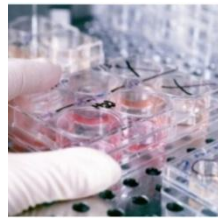




NATIONAL INSTITUTE FOR
COMMUNICABLE DISEASES

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

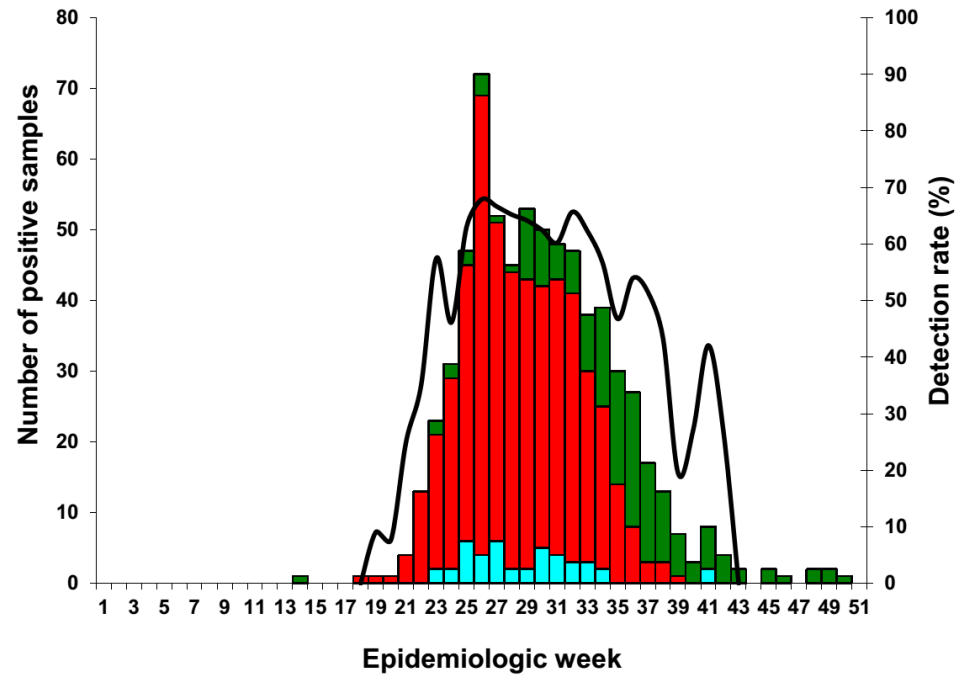
Programme	ILI	Viral Watch	National syndromic surveillance for pneumonia	Private hospital consultations
Start year	2012	1984	2009	2002
Provinces*	KZ NW MP	EC FS GP LP MP NC NW WC	GP KZ MP NW WC	EC FS GP LP MP NW WC
Type of site	Primary health care clinics	General practitioners	Public hospitals	Private 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

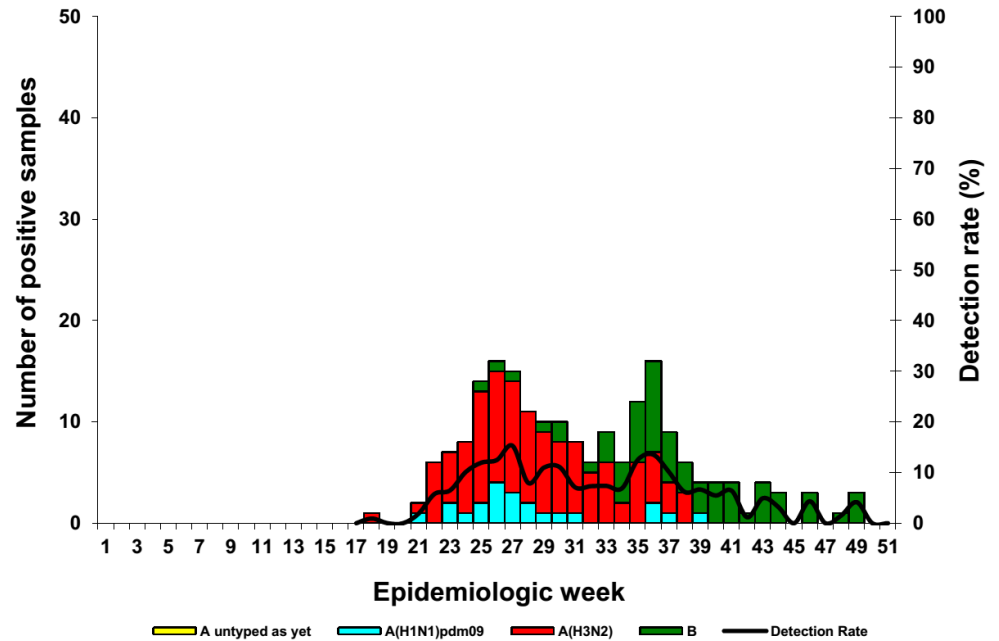
- Season started in week 21 (end May) -detection rate for Viral Watch rose above 10%

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

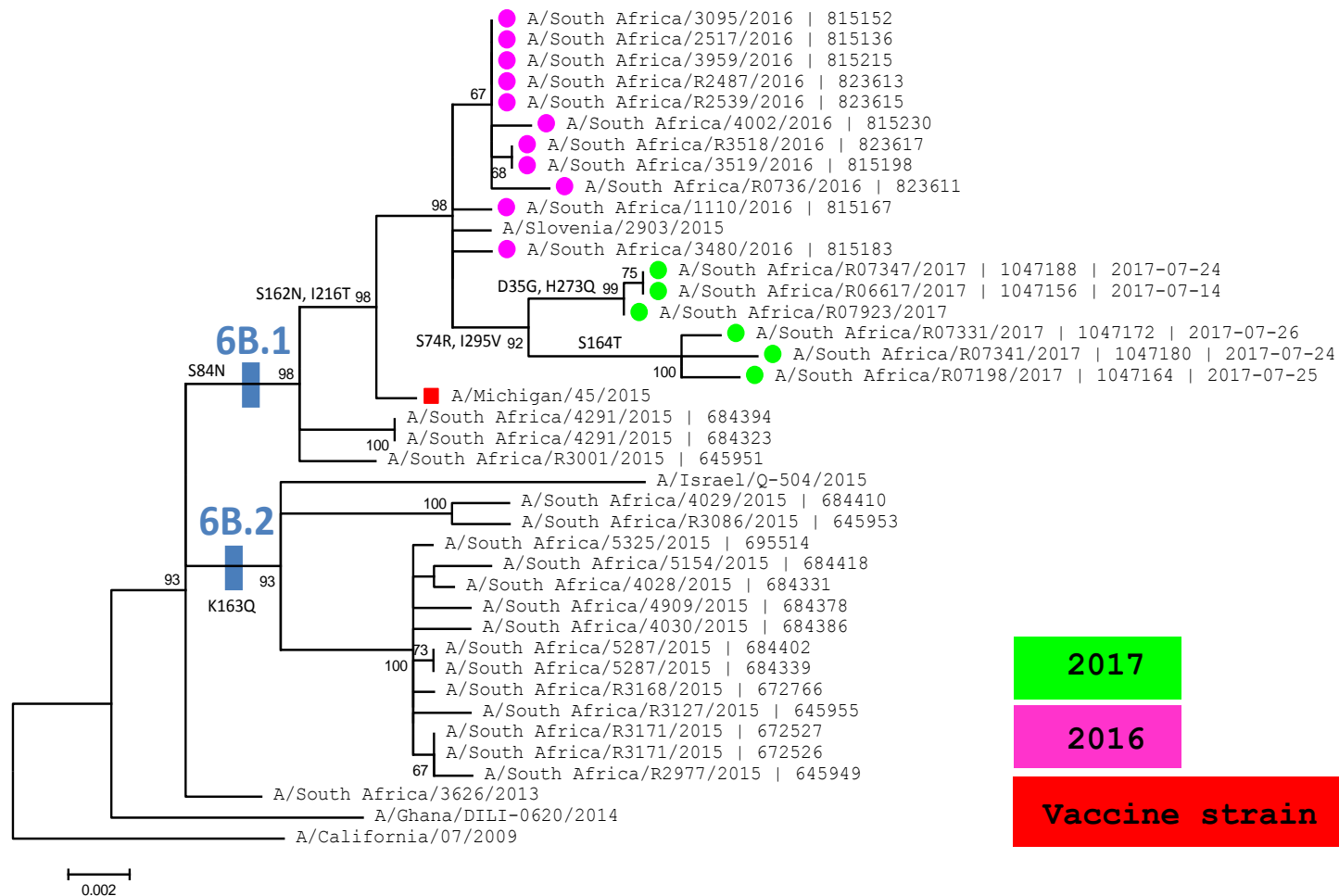


SARI/Pneumonia

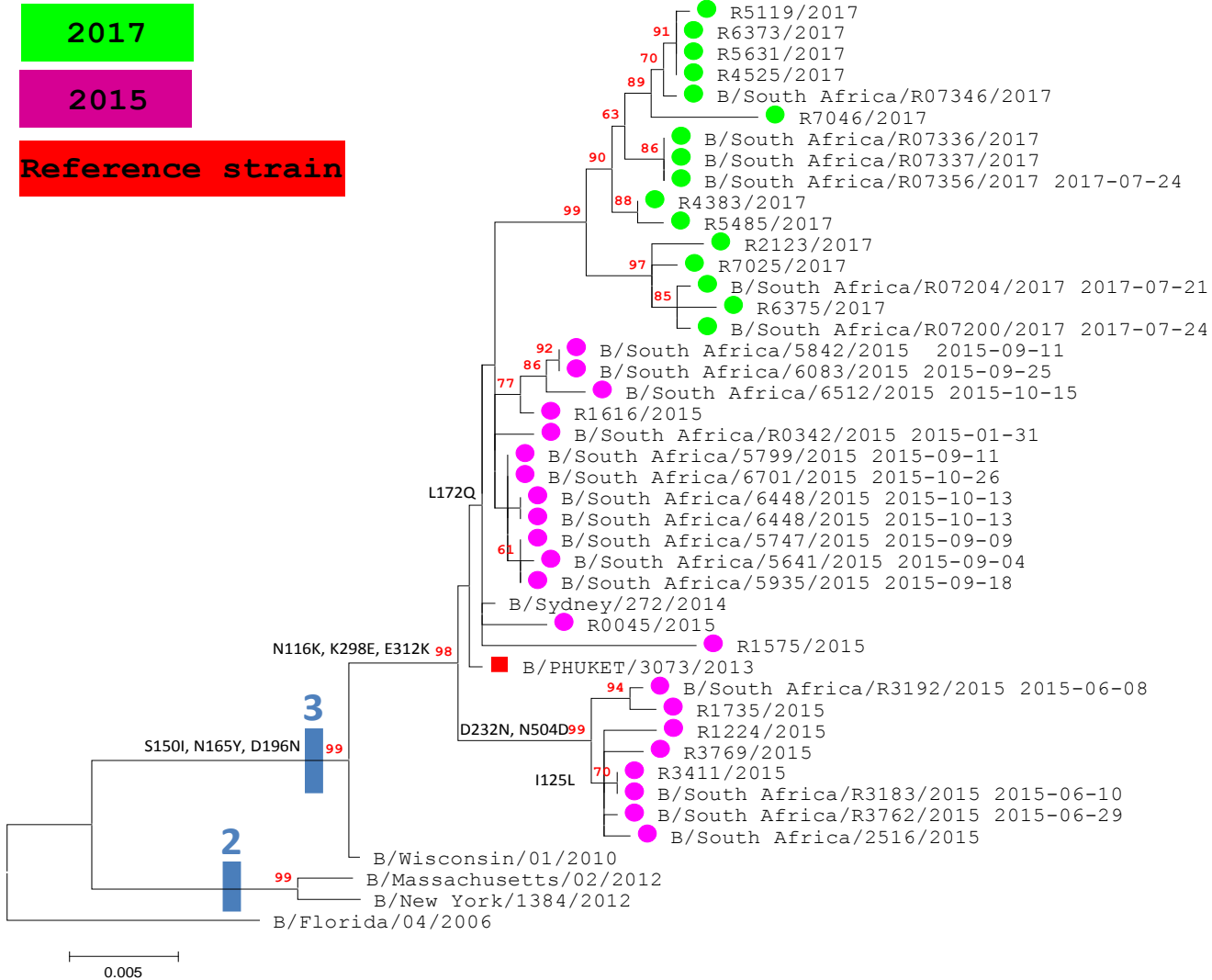


■ A untyped as yet
 ■ A(H1N1)pdm09
 ■ A(H3N2)
 ■ B
 — Detection Rate

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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