisation (WHO) Eighth Meeting of Vaccine Preventable Diseases Laboratory Networks in the Western Pacific held in Manila, Philippines 18-22nd March 2019.

Please find attached as **Appendix 1** – Measles and rubella elimination in New Zealand presentation and **Appendix 2** – New Zealand Country Report from the National measles and Rubella Laboratory (NMRL).

These constitute the two presentations 9(2)(a) gave at the World Health Organisation Eighth Meeting of Vaccine Preventable Diseases Laboratory Networks in the Western Pacific held in Manila, Philippines 18-22nd March 2019.

I trust that this satisfies your interest in this matter.

Please note that this response, or an edited version of this response, may be published on the Canterbury DHB website after your receipt of this response.

Yours sincerely



Carolyn Gullery
Executive Director
Planning, Funding & Decision Support



Measles and rubella elimination in NZ

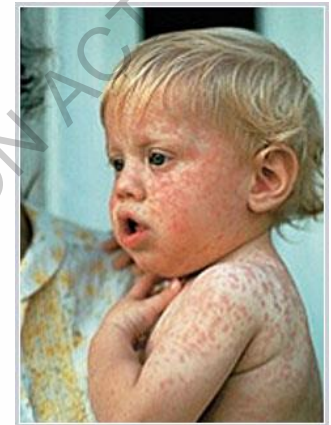
National Measles and Rubella Laboratory (NMRL)

**EIGHTH MEETING ON VACCINE PREVENTABLE DISEASES
LABORATORY NETWORKS IN THE WESTERN PACIFIC REGION
18-22 March 2019, Manila, Philippines**

9(2)(a)

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- CHL is the WHO accredited NMRL for NZ since March 2005
- We provide laboratory support for Measles and/or Rubella surveillance and outbreak investigation and confirmation of Measles/Rubella cases using WHO/CDC recommended methods
- Molecular tests include real-time PCR (screening + Type A) and genotyping via sequencing
- Isolation of viruses from positive patient samples using our cell-culture facility

<https://www.measles.co.nz>

6th Meeting of the Regional Verification Commission

At the sixth RVC meeting in Beijing in September 2017 New Zealand was verified to have achieved the interruption of endemic measles and rubella transmission.



Measles/rubella elimination, WHO criteria

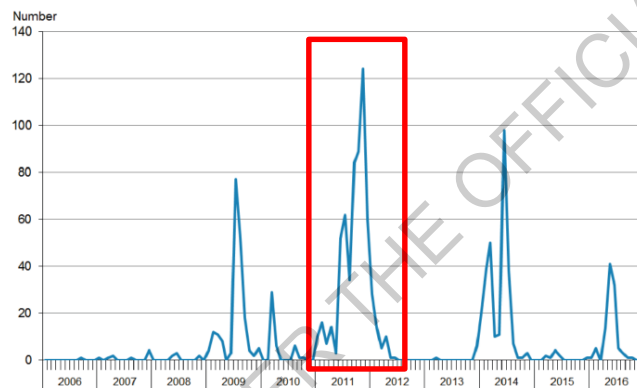
Measles/rubella elimination, WHO criteria

- 1) Documentation of the interruption of endemic measles/rubella virus transmission for a period of at least 36 month from the last endemic case

Measles/rubella elimination, WHO criteria

- 1) Documentation of the interruption of endemic measles virus transmission for a period of at least 36 months from the last endemic case
 - The last such case was notified in June 2012 in NZ

Figure 4: Number of measles cases by month of notification 2006-2016



Endemic measles = existence of continuous transmission of indigenous or imported measles virus that persists for ≥ 12 months

- Measles elimination could be requested since June 2015 in NZ
- In the past 6 years, no reintroduction of measles virus has led to sustained transmission for more than 6 months

BUT: Re-establishment of endemic measles virus transmission can lead to loss of elimination status.

Measles/rubella elimination, WHO criteria

- 1) Documentation of the interruption of endemic measles/rubella virus transmission for a period of at least 36 months from the last endemic case
- 2) The presence of a well-performing surveillance system

National notifiable disease surveillance system (EpiSurv)

- Health professionals and laboratories are required to inform their local Medical Officer of Health of any notifiable disease that they suspect or diagnose.
- Measles and rubella became notifiable on 1 June 1996.
- Notification data are entered at each PHU via a secure web-based portal into a computerised database (EpiSurv). The data are collated and analysed by the Institute of Environmental Science and Research (ESR).
- In practice, when measles or rubella cases occur, they are fully investigated by the local PHU, who try to identify the chain of transmission and the origin of infection, and this detailed information is available for PHU, MoH and NMRL and summarised on EpiSurv.

EpiSurv example

CASE REPORT FORM

Measles, Mumps, Rubella

Measles		EpiSurv No. 18-339485-AK	
Disease Name			
<input checked="" type="radio"/> Measles <input type="radio"/> Mumps <input type="radio"/> Rubella			
Reporting Authority			
Name of Public Health Officer responsible for case			
Notifier Identification			
Reporting source* <input type="radio"/> General Practitioner <input checked="" type="radio"/> Hospital-based Practitioner <input type="radio"/> Laboratory <input type="radio"/> Self-notification <input type="radio"/> Outbreak Investigation <input type="radio"/> Other			
Name of reporting source		Organisation	
Kitty Croison		ACH	
Date reported*		Contact phone	
23/11/2018			
Usual GP		Practice	
GP/Practice address		GP phone	
Number Street Suburb			
Town/City Post Code		<input type="checkbox"/> GeoCode	
Case Identification			
Name of case* Surname ***** Given name(s) *****			
NHI number* ***** Email			
Current address* Number ***** Street ***** Suburb Remuera			
Town/City Auckland Post Code 1050 <input type="checkbox"/> GeoCode EX			
Phone (home) *****		Phone (work) *****	
Phone (other) *****			
Case Demography			
Location TA* Auckland City		DHB* Auckland	
Date of birth* ***** OR Age 30 <input type="radio"/> Days <input type="radio"/> Months <input checked="" type="radio"/> Years			
Sex* <input type="radio"/> Male <input checked="" type="radio"/> Female <input type="radio"/> Indeterminate <input type="radio"/> Unknown			
Occupation*			
Occupation location <input type="radio"/> Place of Work <input type="radio"/> School <input type="radio"/> Pre-school			
Name			
Address Number Street Suburb			
Town/City Post Code <input type="checkbox"/> GeoCode			
Alternative location <input type="radio"/> Place of Work <input type="radio"/> School <input type="radio"/> Pre-school			
Name			
Address Number Street Suburb			
Town/City Post Code <input type="checkbox"/> GeoCode			
Ethnic group case belongs to* (tick all that apply)			
<input checked="" type="checkbox"/> NZ European <input type="checkbox"/> Maori <input type="checkbox"/> Samoan <input type="checkbox"/> Cook Island Maori <input type="checkbox"/> Niuean <input checked="" type="checkbox"/> Chinese <input type="checkbox"/> Indian <input type="checkbox"/> Tongan <input type="checkbox"/> Other (such as Dutch, Japanese, Tokelauan) * (specify)			

Basis of Diagnosis	
CLINICAL CRITERIA	
Fits Clinical Description*	
Measles	Fever $\geq 38.0^{\circ}\text{C}$ present at time of rash onset <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Maculopapular rash <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown If yes, date of onset of rash* 21/11/2018 Cough <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Coryza <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Conjunctivitis <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Koplik's spots <input type="radio"/> Yes <input checked="" type="radio"/> No <input type="radio"/> Unknown
Mumps	Acute swelling of parotid or other salivary gland for more than 2 days <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Orchitis <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown
Rubella	Fever <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Maculopapular rash <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown If yes, date of onset of rash* Arthritis/arthralgia <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Lymphadenopathy <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown Conjunctivitis <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown
LABORATORY CRITERIA	
Laboratory confirmation of disease* <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Not Done <input type="radio"/> Awaiting Results	
Confirmation method	
<input type="checkbox"/> Isolation of virus from clinical specimen <input type="checkbox"/> Positive IgM antibody <input type="checkbox"/> Significant rise in IgG antibody level <input checked="" type="checkbox"/> Nucleic acid testing (NAT/PCR) <input checked="" type="checkbox"/> Genetic characterisation (specify strain) B3	
EPIDEMIOLOGICAL CRITERIA	
Contact with a confirmed case* <input type="radio"/> Yes <input type="radio"/> No <input checked="" type="radio"/> Unknown	
If yes, specify the EpiSurv number of the confirmed case*	
CLASSIFICATION* <input type="radio"/> Under investigation <input type="radio"/> Probable <input checked="" type="radio"/> Confirmed <input type="radio"/> Not a case	
Clinical Course and Outcome	
Date of onset* 18/11/2018 <input checked="" type="checkbox"/> Approximate <input type="checkbox"/> Unknown	
Hospitalised* <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown	
Date hospitalised* 21/11/2018 <input type="checkbox"/> Unknown	
Hospital* Auckland City Hospital	
Died* <input type="radio"/> Yes <input checked="" type="radio"/> No <input type="radio"/> Unknown	
Date died* <input type="checkbox"/> Unknown	
Was this disease the primary cause of death? <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown	
If no, specify the primary cause of death*	

EpiSurv example

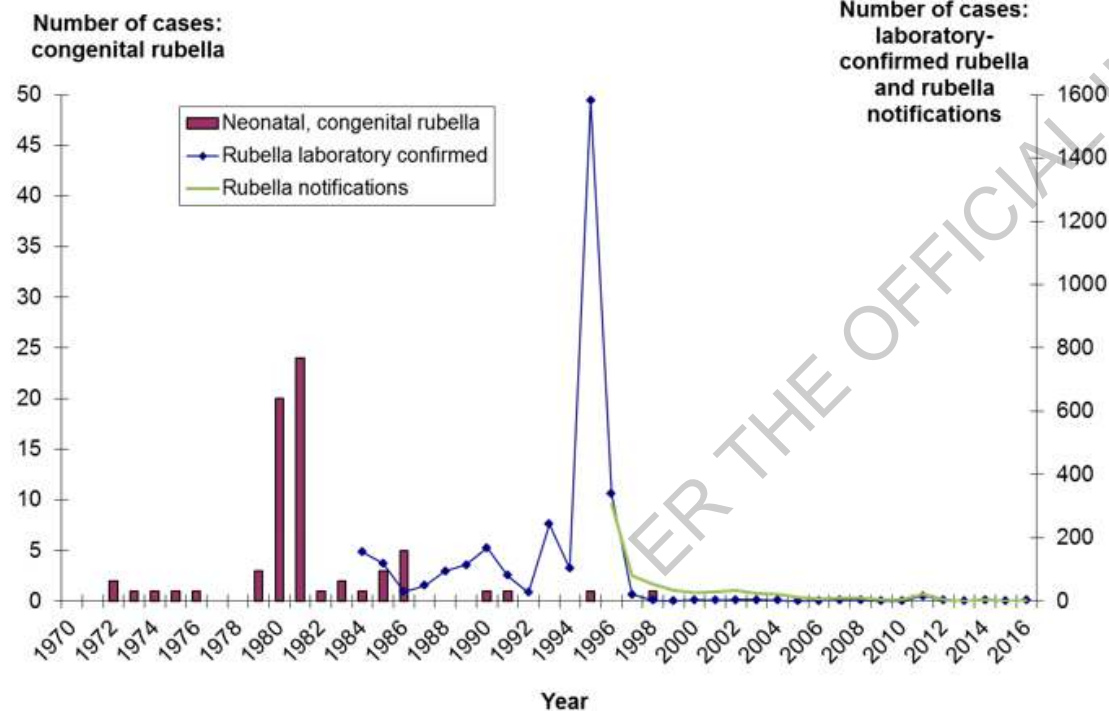
Outbreak Details	Management																																																
Is this case part of an outbreak (i.e. known to be linked to one or more other cases of the same disease)?* <input type="checkbox"/> Yes <input checked="" type="checkbox"/> If yes, specify Outbreak No.* _____	CONTACT MANAGEMENT Did the case have any contacts (measles and rubella only)?* <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown If yes, specify number and management*																																																
Risk Factors Contact with another case of the disease during the incubation period for this disease* <input type="radio"/> Yes <input type="radio"/> No <input checked="" type="radio"/> Unknown Attendance at school, pre-school or childcare during the incubation period for this disease* <input type="radio"/> Yes <input checked="" type="radio"/> No <input type="radio"/> Unknown Was the case overseas during the incubation period for this disease?* <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown If yes, date arrived in New Zealand* _____ Specify countries visited* (from most recent to least recent) <table style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 30%;">Country/Region*</th> <th style="width: 20%;">Date Entered*</th> <th style="width: 20%;">Date Departed*</th> </tr> </thead> <tbody> <tr> <td>Last* Malaysia</td> <td></td> <td></td> </tr> <tr> <td>Second Last* Singapore</td> <td></td> <td></td> </tr> <tr> <td>Third Last* _____</td> <td></td> <td></td> </tr> </tbody> </table> Other risk factors for measles, mumps or rubella (specify)* _____	Country/Region*	Date Entered*	Date Departed*	Last* Malaysia			Second Last* Singapore			Third Last* _____			<table style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 20%;">Category</th> <th style="width: 10%;">Number identified</th> <th style="width: 10%;">Number susceptible</th> <th style="width: 10%;">Number given MMR (measles only)</th> <th style="width: 10%;">Number declined MMR (measles only)</th> <th style="width: 10%;">Number given IG (measles only)</th> </tr> </thead> <tbody> <tr> <td><15 months of age</td> <td>4</td> <td>4</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>15 months and over (not pregnant)</td> <td>141</td> <td>20</td> <td>1</td> <td>1</td> <td></td> </tr> <tr> <td>Pregnant</td> <td>3</td> <td>3</td> <td></td> <td></td> <td>2</td> </tr> </tbody> </table> Flight details if case infectious while on board an international flight (measles only)* <table style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="width: 20%;">Last flight</th> <th style="width: 20%;">2nd to last flight</th> <th style="width: 20%;">3rd to last flight</th> <th style="width: 20%;">4th to last flight</th> </tr> </thead> <tbody> <tr> <td>Flight number(s) _____</td> <td>_____</td> <td>_____</td> <td>_____</td> </tr> <tr> <td>Date of departure _____</td> <td>_____</td> <td>_____</td> <td>_____</td> </tr> </tbody> </table> Unimmunised susceptibles excluded from school/pre-school/childcare for appropriate period* <input checked="" type="radio"/> Yes <input type="radio"/> No <input type="radio"/> NA <input type="radio"/> Unknown	Category	Number identified	Number susceptible	Number given MMR (measles only)	Number declined MMR (measles only)	Number given IG (measles only)	<15 months of age	4	4	1		1	15 months and over (not pregnant)	141	20	1	1		Pregnant	3	3			2	Last flight	2nd to last flight	3rd to last flight	4th to last flight	Flight number(s) _____	_____	_____	_____	Date of departure _____	_____	_____	_____
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Flight number(s) _____	_____	_____	_____																																														
Date of departure _____	_____	_____	_____																																														
Source (measles and rubella only) What was the source of the virus?* <input type="radio"/> Imported <input type="radio"/> Import-related <input type="radio"/> Endemic <input checked="" type="radio"/> Unknown If imported, specify country* _____ Specify region /city* _____ If import-related, specify the EpiSurv number of the source case* _____ If the case was infected in New Zealand, specify the DHB where contact occurred* _____	Comments* We have identified 148 contacts 107 immune 22 not immune 19 unknown (4 awaiting serology, 7 unable to contact, 8 - no serology taken) 2 contacts given immunoglobulin - includes 1 pregnant woman, 1 baby. Was not Infectious on either of her flights.																																																
Protective Factors At any time prior to onset, had the case been immunised with the MMR or appropriate monovalent vaccine?* <input type="radio"/> Yes <input type="radio"/> No <input checked="" type="radio"/> Unknown If yes specify, vaccine details* First administered dose:* <input type="radio"/> MMR/Monovalent <input type="radio"/> Unknown Date given* _____ Or age when first dose was given <input type="radio"/> Weeks <input type="radio"/> Months <input type="radio"/> Years Source of information* <input type="radio"/> Patient/caregiver recall <input type="radio"/> Documented Second administered dose:* <input type="radio"/> MMR/Monovalent <input type="radio"/> Not given <input type="radio"/> Unknown Date given* _____ Or age when second dose was given <input type="radio"/> Weeks <input type="radio"/> Months <input type="radio"/> Years Source of information* <input type="radio"/> Patient/caregiver recall <input type="radio"/> Documented																																																	
Management CASE MANAGEMENT Date case investigation was started* (measles and rubella only) _____ Date case investigation was completed* (measles and rubella only) _____ Case excluded from work or school/pre-school/childcare for appropriate period* <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> NA <input type="radio"/> Unknown Was case pregnant (rubella only)?* <input type="radio"/> Yes <input type="radio"/> No <input type="radio"/> Unknown If yes, gestation period* _____ (weeks) at time of onset																																																	

Measles/rubella elimination, WHO criteria

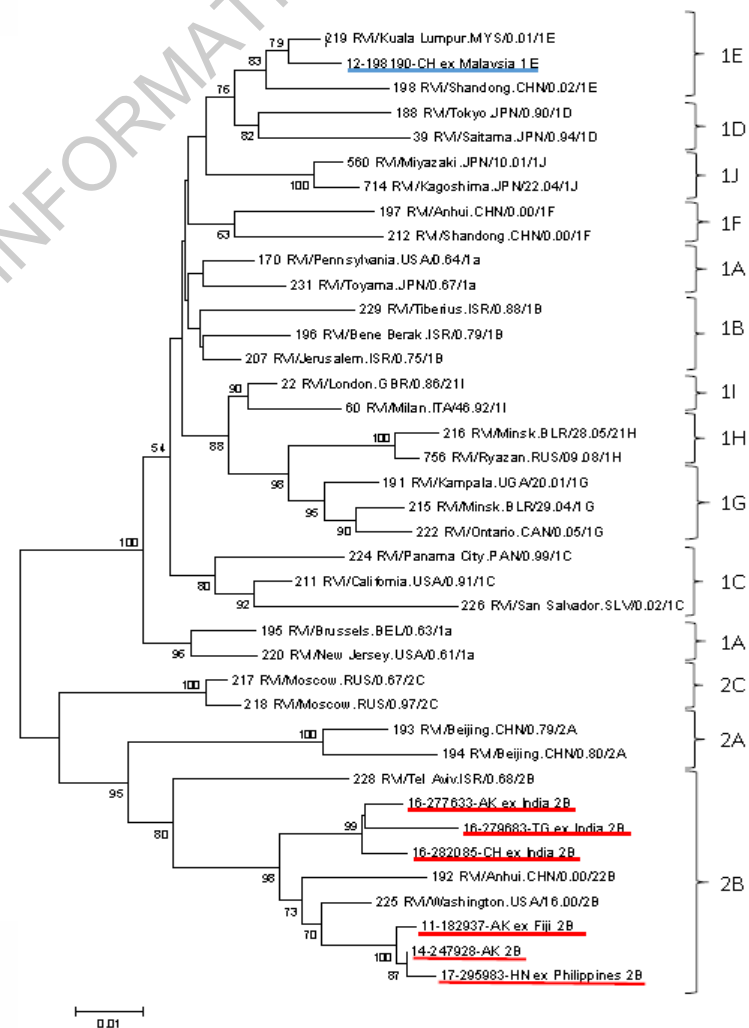
- 1) Documentation of the interruption of endemic measles virus transmission for a period of at least 36 month from the last endemic case
- 2) The presence of a well-performing surveillance system
- 3) Genotyping evidence that supports the interruption of endemic transmission

Rubella genotyping 2011-2017

Notifications of congenital rubella, 1970–2016, notifications of rubella 1996–2016, and laboratory-confirmed cases, 1984–2016



- No CRS in NZ since 1998.
- Last national outbreak 1995/1996.



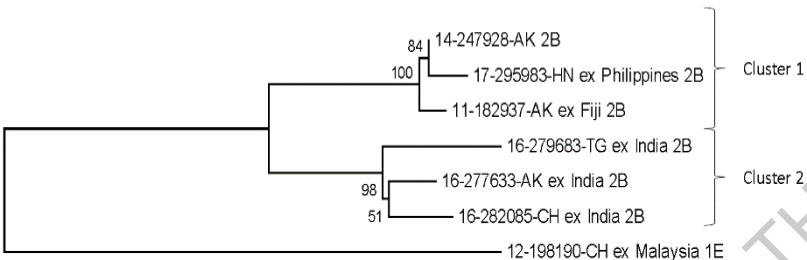
Rubella genotyping 2011-2017

2B Cluster 1

11-182937-AK ex Fiji 2B	G T T C C A C A C G G A A A C C A T A A C C G T G T G C A C T C T C C G T G C C G C G C G C G T G C T G C A A G T C A C G A C C G A A C A T C C G T T
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	C T G C A A C A C G C C G C A C G G A C A A C T C G A G G T C C A G G T C C G C C C G A C C C G G G C G A C C T G G T T G A G T A C A T C A T G A A T T A
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	C A C C G G C A A C C A A C A G T C C C G G T G G G G C C T C G G G A G C C C G A A C T G C C A G G C C C G C A C T G G G C C T C C C G G T T T G C C A
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	G C G C C A C T C T C C A G A C T G T T C G C G G C T C G T G G G G C C A C G C C A G A G C G C C C C G G C T C G T C T C G T C G A T G C T G A C G A
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	C C C C C T T C T G G C C A C T G C C C C G G G C C G G C G A G G T G T G G G T C A C G C C T G T C A T A G G C T C T C A G G C C G G A A G T G C G G
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	A C T C C A C A T A C G C G C C G G A C C G T A C G G C C A C G C C A C C G T C G A A A T G C C G A G T G G A T C C A G C C C A C A C T A C C A G C G A
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	T C C C T G G C A C C G C C C G G C C C T T G G G A C T C A A G T T C A A G A C A G T C C G C C C G G T G G T C C T A C C A G C G C G C T T A G C G C C
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	C C C T C G A A C G T G C G C G T A A C T G G C T G C T A C C A G T G C G G T A C C C C G C G C T G G T G G A G G G C C T C G C C C A G G A G G A G G
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	G A A C T G C C A C C T C A C G T C A A C G G C G A G G A C G T C G G G C C T T C C C C C T G G G A A G T T C G T C A C G C C G C C C T C C T C A A
14-247928-AK 2B
17-295983-HN ex Philippines 2B
11-182937-AK ex Fiji 2B	C A C C C C C G C C C T A C C A A G T G A G T T G C G G G G G T G A G
14-247928-AK 2B
17-295983-HN ex Philippines 2B

2B Cluster 2

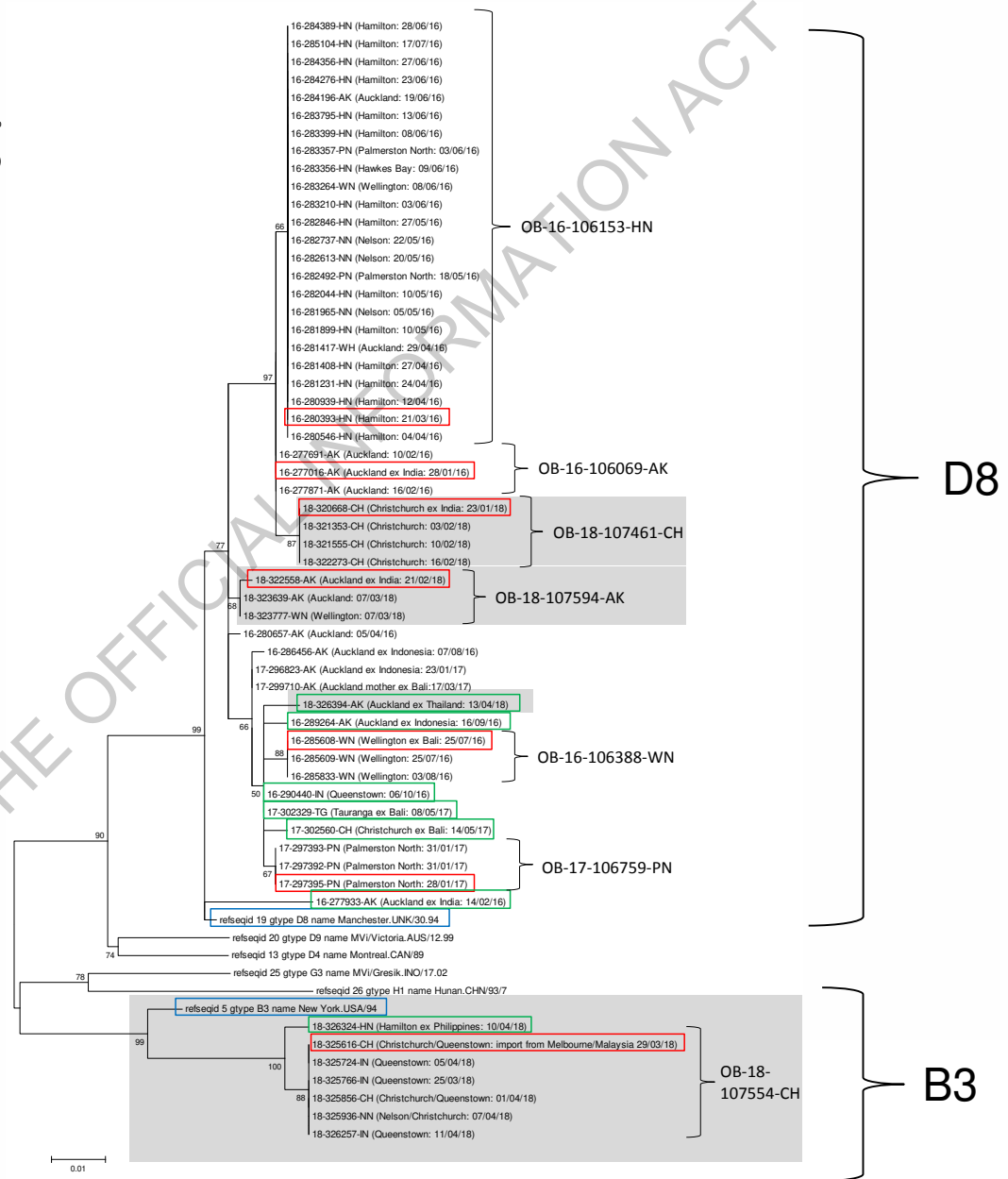
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16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	C T G T A A C A C G C C G C A C G G A C A A C T C G A G G T C C A G G T C C G C C C G A C C C G G G C G A C C T G G T G A G T A C A T C A T G A A T T A
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	C A C G G G C A A T C A A C A G T C C C G G T G G G G C C T C G G G A G C C C G A A C T G C C A G G C C C C G A C T G G G C C T C C C C G G T T T G T C A
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	G C G C C A C T C T C C C G A C T G T T C G G G C T C G T G G G G C C A C G C C A G A G C G C C C G G C T G C G C C T C G T C G A T G C C G A C G A
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	C C C C C T C T G C G C A C G C C C G G G G C G G G C G A G G T G T G G G T C A C G C C T G T C A T A G G C T C T C A G G C G C G C A A G T G C G G
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	A C T C C A C A T A C G C G C C G G A C C G T A C G G C C A C G C C A C C G T C G A A A T G C C T G A G T G G A T C C A C G C C C A C A C T A C C A G C G A
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	T C C T G G C A C C C G C C G G C C C T T G G G A C T C A A G T T C A A G A C A G T C C G C C C A G T G G T C C T A C C G C G C G C T A G C G C C
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	C C C T C G C A A T G T G C G C T A A C T G G C T G C T A C C A G T G T G G A C C C C G C G C T G G T G G A G G G C C T T G C C C A G G A G G A G G
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	G A A C T G C C A C T T T A C C A T C A A C G G C G A G G A C G C C G C G C C T T C C C C C T G G G A A G T T C G T C A C C G C C G C C T C C T C A A
16-279683-TG ex India 2B
16-282085-CH ex India 2B
16-277633-AK ex India 2B	C A C C C C C G C C C T A C C A A G T G A G T T G C G G G G G T G A G
16-279683-TG ex India 2B
16-282085-CH ex India 2B



Measles genotyping 2016-2018

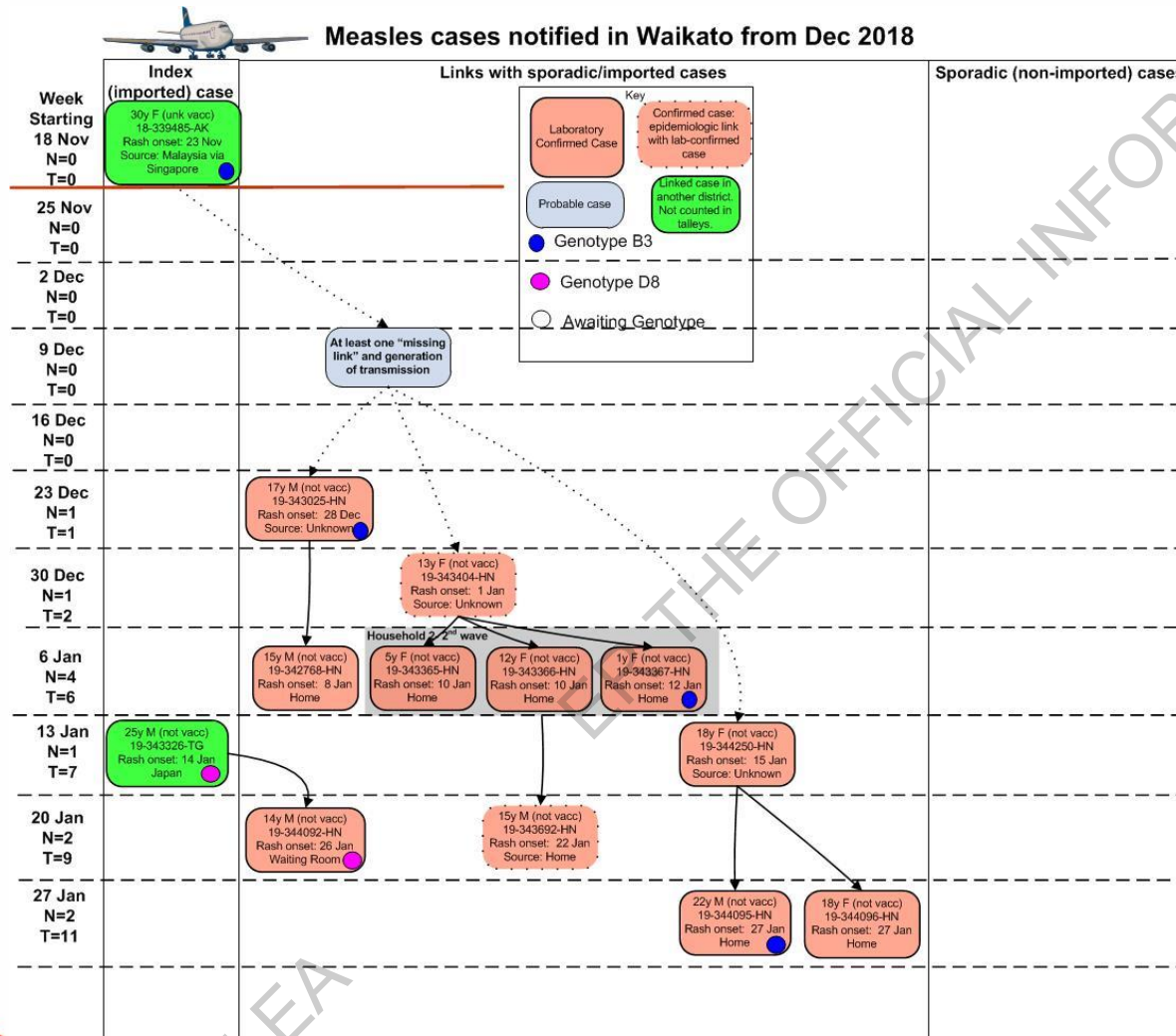
- 2018 outbreaks and sporadic cases are highlighted in grey
- Index cases = red
- Sporadic cases = green
- Reference sequences = blue

-> allows differentiation of lineages within a genotype



Maximum Likelihood Phylogenetic tree, 500 bootstrap replications

Measles transmission networks

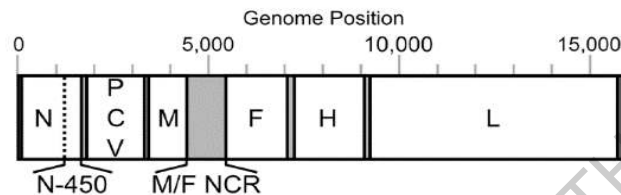


But if outbreaks become too big, e.g. after nosocomial transmission in a hospital, or transmissions at big institutions like universities or factories, it becomes more and more difficult to determine chains of transmission.

Measles cases in Palmerston North 02/2017

Measles outbreak in Japanese students of a boarding school. No travel history.

Genotype: D8



Based on 450 bp window

MeaNS Measles Nucleotide

Charts WHO Map **Data** Sequence analysis

List Search New record Named Strains Submit multiple records

Exact Match Blast Genotype Phylo tree GenBank

If the query sequence matches a genotype reference strain, that match will be shown in green at the top of the first table.
If the query sequence matches a named strain within a genotype, that match will be shown in red at the top of the first table.

You can use the filters underneath this text to limit the results displayed.
Hitting "reset" and "Filter records" will display all results.
The table headers are clickable and will allow the results table to be sorted

Where		When			
WHO region	WPRO	From	yyyy	mon	dd
Country	New Zealand	To	2017	Feb	28
City	All				

Filter records Reset

You can download the filtered and sorted results [HERE](#)

List of records

Number of records - 7

MeaNS Sample Id	WHO name (MeaNS) ▲	Gene	GT	Country	City	Epi year/week	GenBank	Recent Travel
104505	MVs/Palmerstonnorth.NZL/4.17/2	N450	D8	New Zealand	Palmerstonnorth	2017/4	KY656594	
103298	MVs/Palmerston North.NZL/4.17/2/	N450	D8	New Zealand	Palmerston North	2017/4		Nk
104503	MVs/Palmerstonnorth.NZL/5.17/	N450	D8	New Zealand	Palmerstonnorth	2017/5	KY646168	
103272	MVs/Palmerston North.NZL/5.17/	N450	D8	New Zealand	Palmerston North	2017/5		Nk
104504	MVs/Palmerstonnorth.NZL/5.17/2	N450	D8	New Zealand	Palmerstonnorth	2017/5	KY656595	
103297	MVs/Palmerston North.NZL/5.17/2/	N450	D8	New Zealand	Palmerston North	2017/5		Nk
98584	MVs/Queenstown.NZL/41.16/	N450	D8	New Zealand	Queenstown	2016/41	KY115689	Nk

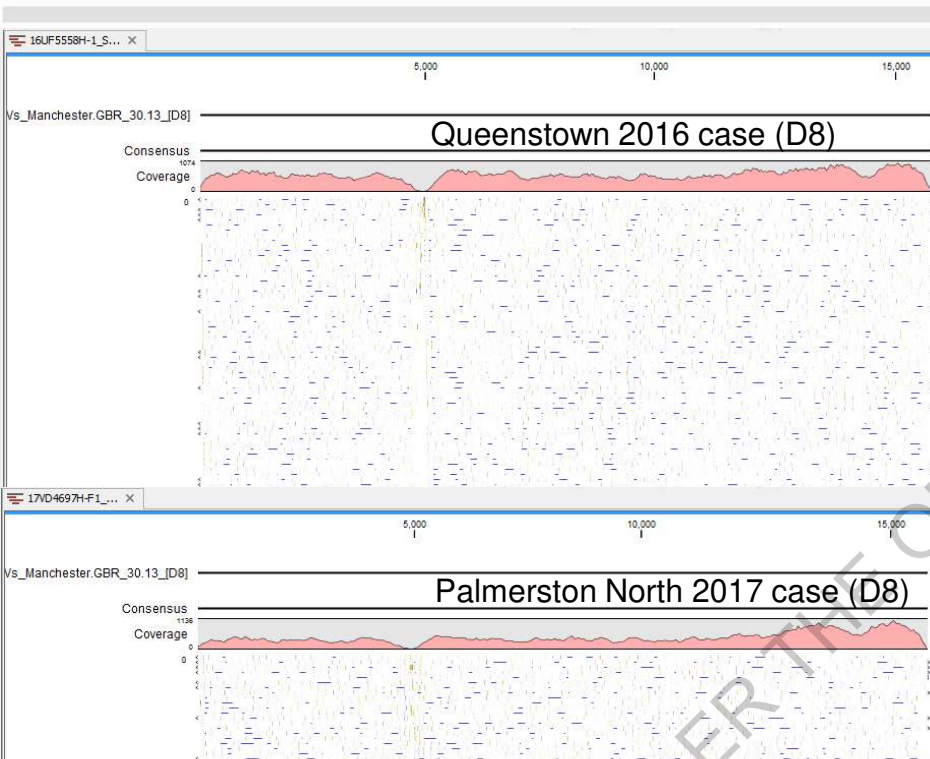
450 bp window genotyping

100% identical

Domain: Data Coding Codon Start: 1	
16UF5558H (Queenstown: 11/10/16)	G T C A G T T C C A C A T T G G C A T C T G A A C T C G G T A T C A C T G C C G A G G A T G C A A G G C T T G T T T C A G A G A T T G C A A T G C A T A C T
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.
16UF5558H (Queenstown: 11/10/16)	A C T G A G G A C A G G A C C A G T A G A G C A G T T G G A C C C A G A C A A G C T C A A G T G T C A T T T T C T A C A C G G T G A T C A A A G T G A G A A T
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.
16UF5558H (Queenstown: 11/10/16)	G A G C T A C C A G G A T T G G G G G G C A A G G A A G A T A G G A G G G T C A G A C A G A G T C G G G G A G G A G C C A G G G A G A G C A A C A G A G A A
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.
16UF5558H (Queenstown: 11/10/16)	A C C G G G T C C A G C A G A T T A A G T G A T G C G A G A G C T G C C C A T C T T C C A A C C A G C A C A C C C T A G A C A T T G A C A C T G C A T C G
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.
16UF5558H (Queenstown: 11/10/16)	G A A T C A G G C C A A G A T C C G C A G G A C A G T C G A A G G T C A G C T G A C G C C C T G C T C A A G C T G C A A G C C A T G G C A G G A A T C C T G
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.
16UF5558H (Queenstown: 11/10/16)	G A A G A A C A A A G T T C A G A C A C G G A C A C C C C A G G G T G T A C A A T G A C A G A G A T C T T C T A G A C
17VC9424U (Palmerston North: 03/02/17)	.
17VD4697H (Palmerston North: 03/02/17)	.
17VD4705G (Palmerston North: 03/02/17)	.

Sequencing a longer stretch of the genome increases the probability of detecting genetic diversity.

Measles NGS whole genome sequencing



A	B
16UF5558H consensus	GTCCAGAGTGACCAAGTCAACATCTGGCCTCAGCTTCGCATCAAGAGGTACCAACATGGAGGATAGGGGGACCAATAG
17VD4697H consensus	TTTTCACATGATGATGCCAAGTAGTAGTCAATCCAGGTTGGAATGGTTCCGAGAACAGGAAATCTCAGATATCGAA
16UF5558H consensus	GTCCAGAGCCCTGAGGGATTTAAACATGATTTCTGGGTACCAATTTCTAGGCCAAATTTGGGTCTTGGCTCGCAAAAGGCGGT
17VD4697H consensus	ACGGCCCAAGACACAGGCAAGTATTTCGGAGCTAAGAAAGTGGATTAAGATACACCAACAAAGAAAGGATAGTTGGTGA
16UF5558H consensus	TTTAGATTGGAGAGAAATGGTTGGATGTGGTGGAGAACAGGATTGGCGAGGACCTCTGCTTACGGCGATTTCATGGTC
17VD4697H consensus	GGCTAATCTGGATATCAAGAGGACACCGGGGAACAAACCTAGGATTGCCGAAATGATATGTACATTGATACATAT
16UF5558H consensus	ATGGTAGAGGCGAGGATTAGCCAGTTTTATGCTGACTATTAAAGTTTGGGATAGAAACTATGATCTGCTCTTGGAGTG
17VD4697H consensus	CATGAATTTGGTGGTGAATATCCACACTTGAATGCTTGAATGATTTTACCAAGCAAAATGGAGAAACTGCACCTAT
16UF5558H consensus	ATGGTAATCTGGAGAACTCAATTCAGAACAAAGTTCAAGTGCAGGATCATACCTCTGTTATGGAGCTATGCCATGGGA
17VD4697H consensus	GTAGGAGTGGAACTTGAAAGCTCTATGGGGGGTTTGAACCTTTGGTGGATCTTACTTTGATCCAGCATATTTTAGATTA
16UF5558H consensus	GGGCAAGAGATGGTGAAGAGGTCAGCTGGGAAGTGCAGTTCCACATTGGCATCTGAACCTCGGTATCACTGCGGAGGAT
17VD4697H consensus	GGCAAGGCTTGTTCAGAGATTGCAATGCATACTACTGAGGACAGGACCAGTAGAGCAGTTGGACCCAGACAAAGCTCAA
16UF5558H consensus	GTGTCAATTTCTACACGGTGATCAAAGTGAAGATGAGCTACCAAGGATTGGGGGGCAAGGAAGATAGGAGGGTCAGACAG
17VD4697H consensus	AGTCGGGGAGGAGCCAGGGAGAGCAACAGAGAAACCGGGTCAGCAGATTAAGTGAATGCGAGAGCTGCCCATCTTCC
16UF5558H consensus	ACCAAGACACCCCTAGACATTGACACTGGCATCGGAATCAGGCCAAGATCCGCAAGGACAGTGGAAAGTCAAGCTGACGCC
17VD4697H consensus	CTGCTCAAGCTCCAGACCATGGCAGGAATCCTGGGAAGAACAAAGTTGACAGACAGGACACCGCCCAAGGTTGTACATGAC
16UF5558H consensus	AGAGATCTTTCTAGACTAGGTGGGAGAGTCCGGAGGACAGAACAAACATCCAGCTGACCTGCATCATTGTATAAAAAAG
17VD4697H consensus	TTAGGAACCAAGTCCACACAGCCGCCACCAACCAATCCACTGCCAGACTGGGGCGATGGCAGAGGAGCAGGGC
16UF5558H consensus	ACGGCATGTCAAAAACGGAGCTGGAAATGCATCCGGGCTCTCAAGGCCAGGCCATCGGGCTCACTGGCGGTGAGGAAGC
17VD4697H consensus	CATGGCAGCATGGTCAGAAATATCAGACAACCCAGGACAGGACCGAGGCCACCTGCAGAGGAAGAGAAAGGACAGGATTC
16UF5558H consensus	GGGTCTCAGCAAAACCATGCTCTCAGCAATTTGATCAACTGAAGGGGTTGACCTCGCATCGCGGTCAGGGATCTGG
17VD4697H consensus	AGAGAGCGATGACGACGGTGAAGCTTTGGGAATCCGCTCAAGAAATGTCGAGGACATCAAGGACTGGGTTCAGTGTTA

Overall 25 nucleotide differences across the whole genome could be detected. In fact, measles virus genomes are very stable. In an outbreak in the UK in 2013 which lasted for 3 months only 5 mutations accumulated within the whole genome.

Only 2320 bp of
15,684 bp depicted

New importations and outbreaks in 2019

- Jan: homeschool outbreak in Waikato
 - unknown source, B3 identical to case from Auckland ex Malaysia in Nov 2018
- Jan: B3 case in Tauranga ex Philippines
- Jan: D8 case in Tauranga ex South-East Asia
- Feb: B3 case in Auckland ex Afghanistan
- Feb: D8 case in Christchurch ex UK
- Feb/March: B3 outbreak in Canterbury and Otago, identical to strain from Philippines from 2018
 - unknown source, 28 cases so far, nosocomial transmissions in hospital

What we have learned from the current outbreak:

- Outbreaks can rapidly get out of control if nosocomial transmission occurs.
- Non-immune hospital staff exposed to confirmed measles cases should stand down from work for at least 21 days.
- It's bad if a measles outbreak coincides with high flu activity, since symptoms can be similar, and the workload for the lab increases dramatically.
- Cases of different outbreaks can have identical N450 sequences if the same strain is imported multiple times. It's fine if travel history is known, but sometimes the index case and travel history can't be identified.



Acknowledgements

- Dr Meik Dilcher, Scientific Officer Virology, CHL
- Rodger Linton, Section Head Virology/Serology, CHL
- Dr Richard Hoskins, Waikato Population Health Service
- Tomasz Kiedrzynski, Communicable Diseases, MoH NZ
- Staff of the National Measles Laboratory, CHL







New Zealand Country Report

National Measles and Rubella Laboratory (NMRL)

**EIGHTH MEETING ON VACCINE PREVENTABLE DISEASES
LABORATORY NETWORKS IN THE WESTERN PACIFIC REGION
18-22 March 2019, Manila, Philippines**

9(2)(a)

Canterbury
District Health Board
Te Poari Hauora o Waitaha

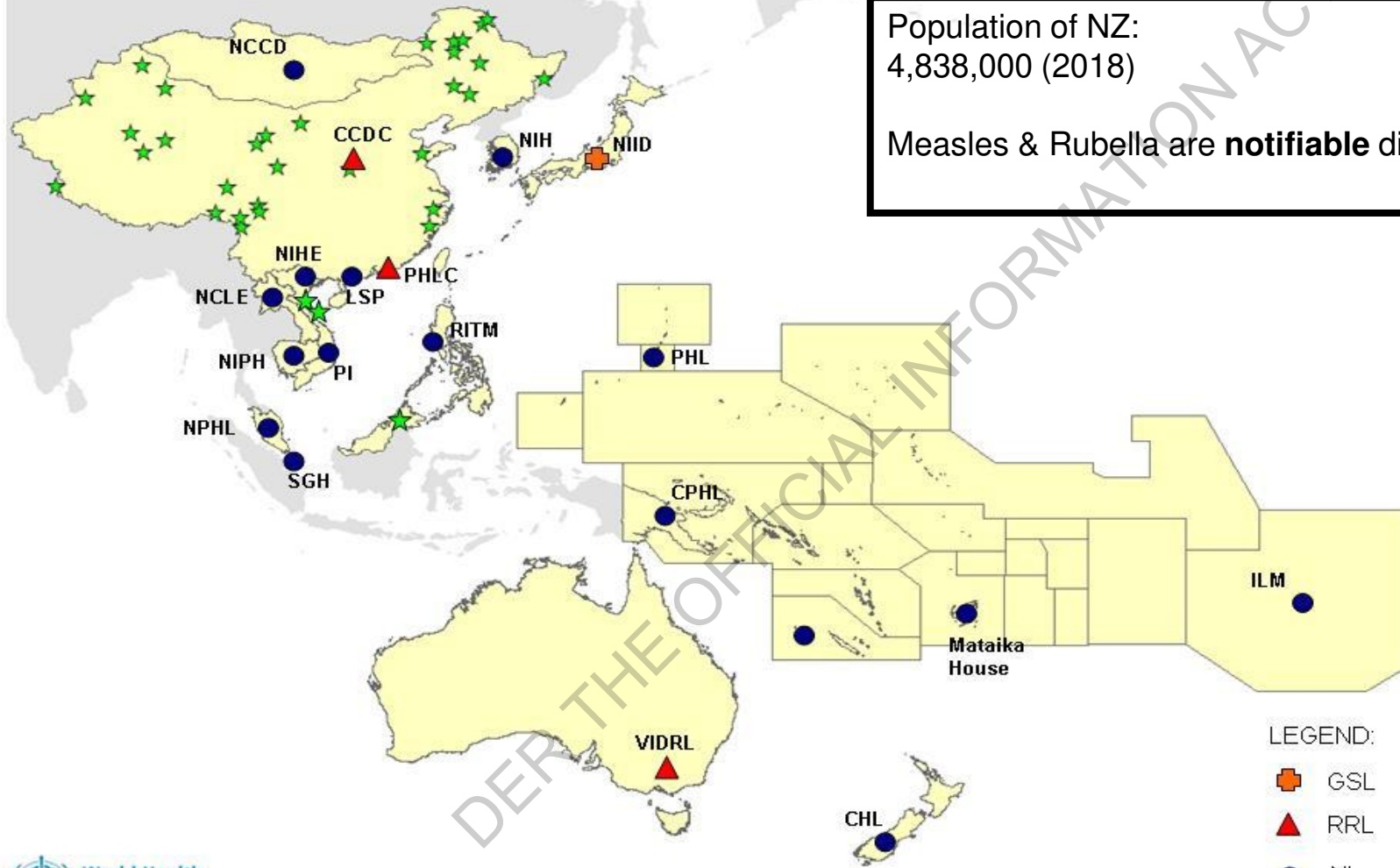


Overview

- National Surveillance Data
- National Immunization Scheme
- Virology Testing Algorithm
- Diagnostic Methods: Molecular
- Serology Testing Algorithm
- Diagnostic Methods: Serology
- NMRL Real-time-PCR and Serology Testing 2014-2018
- Measles Genotyping 2015-2018
- Quality Assurance and Audits
- Data reporting
- Problems, Challenges and Achievements





Population of NZ:
4,838,000 (2018)

Measles & Rubella are **notifiable** diseases



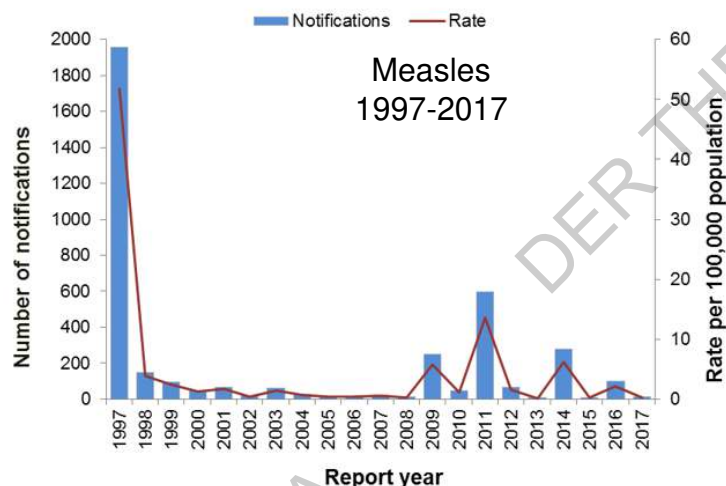
Measles-Rubella Laboratory Network

LEGEND:

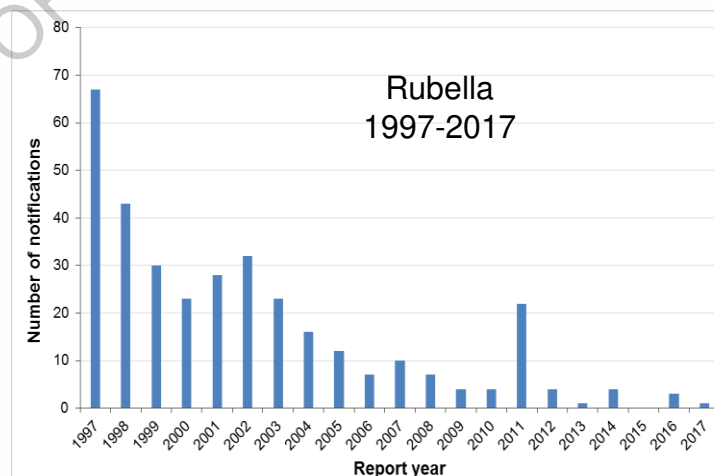
-  GSL
-  RRL
-  NL
-  Prov

National Surveillance Data

Reporting year	2014		2015		2016		2017		2018	
Total Population	4,509,690		4,595,500		4,692,720		4,793,600		4,838,000	
	Measles	Rubella	Measles	Rubella	Measles	Rubella	Measles	Rubella	Measles	Rubella
Total number of suspected cases reported	280	4	10	0	103	3	15	1	30	? 1
Reporting rate per 100,000	6.2	0.08	0.2	0	2.2	0.09	0.3	0.02	0.62	? 0.02



Since 2009 outbreaks of measles in NZ have all resulted from importations.



No CRS in NZ since 1998.



Canterbury Health
Laboratories
www.chl.co.nz | 0800THELAB

New Zealand Immunization Scheme

- > monovalent measles vaccine was introduced in 1969 (rubella vaccine in 1970)
- > between 1969 and 1992 only one dose was given
- > was replaced in 1990 by MMR
- > catch-up campaigns in 1997 and 2001

Two doses

- first at 15 months
- second at 4 years

MMR dose one and dose two coverage by birth cohort and dose (2006 to 2016)

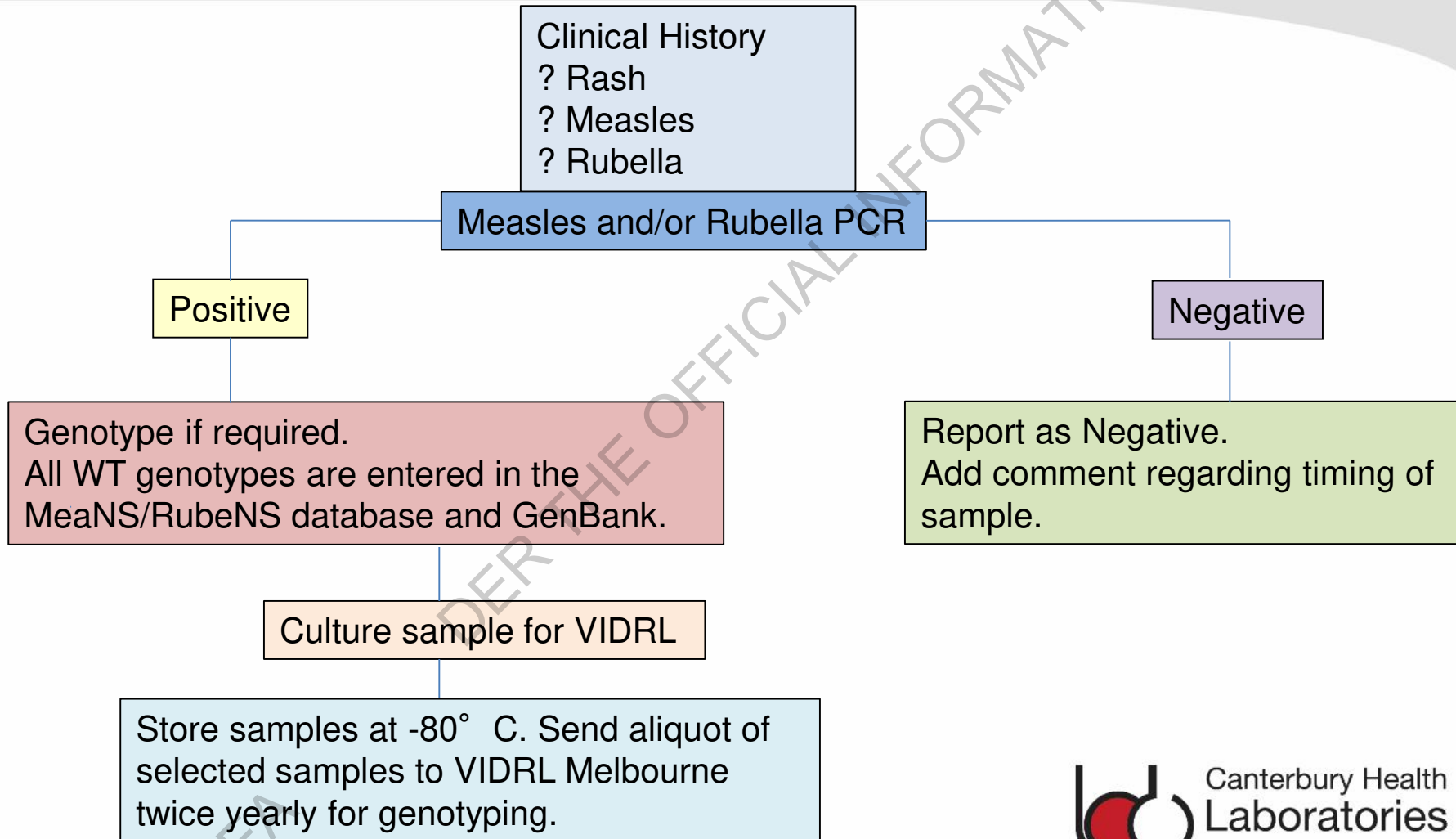
Routine vaccination coverage											
Birth Cohort	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
MMR first dose	90.6%	92.9%	94.1%	94.7%	94.8%	95.2%	95.7%	95.2%	94.9%	94.4%	91.9%
MMR second dose	88.0%	89.9%	90.0%	90.1%	90.6%	91.8%	92.3%	89.7%	N/A	N/A	N/A
a Vaccination coverage is by birth cohort.											
Note: N/A = not applicable											

Target: 90-95% coverage for both doses

But pockets of susceptible, non-immune people

- National Immunization Register exists only since 2005
- in birth cohorts between 1985 and 2005 only 75% – 85% of people are immune
- birth cohorts from 1998 onwards: influenced by Wakefield paper (2/3 of current cases)

Virology Diagnostic Algorithm



NMRL Diagnostic Methods: Molecular

PCR – WHO recommended CDC protocols

• Measles real-time RT-PCR

- Superscript III one-step RT-PCR mix
- Target: nucleoprotein gene
- Positive samples → genotyping and virus isolation in Vero/hSLAM cells

• Rubella real-time RT-PCR

- Superscript III one-step RT-PCR mix
- Target: E1 coding region
- Positive samples → genotyping and virus isolation in Vero/hSLAM cells

Genotyping

• Measles genotyping

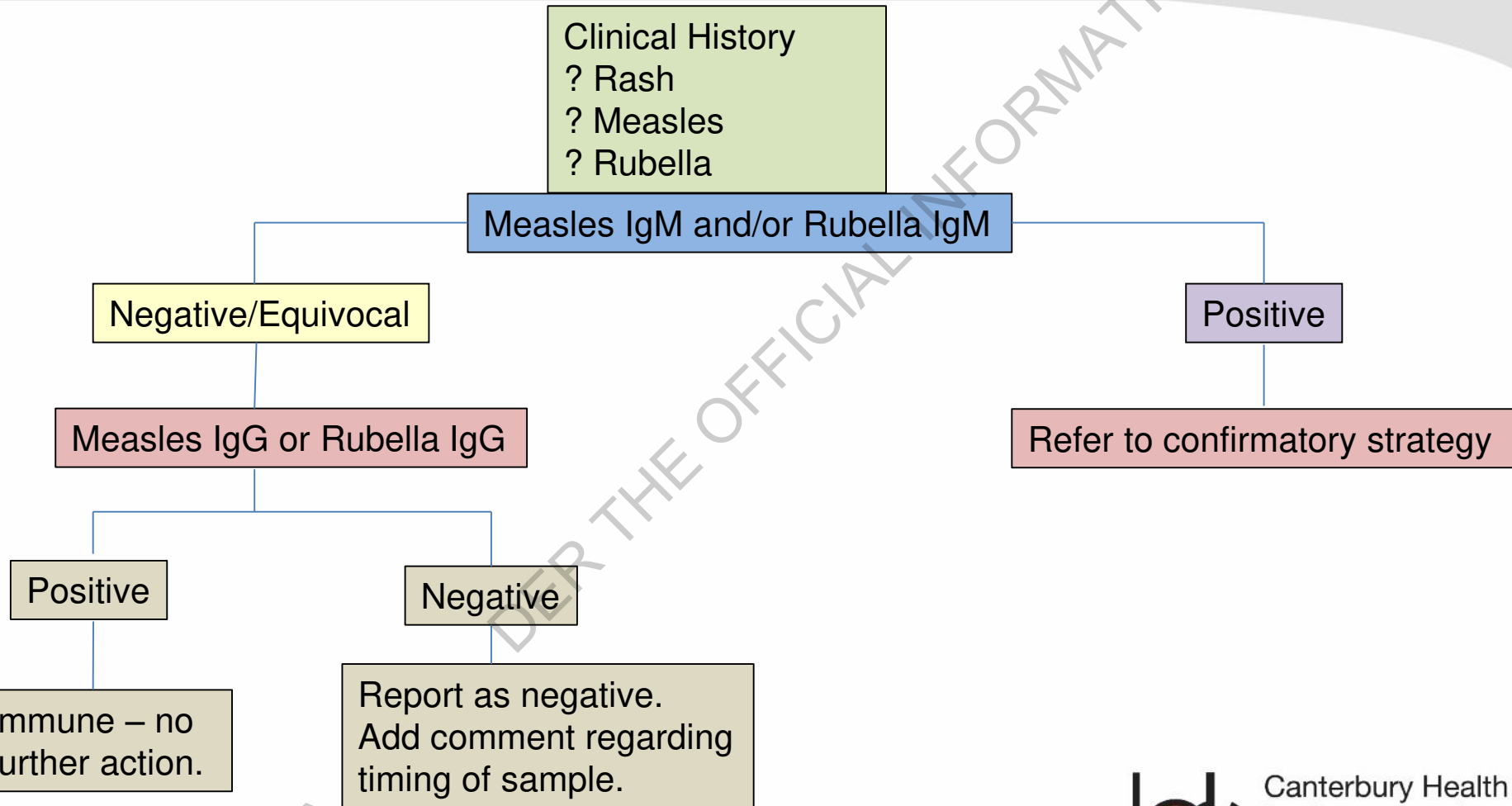
- Conventional RT-PCR (Qiagen one-step RT-PCR kit, primers MeV216 + MeV214)
 - 450 nucleotides at the end of the N gene → sequencing
- Nested PCR with primers MeV210 + MeV217: to further increase the sensitivity → sequencing
- Genotype A-specific real-time RT-PCR for rapid detection of vaccine strains (VIDRL/RRL)

• Rubella genotyping

- Conventional RT-PCR (Qiagen one-step RT-PCR kit)
 - 739 nucleotides of E1 gene derived from 2 fragment method (480 & 633 nts) → sequencing

• NGS whole genome sequencing available (Illumina)

Serology Diagnostic Algorithm



NMRL Diagnostic Methods: Serology

Serum

- Measles IgG: on Triturus using Euroimmun kits
- Measles IgM: Manual ELISA using Siemens Enzygnost kits (WHO recommended)
- Rubella IgG: on Triturus using Euroimmun kits
- Rubella IgM: Manual ELISA using Siemens Enzygnost (WHO recommended)

NMRL Measles and Rubella PCR, Genotyping and Culture

Measles	Tested	Real-time RT-PCR positive	Genotyped (excl. Type A)	Cultured
2014	514	126	63	21
2015	210	10	8	2
2016	597	66	35	34
2017	270	10	7	3
2018	281	29	22	18

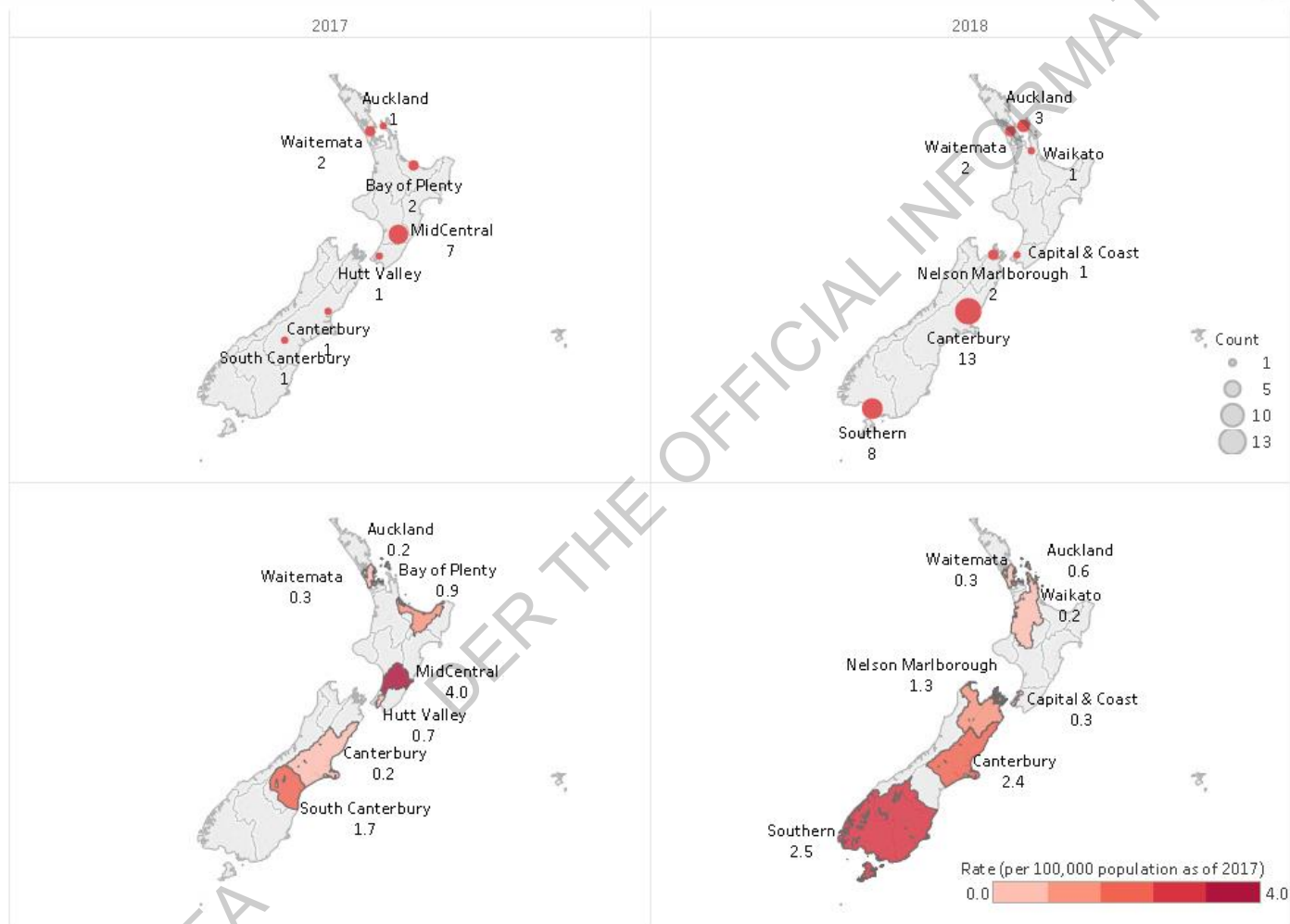
Rubella	Tested	Real-time RT-PCR positive	Genotyped	Cultured
2014	54	1	1 (2B)	0
2015	77	0	0	0
2016	31	3	3 (2B)	0
2017	15	1	1 (2B)	1
2018	8	0	0	0

NMRL Serology Testing 2014-2018

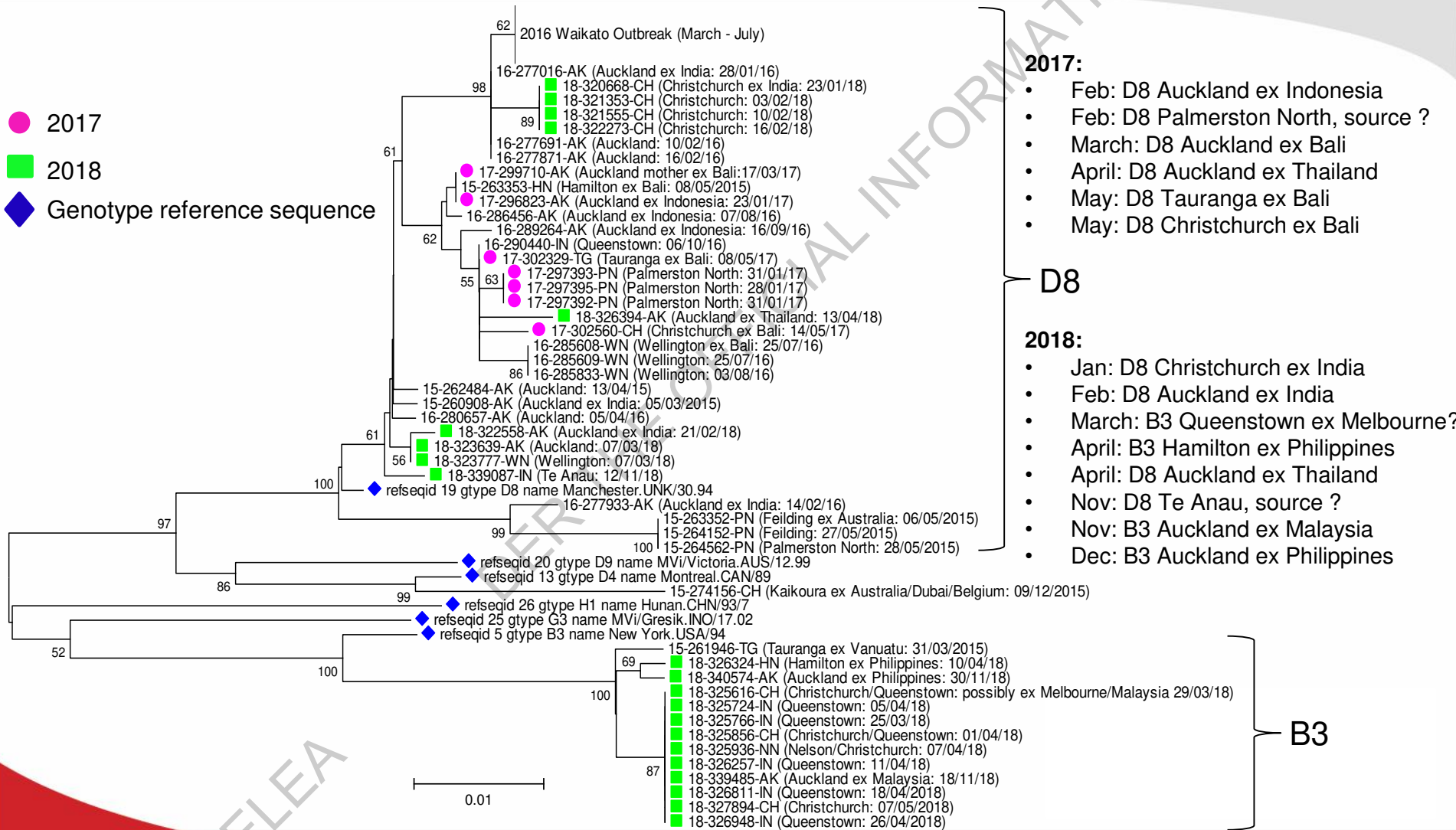
Measles IgM	Tested	Positive	Equivocal
2014	250	45	5
2015	160	8	3
2016	221	22	10
2017	123	4	9
2018	87	10	1

Rubella IgM	Tested	Positive	Equivocal
2014	103	4	1
2015	106	0	1
2016	158	1	0
2017	121	0	1
2018	51	1 (not confirmed)	3

Measles cases and rates 2017 and 2018



Measles Genotyping 2015-2018



Quality Assurance and Audits

QAP

- Annual WHO serum panel
 - 2014 – 2018: 100% correlation
- RCPA Measles and Rubella IgM proficiency panel
 - 2014 – 2018: 100% correlation
- QCMD QAP program
 - New in 2016 for measles only: 100% correlation
- Referred serum and PCR samples to VIDRL RRL
 - 2014 – 2018: 100% correlation
- PCR exchange with Capital Coast, Wellington (including Waikato and Auckland in 2019)
 - 2014 – 2018: 100%
- WHO Molecular Proficiency Panel for Measles and Rubella 2017&2018: Passed
- Internal test QAP: kit positive and negative controls, in-house controls with all batches

Audits

- Internal Audit to ISO 15189 Medical performed annually
- External Audit to ISO 15189 Medical performed annually; Peer review Audit Sept 2016 (Passed); annual accreditation passed for 2017
 - (IANZ accreditation compulsory for all NZ labs)
- WHO Audit 2012+2017; Annual WHO self-assessment (2017/2018)

Measles and rubella testing performed in NZ

Laboratory identification	Measles serology testing	Measles PCR testing	Rubella serology testing	Rubella PCR testing
National Measles and Rubella Reference Laboratory (NMRL) Canterbury Health Laboratories Christchurch	Measles IgG-Euroimmun Siemens Enzygnost Measles IgM Rubella IgG-Euroimmun Siemens Enzygnost Rubella IgM	CDC primers [Hummel et al, 2006, <i>Journal of Virological Methods</i> 132: 166–73]	Rubella IgG-Euroimmun Siemens Enzygnost Rubella IgM	CDC primers [Abernathy et al, 2009, <i>Journal of Clinical Microbiology</i> 47(1):182-88]
LabPLUS Auckland	Trinity Captia Measles IgG (Nov 2015) Trinity Captia Measles IgM (Nov 2015)	CDC primers [Hummel et al, 2006, <i>Journal of Virological Methods</i> 132: 166–73] Forward all genotyping to NMRL/CHL	Roche Laboratories COBAS Rubella IgG Roche Laboratories COBAS Rubella IgM	K. Okamoto et al. 2010. Development of novel TaqMan real-time PCR assay for detection of rubella virus. <i>J Virol Methods</i> 168:267-271
Specialist Services Laboratory Waikato	Vidas Measles IgG Siemens Enzygnost Measles IgM Trinity Captia Measles IgG EIA (Nov 2015)	CDC primers [Hummel et al, 2006, <i>Journal of Virological Methods</i> 132: 166–73] introduced in 2017 Forward all genotyping to NMRL/CHL	Abbott Architect Rubella IgG Vidas Rubella IgM	Sent to NMRL/CHL
SCL Wellington	Vidas Measles IgG (Mar 2016) Trinity Captia Measles IgM (Mar 2016)	CDC primers [Hummel et al, 2006, <i>Journal of Virological Methods</i> 132: 166–73] Forward all genotyping to NMRL/CHL	Abbott Architect Rubella IgG Vidas Rubella IgM	Forward all PCR to LabPLUS, Auckland

Data Reporting

- WHO reporting monthly
 - All positive cases: Serology, PCR & genotype results
- National EpiSurv surveillance data: all notified cases
 - total number of samples tested for Measles in NZ unknown
 - reporting and sending samples to NMRL voluntary
- Selection of samples sent to VIDRL (RMRL) for confirmatory testing
- Genotyped measles results uploaded to MeaNS
- Genotyped rubella results uploaded to RubeNS
- Annual report to MoH NZ

Problems, Challenges and Achievements

- Low level positive real-time-PCR results (not suitable for genotyping)
- Positive results reported from other labs, but samples not sent to NMRL for genotyping/isolation
- Introduction of genotype A specific PCR (VIDRL) has helped to distinguish recent vaccination from clinical disease
- Use of whole genome sequencing to exclude endemic transmission

Acknowledgements

- Dr Meik Dilcher, Scientific Officer Virology, CHL
- Rodger Linton, Section Head Virology/Serology, CHL
- Tomasz Kiedrzyński, Communicable Diseases, MoH NZ
- Liza Lopez, Health Intelligence Team, ESR
- All staff of the National Measles Laboratory, CHL



