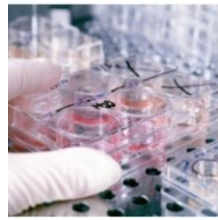




NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES

Division of the National Health Laboratory Service



Epidemiology of influenza A/B viruses during 2017 in South Africa

Florette Treurnicht

Introduction

- Influenza surveillance conducted in South Africa since 1984
- Before that viruses were shared with MRC London since 1950s
- Currently respiratory tract specimens are collected for 3/4 surveillance programs

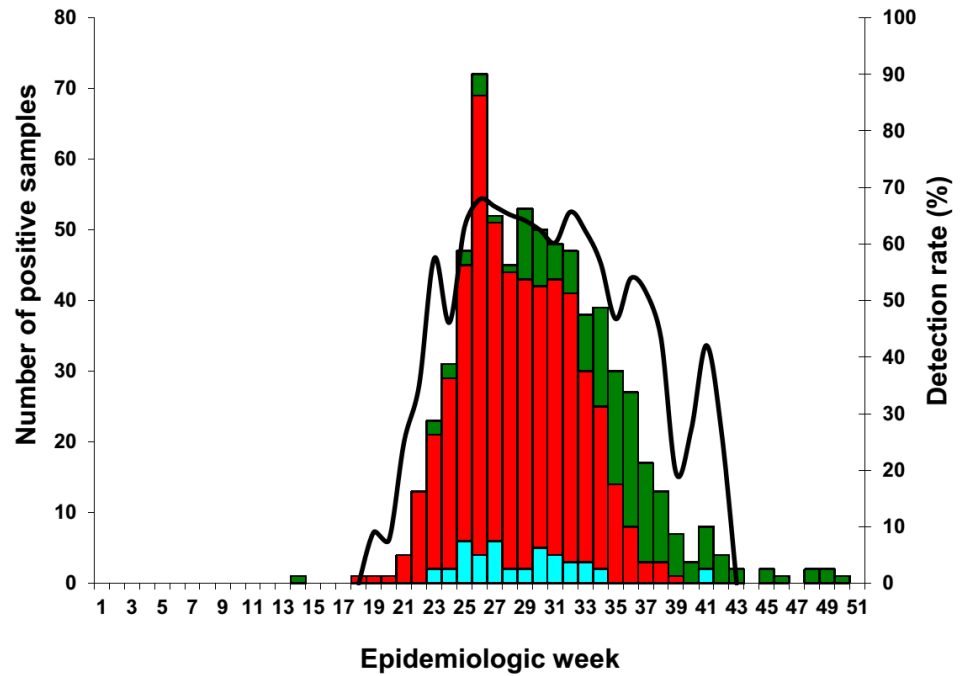
Programme	ILI	Viral Watch	National syndromic surveillance for pneumonia	Private hospital consultations
Start year	2012	1984	2009	2002
Provinces*	KZ NW MP	EC FS GP LP MP NC NW WC	GP KZ MP NW WC	EC FS GP LP MP NW WC
Type of site	Primary health care clinics	General practitioners	Public hospitals	Private hospitals
Case definition	An acute respiratory illness with a temperature ($\geq 38^{\circ}\text{C}$) and cough, & onset ≤ 10 days	An acute respiratory illness with a temperature ($\geq 38^{\circ}\text{C}$) and cough, & onset ≤ 10 days	Acute or chronic lower respiratory tract infection	ICD codes J10-J18

Total number of specimens and cumulative number of influenza types and subtypes, by program in 2017

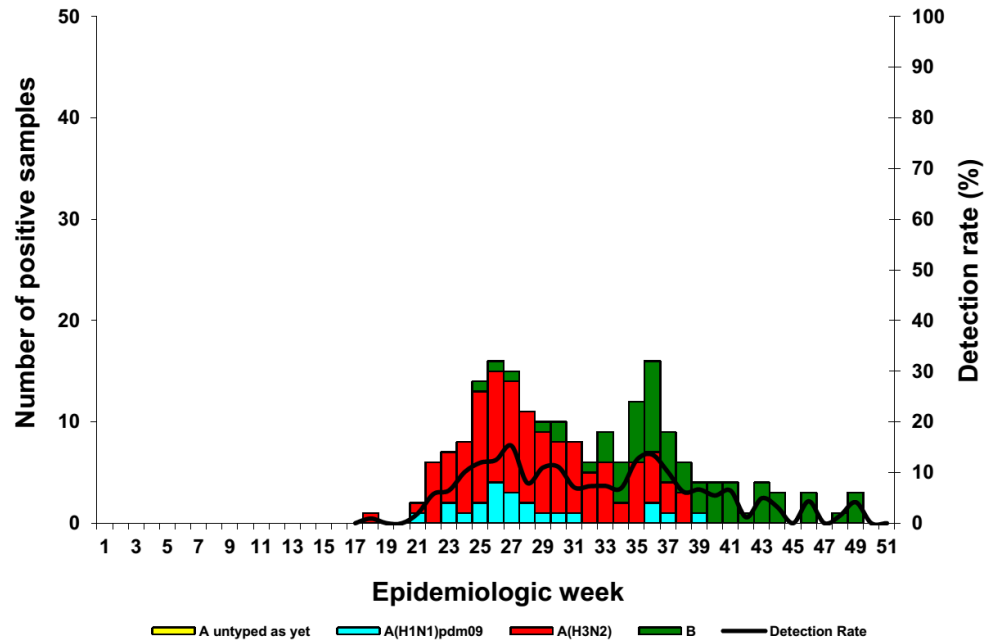
- Season started in week 21 (end May) -detection rate for Viral Watch rose above 10%

Program	Specimens	Influenza Positive	Influenza A	Dual A or A/B	A(H1N1)pdm09	A(H3N2)	Influenza B
	N	N (%)	N (%)	N (%)	N (%)	N (%)	N (%)
ILI/PHC	1781	270 (15)	169 (63)	0	1 (1)	168 (62)	101 (37)
VW	1218	682 (56)	532 (78)	3 (0.4)	41 (6)	488 (72)	150 (22)
SARI/ Pneumonia	4433	200 (4.5)	137 (69)	1 (0.5)	22 (11)	114 (57)	63 (32)
Total	7432	1152 (16)	838 (73)	4 (0.3)	64 (5.6)	770 (69)	314 (27)

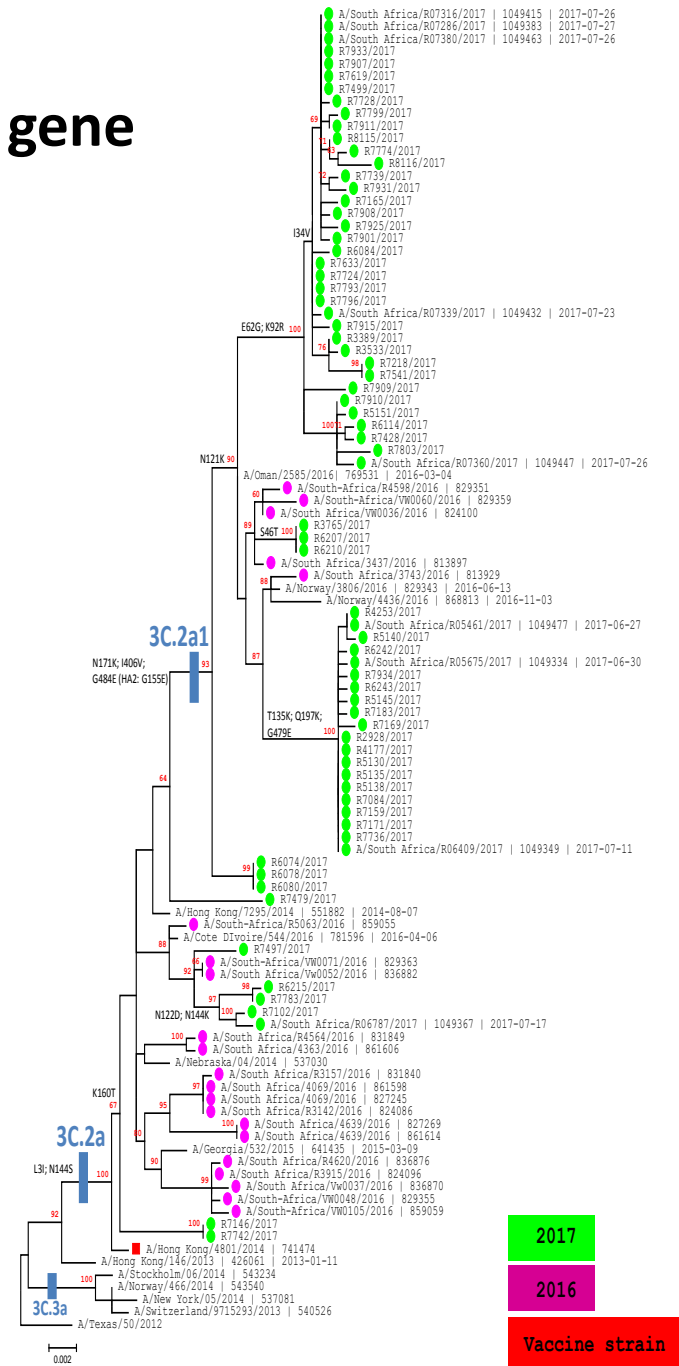
Viral Watch



SARI/Pneumonia

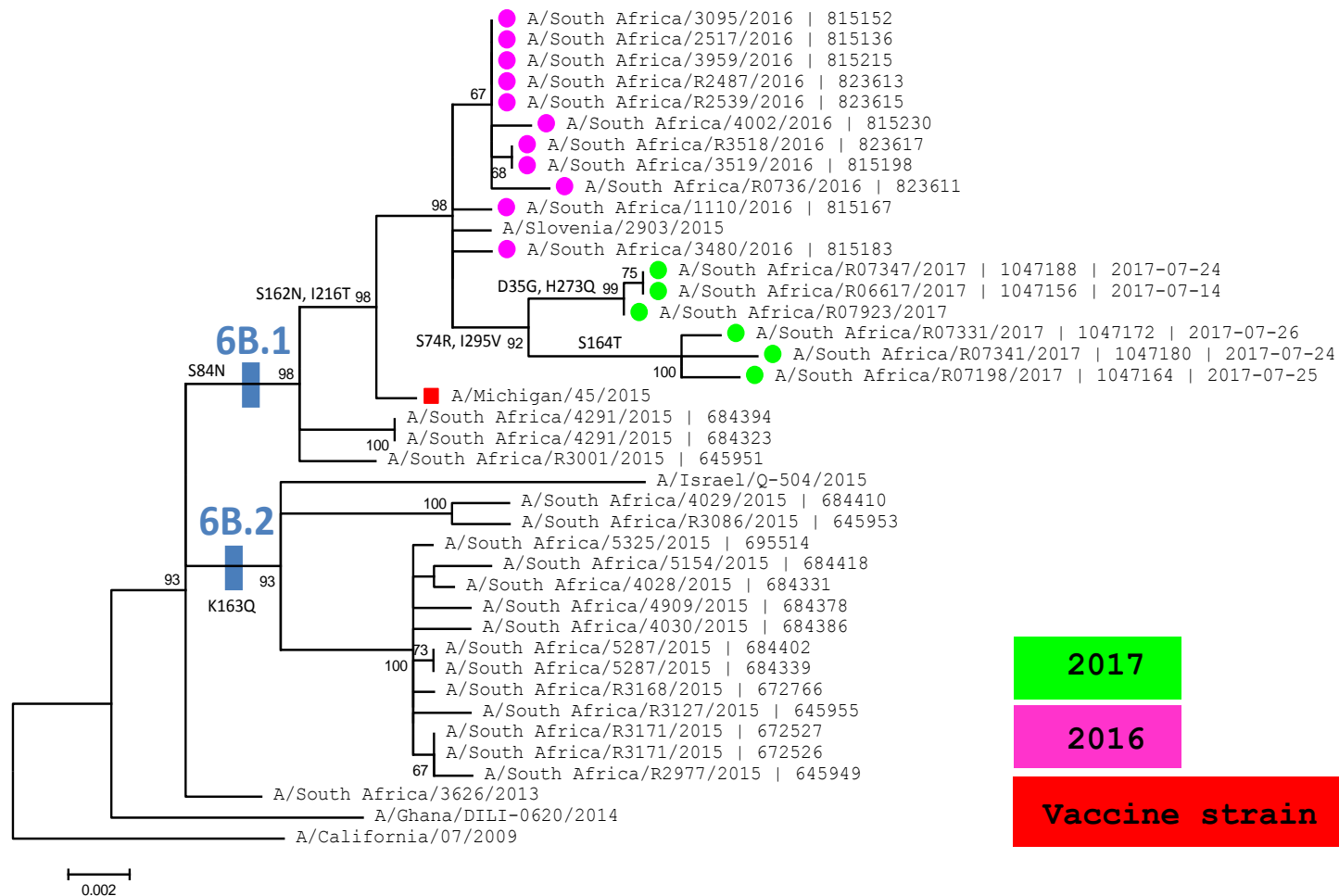


Maximum likelihood tree of the influenza A(H3N2) hemagglutinin gene (1650 bp)

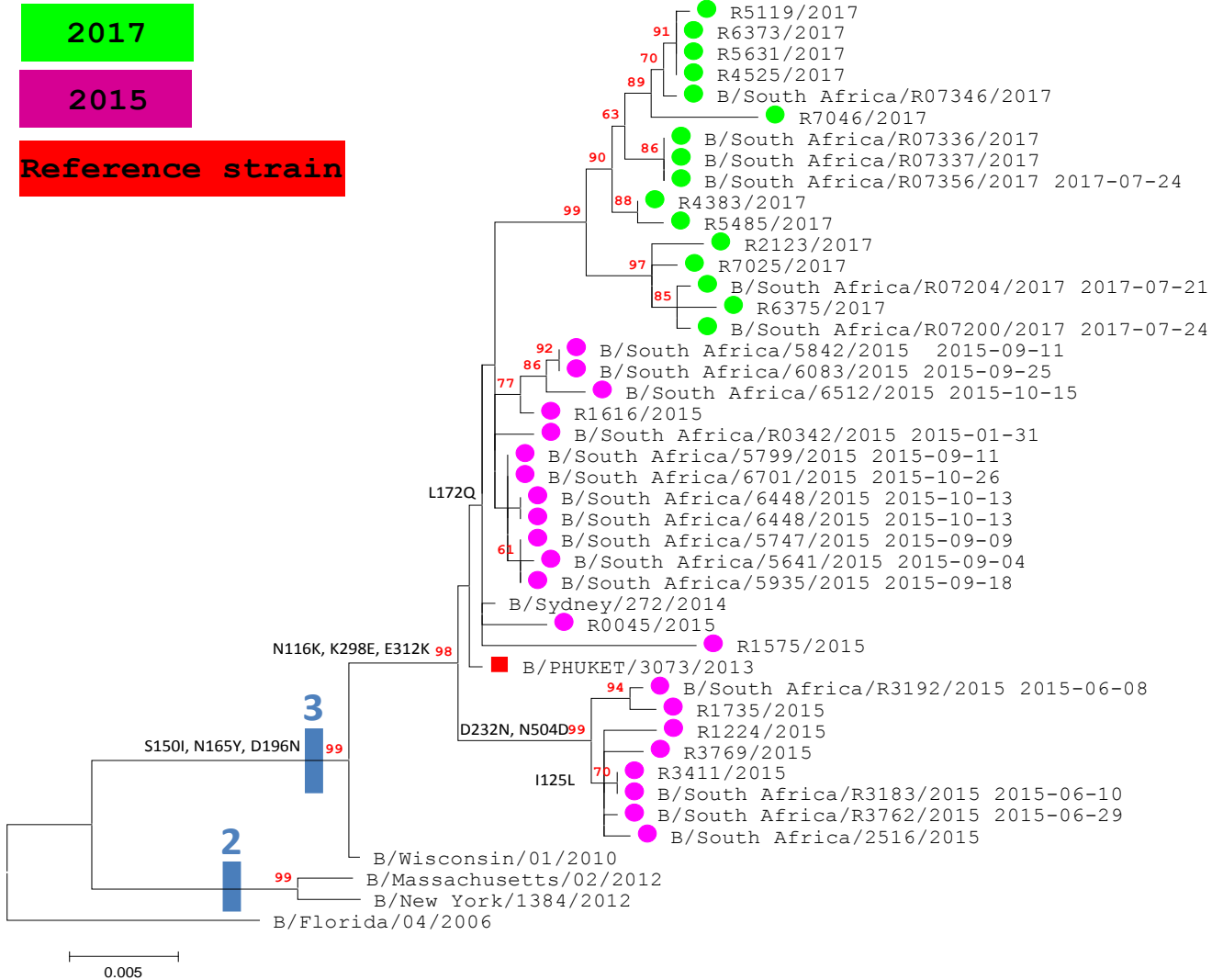


2017
2016
Vaccine strain

Maximum likelihood tree of the influenza A(H1N1)pdm09 hemagglutinin gene (1650 bp)



Maximum likelihood tree of the influenza B/Yamagata hemagglutinin gene (1650 bp)



Summary

- Influenza A dominated and specifically H3N2,
- Very few A(H1N1)pdm09
- Influenza B dominated towards the end of the season

Genetic characterization

- A(H3N2), 3C.2a1 lineage mainly
- A(H1N1)pdm09 lineage 6B.1 viruses
- Influenza B/Yamagata clade 3 viruses
- Same clustering was observed for NA
- No mutations associated with oseltamivir resistance was observed

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