WEEKLY RESPIRATORY PATHOGENS SURVEILLANCE REPORT

SOUTH AFRICA WEEK **42** 2021

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

CONTENTS

HIGHLIGHTS: WEEK 42

- The 2021 influenza season has not yet started although sustained detections of influenza continue in all surveillance programmes. In week 42, transmission is below threshold and impact is low.

- 14 new cases of influenza from Gauteng (n=3), Western Cape (n=3), North West (n=6), Kwa-Zulu Natal (n=1) and Mpumalanga (n=1) surveillance sites were detected in week 42. To date, 183 influenza cases have been detected from Gauteng, Western Cape, North West, Eastern Cape, Mpumalanga and KwaZulu-Natal sentinel surveillance sites. From 1 January 2021 to date, Influenza B (Victoria) was the most commonly detected lineage in both influenza-like illness (ILI) surveillance (n=26/54, 48%) and pneumonia surveillance (n=45/97, 46%).

- RSV activity remains below seasonal threshold in both influenza-like illness (ILI) and pneumonia surveillance programmes. From 1 January 2021 to date, RSV subgroup A was the most commonly detected subgroup in both ILI surveillance (n=40/74, 54%) and pneumonia surveillance (n=211/405, 52%).

- From 2 March 2020 to date, a total of 2 884 COVID-19 cases were detected from all surveillance programmes. A sustained decline in detection rate has been noted in both ILI programme and pneumonia surveillance. Of the 2 003 hospitalised COVID-19 cases reported with available data on outcome, 343 (17%) died.

- From 1 January 2021 to date, of the 1192/1291 (92%) SARS-CoV-2 positive cases with variant type results, Delta (425/871, 49%) and Beta (157/321, 49%), were the most detected variants in pneumonia surveillance and in ILI, respectively. Delta variant predominated in both programmes (from week 22, week starting 31st May 2021 until to date). Beta variant predominated from week 47 of 2020 to week 21 of 2021.

PROGRAMME DESCRIPTIONS

Programme	**Influenza-like illness (ILI)**	**Viral Watch**	**National syndromic surveillance for pneumonia**
Start year	2012	1984	2009
Provinces*	KZ NW WC** MP***	EC FS GP LP MP NC NW WC	GP KZ MP NW WC
Type of site	Primary health care clinics	General practitioners	Public hospitals
Case definition	**ILI:** An acute respiratory illness with a temperature (≥38°C) and cough, & onset ≤10 days **Suspected pertussis** Any person with an acute cough illness lasting ≥14 days (or cough illness of any duration for children <1 year), without a more likely diagnosis AND one or more of the following signs or symptoms: · paroxysms of coughing, · or inspiratory "whoop", · or post-tussive vomiting · or apnoea in children <1 year; OR Any person in whom a clinician suspects pertussis **Suspected SARS-CoV-2** Any person presenting with an acute (≤14 days) respiratory tract infection or other clinical illness compatible with COVID-19$^{\beta}$	**ILI:** An acute respiratory illness with a temperature (≥38°C) and cough, & onset ≤10 days **Suspected SARS-CoV-2** Any person presenting with an acute (≤14 days) respiratory tract infection or other clinical illness compatible with COVID-19$^{\beta}$	**SRI:** Acute (symptom onset≤10 days) or chronic (symptom onset >10) lower respiratory tract infection **Suspected pertussis** Any person with an acute cough illness lasting ≥14 days (or cough illness of any duration for children <1 year), without a more likely diagnosis AND one or more of the following signs or symptoms: · paroxysms of coughing, · or inspiratory "whoop", · or post-tussive vomiting · or apnoea in children <1 year; OR Any person in whom a clinician suspects pertussis. **Suspected SARS-CoV-2** Any person admitted with a physician-diagnosis of suspected COVID-19 and not meeting SRI case definition.
Specimens collected	Oropharyngeal & nasopharyngeal swabs	Throat and/or nasal swabs or Nasopharyngeal swabs	Oropharyngeal & nasopharyngeal swabs
Main pathogens tested****	INF RSV BP SARS-CoV-2	INF RSV BP SARS-CoV-2	INF RSV BP SARS-CoV-2
Testing Methods	**INF and RSV** - Fast-Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay (Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)	**INF and RSV** - Fast-Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)	**INF and RSV** - Fast Track Diagnostics multiplex real-time reverse transcription polymerase chain reaction (until 31 March 2021) ***B. pertussis*** Multiplex real-time PCR (Tatti *et al., J Clin Microbiol* 2011) and culture (if PCR cycle threshold ≤25) **SARS-CoV-2** 1 April 2020 – 31 March 2021: Roche E gene real-time PCR essay (Corman *et al., Euro Surv* 2020) 1 April 2021 to date: Allplex™ SARS-CoV-2/FluA/FluB/RSV PCR kit • positivity assigned if PCR cycle threshold is <40 for ≥1 gene targets (N, S, OR RdRp)

Epidemic Threshold

Thresholds are calculated using the Moving Epidemic Method (MEM), a sequential analysis using the R Language, available from: http://CRAN.R-project.org/web/package=mem) designed to calculate the duration, start and end of the annual influenza epidemic. MEM uses the 40th, 90th and 97.5th percentiles established from available years of historical data to calculate thresholds of activity. Thresholds of activity for influenza and RSV are defined as follows: Below seasonal threshold, Low activity, Moderate activity, High activity, Very high activity. For influenza, thresholds from outpatient influenza like illness (Viral Watch Programme) are used as an indicator of disease transmission in the community and thresholds from pneumonia surveillance are used as an indicator of impact of disease.

* EC: Eastern Cape; FS: Free State; GP: Gauteng; KZ: KwaZulu-Natal; LP: Limpopo; MP: Mpumalanga: NC: Northern Cape; NW: North West; WC: Western Cape

**Started in 2019

***Started in November 2020

****INF: influenza virus; RSV: respiratory syncytial virus; BP: *Bordetella pertussis;* SARS-CoV-2: severe acute respiratory syndrome coronavirus 2

[β] Symptoms include ANY of the following respiratory symptoms: cough, sore throat, shortness of breath, anosmia (loss of sense of smell) or dysgeusia (alteration of the sense of taste), with or without other symptoms (which may include fever, weakness, myalgia, or diarrhoea). Testing for SARS-CoV-2 was initiated in all three surveillance programmes in week 10 of 2020 (week starting 2 March 2020).

COMMENTS

Influenza

The 2021 influenza season has not yet started although sustained detections of influenza continue in all surveillance programmes. Since the first influenza positive case of 2021 was detected in pneumonia surveillance in week 9 of 2021 (week ending on the 07 March 2021), sporadic cases have been reported from week 16 to date. Of the 183 influenza cases detected in surveillance sites in 2021, the majority (n=93, 51%) were influenza B(Victoria). In week 42, transmission is below threshold and impact is low.

ILI programme: In 2021 to date, specimens from 1 550 patients meeting ILI case definition were received from 4 ILI sites. Influenza was detected in 54 (3%) patients, of which four (7%) were influenza A(H1N1)pdm09, five (9%) influenza A(H3N2), one (2%) influenza A(inconclusive), 13 (24%) influenza A(pending subtype results), 26 (48%) influenza B(Victoria) and four (7%) influenza B(lineage inconclusive). (Fig1, Table1).

Viral Watch programme: In 2021 to date, specimens were received from 185 patients from Viral Watch sites in 5 of the 8 provinces participating in surveillance. Influenza was detected in 15 (8%) patients, of which two (13%) were influenza A(H1N1)pdm09, three (20%) influenza A(pending results), five (33%) influenza B(Victoria), four (27%) influenza B(lineage inconclusive) and one (7%) influenza B(lineage pending results). (Fig7, Table5)

Pneumonia surveillance: Since the beginning of 2021, specimens from 5 129 patients with severe respiratory illness (SRI) were received from the 6 sentinel sites. Influenza was detected in 97 (2%) patients, of which 21 (22%) were influenza A(H1N1)pdm09, 14 (14%) influenza A(H3N2), one (1%) influenza A(subtype inconclusive), 10 (10%) influenza A(pending subtype results), 45 (46%) influenza B(Victoria), four (4%) were influenza B(lineage inconclusive) and two (2%) influenza B(lineage pending results). (Fig12, Table9)

In addition, influenza B(Victoria) was detected in 17 of 765 (2%) patients who met suspected SARS-CoV-2 case definition but did not meet the pneumonia/ILI surveillance case definitions.

Respiratory syncytial virus

In 2021 to date, RSV detection has been reported from all surveillance programmes, activity remains below seasonal threshold. Of the 485 RSV cases detected in 2021, the majority (n=254, 52%) were RSV subgroup A.

ILI programme: In 2021 to date, 1 550 specimens from patients meeting the ILI case definition were tested and RSV was detected in 74 (5%) patients. Of which, 40 (54%) were RSV subgroup A, 31 (42%) RSV subgroup B, two (3%) RSV subgroup A and B and one (1%) was RSV (subgroup inconclusive). (Fig4, Table2)

Viral Watch programme: In 2021 to date, 185 specimens from viral watch patients were tested and RSV was detected in specimens of six (3%) patients. Of which, three (50%) were RSV subgroup A, two (33%) RSV subgroup B and one (17%) was RSV (subgroup inconclusive). (Fig9, Table6)

Pneumonia surveillance: Since the beginning of 2021, 5 129 specimens were tested and RSV was detected in specimens of 405 (8%) patients. Of which, 211 (52%) were RSV subgroup A, 187 (46%) RSV subgroup B, five (1%) RSV (subgroup inconclusive) and two (1%) RSV (subgroup pending). (Fig14, Table10)

In addition, RSV was detected in 21 of 765 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet the pneumonia/ILI surveillance case definitions.

SARS-CoV-2 (Severe acute respiratory syndrome coronavirus 2)

ILI programme: From March 2020 to date, 2 861 patients were tested and SARS-CoV-2 was detected in 568 (20%) patients. From 1 January 2021 to date, of the 321/338 (95%) with data on variant type, majority (157/321, 49%) were Beta variant which predominated from week1 to week 24, followed by Delta (139/321, 43%) variant which predominated from week 25 to week 36. (Fig6, Table4)

Viral Watch programme: From March 2020 to date, 464 patients presenting with ILI were tested and SARS-CoV-2 was detected in 84 (18%) patients. From 1 January 2021, of the 21/84 (25%) with data on variant type, majority were (19/21, 90%) were Delta variant which dominated from week 25 to week 30. (Fig11, Table8)

Pneumonia surveillance: From March 2020 to date, 9 142 patients with severe respiratory illness (SRI) were tested and SARS-CoV-2 was detected in 2 048 (22%) patients. From 1 January 2021 to date, of the 871/954 (91%) with data on variant type, majority were (425/871, 49%) were Delta variant which dominated from week 22 to week38 followed by Beta (401/871, 46%) variant which dominated from week 1 to 25. (Fig17, Table12)

In addition, SARS-CoV-2 was detected in 192 of 968 (20%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet the pneumonia/ILI surveillance case definitions.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

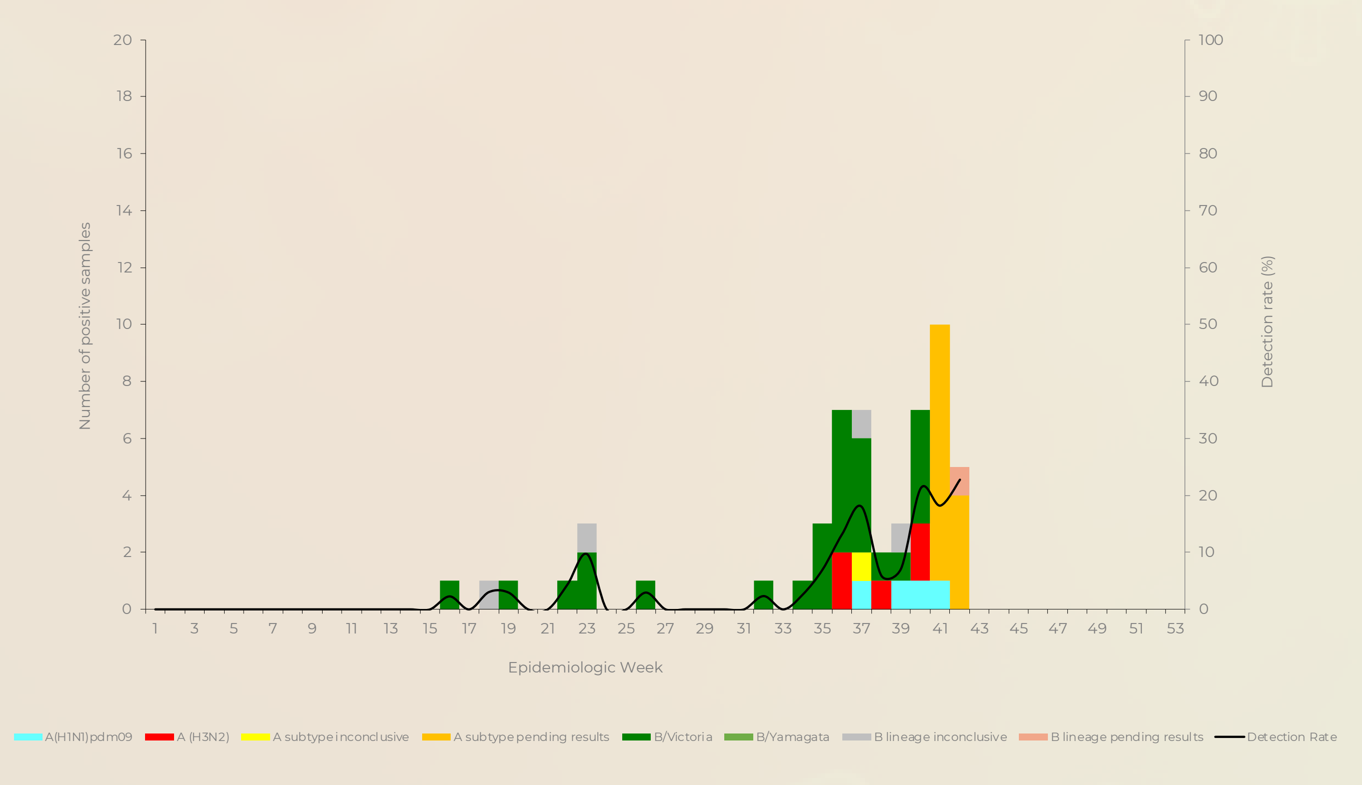

Figure 1. Number of influenza positive cases* by influenza subtype and lineage** and detection rate*** by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

*Specimens from patients with influenza-like illnesses at 5 sentinel sites in 4 provinces
**Influenza B (Victoria) was detected in 13 (2%) of 591 specimens, from patients who met suspected SARS-CoV-2 case definition but did not meet Influenza-like illness (ILI) case definition. These are not included in the epidemiological curve.
***Only reported for weeks with >10 specimens submitted
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 1. Number of laboratory confirmed influenza cases by subtype and lineage** and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

Clinic (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results^β	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results^β	Total samples
Agincourt (MP)	0	0	0	1	0	0	0	0	210
Eastridge (WC)	0	2	0	0	6	0	0	0	214
Edendale Gateway (KZ)	0	1	0	0	5	0	2	1	204
Jouberton (NW)	4	2	1	11	12	0	1	0	711
Mitchell's Plain (WC)	0	0	0	1	3	0	1	0	211
Total:	**4**	**5**	**1**	**13**	**26**	**0**	**4**	**1**	**1 550**

KZ: KwaZulu-Natal; NW: North West; WC: Western Cape; MP: Mpumalanga
Inconclusive: insufficient viral load in sample and unable to characterise further

**Influenza B (Victoria) was detected in 12 (2%) of 591 specimens, from patients who met suspected SARS-CoV-2 case definition but did not meet Influenza-like illness (ILI) case definition. These are not included in the table.
^β influenza A subtype or B lineage results are pending

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

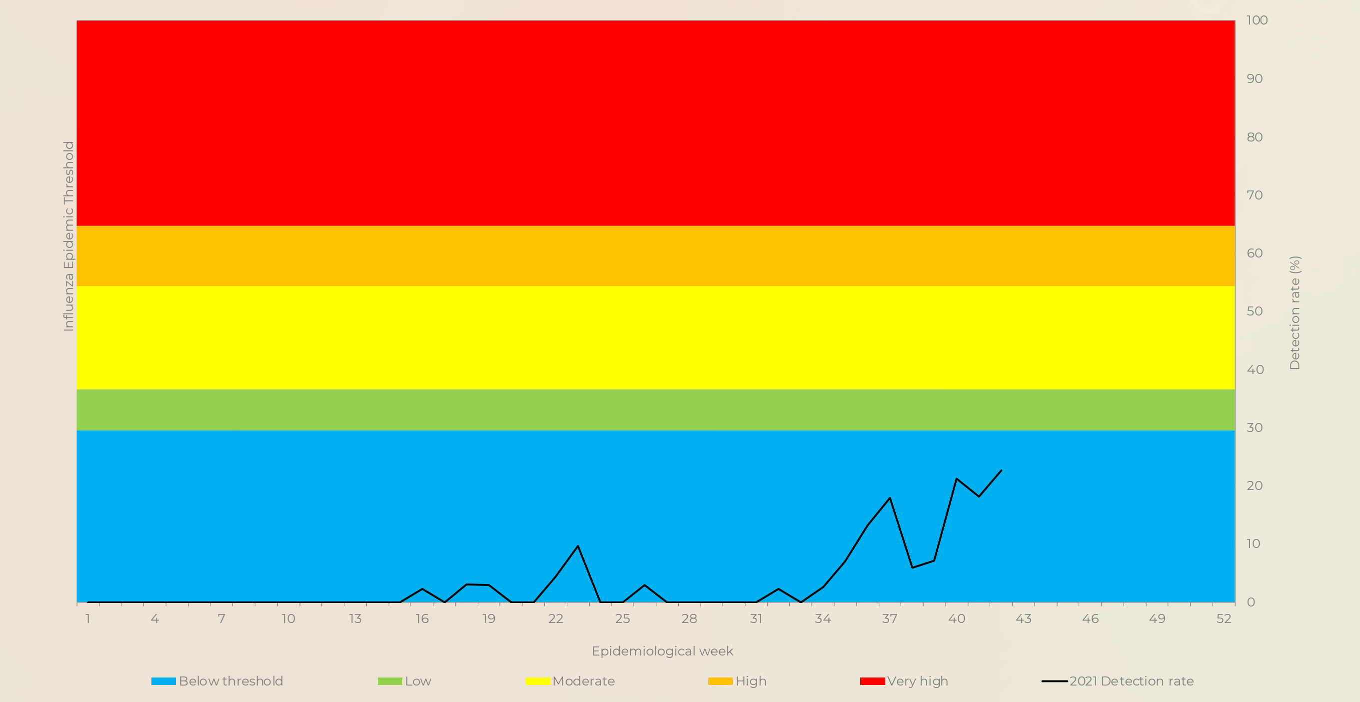

Figure 2. Influenza percentage detections and epidemic thresholds*, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

*Thresholds based on 2012-2019 data

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

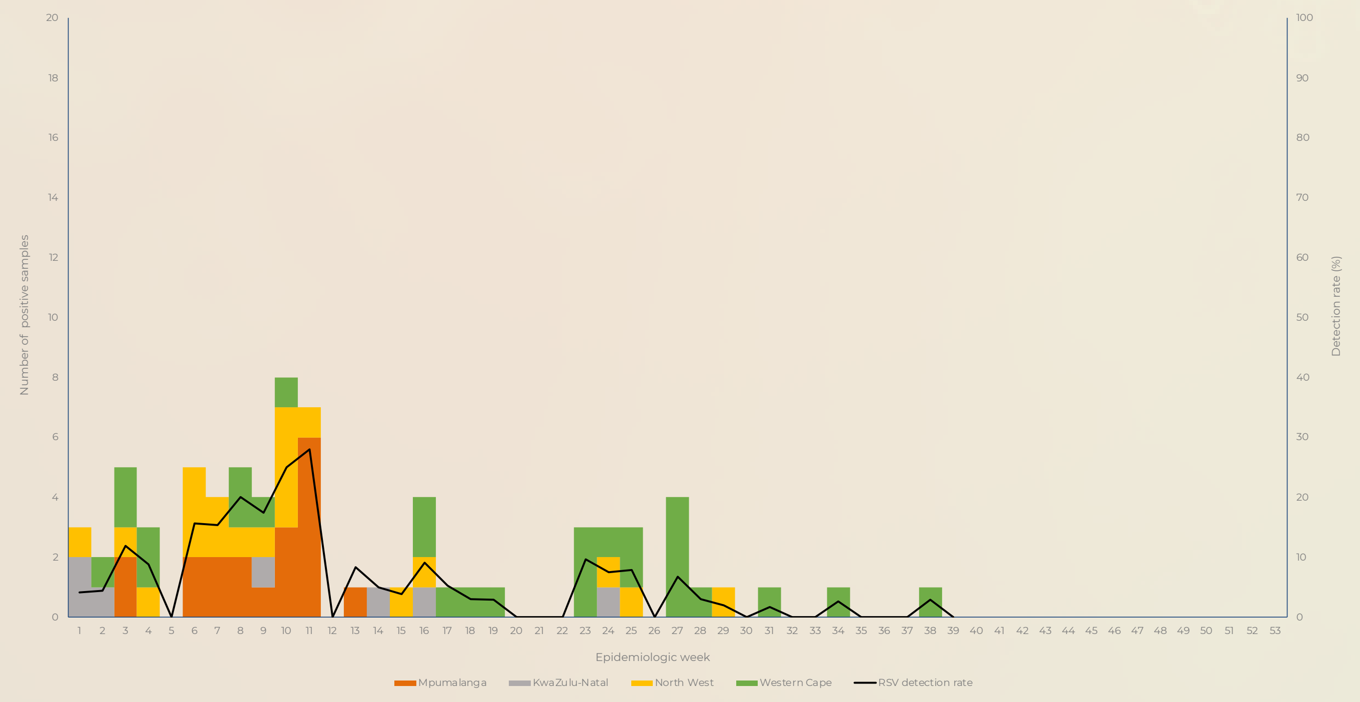

Figure 3. Number of patients testing positive for respiratory syncytial virus* by province and detection rate** by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

**RSV was detected from 15 of 591 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the epidemiological curve.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

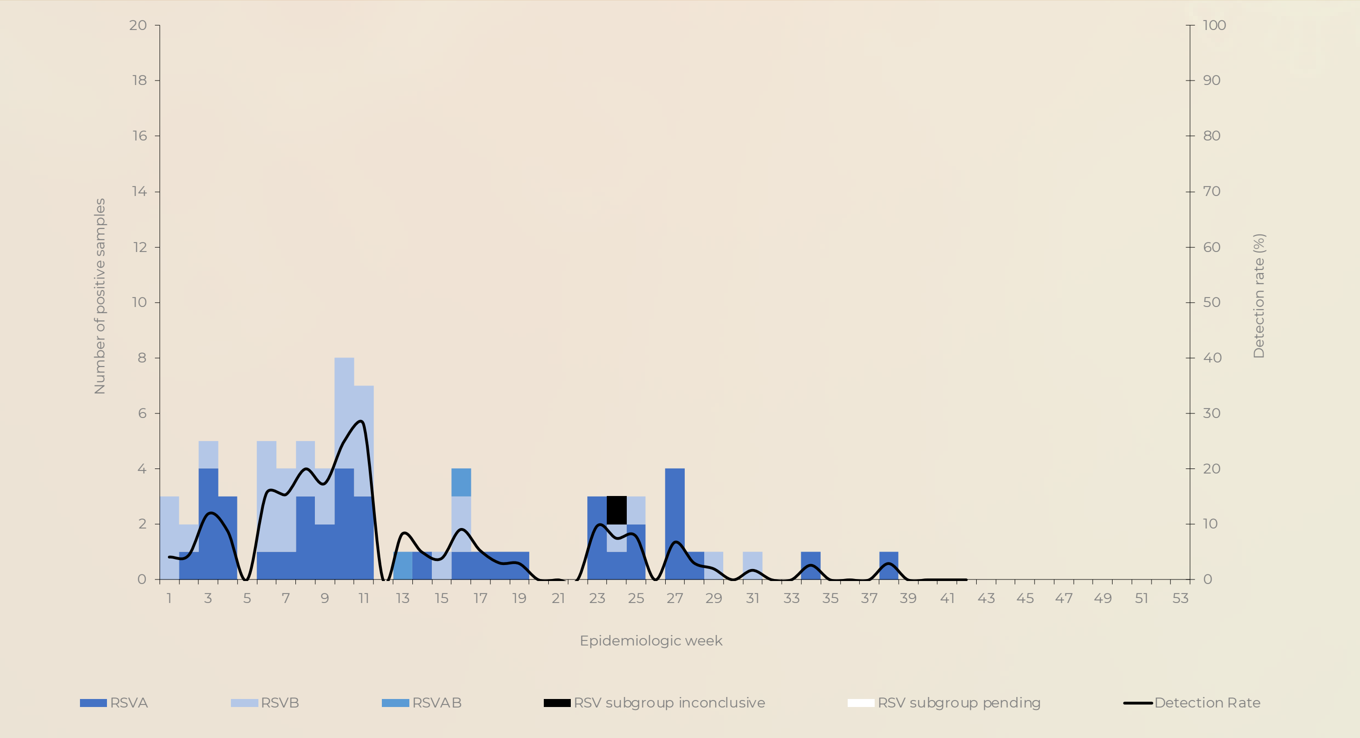

Figure 4. Number of patients testing positive for respiratory syncytial virus** by subgroup and detection rate by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified

**RSV was detected from 15 of 591 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the epidemiological curve.

Table 2. Number of patients testing positive for respiratory syncytial virus (RSV) by subgroups** identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance in primary health care clinics, 04/01/2021 – 24/10/2021

Clinic (Province)	RSVA	RSVB	RSVAB	RSV subgroup inconclusive	RSV subgroup pending*	Total samples
Agincourt (MP)	11	7	1	0	0	210
Eastridge (WC)	23	1	1	0	0	214
Edendale Gateway (KZ)	1	6	0	0	0	204
Jouberton (NW)	2	17	0	1	0	711
Mitchell's Plain (WC)	3	0	0	0	0	211
Total	**40**	**31**	**2**	**1**	**0**	**1 550**

KZ: KwaZulu-Natal; NW: North West; WC: Western Cape; MP: Mpumalanga
Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
*RSV results for subgroups are pending

**RSV was detected from 15 of 591 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the table.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

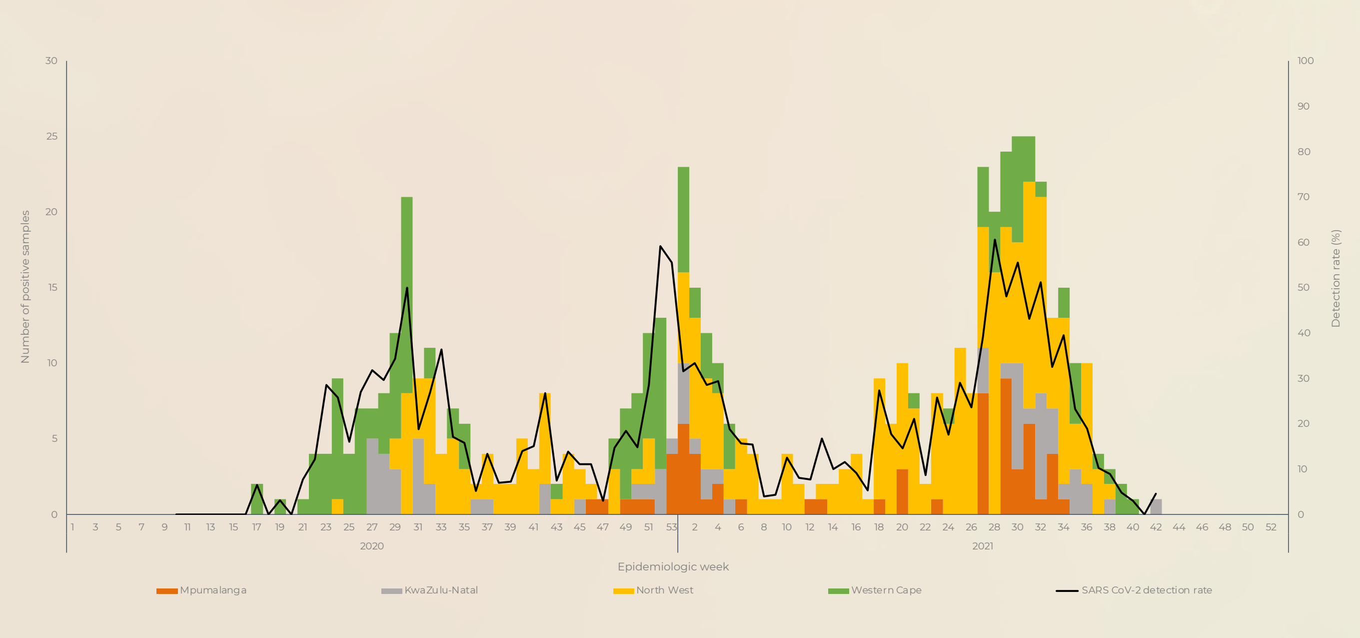

Figure 5. Number of patients testing positive for SARS-CoV-2* by province and detection rate by week, Influenza-like illness (ILI) surveillance in primary health care clinics, 02/03/2020 – 24/10/2021

*Specimens from patients with influenza-like illnesses at 5 sentinel sites in 4 provinces

**SARS-CoV-2 was detected in 148 of 723 (20%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the epidemiological curve.

Table 3. Number of patients positive for SARS-CoV-2 identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance primary health care clinics, 02/03/2020 – 24/10/2021

Clinic (Province)	SARS-CoV-2 positive	Total samples tested
Agincourt (MP)	62	240
Eastridge (WC)	59	702
Edendale Gateway (KZ)	69	346
Jouberton (NW)	288	1034
Mitchell’s Plain (WC)	90	539
Total:	**567**	**2 861**

KZ: KwaZulu-Natal; NW: North West; WCP: Western Cape; MP: Mpumalanga (started enrolling on the 10th November 2020)

**SARS-CoV-2 was detected in 148 of 723 (20%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet influenza-like illness (ILI) case definition. These are not included in the table.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE PRIMARY HEALTH CARE CLINICS

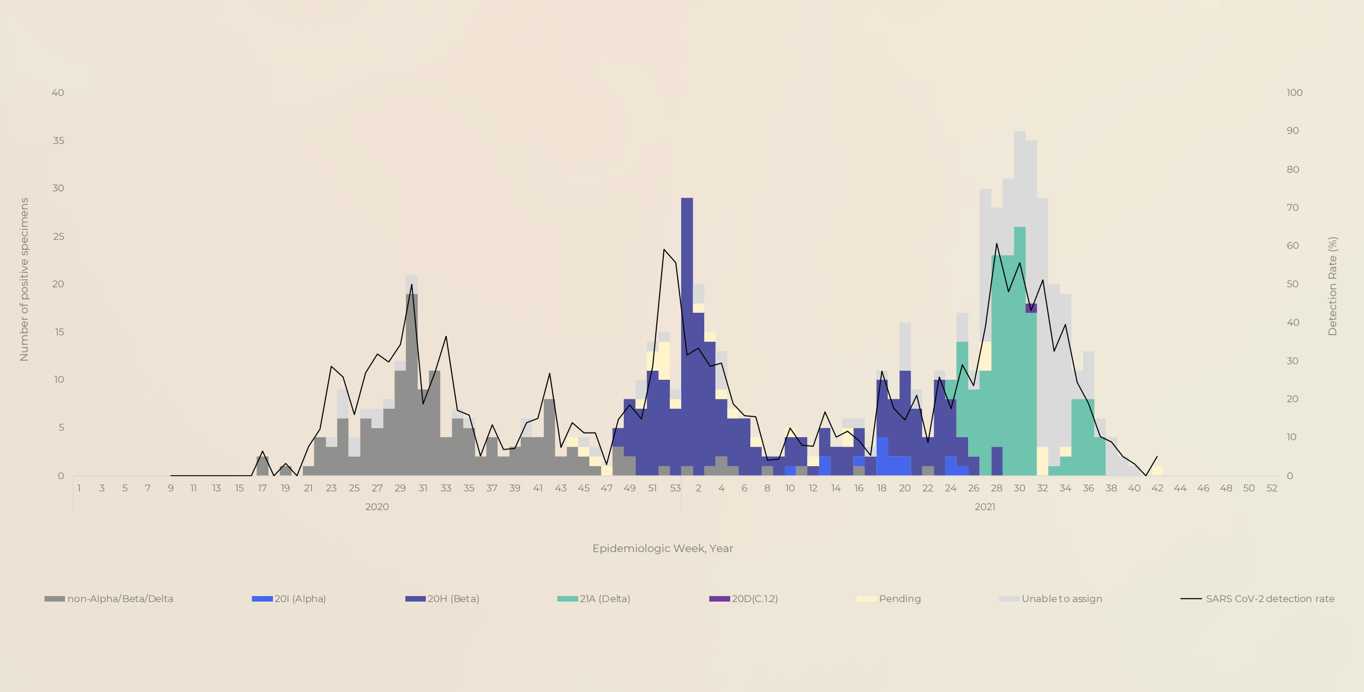

Figure 6. Number and detection rate of laboratory confirmed SARS-CoV-2* cases by variant type (variant PCR/sequencing) and week, Influenza-like illness (ILI) surveillance in primary health care clinics, 02/03/2020 – 24/10/2021

*Specimens are from patients with influenza-like illness at 5 sentinel sites in 4 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the ILI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

Table 4. Number of SARS-CoV-2* positive cases by variant (variant PCR and/or sequencing) identified and total number of samples tested by clinic and province, Influenza-like illness (ILI) surveillance primary health care clinics, 02/03/2020 – 24/10/2021

Clinic (Province)	Non-Alpha/ Beta/Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	Pending	Unable to assign	Total SARS-CoV-2 positive
Agincourt (MP)	3	0	29	17	0	7	31	87
Eastridge (WC)	20	0	17	7	0	3	13	60
Edendale Gateway (KZ)	27	0	22	31	0	4	29	113
Jouberton (NW)	67	15	104	73	1	14	89	363
Mitchell’s Plain (WC)	35	0	27	11	0	1	19	93
Total:	**152**	**15**	**199**	**139**	**1**	**29**	**181**	**716**

KZ: KwaZulu-Natal; NW: North West; WCP: Western Cape; MP: Mpumalanga (started enrolling on the 10th November 2020)
*Specimens are from patients with influenza-like illness at 5 sentinel sites in 4 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the ILI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

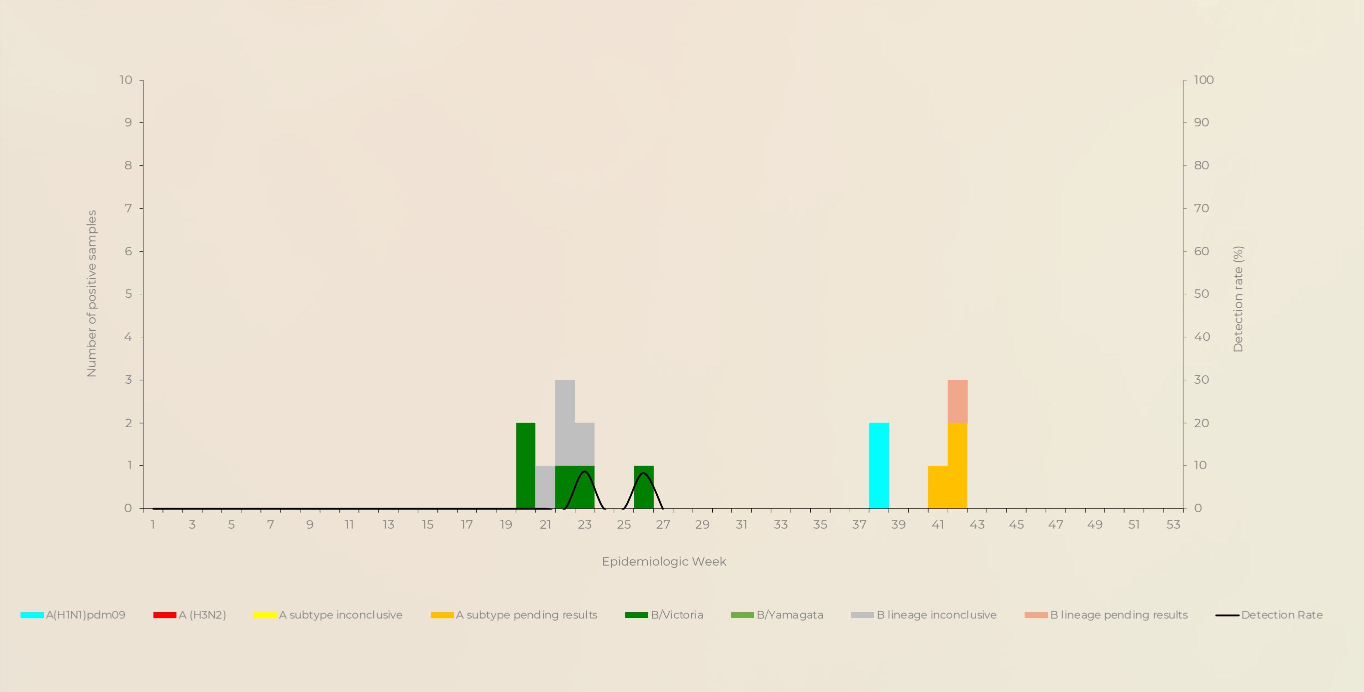

Figure 7. Number of positive patients* by influenza subtype and lineage and detection rate** by week, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

*Specimens from patients with Influenza-like illnesses at 90 sentinel sites in 8 provinces
** Only reported for weeks with >10 specimens submitted.
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 5. Number of laboratory confirmed influenza cases by influenza subtype and lineage and total number of samples tested by province, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

Province	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results*	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results*	Total samples
Eastern Cape	0	0	0	0	1	0	0	1	2
Free State	0	0	0	0	0	0	0	0	0
Gauteng	2	0	0	2	4	0	4	0	149
Limpopo	0	0	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	0	0	0	3
North West	0	0	0	0	0	0	0	0	2
Northern Cape	0	0	0	0	0	0	0	0	0
Western Cape	0	0	0	1	0	0	0	0	29
Total:	**2**	**0**	**0**	**3**	**5**	**0**	**4**	**1**	**185**

Inconclusive: insufficient viral load in sample and unable to characterise further
*Influenza A subtype or B lineage results are pending

From 04 January 2021 to date, no patients were tested for influenza at the time of entry into South Africa following travel abroad.

Patients known to have acquired influenza abroad are not included in the table or epidemiological curve.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

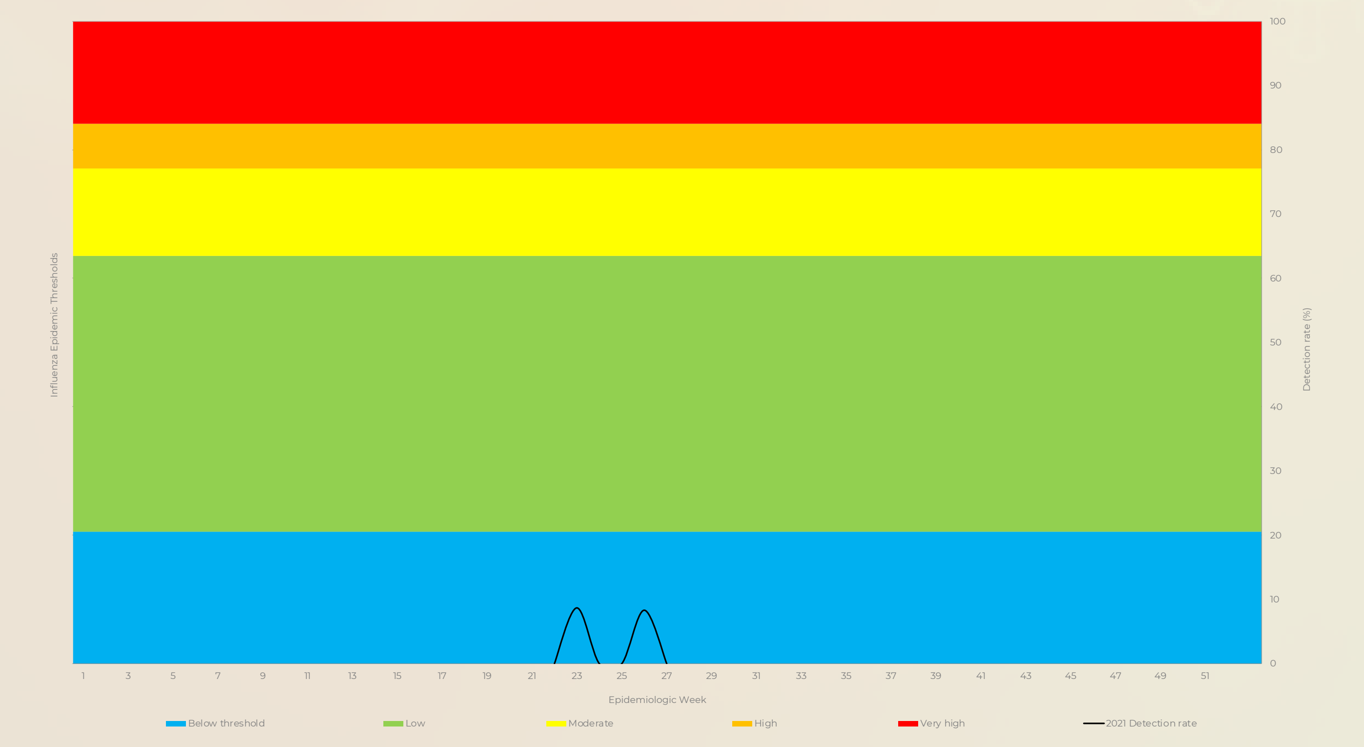

Figure 8. Influenza percentage detections and epidemic thresholds*, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

*Thresholds based on 2010-2019 data

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

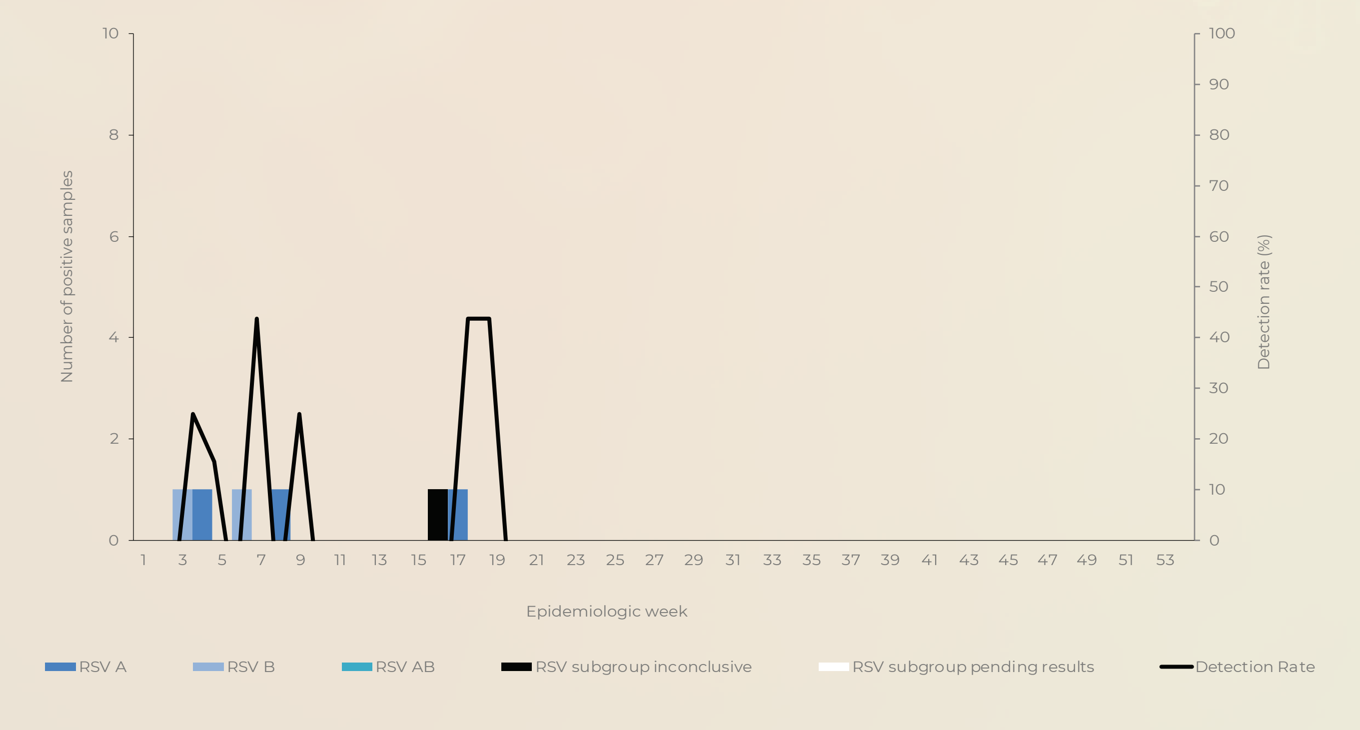

Figure 9. Number of RSV positive cases testing positive for respiratory syncytial virus (RSV)* by subgroup and detection rate by week, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

*RSV results for subgroups are pending

Table 6. Number of RSV positive cases identified and total number of samples tested by province, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

Province	RSV A	RSV B	RSV AB	RSV subgroup inconclusive	RSV subgroup pending results*	Total samples tested
Eastern Cape	0	0	0	0	0	2
Free State	0	0	0	0	0	0
Gauteng	2	2	0	0	0	149
Limpopo	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	3
North West	0	0	0	0	0	2
Northern Cape	0	0	0	0	0	0
Western Cape	1	0	0	1	0	29
Total:	**3**	**2**	**0**	**1**	**0**	**185**

*RSV results for subgroups are pending

**Inconclusive: insufficient viral load in sample and unable to characterise further

Data are provisional as reported to date (Data for this report drawn on (26/10/2021). Number of consultations/specimens are reported/analysed by date of consultation/specimen collection.

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

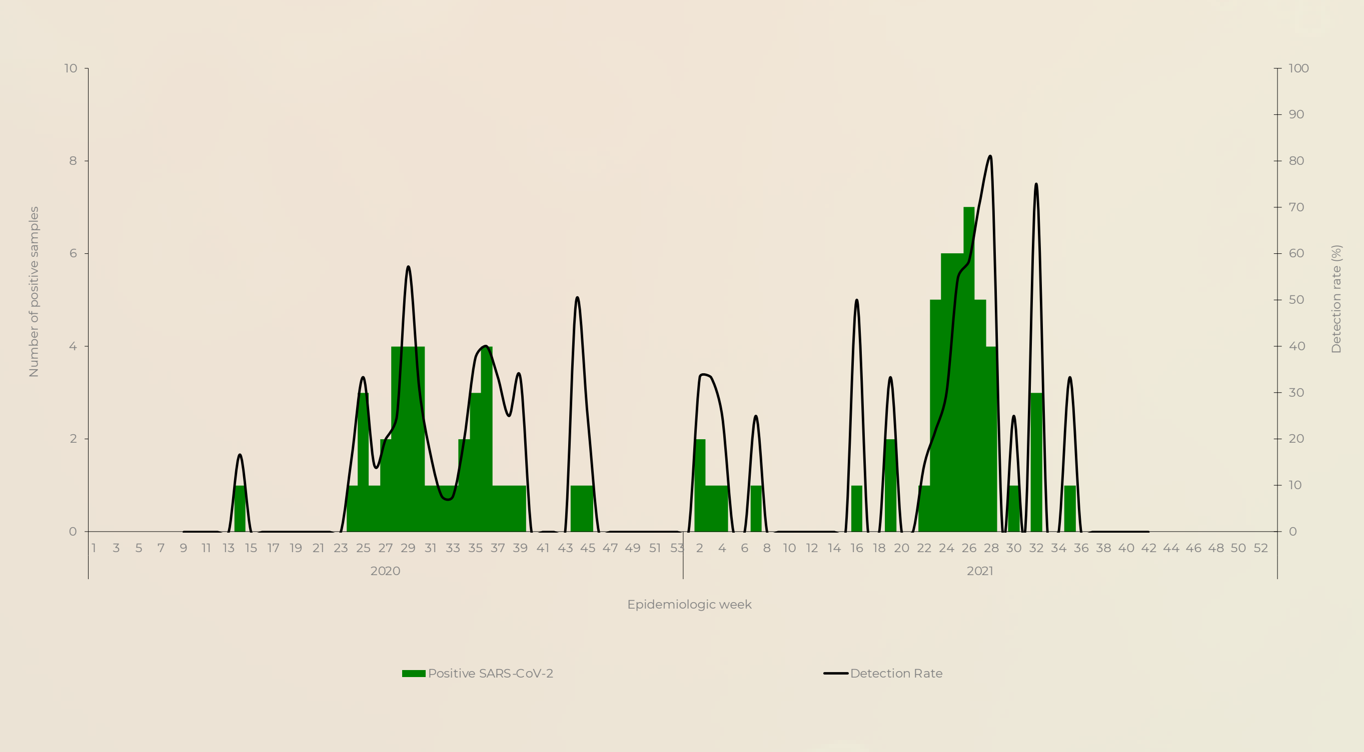

Figure 10. Number of patients testing positive for SARS-CoV-2*, by site and detection rate by week, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Table 7. Number of SARS-CoV-2 positive cases identified and total number tested by province, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

Province	SARS-CoV-2 positive	Total samples tested
Eastern Cape	1	6
Free State	1	14
Gauteng	65	309
Limpopo	0	2
Mpumalanga	1	8
North West	0	2
Northern Cape	0	2
Western Cape	16	121
Total:	**84**	**464**

INFLUENZA-LIKE ILLNESS (ILI) SURVEILLANCE VIRAL WATCH

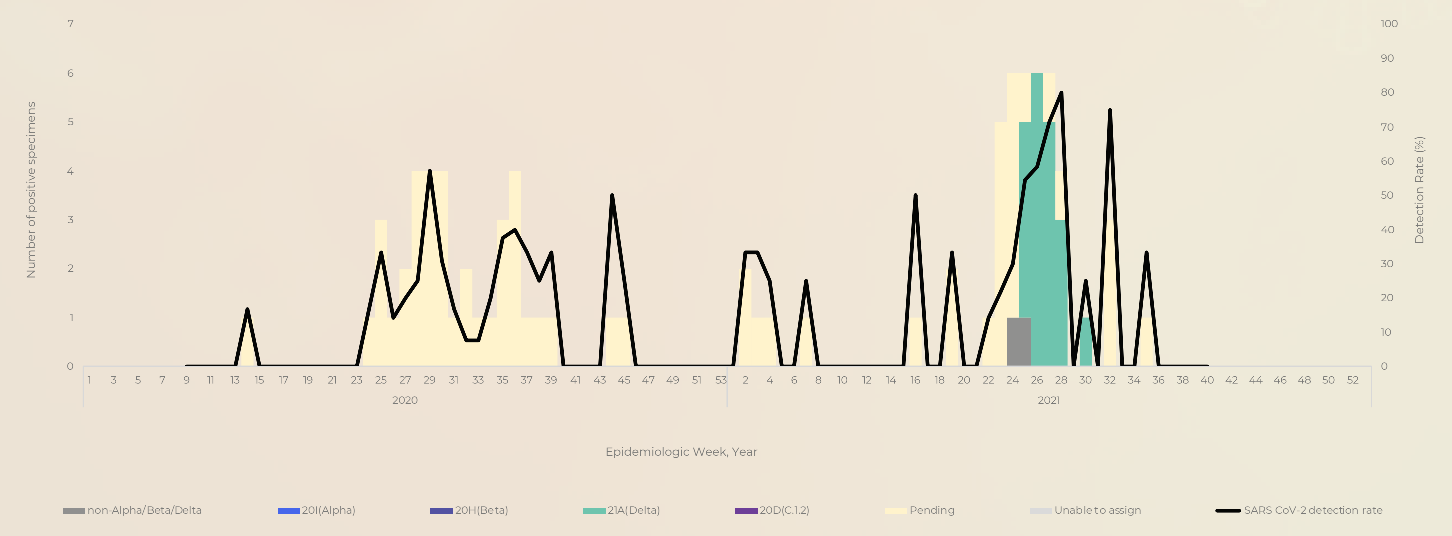

Figure 11. Number and detection rate of laboratory confirmed SARS-CoV-2* cases by variant type (variant PCR/sequencing) and week, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

Table 8. Number of SARS-CoV-2* positive cases by variant (variant PCR and/or sequencing) identified and total number of samples tested by province, ILI surveillance - Viral Watch, 04/01/2021 – 24/10/2021

Clinic (Province)	Non-Alpha/ Beta/Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	Pending	Unable to assign	Total SARS-CoV-2 positive
Eastern Cape	0	0	0	0	0	1	0	1
Free State	0	0	0	0	0	1	0	1
Gauteng	2	0	0	18	0	45	0	65
Limpopo	0	0	0	0	0	0	0	0
Mpumalanga	0	0	0	0	0	1	0	1
North West	0	0	0	0	0	0	0	0
Northern Cape	0	0	0	0	0	0	0	0
Western Cape	0	0	0	1	0	1	0	16
Total:	**2**	**0**	**0**	**19**	**0**	**63**	**0**	**84**

*Specimens from patients with Influenza-like illnesses at 92 sentinel sites in 8 provinces

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

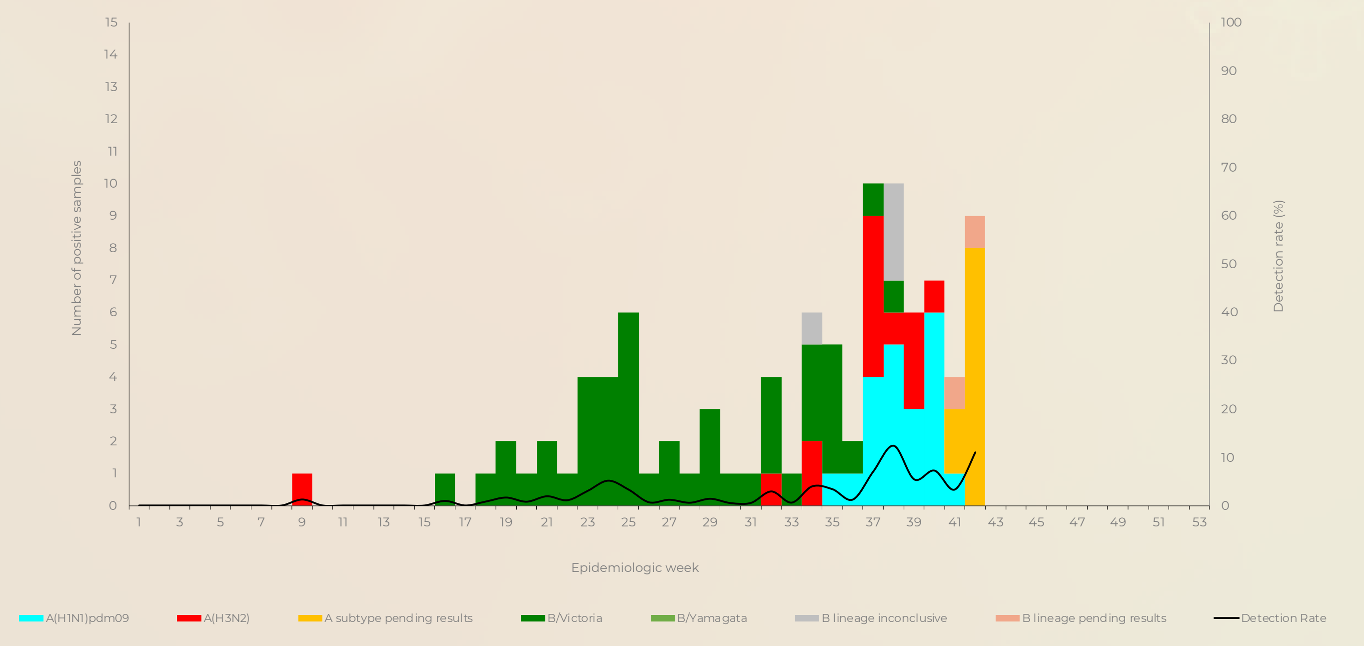

Figure 12. Number of positive influenza positive cases* by influenza subtype and lineage** and detection rate*** by week, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

*Specimens from patients hospitalised with pneumonia at 7 sentinel sites in 5 provinces
**Influenza B(Victoria) was detected from four of 174 (2%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.
***Only reported for weeks with >10 specimens submitted
Inconclusive: insufficient viral load in sample and unable to characterise further

Table 9. Number of laboratory confirmed influenza cases by subtype and lineage** and total number of samples tested by hospital, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

Hospital (Province)	A(H1N1) pdm09	A(H3N2)	A subtype inconclusive	A subtype pending results***	B/ Victoria	B/ Yamagata	B lineage inconclusive	B lineage pending results***	Total samples
Edendale (KZ)	0	0	0	0	9	0	0	0	796
Helen Joseph-Rahima Moosa (GP)	19	10	1	4	17	0	3	2	1344
Klerksdorp-Tshepong (NW)	1	1	0	4	4	0	1	0	831
Mapulaneng-Matikwana (MP)	1	0	0	0	1	0	0	0	501
Red Cross (WC)	0	1	0	1	12	0	0	0	665
Mitchell's Plain (WC)	0	2	0	1	1	0	0	0	791
Tintswalo (MP)	0	0	0	0	1	0	0	0	201
Total:	**21**	**14**	**1**	**10**	**45**	**0**	**4**	**2**	**5 129**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
Inconclusive: insufficient viral load in sample and unable to characterise further

**Influenza B(Victoria) was detected from four of 174 (2%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the table.
***influenza A subtype or B lineage results are pending

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

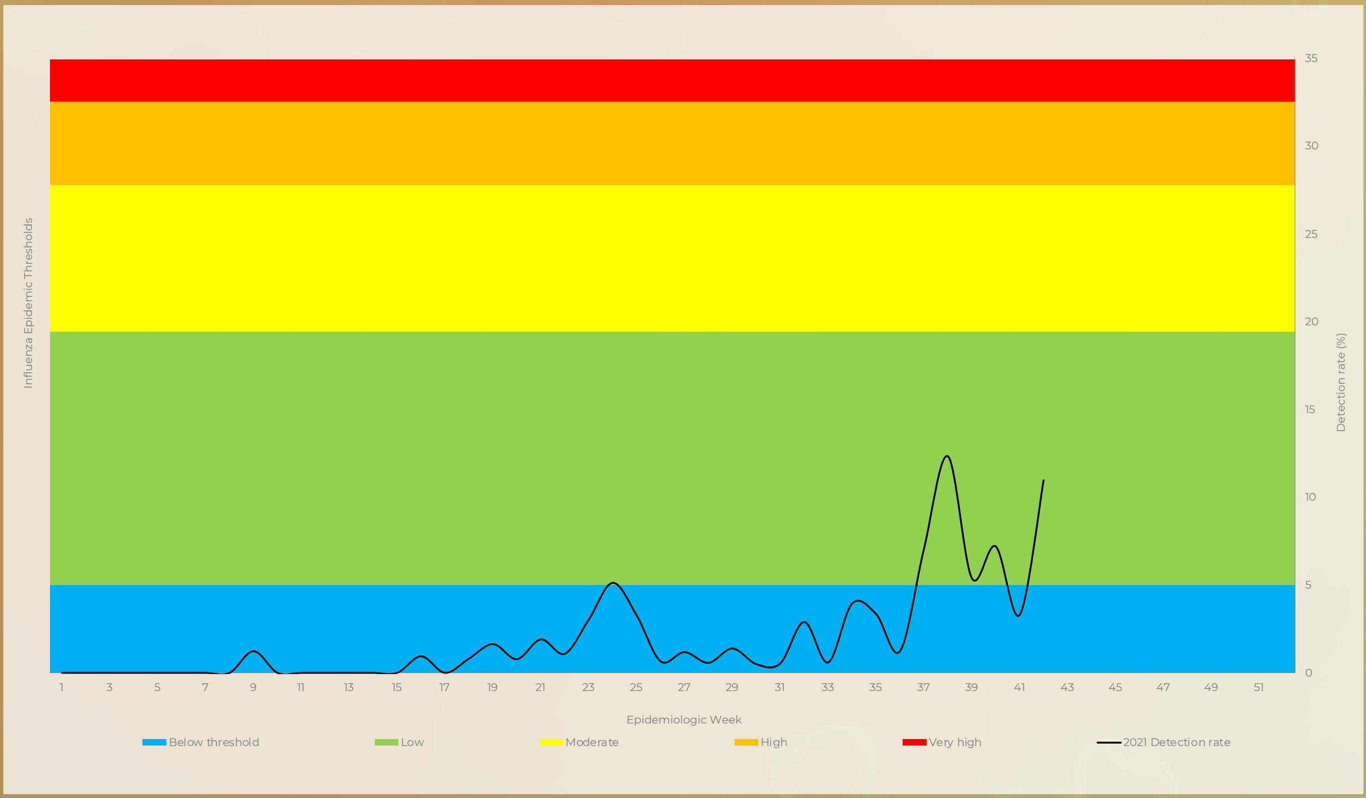

Figure 13. Influenza percentage detections and epidemic thresholds*, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

*Thresholds based on 2010-2019 data

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

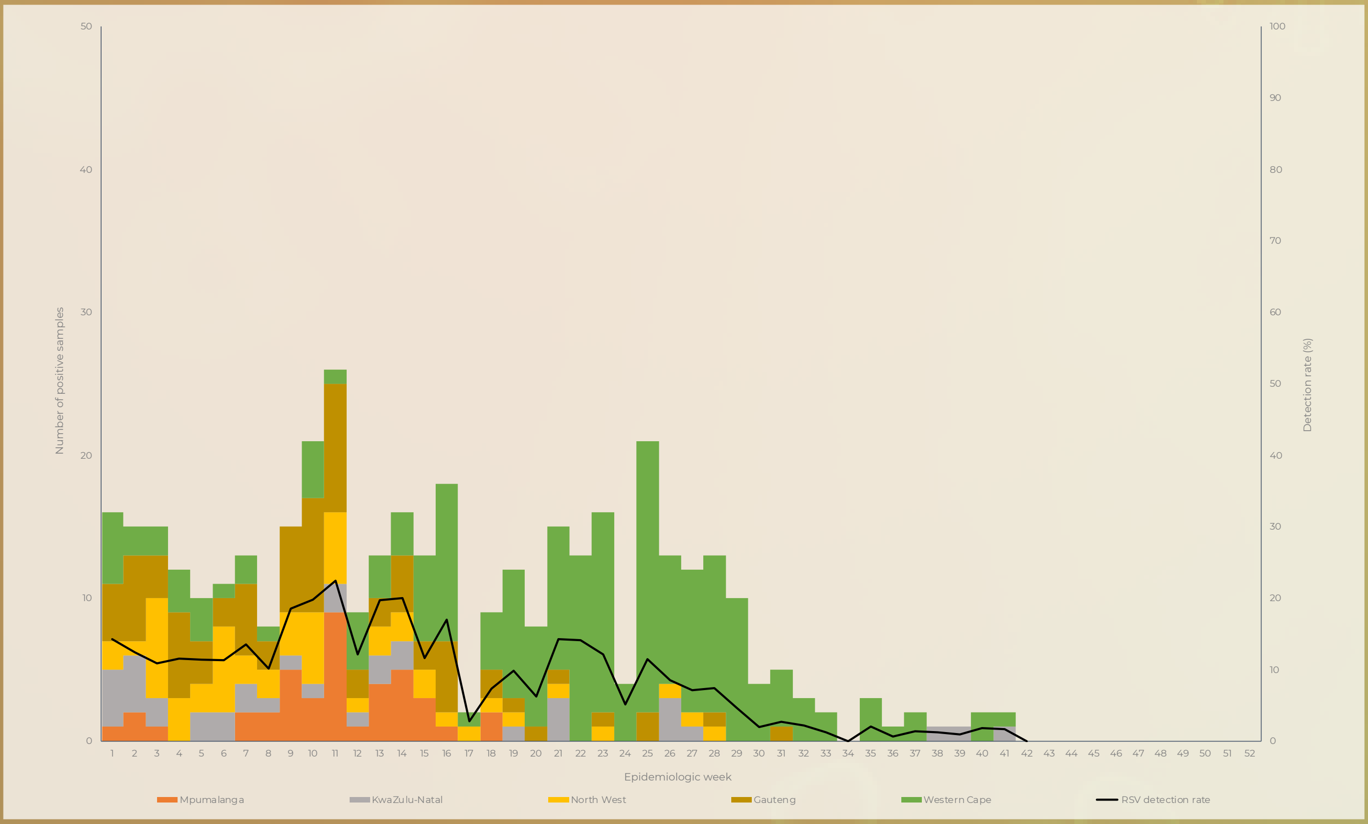

Figure 14. Number of patients testing positive for respiratory syncytial virus* by province and detection rate by week, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

*RSV was detected in six of 174 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

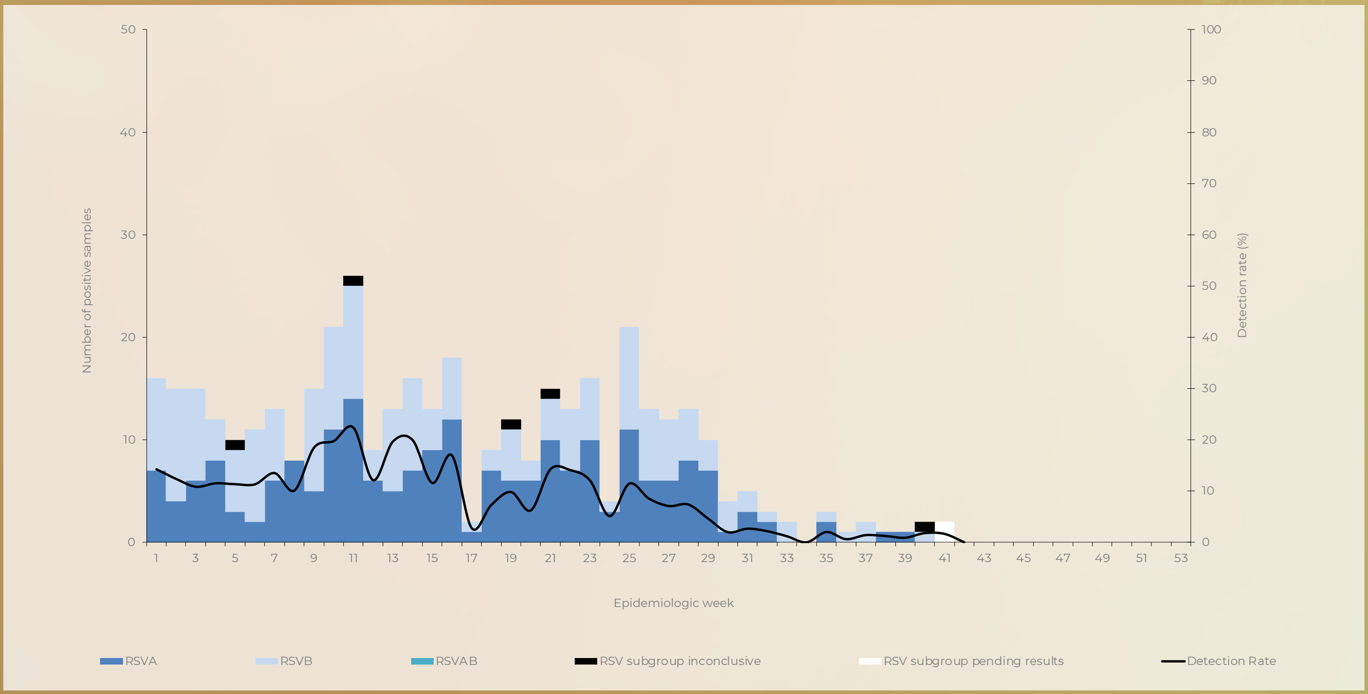

Figure 15. Number of patients testing positive for respiratory syncytial virus* by subgroup and detection rate by week, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
RSV subgroup pending: RSV results for subgroups are pending

*RSV was detected in six of 174 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.

Table 10: Number of patients positive for respiratory syncytial virus subgroups** by subgroups identified and total number of samples tested by hospital, pneumonia surveillance public hospitals, 04/01/2021 – 24/10/2021

Hospital (Province)	RSVA	RSVB	RSVAB	RSV subgroup inconclusive	RSV subgroup pending*	Total samples
Edendale (KZ)	7	29	0	0	1	796
Helen Joseph-Rahima Moosa (GP)	37	42	0	0	0	1344
Klerksdorp-Tshepong (NW)	8	44	0	2	0	831
Mapulaneng-Matikwana (MP)	21	7	0	0	0	501
Red Cross (WC)	87	50	0	2	1	665
Mitchell's Plain (WC)	41	12	0	1	0	791
Tintswalo (MP)	10	3	0	0	0	201
Total:	**211**	**187**	**0**	**5**	**2**	**5 129**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
Inconclusive: insufficient viral load in sample and unable to characterise further
RSV AB: Both RSV A and B subgroup identified
*RSV results for subgroups are pending

**RSV was detected in six of 174 (3%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the table

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

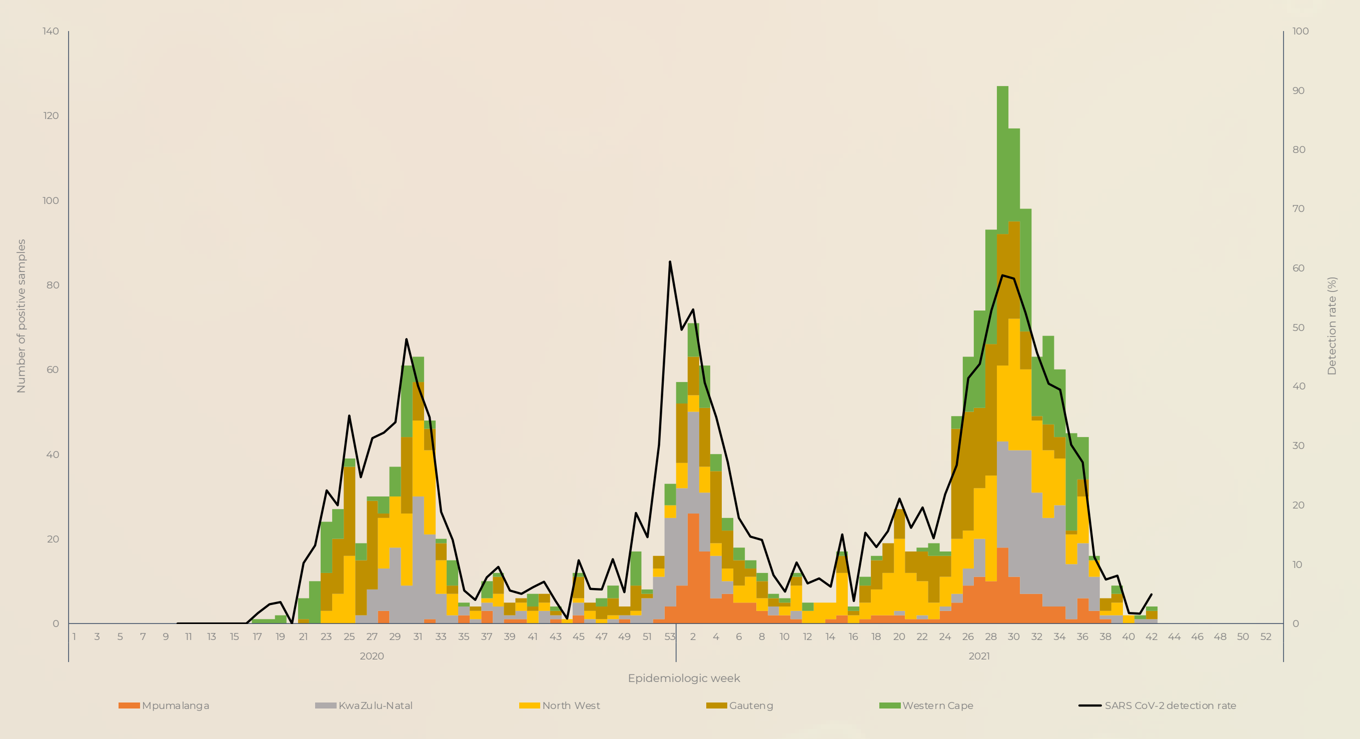

Figure 16. Number of patients testing positive for SARS-CoV-2*ᵝ by province and detection rate by week, pneumonia surveillance public hospitals, 02/03/2020 – 24/10/2021

*Specimens from patients hospitalized with pneumonia at 6 sentinel sites in 5 provinces

*ᵝSARS-CoV-2 was detected in 44 of 245 (18%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the epidemiological curve.

Table 11. Number of patients positive for SARS-CoV-2** and total number of samples tested by hospital, pneumonia surveillance public hospitals, 02/03/2020 – 24/10/2021

Hospital (Province)	SARS-CoV-2 positive	Total samples tested
Edendale (KZ)	460	1 640
Helen Joseph-Rahima Moosa (GP)	485	2 185
Klerksdorp-Tshepong (NW)	476	1 424
Mapulaneng-Matikwana (MP)	165	803
Red Cross (WC)	61	1 629
Mitchell's Plain (WC)	350	1 260
Tintswalo (MP)	51	201
Total:	**2 048**	**9 142**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga; WC: Western Cape

**SARS-CoV-2 was detected in 44 of 245 (18%) specimens from patients who met suspected SARS-CoV-2 case definition but did not meet pneumonia (SRI) case definition. These are not included in the table.

NATIONAL SYNDROMIC SURVEILLANCE FOR PNEUMONIA

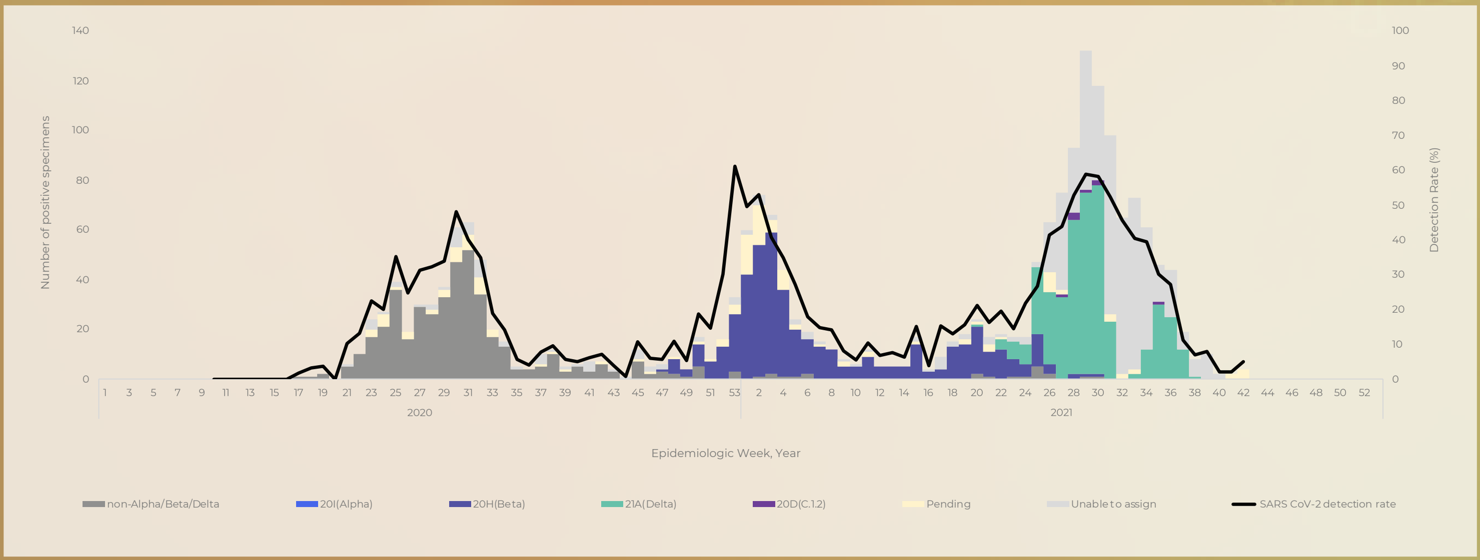

Figure 17. Number and detection rate of laboratory confirmed SARS-CoV-2 cases* by variant type (variant PCR/sequencing), pneumonia surveillance public hospitals, 02/03/2020 – 24/10/2021

*Specimens are from hospitalized patients at 7 sentinel sites in 5 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the SRI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result

Pending: outstanding variant results

Table 12. Number of SARS-CoV-2 positive cases* by variant (variant PCR and/or sequencing) identified and total number of samples tested by hospital, pneumonia surveillance public hospitals, 02/03/2020 – 24/10/2021

Hospital (Province)	Non-Alpha/ Beta/Delta	20I (Alpha)	20H (Beta)	21A (Delta)	20D (C.1.2)	Pending	Unable to assign	Total SARS-CoV-2 positive
Edendale (KZ)	102	1	75	83	2	59	145	467
Helen Joseph-Rahima Moosa (GP)	134	5	120	101	4	21	101	487
Klerksdorp-Tshepong (NW)	130	9	112	94	2	15	116	478
Mapulaneng-Matikwana (MP)	16	0	90	29	0	17	47	199
Red Cross (WC)	15	0	5	7	0	7	27	61
Mitchell's Plain (WC)	50	0	49	96	0	14	140	349
Tintswalo (MP)	0	1	12	15	0	5	18	51
Total:	**447**	**16**	**463**	**425**	**8**	**138**	**594**	**2092**

GP: Gauteng; KZ: KwaZulu-Natal; NW: North West; MP: Mpumalanga (Tintswalo started enrolling on the 10th Feb 2021); WC: Western Cape
*Specimens are from hospitalized patients at 7 sentinel sites in 5 provinces who met suspected SARS-CoV-2 case definition and met pneumonia (SRI) case definition as well as those that did not meet the SRI case definition.

Unable to assign: no lineage assigned due to poor- sequence quality OR low viral load (ct=>35) OR variant PCR could not assign variant and no sequencing result
Pending: outstanding variant results

SUMMARY OF LABORATORY CONFIRMED SARS-COV-2 CASES

Table 13. Characteristics of individuals with laboratory-confirmed SARS-CoV-2, enrolled in influenza-like illness (ILI) and pneumonia surveillance programmes, South Africa, 2 March 2020 - 24 October 2021

Characteristic	Influenza–like illness (ILI), public-sector, n=716 (%)	Pneumonia, n=2 092 (%)
Age group		
0-9	52/716 (7)	138/2092 (6)
10-19	53/716 (7)	15/2092 (1)
20-39	334/716 (47)	379/2092 (18)
40-59	222/716 (31)	785/2092 (38)
60-79	53/716 (7)	699/2092 (33)
≥80	2/716 (<1)	76/2092 (4)
Sex-female	432/716 (60)	1277/2092 (61)
Province*		
Gauteng	N/A	486/2092 (23)
KwaZulu-Natal	113/716 (16)	467/2092 (22)
Mpumalanga**	87/716 (12)	251/2092 (12)
North West	363/716 (51)	476/2092 (23)
Western Cape	153/716 (21)	412/2092 (20)
Race		
Black	538/709 (76)	1645/2075 (79)
Coloured	140/709 (20)	326/2075 (16)
Asian/Indian	4/709 (1)	50/2075 (2)
White	22/709 (3)	41/2075 (2)
Other	5/709 (1)	13/2075 (<1)
Variant$$		
Non-Alpha/Beta/Delta	152/535 (28)	447/1497 (30)
20I(Alpha)	15/535 (3)	16/1497 (1)
20H(Beta)	199/535 (37)	463/1497 (31)
21A(Delta)	139/535 (26)	425/1497 (28)
20D(C.1.2)	1/535 (0.2)	8/1497 (1)
Pending results	29/535 (5)	138/1497 (9)

Characteristic	Influenza–like illness (ILI), public-sector, n=716 (%)	Pneumonia, n=2 092 (%)
Presentation		
Fever	556/709 (78)	964/2075 (46)
Cough	690/709 (97)	1990/2075 (96)
Shortness of breath	257/709 (36)	1626/2075 (78)
Chest pain	310/709 (44)	845/2075 (41)
Diarrhoea	54/709 (8)	132/2075 (6)
Underlying conditions		
Hypertension[$]	17/690 (2)	249/1895 (13)
Cardiac	2/709 (<1)	47/2075 (2)
Lung disease	0/709 (0)	3/2075 (<1)
Diabetes	17/709 (2)	435/2075 (21)
Cancer	2/709 (<1)	13/2075 (1)
Tuberculosis	11/709 (2)	54/2075 (3)
HIV-infection	132/709 (19)	456/2075 (22)
Other ***	12/709 (2)	90/2075 (4)
Management		
Oxygen therapy	9/709 (1)	1630/2075 (79)
ICU admission	N/A	50/2075 (2)
Ventilation	N/A	55/2075 (3)
Outcome* **		
Died	0/702 (0)	343/2003 (17)

*ILI surveillance not conducted in Gauteng province

**Mpumalanga (ILI site started enrolling on the 10th November 2020 and an additional SARI site started enrolling on the 10th February 2021)

***Chronic lung, liver and kidney disease, organ transplant, pregnancy, malnutrition, obesity, tracheostomy, prematurity, seizure, stroke, anaemia, asplenia, burns, Systemic lupus erythematosus, seizures

****Outcome includes patients who are still hospitalised, have been discharged or referred, and those who died

[$] Data on hypertension was not collected on all cases.

[$$] These individuals with unassigned sequence are not included, ILI (n=181) and SRI (n=594)

Note: Children may be over-represented amongst hospitalised patients due to the inclusion of a large paediatric hospital in Cape Town.
Of the 343 patients who died, three were in <20 age group, 25 in the 20-39 year age group, 116 in the 40-59 year age group, and 199 were ≥60 years; 197/343 (57%) were female.

Of the 1170 hospitalised cases with COVID19 vaccine status, 96 (8%) received vaccine. 11 (11%) received Johnson & Johnson, 74 (77%) received the first dose of Pfizer-BioNTech, 3 (3%) Astra Zeneca and 8 (8%) could not remember the vaccine type received. 18 (19%) of the 96 cases had full vaccination (n=11, J&J and n=7, Pfizer-BioNTech). Cases age varied from 35 years to >60 years old and the majority (72%, 69/96) were >60 years old. Females were a majority 57% (55/96) and 11% (11/96) cases were HIV infected.

METHODS

SARS-CoV-2 Testing

March 2020 – March 2021: SARS-CoV-2 was detected using the Roche E gene real-time PCR assay (Corman et al. Euro Surveillance 2020) with cycle threshold (Ct) <40 interpreted as positive for SARS-CoV-2. From April 2021 to date the laboratory changed to the Allplex™ SARS-CoV-2/FluA/FluB/RSV kit (Seegene Inc., Seoul, South Korea), with positivity assigned if the PCR cycle threshold (Ct) was <40 for ≥1 gene targets (N, S or RdRp).

A confirmed SARS-CoV-2 case is a person of any age enrolled in surveillance with laboratory confirmation of SARS-CoV-2 infection by PCR. Only positive SARS-CoV-2 specimens on PCR are further tested to determine variant/lineage type by variant PCR or genomic sequencing.

Variant PCR

Allplex™ SARS-CoV-2 Variants I PCR detects Alpha and Beta/Gamma variants. The assay was conducted on all SARS-CoV-2-positive samples from 1 March 2020 – 30 June 2021.

Allplex™ SARS-CoV-2 Variants II PCR detects Delta variant and distinguishes Beta from Gamma. The assay was conducted on SARS-CoV-2-positive samples from 1 Jan to 30 June 2021.

Extraction: Total nucleic acids were extracted from 200µl NP/OP samples in universal or viral transport medium using a MagNA Pure 96 automated extractor and DNA/Viral NA Small Volume v2.0 extraction kit (Roche Diagnostics, Mannheim, Germany).

SARS-CoV-2 genomic surveillance

SARS-CoV-2 Whole-Genome Sequencing and Genome Assembly

RNA Extraction

RNA was extracted either manually or automatically in batches, using the QIAamp viral RNA mini kit (QIAGEN, CA, USA) or the Chemagic 360 using the CMG-1049 kit (PerkinElmer, MA, USA). A modification was done on the manual extractions by adding 280 µl per sample, in order to increase yields. 300 µl of each sample was used for automated magnetic bead-based extraction using the Chemagic 360. RNA was eluted in 60 µl of the elution buffer. Isolated RNA was stored at -80 °C prior to use.

PCR and Library Preparation

Sequencing was performed using the Illumina COVIDSeq protocol (Illumina Inc., CA, USA) or nCoV-2019 ARTIC network sequencing protocol v3 (https://artic.network/ncov-2019). These are amplicon-based next-generation sequencing approaches. Briefly, for the nCoV-2019 ARTIC network sequencing protocol, the first strand synthesis was carried out on extracted RNA samples using random hexamer primers from the SuperScript IV reverse transcriptase synthesis kit (Life Technologies, CA, USA) or LunaScript RT SuperMix Kit (New England Biolabs (NEB), MA , USA). The synthesized cDNA was amplified using multiplex polymerase chain reactions (PCRs) using ARTIC nCoV-2019 v3 primers. For the COVIDSeq protocol, the first strand synthesis was carried out using random hexamer primers from Illumina and the synthesized cDNA underwent two separate multiplex PCR reactions.

For Illumina sequencing using the nCoV-2019 ARTIC network sequencing protocol, the pooled PCR products underwent bead-based tagmentation using the Nextera Flex DNA library preparation kit (Illumina Inc., CA, USA). The adapter-tagged amplicons were cleaned up using AmpureXP purification beads (Beckman Coulter, High Wycombe, UK) and amplified using one round of PCR. The PCRs were indexed using the Nextera CD indexes (Illumina Inc., CA, USA) according to the manufacturer's instructions. For COVIDSeq sequencing protocol, pooled PCR amplified products were processed for tagmentation and adapter ligation using IDT for Illumina Nextera UD Indexes. Further enrichment and cleanup was performed as per protocols provided by the manufacturer (Illumina Inc., CA, USA). Pooled samples from both COVIDSeq protocol and nCoV-2019 ARTIC network protocol were quantified using Qubit 3.0 or 4.0 fluorometer (Invitrogen Inc., MA, USA) using the Qubit dsDNA High Sensitivity assay according to manufacturer's instructions. The fragment sizes were analyzed using TapeStation 4200 (Invitrogen Inc., MA, USA). The pooled libraries were further normalized to 4nM concentration and 25 µl of each normalized pool containing unique index adapter sets were combined in a new tube. The final library pool was denatured and neutralized with 0.2 N sodium hydroxide and 200 mM Tris-HCL (pH7), respectively. 1.5 pM sample library was spiked with 2% PhiX. Libraries were loaded onto a 300-cycle NextSeq 500/550 HighOutput Kit v2 and run on the Illumina NextSeq 550 instrument (Illumina Inc., CA, USA).

Assembly, Processing and Quality Control of Genomic Sequences

Raw reads from Illumina sequencing were assembled using the Exatype NGS SARS-CoV-2 pipeline v1.6.1, (https://sars-cov-2.exatype.com/). The resulting consensus sequence was further manually polished by considering and correcting indels in homopolymer regions that break the open reading frame (probably sequencing errors) using Aliview v1.27, (http://ormbunkar.se/aliview/) (Larsson, 2014). Mutations resulting in mid-gene stop codons and frameshifts were reverted to wild type. All assemblies determined to have acceptable quality (defined as having at least 1 000 000 reads and at least 40 % 10 X coverage) were deposited on GISAID (https://www.gisaid.org/) (Elbe & Buckland-Merrett, 2017; Shu & McCauley, 2017).

Classification of Lineage, Clade and Associated Mutations

Assembled genomes were assigned lineages using the 'Phylogenetic Assignment of Named Global Outbreak Lineages' (PANGOLIN) software suite (https://github.com/hCoV-2019/pangolin) (Rambaut et al., 2020), a tool used for dynamic SARS-CoV-2 lineage classification. The SARS-CoV-2 genomes in our dataset were also classified using the clade classification proposed by NextStrain (https://nextstrain.org/), a tool built for real-time tracking of the pathogen evolution (Hadfield et al., 2018).