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

COMMUNICABLE DISEASES

November 2021, Vol. 20 (11)

COMMUNIQUÉ

CONTENTS

Editor's Note

Dr Michelle Groome

Dreams of a quiet December, languishing in a period of low COVID-19 cases, have been dashed by the appearance of the new SARS-CoV-2 variant of concern which threatens to steal a restful festive season from us. News of the detection of Omicron (B.1.1.529) variant catapulted into world headlines last Thursday amidst concerns over the number of mutations it contains. Daily case numbers in South Africa are rising steadily, percent positivity is climbing and we are waiting with baited breath for data on transmissibility, possible immune escape and severity of Omicron. Read more about the variant at https://www.nicd.ac.za/frequently-asked-questions-for-the-b-1-1-529-mutated-sars-cov-2-lineage-in-south-africa/

In this issue, we provide an update on rabies, which continues to be a concern with six new human cases confirmed from Eastern Cape, KwaZulu-Natal and Limpopo provinces. There is also a detailed report on the emergence of non-epidemic Vibrio cholerae O1 ST75 in South Africa.

With the fourth wave looming, we propose a COVID-19 wave definition for use in retrospective analyses. We hope that this simple working definition may help researchers to communicate consistent messages about COVID-19.

There has been a sustained increase in influenza cases in recent weeks, which is unusual for this time of year. Likely this is as a result of relaxation of COVID-19 restrictions combined with an immunity gap because influenza has not circulated for two years. It is not too late to vaccinate against influenza.

Beyond our borders, there have been no new cases Ebola virus disease in the Democratic Republic of the Congo in the past 14 days. Thirty-three cases of visceral leishmaniasis have been reported in Kenya, a case of monkeypox virus in the United States and a case of melioidosis from the United Kingdom.

Enjoy this issue of the Communiqué and please remember to get your COVID-19 vaccine if you haven't done so already, encourage those around you to get vaccinated, continue wearing your masks, and practice social distancing.

ZOONOTIC AND VECTOR-BORNE DISEASES

An update on rabies in South Africa, 2021

In the past month, six new cases of human rabies were laboratory confirmed, originating from the Eastern Cape, KwaZulu-Natal and Limpopo provinces. The total number of laboratory-confirmed cases for 2021 up to 23 November is 17 (including the six cases mentioned here). The provincial distribution of these cases is as follows: Eastern Cape (n=9), KwaZulu-Natal (n=4) and Limpopo (n=4) (Figure 1). Three probable cases from KwaZulu-Natal Province have been documented (Figure 1), in which rabies was suspected on clinical signs and fatal outcome, as well as a history of dog/cat bites, without laboratory confirmation.

The histories for the recent cases are as follows. A case of rabies was confirmed in a 7-year-old boy from Greater Letaba, Mopani District, Limpopo Province in the last week of October. He died following hospitalisation with hydrophobia, hypersalivation, and muscle spasms. No animal exposure history or rabies post-exposure prophylaxis (PEP) was available for this patient. The case was confirmed by testing of a post-mortem-collected brain sample.

An 18-month-old boy from KwaNtabangwangwa, Zululand District, KwaZulu-Natal Province, was bitten in the face and on the hand by a dog on 8 October. He received one dose of rabies vaccine on the same day as the incident, and it was unclear whether rabies immunoglobulin (RIG) was given and if the patient received all doses of vaccine. The child was brought to the hospital two weeks later with fever, shortness of breath, hypersalivation, encephalopathy, and diaphragm paralysis, and died on 31 October. The case was confirmed by testing of a post-mortem-collected brain sample.

The remaining four cases were reported from the Amathole District (n=2) and Nelson Mandela Bay Metropolitan Municipality (n=2), Eastern Cape Province. A 44-year-old woman was bitten on the face and hands by a wild animal (details are being investigated) in Ngxingxolo, Amathole, in mid-September. Five weeks later, she suffered malaise, nausea, muscle spasms, dysphasia, hydrophobia, hyperactivity, and hypersalivation before demising in hospital on 27 October. PCR testing on two saliva specimens was positive. On 17 October, a 10-year-old child was attacked in the face and abdomen by a dog in Silatsha, Mooiplaas. The child received rabies PEP, which included the full course of vaccine (4 doses) although it was unclear whether RIG was administered. Three weeks later, he died in hospital after suffering from fever, malaise, vomiting, muscle spasms, autonomic instability, nausea, and localised pain/paresthesia at the bite sites. PCR testing on two saliva samples were positive for rabies. A 6-year-old girl died on 13 November after being bitten by a stray dog in the beginning of the month near her home in Rosendal, Gamble, Kariega, Nelson Mandela Bay. The wounds were inflicted under the eye and in the back, and only rabies vaccination was started but no RIG was reportedly provided. The child presented with fever, nausea, hypersalivation, vomiting, and dysphasia.

The case was confirmed by testing of a post-mortem-collected brain sample. A 17-year-old man from Kwazakhele, Gqerberha, Nelson Mandela Bay, was bitten on the hand by a dog in September. The patient was hospitalised with fever, nausea, muscle spasms, anxiety, hypersalivation, aggressiveness, vomiting, disorientation, agitation, localized weakness, headache, anorexia, ataxia, sleeplessness, delirium, hydrophobia, hyperactivity and autonomic instability in the second week of November. The case was confirmed by testing of a post-mortem-collected brain sample.

In the eastern provinces of South Africa, rabies is a re-emerging public health problem associated with dog rabies (see https://www.kzndard.gov.za/latest-news/item/327-rabies-update). Increases in cases have been reported in the municipalities of Buffalo City, Nelson Mandela Bay and eThekwini, as well as King Cetshwayo and Vhembe districts in 2021 (Figure 1). Cases of rabies in dogs were also reported from the Western Cape Province, specifically Khayelitsha and Gordon's Bay, earlier this year. These were the first reports of dog rabies in this province for decades. No new cases have been reported since mid-October 2021. No human cases of rabies have been identified from the Western Cape Province.

Mass-vaccination campaigns for dogs (and cats) are underway in affected areas. Vaccination of dogs (and cats) is the most important intervention for rabies prevention and control. When possible exposure occurs, infection may be prevented through rabies post-exposure prophylaxis. This requires thorough washing of all wound sites with soap and water followed by rabies vaccination and immunoglobulin therapy. More rabies information, including how rabies is prevented through rabies post-exposure prophylaxis, is on the NICD website at www.nicd.ac.za.

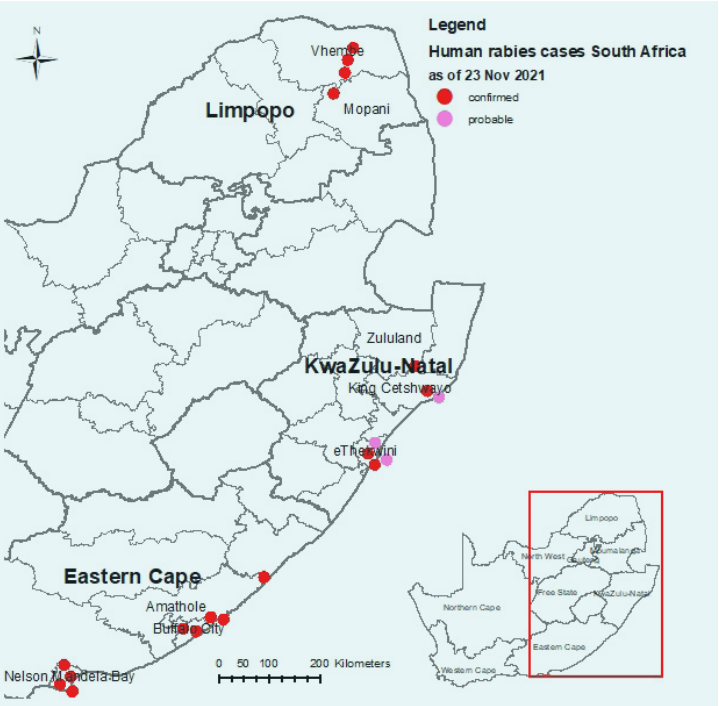

Figure 1. Human rabies cases in South Africa for 2021 until 23 November (created from NICD data)

Source: Centre for Emerging Zoonotic and Parasitic Diseases, NICD-NHLS; januszp@nicd.ac.za

CORONAVIRUS DISEASE (COVID-19) PANDEMIC

Proposed definition of COVID-19 wave in South Africa

South Africa reported its first case of COVID-19 on 5 March 2020, and as of 20 November 2021, the country had reported 2 929 862 cases including 94 471 deaths.

To date, there have been three periods of increased transmission (waves). There have been several different definitions proposed for the start of a COVID-19 wave in South Africa, which may cause inconsistences amongst researchers or policy makers. A clear simple working definition for retrospective analyses describing wave characteristics can be very helpful for researchers to communicate consistent messages about COVID-19. The aim of this article is to propose a simple working definition for a COVID-19 wave (upward and downward periods) in South Africa for use in retrospective analyses of wave characteristics. We do not propose that this wave definition be used prospectively to define the start of a new wave or to guide any public health action.

Some different wave definitions that have been used are described here. Based on the South African resurgence plan, a wave can be defined as the period from when COVID-19 weekly incidence is equal to or greater than 30 cases per 100 000 persons until the weekly incidence is equal to or below 30 cases per 100 000 persons (resurgence plan not published). A similar definition was used to describe a COVID-19 wave among hospitalized cases;[1] however, they used a weekly incidence of 5 cases per 100 000 persons (upward and downward trends) as a cutoff, probably because they were looking at a subset of COVID-19 cases (admissions only) in whom the rate is lower. This definition correlated well with the case-based rate definition. The South African Ministerial Advisory Committee on COVID-19 proposed the following definition: a wave starts when cases reach 30% of the previous wave's peak, and ends when cases reach 15% of the peak (in the ending wave/ downward trend) (https://sacoronavirus.co.za/wp-content/uploads/2020/12/Secondwave-Appendix.pdf).

We would like to propose that for retrospective analyses describing wave characteristics the following definition could be used - a wave can be defined as the period from when COVID-19 weekly incidence is equal to or greater than 30 cases per 100 000 persons until the weekly incidence equal or below 30 cases per 100 000 persons. The reason we are proposing the above definition is that it is not computationally difficult, can be applied to different geographic areas and time scales and can be easily estimated using available data on case counts. The incidence should be determined by dividing the number of new cases (weekly) by population at risk (mid-year population estimates-2020) per 100 000 persons. Epidemiologic weeks should be computed using USA Centre for Disease Control (CDC) epidemiologic week definition (Sunday-Saturday). A limitation of the proposed definition is that it is dependent on testing volumes remaining at a constant level. For this reason we do not propose using this measure for potential future waves pending evaluation of its performance as compared to other metrics.

Using the above proposed COVID-19 wave definition in South Africa, the first wave was from week 24 of 2020 (35.7 cases per 100 000 persons) to week 34 of 2020 (<30 cases per 100 000 persons), second wave from week 47 of 2020 (30.2 cases per 100 000 persons) to week 5 of 2021 (<30 cases per 100 000 persons), and third wave from week 19 of 2021 (30.9 cases per 100 000 persons) to week 37 of 2021 (<30 cases per 100 000 persons), see Figure 2.

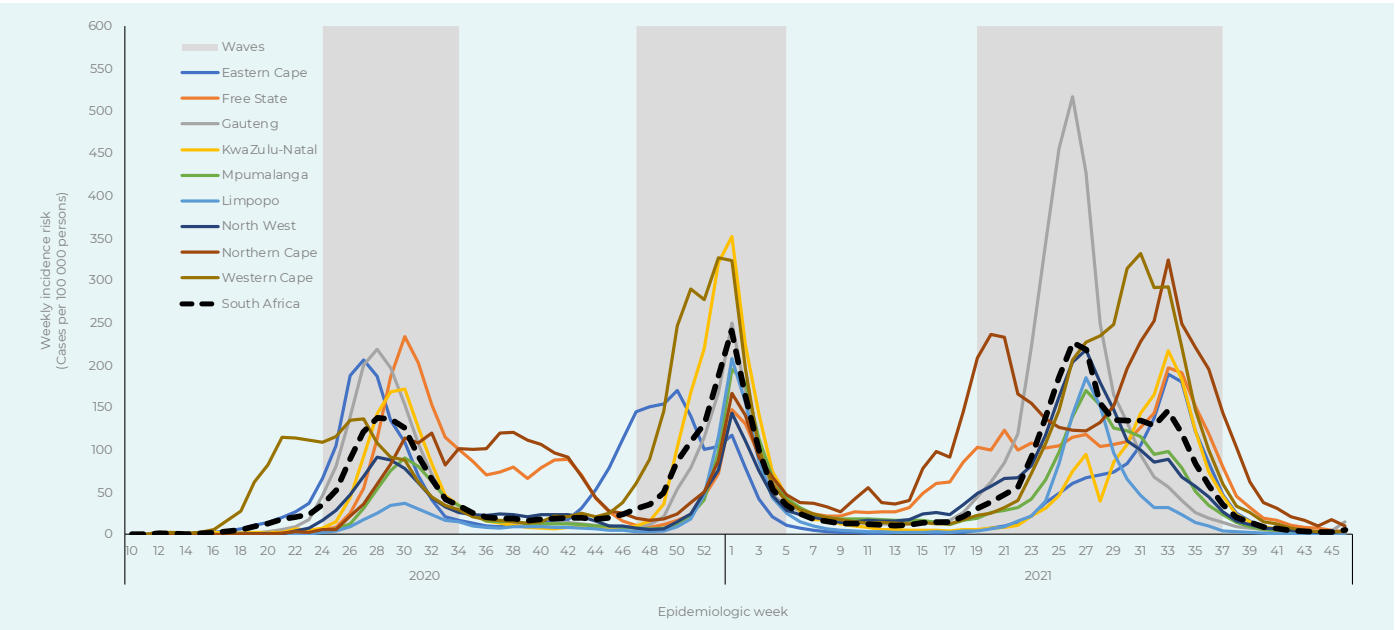

Figure 2. Weekly incidence risk of laboratory-confirmed cases of COVID-19 by province and epidemiologic week, South Africa, 2 March 2020 – 20 November 2021 (n=2 929 862)

CORONAVIRUS DISEASE (COVID-19) PANDEMIC

The provinces experienced the beginning and ending of the waves at different weeks (periods). The first province to enter first wave was the Western Cape in week 19 of 2020 (61.8 cases per 100 000 persons), and Limpopo was the last to enter first wave in week 29 of 2020 (34.1 cases per 100 000 persons), and first to exit first wave in week 31 of 2020 (30.1 cases per 100 000 persons), and the last provinces to exit first wave were Free State and Northern Cape in week 44 of 2020 (43.1 cases per 100 000 persons) and (43.7 cases per 100 000 persons), respectively, table 1.

In the second wave Eastern Cape was the first province to enter the second wave in week 43 of 2020 (31.1 cases per 100 000 persons), and Northern Cape was the last province to exit second wave in week 8 of 2021 (32.6 cases per 100 000 persons). In the third wave, Northern Cape was the first and last province to enter and exit the third wave in week 10 of 2021 (42.1 cases per 100 000 persons) and week 41 of 2021 (30.9 cases per 100 000 persons), respectively.

To date the province that has experienced the shortest wave was Limpopo in the first wave n=3 weeks (weeks 29-31 of 2020), and the province that experienced the longest wave was Northern Cape in the third wave n=32 weeks (weeks 10-41 of 2021).

Table 1: COVID-19 wave periods by weekly incidence, South Africa, 2 March 2020 – 20 November 2021

Province	First wave		Second wave		Third wave	
	Week[1] number (year 2020)	Weekly incidence (100 000 persons)	week number (year 2020-2021)	Weekly incidence (100 000 persons)	week number (year 2021)	Weekly incidence (100 000 persons) 6 734 001
Eastern Cape	23-32	37.0 - 40.7	43 - 3	31.1-41.5	24-37	37.3-46.5
Free State	27-44	54.6-43.1	52 - 6	45.0-31.2	14-39	32.0-31.8
Gauteng	24-34	45.8-34.1	50 - 5	53.5-35.2	19-34	44.4-40.4
KwaZulu-Natal	26-34	43.5-34.2	49 - 5	36.2-45.6	24-37	31.1-44.9
Limpopo	29-31	34.1-30.1	52 - 4	47.0-43.6	24-33	39.3-31.6
Mpumalanga	27-34	30.6-34.0	52 - 6	41.0-32.2	22-36	31.9-34.6
North West	26-33	46.9-32.4	53 - 4	49.9-46.0	18-36	34.9-44.3
Northern Cape	27-44	35.9-43.7	51 – 8	37.8-32.6	10-41	42.1-30.9
Western Cape	19-33	61.8-34.5	46 - 5	37.4-39.0	21-38	31.5-33.1
South Africa	**24-34**	**35.7-33.9**	**47-5**	**30.2-34.3**	**19-37**	**30.9-35.7**

Epidemiologic weeks constructs using America's Centre for Disease Control week definition (Sunday-Saturday)

In summary, the proposed COVID-19 wave definition will aid researchers and policy makers to communicate consistent messages re-COVID-19 waves. As demonstrated by provinces as they entered and exited waves at different time periods, the definition should be applied in a specified geographic area e.g. national, province or district.

1. Jassat W, Mudara C, Ozougwu L, Tempia S, Blumberg L, Davies M-A, et al. Difference in mortality among individuals admitted to hospital with COVID-19 during the first and second waves in South Africa: A cohort study. The Lancet. Global health. 2021; 9(9):e1216-e25.

Source: Centre for Respiratory Diseases and Meningitis, NICD-NHLS; cherylc@nicd.ac.za

ENTERIC DISEASES

The emergence of non-epidemic *Vibrio cholerae* O1 ST75 in South Africa

Cholera is a potentially fatal acute diarrhoeal disease resulting in large volumes of watery stool, causing rapid dehydration that can progress to hypovolaemic shock and metabolic acidosis. Every year, an estimated 3-5 million people worldwide contract cholera, with ~100 000 deaths. Cholera is caused by toxin-producing *Vibrio cholerae* serogroups O1 or O139. *V. cholerae* is a highly motile, comma-shaped Gram-negative bacterium with a single polar flagellum. It has more than 200 serogroups, based on the O-antigen of lipopolysaccharide. The serogroup O1 is classified into two biotypes (biological variants), termed classical and El Tor; each biotype is subdivided into two serotypes, Ogawa and Inaba.

Over the last 200 years, cholera has spread globally beyond Asia seven times, resulting in seven cholera pandemics. The first six pandemics (which began in 1817, 1829, 1852, 1863, 1881, and 1889 respectively) were caused by the classical biotype of *V. cholerae* serogroup O1. The seventh cholera pandemic (which is still ongoing) began in 1961, appearing first in Indonesia and subsequently spreading to South Asia, Africa, South America and the Caribbean islands. It is caused by *V. cholerae* serogroup O1 of the El Tor biotype, and named 7PET; it has been identified through whole-genome sequencing as *V. cholerae* sequence type 69 (ST69). The seventh pandemic continues to be a major public health threat for 175 countries in Asia, Africa and the Americas. In late 1992, *V. cholerae* serogroup O139 (Bengal) caused large outbreaks of cholera in India and Bangladesh; but never spread out of Asia and is now seldom isolated. Recently, there has been increased recognition of the role that non-01 and non-O139 serogroups may be playing in diarrhoeal disease.

The first laboratory-confirmed cholera case in South Africa was reported in 1974. South Africa is not considered endemic for cholera; outbreaks are typically associated with importation events, particularly from neighbouring countries. Large outbreaks have previously occurred in three provinces (Mpumalanga, Limpopo, and KwaZulu-Natal) caused by importation events from neighbouring countries, particularly Zimbabwe and Mozambique. The last cholera outbreak in South Africa was initiated by an importation of cases from a large outbreak in Zimbabwe during 2008. From November 2008 to April 2009, >12000 cases and 65 deaths were reported nationally, primarily from Mpumalanga and Limpopo provinces. Since the 2008-2009 outbreak, very few cases have been identified. From 2010 through 2014, five cases of cholera were reported (most proven to be imported), and from 2015 through 2017 no cases were identified.

Cholera is a category 1 notifiable medical condition in South Africa. All *V. cholerae* isolates (human and environmental) identified at private sector and NHLS laboratories in South Africa, are submitted to the Centre for Enteric Diseases, National Institute for Communicable Diseases (NICD), for further investigation. The case definition for confirmed cholera is the isolation of *V. cholerae* O1 or O139 from a person with diarrhoea.

From February 2018 through January 2020, the NICD received a total of 102 *V. cholerae* isolates for testing, of which nine were identified as *V. cholerae* O1. The isolates were phenotypically and genotypically characterised, including whole-genome sequencing (WGS), comparative genomics and phylogenetic analysis.

Of the nine *V. cholerae* O1 isolates tested, two isolates were identified as ST69 (7PET lineage) and seven as ST75. The ST69 isolates were recovered from two patients with cholera in a family cluster in October 2018. The index case-patient had travelled to Zimbabwe, where a cholera outbreak was ongoing, within the incubation period (7 days) before onset of symptoms. These ST69 isolates were confirmed as belonging to the highly resistant outbreak strain identified during the 2018 cholera outbreak in Zimbabwe. The seven ST75 isolates originated from KwaZulu-Natal and Limpopo provinces. Five isolates were recovered from patients with cholera, and two isolates were recovered from environmental samples collected during two of the case investigations (on-site sewage in Limpopo Province, and river water in KwaZulu-Natal Province, respectively). Case-patients were adults 37-57 years of age. The three cases in KwaZulu-Natal Province were located ~200-600 km apart, the first occurring in February 2018 and the last in January 2020. The 2 cases in Limpopo Province were located in the same district ~70 km apart and both occurred in November 2018. The cases in Limpopo Province were ≥900 km from the cases in KwaZulu-Natal Province. Epidemiological investigations included interviewing case-patients using a standardised case investigation form, visiting their places of residence to inspect water and sanitation services and interview other household members, collection of stool samples from household members and collection of environmental samples when indicated. There was no evidence of importation from another country, no epidemiological links between cases, no secondary transmission and no evidence of increased diarrhoea cases in local clinics and hospitals in the respective districts. Phenotypic characterisation of the O1 ST75 strains confirmed toxigenic *V. cholerae* 01 serotypes Ogawa and Inaba. All seven O1 ST75 isolates showed susceptibility to all antimicrobials tested, in contrast to African 7PET isolates which are reported to have become increasingly antimicrobial-resistant over time.

Further phylogenetic analysis showed the South African O1 ST75 isolates to be very closely related to each other but split into two clusters based on province of origin, with Limpopo Province isolates differing from the KwaZulu-Natal isolates by 4-5 alleles on core-genome multilocus sequence typing (cg-MLST). On single nucleotide polymorphism (SNP) analysis, all isolates clustered into a previously defined L3b.1 clade (Figure 1). Further comparison of the South African O1 ST75 isolates with a larger global collection of O1 ST75 of closely related genomes showed the closest relationship with isolates collected from the Russian Federation in 2005 and 2011. The L3b.1 isolates from

ENTERIC DISEASES

Taiwan and China were genetically more distant (Figure 1).

The first *V. cholerae* O1 ST75, the US Gulf Clone, was identified in the United States in 1973. Since then clinical and environmental isolates have been identified in multiple countries in several regions including South America, Europe, Asia and South East Asia. Cases due to *V. cholerae* O1 ST75 are reported to be primarily sporadic, although small clusters have been reported (usually household transmission) and the isolates are typically drug susceptible. This is the first report of *V. cholerae* O1 ST75 isolates from Africa.

Recent reports from Taiwan and Argentina provide further insight into the epidemiological characteristics of O1 ST75. Taiwan investigated the epidemiology of cholera during 2002-2018 and described the emergence of an ST75 clone in 2009. This clone has since become more prevalent than the O1 ST69 clone from a previous pandemic. Sixty-one of the sixty-three ST75 cases were sporadic; two were part of a family cluster. Closely related ST75 strains had been identified in China and two other South East Asia countries suggesting the ST75 clone may be spreading more widely in Asia. Argentinian scientists describe that during the cholera epidemic of 1992-1998, the epidemic clone (7PET lineage) co-existed alongside highly diverse non-7PET *V. cholerae* strains. Four of sixty-five non-7PET isolates sequenced were serogroup O1 and two were members of the Gulf Coast lineage of O1. The authors suggest that these non-7PET strains lack the propensity to cause epidemics and do not pose the same relative risk to public health as 7PET, and that this difference should be accounted for in epidemic preparedness responses.

The findings from South Africa align with those from Taiwan in that ST75 cholera cases now outnumber ST69 cholera cases. In addition, in keeping with observations in the literature, all South African O1 ST75 cases have been sporadic, with no secondary cases and no demonstrable epidemiological links. No associated outbreaks occurred, even when the strains were present in surface water sources used by multiple vulnerable communities with very poor WaSH (safe water, sanitation and hygiene). The O1 ST75 isolates were found across large spatial and geographical distances, suggesting local spread.

The emergence and dominance of non-epidemic (non-7PET) *V. cholerae* O1 ST75 in South Africa has major implications for the public health response to cholera cases. The level of public health response must be commensurate with the risk of outbreak, and WGS and cgMLST will need to be expedited to guide the response. Ongoing WGS of all clinical and environmental *V. cholerae* isolates is essential to describe the dynamics of O1 ST75 in South Africa and to identify emergence of other non-7PET strains.

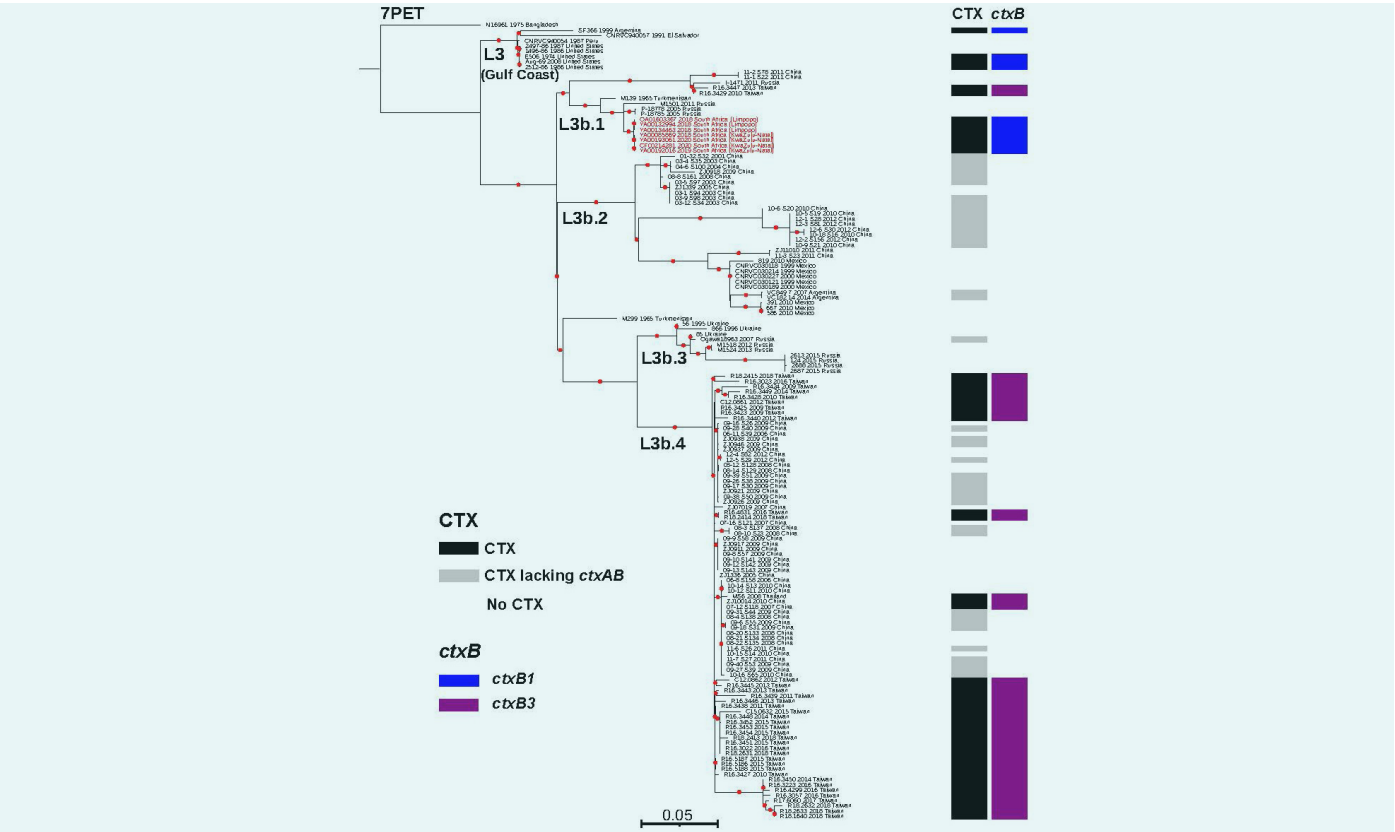

Figure 3. Phylogenomics of *V. cholerae* O1 ST75 isolates from South Africa, 2018-2020. Maximum likelihood phylogeny for 151 ST75 (or closely related STs) and one ST69 *V. cholerae* O1 genomic sequences. The seventh pandemic *V. cholerae* O1 El Tor (7PET) genome N16961 (ST69) was used as an outgroup. For each genome, its name, year (when known), and country of isolation (plus province of isolation for the South African isolates) are orderly shown at the tips of the tree. The genomes from South Africa are highlighted in red. The lineages, presence of the CTX prophage or its variant form, types of *ctxB* allele are also shown. The 7PET outgroup genome, N16961 contains CTX with an *ctxB3* allele (not represented in the figure). Bootstrap values greater than or equal to 95% are shown at the branch of the nodes as a red dot. The scale bar denotes substitutions per variable site (SNVs).

Source: Centre for Enteric Diseases, NICD-NHLS; junot@nicd.ac.za

INTERNATIONAL OUTBREAKS OF IMPORTANCE

An update on Ebola virus disease, DRC

There have been no new cases of Ebola virus disease in Beni Health Zone in North Kivu Province in the Democratic Republic of the Congo in the past 14 days. The last known confirmed case was reported on 30 October 2021, with the case discharged on 4 November 2021.

As of 13 November 2021, a total of 11 cases (eight confirmed and three probable) including four community deaths) has been reported in the Beni Health zone. The case fatality rate among confirmed cases is 75.0% (6/8). Since the start of the outbreak, three out of the 11 health areas in Beni Health Zone have reported at least one confirmed EVD case.

A total of 227 contacts has been identified and 205 are under active follow up in 11 health areas. Of the total contacts, 13 contacts had never been seen in the past 21 days, and three were lost to follow up.

The North Kivu Provincial health authorities are leading the current response with support from WHO and its partners. The head of the Provincial Health division of North Kivu conducted a press briefing highlighting the EVD outbreak response and prevention measures with emphasis on vaccination.

Source: World Health Organization, Regional Office for Africa (www.afro.who.int)

SEASONAL DISEASES

Influenza, 2021 – Influenza activity increases

There has been a sustained increase in influenza cases from the influenza-like illness (ILI) (outpatient in public health clinics) and pneumonia (hospital) surveillance sentinel sites in recent weeks. The total number of influenza cases detected by the syndromic sentinel surveillance programmes conducted by the NICD as of week 45 of 2021 (week ending 14 November 2021) has increased from 154 in week 41 (date of last Communiqué) to 246.

As of week 45 2021, 131 influenza detections at pneumonia surveillance sentinel sites have been reported with the predominant subtype and lineage being B Victoria (50/131, 38.2%) followed by A (H1N1)pdm09 (33/131, 25.2%) and A (H3N2) (21/131, 16.0%) (Figure 4). For the ILI sentinel sites, 115 influenza cases have been reported, with the predominant subtype and lineage being B Victoria (44/115, 38.3%) followed by A (H3N2) (39/115, 33.9%) and A (H1N1)pdm09 (11/115, 9.6%) (Figure 4).

Clinicians are encouraged to consider influenza as part of a differential diagnosis when managing patients presenting with respiratory illness. It is also important to encourage patients, especially those at high risk for developing severe influenza illness and complications to take the influenza vaccine. Because of the recent changes in respiratory virus epidemiology as a result of non-pharmaceutical interventions (NPI) to control COVID-19, it is possible that we may see increasing influenza detections even as we enter the summer months, especially if compliance to NPIs is relaxed. For this reason, it is still not too late to vaccinate against influenza as long as influenza is circulating. Updated guidelines on influenza diagnosis and management are available at:

https://www.nicd.ac.za/wp-content/uploads/2021/07/Influenza-guidelines_-April-2021-final.pdf

The composition of the 2022 southern hemisphere influenza vaccines has been updated. WHO recommends that the egg-based trivalent vaccines should contain the following:

- an A/Victoria/2570/2019 (H1N1) pdm09-like virus;
- an A/Darwin/9/2021 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

In addition to the above, the quadrivalent vaccine should include a B/Phuket/3073/2013 (B/Yamagata lineage)-like virus. These recommendations included two updates compared to the 2021 southern hemisphere vaccines, influenza A(H3N2) and B/ Victoria lineage components were updated. https://www.who.int/publications/m/item/recommended-composition-of-influenza-virus-vaccines-for-use-in-the-2022

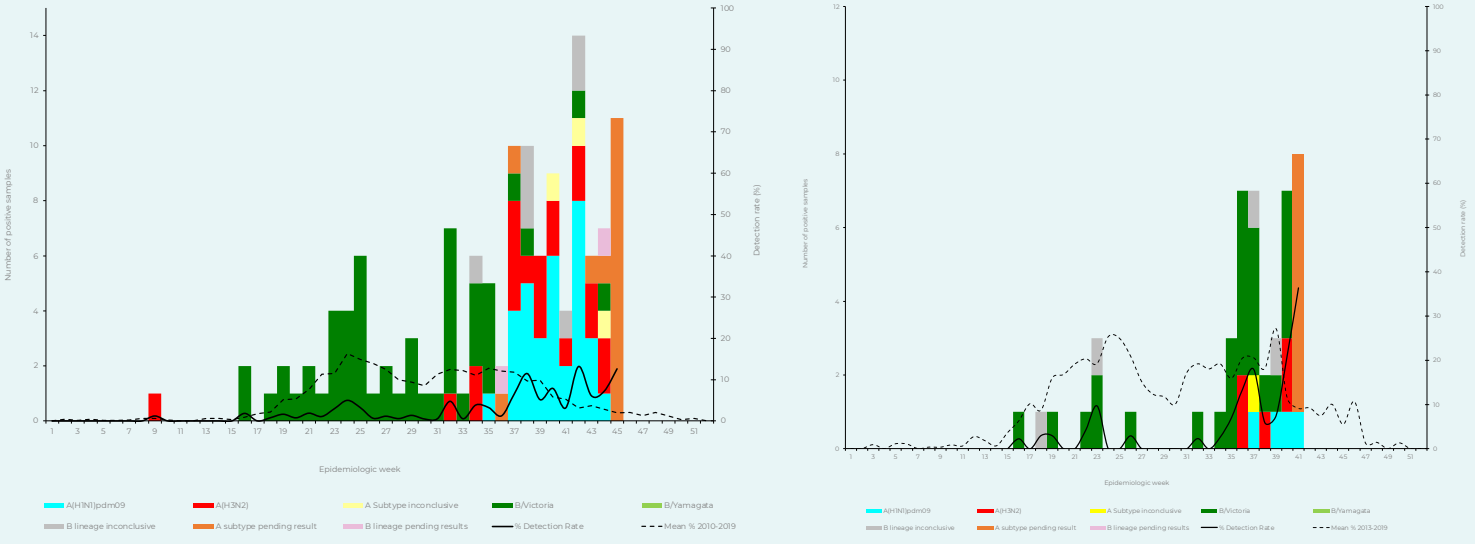

Figure 4. Number of positive cases by influenza subtype and lineage and detection rate, pneumonia surveillance (left) and ILI surveillance (right), 01 January – 14 November 2021

SEASONAL DISEASES

Respiratory syncytial virus (RSV) 2021 - RSV activity remains low

As of week 45 2021 (week ending 14 November 2021), 482 RSV cases have been detected at pneumonia and ILI surveillance sentinel sites. The majority of RSV positive cases were subgroup A (255/482, 52.9%), followed by subgroup B (221/482, 45.9%).

The detection rate continues to decrease these past few weeks to rates below 10% since week 26 (Figure 5).

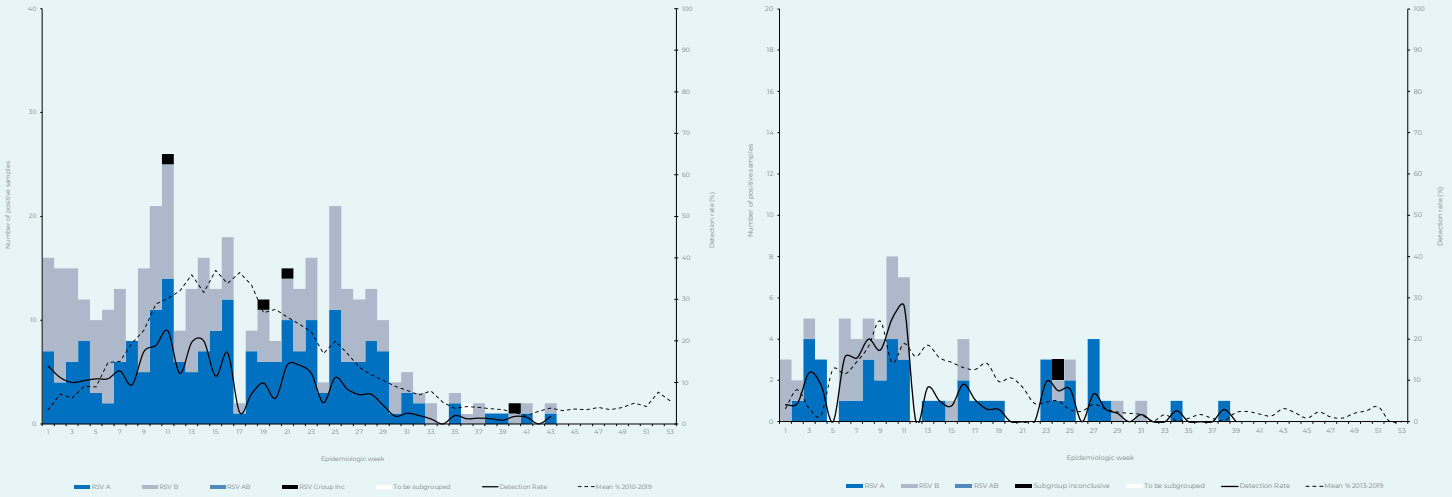

Figure 5. Number of samples testing positive for respiratory syncytial virus by subgroup and detection rate by week for pneumonia surveillance (left) and ILI surveillance (right), 01 January – 14 November 2021

Source: Centre for Respiratory Diseases and Meningitis, NICD-NHLS; cherylc@nicd.ac.za

Malaria

The southern African malaria season has started and the number of cases is expected to rise following the onset of summer rains. The numbers of reported malaria cases are, however, still comparatively low compared to previous years. It is important to note that many of the variables that contribute to malaria incidence are unstable or unpredictable - these include climatic, economic and political factors, and the state of the SARS-CoV-2 pandemic, and so the rate of incidence can increase substantially in a short period of time. People intending to visit malaria risk areas should therefore familiarise themselves with malaria-preventive measures (https://www.nicd.ac.za/wp-content/uploads/2019/03/National-Guidelines-for-prevention-of-Malaria_updated-08012019-1.pdf). While COVID-19 is often the main concern when a person becomes ill with non-specific symptoms, it is also important to remind healthcare workers of the need to consider malaria in a febrile patients living in or travelling from a malaria-endemic region. Missed or delayed recognition of malaria has the potential for serious illness or death. Any person presenting with fever and progressive 'flu-like symptoms who lives in, or has recently visited, a malaria-endemic area, should be checked for malaria, irrespective of pending or completed tests for SARS-CoV-2 infection. The ability of vector mosquitoes to hitchhike to non-malaria areas and infect local residents, frequently with serious medical consequences, also should not be forgotten. This type of malaria should be considered in a patient with a progressively worsening febrile illness of unknown cause, particularly if thrombocytopenia is evident.

Source: Centre for Emerging Zoonotic and Parasitic Diseases, NICD-NHLS; johnf@nicd.ac.za / basilb@nicd.ac.za

BEYOND OUR BORDERS

The 'Beyond our Borders' column focuses on selected and current international diseases that may affect South Africans travelling abroad. Numbers correspond to Figure 6 on page 11.

Monkeypox virus – Maryland, USA

A case of monkeypox virus has been reported from Maryland, USA, in a resident who recently returned from Nigeria. This is the second case of monkeypox virus imported into the USA from Nigeria. Monkeypox is endemic mostly in central and western African countries, with majority of infections reported in the Democratic Republic of Congo. In Africa, monkeypox has been shown to cause death in as many as 1 in 10 people who contract the disease.

Monkeypox virus belongs to the Orthopoxvirus in the family Poxviridae, the same family of viruses as smallpox; however, monkeypox generally causes a milder infection than smallpox. The main reservoir of the virus is unknown, although rodents are largely suspected to play a role in transmission. Transmission can occur from animal-to-human or human-to-human. Animal-to-human transmission occurs by bites, scratches or bushmeat preparation, whilst human-to-human transmission mainly occurs through respiratory droplets, or direct contact with contaminated bodily fluids or lesion material.

The incubation period for monkeypox can range from five to 21 days and symptoms are mostly nonspecific, such as fever, headache, muscle aches and exhaustion. The main difference between symptoms of smallpox and monkeypox is that monkeypox causes lymphadenopathy, whilst smallpox does not. Within a few days after the appearance of the rash, patients develop a rash that often starts on the face then spreads to the rest of the body. The lesions progress through four stages, namely the macular – papular – vesicular and pustular stages, then finally the lesions form scabs and fall off. The duration of illness typically lasts 2 to 4 weeks.

There is no specific treatment for monkeypox virus; however, the smallpox vaccine and immunoglobulin can be used during outbreaks.

Melioidosis – United Kingdom

A case of melioidosis has been reported from the UK in a 33-year-old man, who emigrated from Ghana 14 months prior to his presentation. The patient presented with femoral osteomyelitis and melioidosis was diagnosed from bone marrow aspirate samples that yielded the causative agent *Burkholderia pseudomallei*, a Gram-negative, aerobic bacillus.

Melioidosis, also referred to as Whitmore's disease, is a bacterial disease that can infect both humans and animals. It is predominately found in tropical climates, such as Southeast Asia and northern Australia. Transmission occurs through inhalation of contaminated dust particles or water droplets or through their ingestion. Human-to-human transmission is very rare.

The incubation period is highly variable; generally, symptoms may appear 2 to 4 weeks after exposure but years can elapse between presumed exposure and appearance of disease. Melioidosis has a wide range of signs and symptoms and can mimic other diseases such as tuberculosis and pneumonia. The disease may manifest either as an acute localized infection, acute pulmonary infection, acute bloodstream infection, or disseminated infection. Sub-clinical infections are also possible.

The type of infection and manifestation of the illness will determine the course and duration of treatment. Treatment usually starts with parenteral antibiotics for two weeks, followed by oral antibiotics for 3 to 6 months.

BEYOND OUR BORDERS

Visceral leishmaniasis – Tharaka Nithi County, Kenya

A total of 33 cases of visceral leishmaniasis has been reported from Tharaka Nithi County in Kenya. Health officials from the region have also reported associated five deaths. The spread of the disease is attributed to poor hygienic conditions, malnutrition, and environmental changes.

Visceral Leishmaniasis, also called kala-azar, is a vector-borne disease, caused by obligate intracellular protozoa and is transmitted through the bites of infected female sandflies. Human infection has been found to be caused by more than 20 species of *Leishmania* parasites. Visceral leishmaniasis is commonly caused by the species *L. donovani* and *L. infantum*, which affect the spleen, liver and bone marrow. The incubation period ranges from weeks to months. Asymptomatic infection can occur and manifest years after exposure, in people who become immunocompromised from other illnesses such as HIV/AIDS or cancer.

Visceral leishmaniasis is characterized by irregular bouts of fever and anaemia. Symptoms typically include fever, weight loss and fatigue and clinical signs involve the appearance of hepatomegaly, splenomegaly, anaemia, leukopenia and thrombocytopenia.

The disease is diagnosed by detecting *Leishmania* parasites in tissue specimens. Visceral leishmaniasis, is most often diagnosed using bone marrow aspirates. Treatment depends on the *Leishmania* species causing the disease, the underlying host factors, and the severity of the disease. Thus, treatment decisions are individualised; however, the use of effective systemic therapy is important as well as supportive care.

Figure 6. Current outbreaks/events that may have implications for travellers. Numbers correspond to text above. The red dot is the approximate location of the outbreak or event.

Source: Promed (www.promedmail.org), World Health Organization (www.who.int), Centres for Disease Control and Prevention (www.cdc.gov), World Organisation for Animal Health (www.oie.int), National Institute for Communicable Diseases (www.nicd.ac.za); Outbreak News Today (www.outbreaknewstoday.com)

WHO AFRO UPDATE

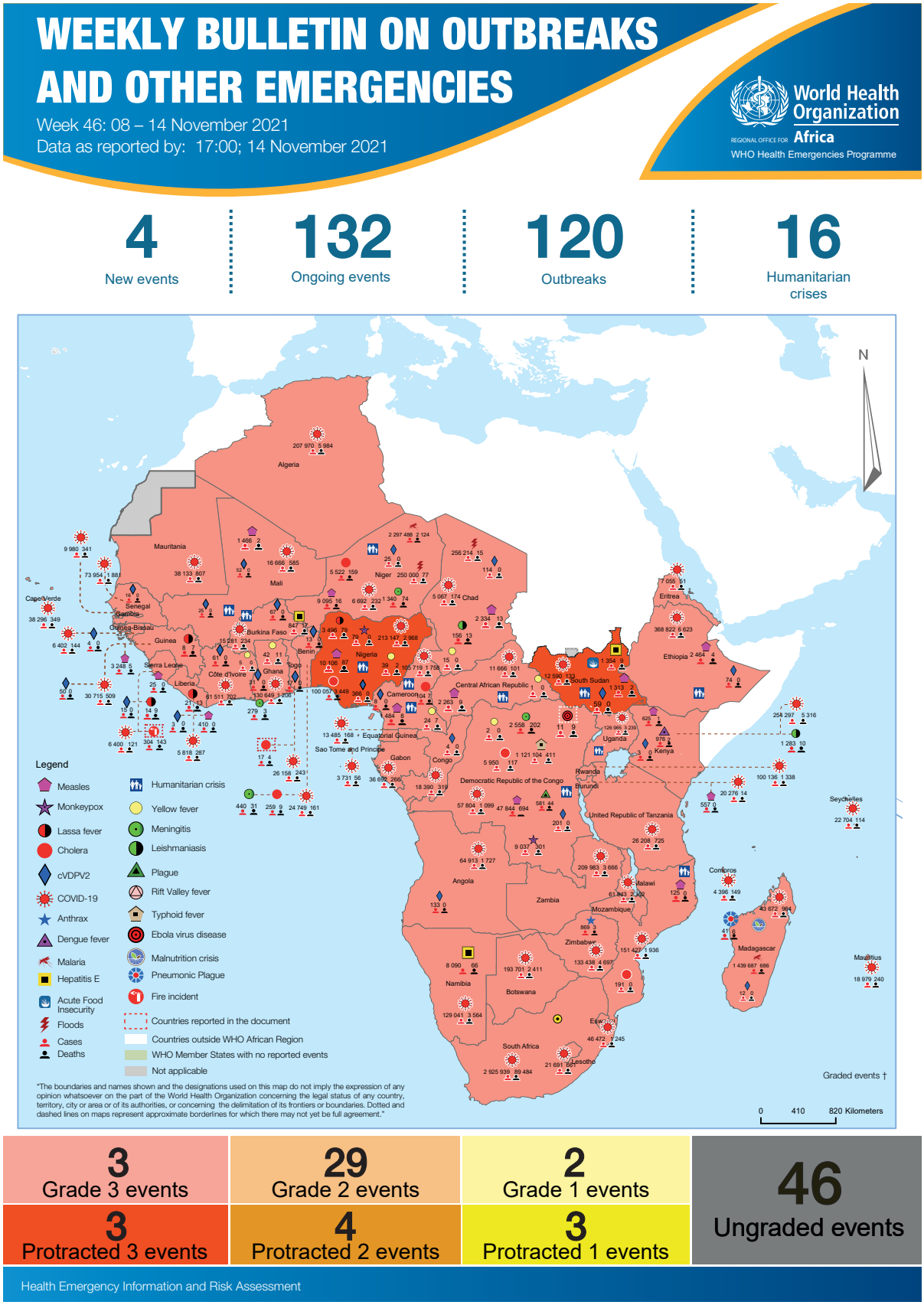

Figure 7. The Weekly WHO Outbreak and Emergencies Bulletin focuses on selected public health emergencies occurring in the WHO African Region. The African Region WHO Health Emergencies Programme is currently monitoring 136 events. For more information, see link below:
http://apps.who.int/iris/bitstream/handle/10665/348840/OEW46-0814112021.pdf

The Communicable Diseases Communiqué offers up-to-date information regarding communicable diseases in South Africa and abroad. It forms part of the NICD's key mandate of disease surveillance, outbreak response and research on communicable diseases. The publication is released on a monthly basis and can be accessed via the NICD website on http://www.nicd.ac.za/publications/internal-publications/

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