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FOREWORD

Outbreak report: This issue describes an astrovirus-associated foodborne outbreak at a childcare facility in South Africa's Gauteng Province. There were 279 gastroenteritis cases identified, the vast majority of whom were children less than five years old. The likely route of infection was from contaminated food delivered to the crèche, followed by person-to-person transmission.

Surveillance reports: The incidence of hepatitis C virus (HCV) in South Africa was surveyed using data mined from the National Health Laboratory Service central data warehouse. Overall prevalence for South Africa in 2017 is given in this issue as 5/100 000 population for those seeking care in the public sector. Also in this issue is surveillance data for 2018 from the syndromic respiratory illness surveillance programmes coordinated by the National Institute for Communicable Diseases. These show that South Africa's 2018 influenza season started in week 18 and was predominated initially by influenza A(H1N1)pdm09 with circulation of influenza B towards the end of the season. Last but not least is the annual malaria vector surveillance report for South Africa for 2018, showing the geographical distribution of four vector species. These include *Anopheles parensis*, which has only very recently, and unexpectedly, been implicated as a minor vector of malaria in South Africa.

We trust that you will find these diverse reports interesting and informative. All authors and reviewers are thanked for their contributions.

Basil Brooke,

Editor

A SUSPECTED ASTROVIRUS-ASSOCIATED FOODBORNE OUTBREAK AMONG CHILDREN AND STAFF ATTENDING A GROUP OF CHILDCARE CENTRES IN GAUTENG PROVINCE, NOVEMBER 2018

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Executive summary

In November 2018 a suspected outbreak of gastroenteritis, reported from multiple branches of a childcare and education facility (crèche) chain in Gauteng Province, was investigated. The outbreak affected children attending the crèches as well as adult employees. A standardised questionnaire was used to collect food history from the adult cases at selected crèche branches. A single caterer pre-prepared meals and delivered to all crèches. Food retention samples collected from the caterer were tested for pathogens commonly associated with foodborne disease, and stool specimens collected from adults and children at several crèches were tested for selected enteric viruses, bacteria and parasites. A total of 279 cases was identified. Where date of birth was available, 87% (235/270) of case-patients were children and 13% (35/270) were adults. The median age among children was 3 years (range 8 months – 5 years) and the median age among adults was 30 years (range 19-62 years). Illness in children preceded that in adults, suggesting secondary infection in adults. No pathogens were detected in the food samples; however, these samples were collected well after the outbreak was reported, and no food retention samples dating to the start of the outbreak were available for testing. Human astroviruses (HAstVs) were detected in 54% (7/13) of the stool specimens. Nucleic acid sequence analysis and phylogenetic tree comparisons showed that the HAstVs identified were highly related (99%) to each other and to another HAstV type 8 strain that was detected in South Africa in 1998. The HAstV strains were detected in case-patients (six adults and one child) from two crèches. These data strongly suggest that catered food from a single supplier was the source of the HAstV outbreak, perpetuated by person-to-person transmission.

Introduction

Human astroviruses (HAstVs) are transmitted by the faecal-oral route, either directly from person-to-person or indirectly via contaminated food and water, and have been implicated in large foodborne gastroenteritis outbreaks.[1] In 1991, HAstV-contaminated school lunches resulted in an outbreak of acute gastroenteritis that involved 10 primary and four junior high schools in Katano City, Japan. More than 4 700 people, including pupils and adults, were affected. The primary source of the HAstV outbreak was contaminated food from a common supplier.[2] The ability of the virus to spread from person-to-person is well described and has been demonstrated by human volunteer studies.[3]

Astrovirus (AstV) infection has an incubation period of 1-4 days and typically presents as watery diarrhoea that resembles a mild form of rotavirus gastroenteritis. Astrovirus diarrhoea is usually seen in young children aged 6 months to 2 years and may be associated with anorexia, fever, vomiting and abdominal pain. Although AstV diarrhoea does not normally result in significant dehydration or hospitalisation, persons with poor nutritional status, immunodeficiency, mixed infections, or underlying gastrointestinal disease are at risk for developing complications.[4] In individuals with immunosuppression (other than HIV), AstVs have been associated with non-diarrhoeal symptoms such as coeliac disease and neurotropic conditions.[5]

Human AstVs are classified into eight classic strains, HAstV-1 to HAstV-8, and recombinant and novel strains have also been identified.[4-5] Classic HAstVs are globally distributed and are the third most common cause of viral gastroenteritis, following rotavirus and norovirus.[6]

There is limited data on the epidemiology of HAstVs in South Africa (SA). Most investigations have reported the rates of HAstVs detection for specific geographical areas.[7-11] HAstVs were first detected in SA in 1979, when the star-shaped virions were viewed by electron microscopy in stool specimens collected from a six-month-old baby.[12] Since then, several small studies have investigated the presence of HAstVs in SA, reporting detection of HAstVs in human stool specimens and environmental water samples.[7-9, 11, 13-15] In 1997, HAstVs were detected in 37% of stool specimens collected in a diarrhoeal disease outbreak in a child care centre in Tshwane, Gauteng Province.[16]

A study carried out between 2009 and 2014 reported HAstVs in 7% of stool specimens collected from hospitalised patients under the age of five years.[17] The study was conducted in selected areas in SA and included sites from Mpumalanga, Gauteng and KwaZulu-Natal provinces. However, since these pathogens are typically associated with milder infections, community and outpatient-focused studies are required to determine the broader epidemiology of HAstVs.

Outbreak background

The Outbreak Response Unit of the National Institute for Communicable Diseases (ORU-NICD) received a notification of a suspected outbreak of gastroenteritis on 6 November 2018, reportedly affecting multiple branches of a childcare and education facility (crèche) chain in Gauteng Province. There are ten branches in total: four in the City of Johannesburg, four in the City of Tshwane, one on the West Rand and one in Ekurhuleni District (Figure 1). The cases included children attending the crèches as well as adult employees. All crèches received food from the same caterer daily. The caterer provided pre-prepared lunch and snacks to the crèches, while each crèche prepared their own breakfast (which included porridge made from either Mabele, oats or mielie-meal). All crèches have a similar menu, rotated on a two-weekly basis.

Food supply was identified as the only common epidemiological link between the crèches. The investigating team hypothesised that contaminated food from the caterer was the likely vehicle of infection. An epidemiological investigation was thus conducted with the aim of determining the magnitude of the outbreak, identifying the source of the outbreak, and providing recommendations to prevent occurrence of similar outbreaks.

Methods

Study setting

The outbreak affected both children and adults at the ten crèches. The crèches are distributed across Gauteng Province (Figure 1) and enrol children aged six weeks to five years. The children are categorised by age into separate classes, namely: baby (3 weeks – 12 months), young toddler (1–2 years) and 2 to 5 year olds.

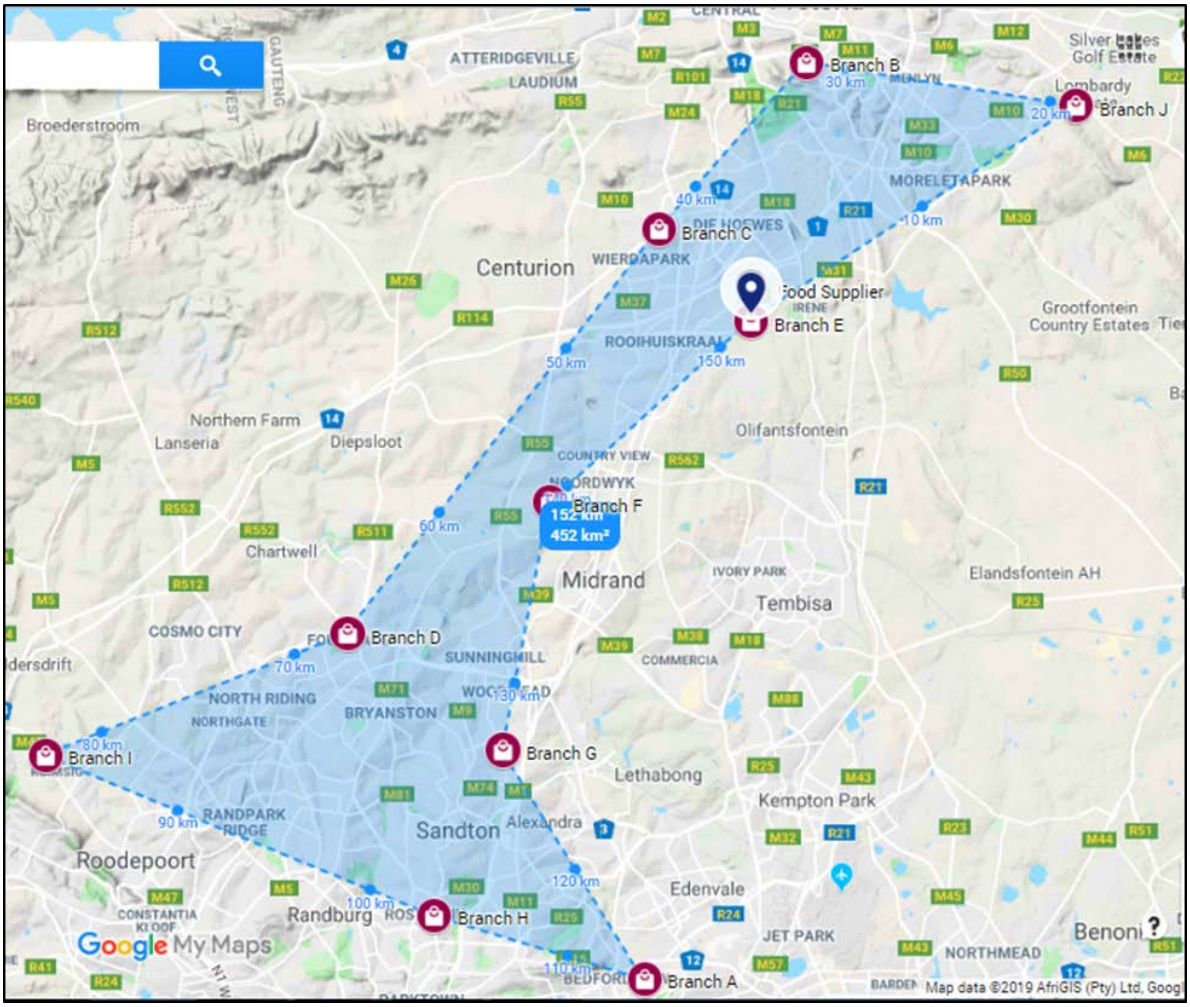

Figure 1: Distribution of crèche branches, human astrovirus (HAstV) outbreak, Gauteng Province, South Africa, November 2018.

Study design

A descriptive study was conducted amongst children and adults from all ten branches, and a case-control study was conducted amongst adults at four of the ten branches. A case was defined as a person of any age who presented with diarrhoea or vomiting with/without fever between 17 October and 23 November 2018. A control was defined as any adult crèche employee working between 17 October and 23 November who did not develop symptoms of gastroenteritis.

Data collection

Epidemiological investigation

A line list including cases (children and adults) from all branches was compiled. The investigating team visited four of the ten branches and completed a detailed hard-copy semi-standardised questionnaire with consenting adults for cases and controls. The team also visited the caterer and

completed questionnaires with food handlers working at the facility. Data collected through the questionnaire included demographic, clinical and food history.

Laboratory investigations

Clinical specimens

Stools specimens and rectal swabs were collected between 13 and 29 November 2018 from four crèches and from food handlers at the caterer's premises. These specimens were sent to the Centre for Enteric Diseases (CED) for enteric pathogens testing.

In total, 13 specimens were received at CED. Nucleic acid extracts from these specimens were screened using one-step multiplex real-time kits (Fast Track Diagnostics; Luxembourg) for the presence of selected enteric viruses (FTlyo Viral gastroenteritis), bacteria (FTlyo Bacterial gastroenteritis) and parasites (FTlyo Stool parasites).

The HAstVs detected were further characterised by reverse transcriptase-polymerase chain reaction (RT-PCR) and nucleotide sequence analysis. Amplicons were sequenced and analysed on an ABI 3500 Genetic Analyser (Applied Biosystems). Nucleotide sequence data were compared with published sequences. Phylogenetic analyses was performed to establish relatedness between the outbreak strains and reference sequences. A phylogenetic tree was drawn using the aligned sequences and reference HAstVs strains obtained from the NCBI databases using MEGA5 analysis software.

Environmental investigations

Environmental Health Practitioners from the City of Tshwane conducted an environmental assessment of the caterer's facility and collected environmental surface swabs from the kitchen. Food retention samples collected for 29 and 30 October 2018 by the caterer, which included fish cakes and chicken á la King, were sent to a private food laboratory for *Salmonella* spp., *Staphylococcus aureus* and *Listeria monocytogenes* testing. Eggs collected from the caterer were also tested for *S. aureus*, aerobic bacteria, *Salmonella* spp., yeasts and moulds. Environmental assessments were also conducted at six of the ten crèches, but no environmental samples were collected.

Data analysis

Descriptive analysis was conducted using Microsoft Excel and STATA version 14. The Chi-square test was used to assess risk factors associated with illness between cases and controls.

Results

Epidemiological investigation

A total of 279 cases from all ten crèches was captured on the line list (Table 1). Where date of birth was available, 87% (235/270) cases were children and 13% (35/270) were adults. The median age among children was 3 years (range 8 months – 5 years) and the median age among adults was 30 years (range 19-62 years). All adult cases were females, and females accounted for 52% (112/216) of cases among children. The epidemic curve suggests a propagated outbreak in which the causative agent is transmitted by person-to-person contact (Figure 2).

Table 1: Proportion of human astrovirus (HAstV) cases across ten crèches, City of Tshwane, Gauteng Province, South Africa, November 2018.

Crèche branches	Adults n (%)	Children n (%)	Age unknown	Grand Total
Branch A	4 (7)	44 (82)	6 (11)	54 (19)
Branch J	7 (15)	39 (85)		46 (16)
Branch I	9 (21)	33 (77)	1 (2)	43 (15)
Branch C		36 (97)	1 (3)	37 (13)
Branch G	4 (13)	26 (84)	1 (3)	31 (11)
Branch H	5 (21)	19 (79)		24 (9)
Branch E		16 (100)		16 (6)
Branch B	3 (21)	11 (79)		14 (5)
Branch D	2 (22)	7 (78)		9 (3)
Branch F	1 (20)	4 (80)		5 (2)
Grand Total	**35 (13)**	**235 (84)**	**9 (3)**	**279**

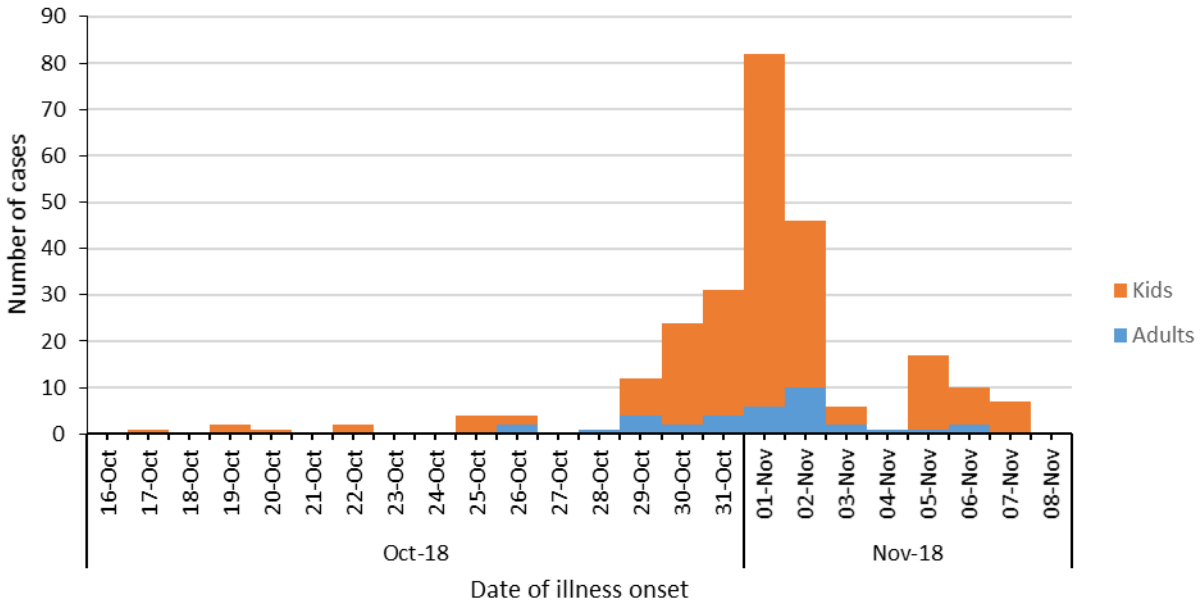

Figure 2: Epidemiological curve of human astrovirus (HAstV) cases by date of illness onset stratified by age group, Gauteng Province, South Africa, November 2018.

A total of 21 questionnaires was completed for adult cases (n=13) and controls (n=8). These included nine assistant teachers, six teachers, two managers, three caregivers and a health-hygiene assistant. The most common symptoms amongst cases were diarrhoea (92%, 12/13), abdominal cramps (92%, 12/13), nausea (46%, 6/13) and vomiting (23%, 3/13). The daily functions of most adults involved close contact with the children (90%, 19/21), while the remaining adults performed management functions and had limited or no contact with the children. The caterer reported that food is prepared every morning from 04h00 and transported to all the crèches before 10h00. The food includes lunch meals, afternoon snacks and snacks for the following day. Food is transported in cooler units with thermometers for temperature control and is reheated to 70 °C by the health-hygiene personnel at the crèches.

Laboratory findings

1. Clinical samples

a) Screening assays

Of the 13 specimens received, seven (7/13, 54%) tested positive for HAstVs, five (5/13, 39%) were positive for adenovirus, one (1/13, 8%) was positive for sapovirus and one (1/13, 8%) was positive for norovirus GI. Of the seven HAstV-positive specimens, four were detected as mixed viral

infections and the remaining three were single HAstV infections. All specimens were negative for enteric bacteria and parasites. Five specimens were negative for all pathogens screened.

b) RT-PCR amplification and Sanger sequencing

Only six of the seven HAstVs detected could be amplified for further characterisation. Sanger sequencing reactions were performed using these six RT-PCR products. Of these, nucleotide sequence contigs could be constructed for three strains and all three were identified as HAstV genotype 8 (HAstV-8) by comparison with BLAST

c) Phylogenetic analysis

The results for analysis of the capsid region showed that the strains detected from the outbreak were highly similar to each other (99%) and grouped together in a single clade with the highest similarity to a HAstV -8 strain identified in Hungary (AJ620757). Furthermore, this reference strain was most closely related to a HAstV-8 isolate identified previously in SA in 1998. Figure 3 shows the phylogenetic tree drawn using nucleotide sequence similarities from the capsid region of the genome. The three HAstVs identified as genotype 8 were collected from two of the crèches where the gastroenteritis outbreaks occurred.

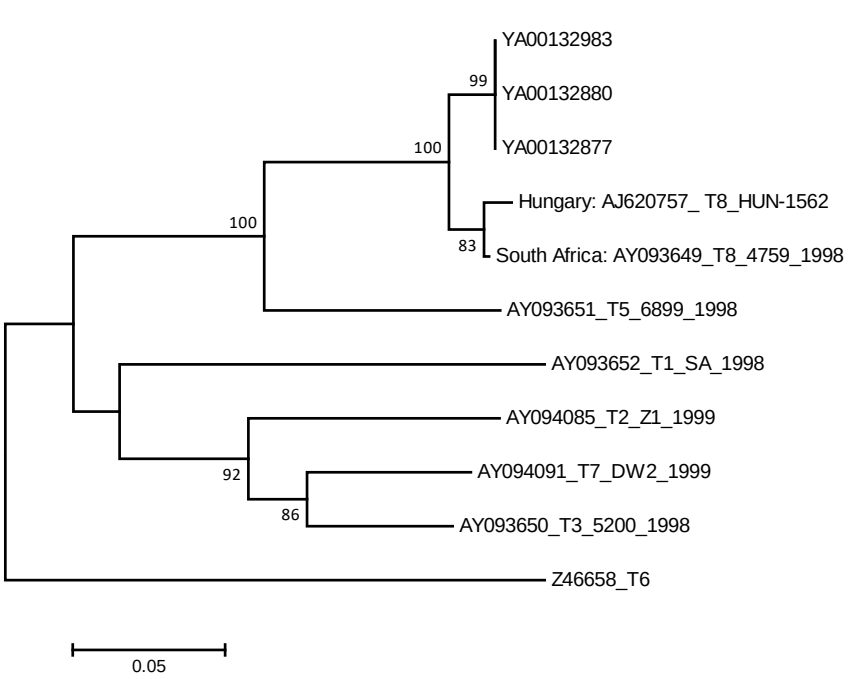

Figure 3: Molecular characterisation of human astrovirus identified in human stool specimens showing the clustering of related outbreak strains (YA00132983, YA00132880, YA00132877) and similarity to other human astrovirus type 8 strains (Hungarian and South African). Outbreak specimens highlighted in brackets.

Environmental findings

The caterer reported that the retention samples they had submitted were negative for all pathogens that were tested. Although environmental and food hygiene practice at most of the crèches was satisfactory, several concerns were noted. Thermometers were not always available for temperature monitoring on food delivery, and Certificates of Acceptability and health certificates were not available at some of the crèches. At one crèche, temperatures of delivered food and refrigerators were not recorded for more than a month prior to the onset of the outbreak.

Discussion

In this outbreak, children and adults from multiple crèches in a childcare facility chain presented with gastroenteritis. A caterer was identified as the only common link between the crèches. The epidemiological curve and analysis of the questionnaire data shows that the adult cases were likely secondary infections following contact with ill children. Interviewed adults reported that they typically consume food from their home-prepared lunch boxes and rarely eat the pre-prepared food from the caterer. The most plausible route of transmission is likely from contaminated food to the crèche children, and then person-to-person spread from the children to adult employees.

The molecular results suggest that the HAstV-8 strain identified from the three stool specimens was from a single source. The strain detected in one child was identical to the HAstV strain detected in the two teachers. The child and one teacher were from Branch J and the other teacher was from Branch I. The distance between the two crèches is approximately 152 km, which further supports the hypothesis that contaminated food from the caterer was the likely source of infection.

Food handlers were reluctant to provide stool specimens, so by the time they consented and specimens were collected the outbreak was over and the likelihood of detecting HAstV extremely low. Astrovirus is able to survive on inert surfaces and fomites[18], which may lead to contamination of the food preparation environment and food items. Unfortunately, environmental surface swabs were not tested for HAstV. Food retention samples from the food supplier that were sent for testing were negative for foodborne pathogens, but were also not tested for HAstV.

Further molecular analysis of the HAstV-positive strains was restricted by the quality of specimens submitted for testing and the delay in specimen receipt.

This investigation highlights the importance of collecting good quality clinical specimens during an outbreak. It also serves as an important reminder that food specimens (and, often, clinical specimens) are not routinely tested for viral enteric pathogens and so many viral foodborne infections and outbreaks are missed.

Conclusion

This was an HAstV-8 associated foodborne outbreak spread by a common food source and further propagated by person-to-person transmission.

Acknowledgements

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LABORATORY-BASED HEPATITIS C SURVEILLANCE FOR SOUTH AFRICA, 2017

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Executive summary

There is no active national surveillance for hepatitis C virus (HCV) in South Africa. Analysing laboratory data can assist with estimating the prevalence of HCV amongst patients who seek medical attention in healthcare facilities. National Health Laboratory Service (NHLS) HCV data were analysed to understand the testing pattern and demographic distribution of the disease for the year 2017. HCV data were extracted from the NHLS central data warehouse. Patients were considered exposed to HCV if they were positive for anti-HCV antibody. Patients positive with HCV viral load test were regarded as viraemia with active infection. Demographic analysis was based on age, gender, province, district or sub-district. HCV genotyping data were analysed to describe genotype circulation in South Africa. Of 10 138 patients tested for HCV exposure, 28% (2 917/10 138) were shown to be anti-HCV positive. Overall prevalence for South Africa was 5/100 000 population for those seeking care in the public sector in 2017. Gauteng Province had the highest prevalence at 11/100 000 population, with other provinces ranging from 2 to 4/100 000 population, likely reflecting referral patterns to tertiary healthcare facilities in Gauteng Province. Peak age distribution in males was 25-29 years and in females 30-34 years. Genotypes 1 (34%) and 5 (29%) were commonly detected in South Africa in 2017. It is concluded that HCV testing data from public health sector facilities can be used to monitor the prevalence of HCV in South Africa. Monitoring HCV data can be used to improve screening and treatment guidelines in support of the target of viral hepatitis elimination by 2030.

Introduction

Hepatitis C virus (HCV) causes acute and chronic hepatitis, ranging in severity from a mild illness lasting a few weeks to a serious, lifelong illness. Acute HCV infection is usually asymptomatic and is only rarely associated with life-threatening disease. About 15-45% of infected persons spontaneously clear the virus within 6 months of infection without any treatment. However, 60-80% of infected people will develop chronic HCV infection, of which 15-30% have the risk of developing liver cirrhosis within 20 years.[1] The use of unsafe healthcare procedures and drug injection with non-sterile needles were the leading causes of new HCV infections, accounting for approximately 1.75 million new infections in 2015. Globally, 71 million people have chronic hepatitis C, of which 2.3 million persons are co-infected with HIV.[2]

The prevalence of HCV is unknown in South Africa, with estimates of 0.1% in the general population and 0.03% in blood donors.[3,4] HCV prevalence information in high-risk groups is also limited in South Africa. High-risk groups for HCV infection include intravenous drug users, men having sex with men (MSM), HIV-infected persons, patients on haemodialysis, patients with a history of blood transfusions or organ transplantation, health care workers after needlestick injuries, and children born to HCV-infected mothers. HCV prevalence in HIV co-infected persons is low in South Africa.[5] From a study in Cape Town, HCV prevalence in MSM showed a high prevalence of 27% of whom 37% were co-infected with HIV.[6] This is pertinent because high HCV prevalence in high-risk groups may have an impact on transmission of the disease and planning for other prevention and treatment strategies.

The 67th World Health Assembly of the World Health Organization (WHO) recognized viral hepatitis as a public health threat and targeted elimination by 2030.[7] One of the action plans for the WHO African Region (2016-2020) focuses on setting up strong and reliable information systems to estimate the prevalence of HCV.[8] The WHO guideline 2017[9] provides an algorithm for screening using serological tests, in which a positive HCV-antibody result indicates a current or past infection. In order to confirm a current infection, a nucleic acid test (NAT) for the detection of HCV ribonucleic acid (RNA) should be performed directly following a positive HCV serological test to establish active infection (viraemia).

The aim of this project was to extract data from the National Health Laboratory Service (NHLS) Central Data Warehouse (CDW) for 2017 to determine the number of patients with hepatitis C antibody (seroprevalence), the number of patients with viraemia in public health facilities and the demographic distribution of HCV exposure and infection. These data represent HCV laboratory testing performed in all NHLS laboratories countrywide.

Methods

HCV data extracted from the NHLS CDW was de-duplicated to ensure that each patient was counted only once. De-duplication utilised a matching system that included name, surname, gender and date of birth followed by the assignation of a unique identifier. Those that did not match were further validated by checking the hospital identifier. Data for patients managed clinically in more than one health facility may have been missed due to lack of a unique patient identifier.

Patients were considered exposed to HCV if they were positive for anti-HCV antibody. Patients positive for HCV viral load and/or genotype were regarded as having active infection. Data analysis was performed on anti-HCV tests and HCV viral load test using Stata 14 and Microsoft Excel. Demographic analysis was based on age, gender, province, district or sub-district. HCV genotyping data were analysed to describe genotype circulation in South Africa.

Results

HCV antibody testing

A total of 10 401 patients was tested for HCV antibody or viral load, of which 10 138 were tested by HCV serology and 744 had an HCV nucleic test (Figure 1). The hepatitis C seropositivity rate amongst samples tested was 28% (2 917/10 401). Eighty-four percent (2 462/2 917) of the patients who tested positive by HCV serology were not followed up with a HCV viral load or any other nucleic acid test for confirmation.

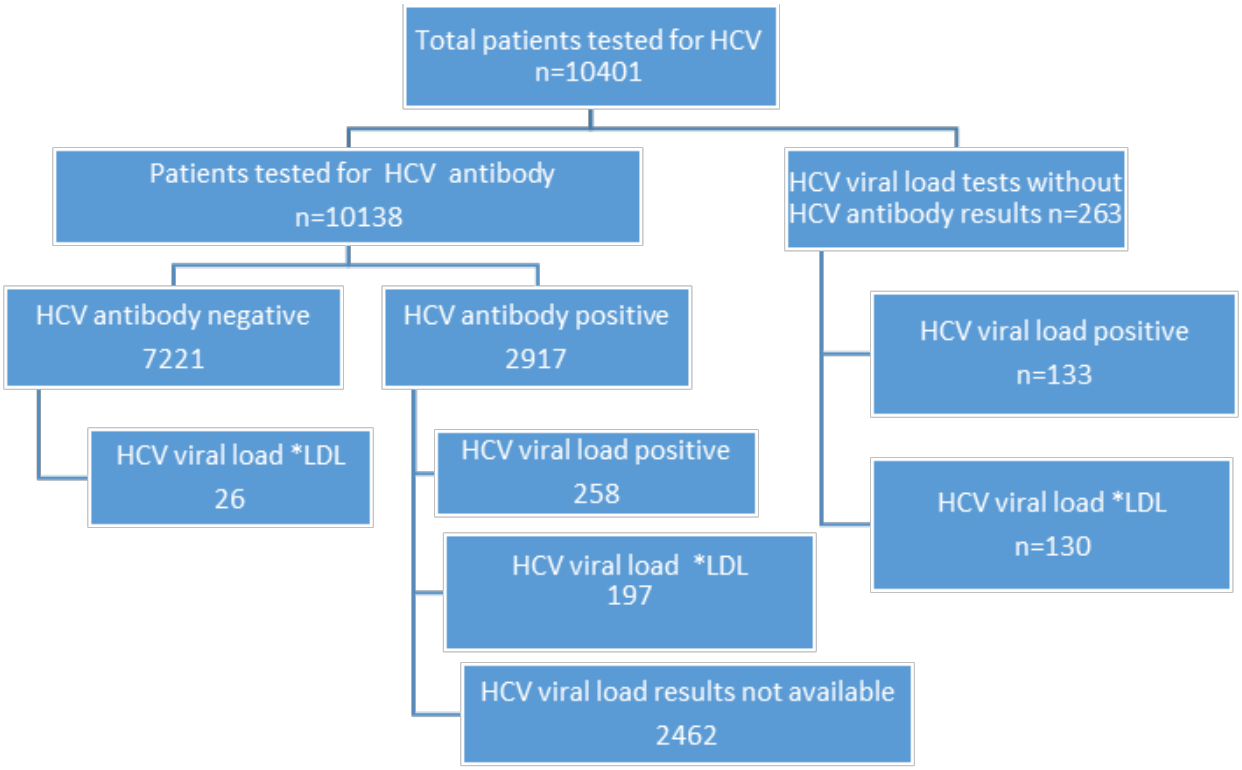

Figure 1: Patients tested for hepatitis C virus by test method from the public health sector in South Africa, 2017. *LDL = lower than detectable limit.

Gauteng Province showed the highest number of patients that tested positive by HCV serology and HCV viral load, accounting for 51% and 58% prevalence respectively (Table 1). HCV antibody prevalence in South Africa for 2017 was 5/100 000 population. Gauteng Province had the highest HCV seroprevalence with 11/100 000 population compared to other provinces that ranged from 2-4 per 100 000 population (Table 2). Information on gender was available on 99% (2 896/2 917) of HCV seropositive patients of whom 65% (1 880/2 896) were males. For HCV antibody-positive males, the most predominant age groups were 20-44 years, and for females, 30-34 years.

Table 1: Provincial distribution of hepatitis C seropositive and viraemic patients in South Africa, 2017.

Province	Hepatitis C Antibody		Hepatitis C Viral Load	
	HCV antibody positive (Number)	HCV antibody positive (Percentage)	HCV viral load test positive (Number)	HCV viral load test positive (Percentage)
Eastern Cape	265	9	33	8
Free State	80	3	5	1
Gauteng	1497	51	230	58
KwaZulu-Natal	346	12	25	6
Limpopo	232	8	6	2
Mpumalanga	149	5	2	1
North West	125	4	10	3
Northern Cape	34	1	1	0
Western Cape	189	6	82	21
Total	**2 917**	**100**	**394**	**100**

Table 2: Hepatitis C virus (HCV) seroprevalence by province, South Africa, 2017.

Province	Population	Anti-HCV positive cases	Anti-HCV prevalence Per 100 000 population
Eastern Cape	6,773,279	265	4
Free State	2,765,817	80	3
Gauteng	13,820,216	1,497	11
KwaZulu-Natal	10,924,776	346	3
Limpopo	5,789,937	232	4
Mpumalanga	4,344,146	149	3
North West	3,809,369	125	3
Northern Cape	1,202,802	34	3
Western Cape	6,478,870	189	3
South Africa	**55,909,212**	**2,917**	**5**

Hepatitis viral load testing

Sixteen percent (455/2 917) of the patients who tested positive by HCV serology had a viral load test. Of the 747 patients tested for viral load, 53% (394) were positive. Males accounted for 63% (251/394) of viraemic patients, showing two age group peaks at 20-39 and 65-69 years. For viraemic females, the peak age group was 55-74 years (Figure 2).

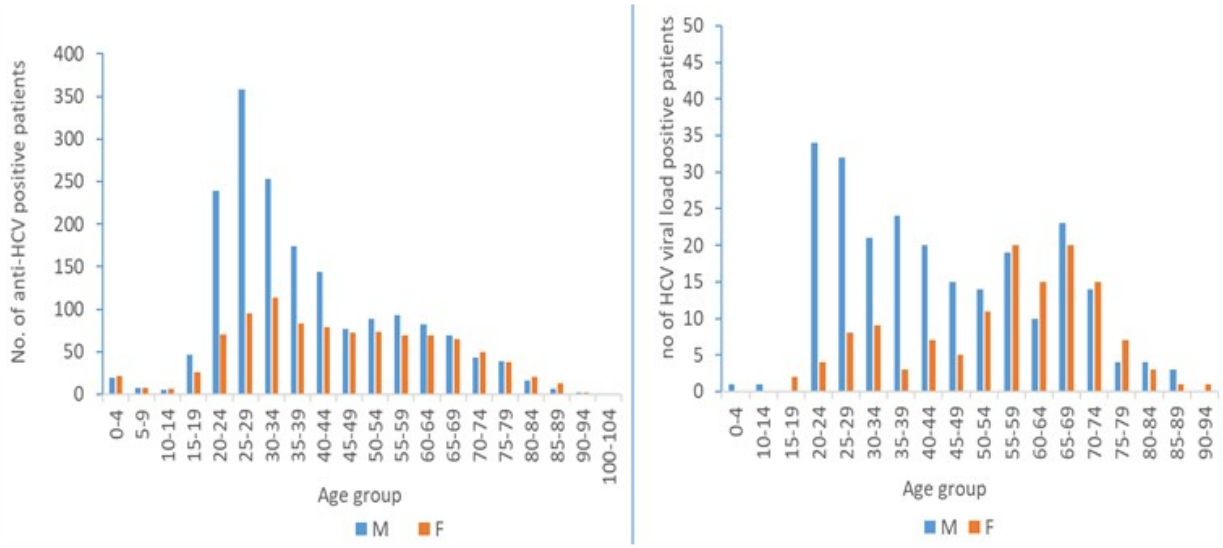

Figure 2: Age and gender of hepatitis C virus (HCV) antibody-positive (N=2738) and HCV viral load (N=394) patients in South Africa, 2017. The left block shows anti-HCV-positive patients and the right block shows HCV viraemic patients.

HCV genotypes

Of the 747 viraemic patients, 160 had an HCV genotype test. Circulating HCV genotypes were identified from six of South Africa's nine provinces. There were no genotype data information from Limpopo, Mpumalanga and Northern Cape provinces. HCV genotypes 1-5 were found to be circulating. Genotypes 1 (34%) and 5a (29%) were common (Figure 3). Genotype 2 was detected in the North West and Western Cape provinces. The common subtypes were genotype 1a (34%), 1b (13%) and 3a (10%) (Table 3).

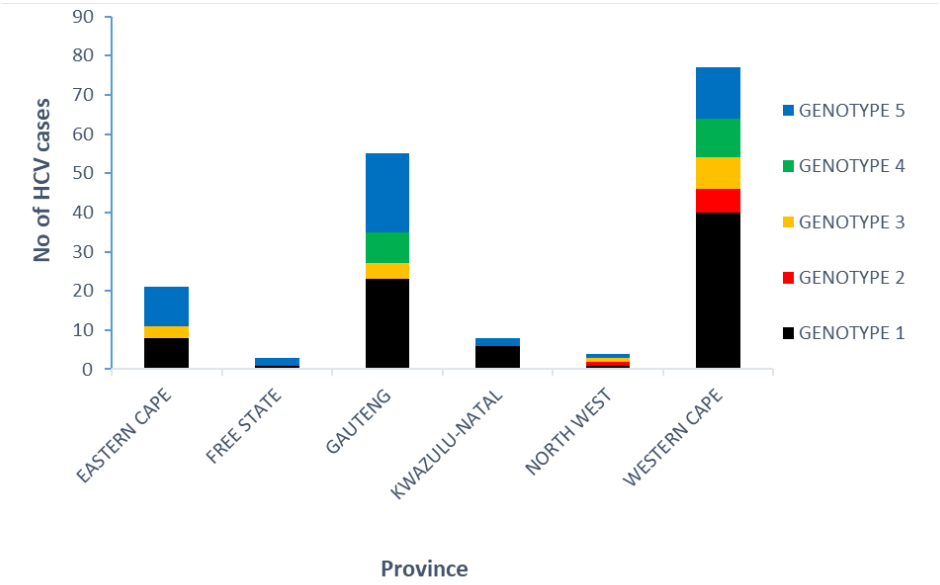

Figure 3: Hepatitis C virus (HCV) genotypes from diagnostic tests by province, South Africa, 2017. n=168 HCV cases.

Table 3: Hepatitis C virus (HCV) sub-genotypes detected by province, South Africa, 2017. n=168.

HCV genotype	HCV sub genotyping	Eastern Cape province	Free State province	Gauteng province	Kwazulu-Natal province	North West province	Western Cape province	Sub genotype Total	Sub genotype percentage	HCV genotype Total
1	genotype 1a	3	1	18	2	0	33	**57**	34%	**79**
	genotype 1b	5	0	5	4	1	7	**22**	13%	
2	genotype 2 (no sub genotype ascribed)	0	0	0	0	1	2	**3**	2%	**23**
	genotype 2a/c	0	0	0	0	0	2	**2**	1%	
	genotype 2b	0	0	0	0	0	2	**2**	1%	
3	genotype 3a	3	0	4	0	1	8	**16**	10%	**16**
4	genotype 4 (no sub genotype ascribed)	0	0	8	0	0	5	**13**	8%	**18**
	genotype 4a	0	0	0	0	0	1	**1**	1%	
	genotype 4b	0	0	0	0	0	1	**1**	1%	
	genotype 4c/d	0	0	0	0	0	3	**3**	2%	
5	genotype 5a	10	2	20	2	1	13	**48**	29%	**48**

Discussion

The NHLS laboratories, which serve approximately 80% of the South African population, were a useful source for national hepatitis C data. The study showed an overall HCV seroprevalence rate for 2017 of 5/100 000 persons.

Hepatitis C antibody tests do not discriminate between IgM or IgG presence. It is therefore difficult to conclude from an antibody result alone whether an individual is actively infected with the virus. A confirmatory nucleic acid test is necessary to indicate current infection. NHLS laboratory data shows that only 8% (258/2917) of anti-HCV positive test results have an active infection confirmed by a HCV viral load test. This suggests that the testing algorithm to confirm an HCV antibody-positive case was seldom followed by a confirmatory nucleic acid test. There are several factors that may affect this testing pattern. The study interrogated data from 01 January 2017 to 31 December 2017 - it is possible that antibody tests were done in previous years and viral load performed in 2017. The testing algorithm for hepatitis C is not widely understood, the viral load test is expensive and there is no public treatment programme for HCV in South Africa.

The number of patients having a viral load test was high in Western Cape (45%) and Gauteng (21%) provinces, where there are established liver clinics to manage the disease.[9] The heterogeneous circulation of HCV genotypes 1-5 in South Africa during 2017 corroborates data from earlier studies.[10] In this study, sub-genotypes 1a and 5a were predominant. A recent study on key populations found that genotypes 1a and 3a were prevalent among people who inject/use drugs. Data concerning circulating genotypes can assist in the planning of HCV therapeutic programmes.

It is concluded that the NHLS Central Data Warehouse can be used for surveillance purposes to understand the prevalence and epidemiology of hepatitis C in South Africa. This information can assist in the development of guidelines for prevention, screening and treatment.

Acknowledgments

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EPIDEMIOLOGY OF RESPIRATORY PATHOGENS FROM INFLUENZA-LIKE ILLNESS AND PNEUMONIA SURVEILLANCE PROGRAMMES, SOUTH AFRICA, 2018

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Executive summary

Syndromic respiratory illness surveillance programmes coordinated by the National Institute for Communicable Diseases include pneumonia surveillance, influenza-like illness (ILI) (2 programmes-systematic ILI at public health clinics and the Viral Watch programme) and the respiratory morbidity surveillance system. South Africa's 2018 influenza season started in week 18 and was predominated initially by influenza A(H1N1)pdm09 with circulation of influenza B towards the end of the season (week 40). There were 20 sporadic cases of A(H3N2). The overall vaccine effectiveness (VE), adjusted for age and seasonality, was 57% (95% CI 19% to 77%) against influenza A(H1N1)pdm09 and 14% (95% CI -120 % to 67%) against influenza B. The respiratory syncytial virus (RSV) season preceded the influenza season, starting in week 7. There was no obvious seasonality identified for *Bordetella pertussis.* However, an increase in pertussis cases was noted among patients enrolled in pneumonia surveillance from July onwards. Among ILI cases, the commonest pathogen identified in individuals aged <15 years was influenza (17%; 73/428) and RSV (10%; 42/428) followed by *B. pertussis* (3%; 11/428). Among individuals aged ≥15 years influenza (10%) was also most commonly detected followed by RSV (3%; 7/292) and *B. pertussis* (2%; 5/292%). Among individuals enrolled as part of pneumonia surveillance aged <5 years, the most common pathogen was RSV (27%; 792/2901) followed by influenza (7%; 206/2901) and *B. pertussis* (3%; 81/2901). Among individuals aged ≥15 years, influenza (6%; 103/1729) was most common, followed by RSV (2%; 28/1729) and *B. pertussis* (1%; 17/1729). Overall in-hospital case fatality ratio among individuals enrolled as part of pneumonia surveillance was 3% (153/4627).

Introduction

The Centre for Respiratory Diseases and Meningitis (CRDM) of the National Institute for Communicable Diseases (NICD) coordinates the following syndromic respiratory illness programmes: pneumonia surveillance, influenza-like illness (ILI) (2 programmes: systematic ILI at public health clinics and the Viral Watch programme, private general practitioners) and the respiratory morbidity surveillance system. This report describes the findings from these programmes for the year 2018 for the following core respiratory pathogens: influenza virus, respiratory syncytial virus (RSV) and *Bordetella pertussis* (pertussis).

Methods

A brief summary of each surveillance programme is included below. Respiratory specimens from all sites were tested for three core pathogens: influenza virus, RSV and *B. pertussis*.

Description of the surveillance programmes

The primary objectives of the pneumonia and systematic ILI surveillance programmes are to describe the burden and aetiology of inpatient severe respiratory illness and outpatient ILI, respectively, in HIV-infected and HIV-uninfected individuals of all ages at selected sentinel sites in South Africa. In addition, specific objectives include describing the timing and severity of the influenza and RSV seasons, describing the epidemiology of *B. pertussis,* characterising circulating influenza virus strains to guide decisions around Southern Hemisphere influenza vaccine composition, annual estimates of influenza vaccine effectiveness and detecting outbreaks caused by the pathogens included as part of surveillance.

Pneumonia surveillance is an active, prospective, hospital-based surveillance programme for severe respiratory illness. Patients admitted at the surveillance sites meeting the standardized clinical case definition of severe respiratory illness (SRI) are prospectively enrolled (Table1). For the purpose of comparison SRI is further divided into severe acute respiratory illness (SARI), in those with symptom duration of ≤10 days, and severe chronic respiratory illness (SCRI) in those with symptom duration of >10 days. Dedicated staff screened and enrolled patients from Monday to Friday each week. Clinical and epidemiological data were collected using standardized questionnaires. Information on in-hospital management and outcome were collected. All completed forms were shipped to NICD for data entry. Samples collected and tested varied by site and case definition (Table 2). Combined

nasopharyngeal (NPS) and oropharyngeal swabs (OPS) were collected at all sites that conduct core surveillance. At the three enhanced sites, nasopharyngeal aspirates were collected instead of combined NPS and OPS from children aged <1 year. Sputum samples (induced or expectorated) were collected at enhanced sites (Table 2).

The systematic ILI surveillance programme was established in 2012. It is currently active at public health clinics serviced by Edendale Hospital (EDH) and Klerksdorp-Tshepong Hospital Complex (KTHC). Patients presenting at these sites meeting the ILI and suspected pertussis case definitions (Table 1) were enrolled prospectively. Dedicated staff screened and enrolled patients for systematic ILI surveillance from Monday to Friday. Clinical and epidemiological data were collected using standardized questionnaires and nasopharyngeal samples were collected for testing (Table 2).

The Viral Watch sentinel surveillance programme was started in 1984 to monitor influenza activity. The programme is mainly composed of general practitioners who voluntarily submit NPS or OPS from patients who meet the ILI definition (Table1). Data from this programme have been used since 2005 to estimate the effectiveness of trivalent seasonal influenza vaccine (TIV) against influenza-associated medically-attended acute respiratory illness using a test-negative case control study design.[1,2] For this report, patients with ILI presenting to the sentinel surveillance sites during the 2018 influenza season were used to calculate vaccine effectiveness (VE). During 2018, 89 practitioners registered across South Africa submitted specimens throughout the year.

The start of the RSV seasons is defined as at least two consecutive weekly detection rates of ≥10%. The season is considered to have ended when the detection rate of RSV drops below 10% for two consecutive weeks. The influenza season was declared by applying the Moving Epidemic Method (MEM) method by which thresholds are calculated through a sequential analysis using the R Language (available from: http://CRAN.R-project.org/web/package=mem). This method is designed to calculate the duration, start and end of an 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 are categorized as follows: Below seasonal threshold, low activity, moderate activity, high activity and 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.

The respiratory morbidity surveillance system tracks trends in the number of pneumonia and influenza hospitalizations using anonymised data from a private hospital group.

Table 1: Case definitions by age group and surveillance site/programme for the clinical syndromes included in the influenza-like illness (ILI) and pneumonia surveillance programmes, South Africa, 2018.

Case definition	Criteria	Surveillance site/programme
Influenza-like illness (ILI)	**Patients of all ages** Acute fever of ≥38°C and/or self-reported fever within the last 10 days AND cough	Viral Watch programme and public health clinics for systematic ILI surveillance: Jouberton and Edendale Gateway
Severe respiratory illness (SRI)	**2 days - <3 months** Any child hospitalised with diagnosis of suspected sepsis or physician diagnosed LRTI irrespective of signs and symptoms.	EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, RCH/MPH Pneumonia surveillance
	3 months - <5 years Any child ≥3 months to <5 years hospitalised with physician-diagnosed LRTI including bronchiolitis, pneumonia, bronchitis and pleural effusion	EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, RCH/MPH Pneumonia surveillance
	≥5 years Any person hospitalised with a respiratory infection with fever (≥38ºC) or history of fever AND cough	EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, RCH/MPH Pneumonia surveillance
Suspected pertussis	Any patient presenting with cough illness of any duration and at least one of the following: paroxysms of cough, post-tussive vomiting, inspiratory whoop **OR** Infants <1 year with apnoea, with or without cyanosis.	Public health clinics for systematic ILI surveillance: Jouberton and Edendale Gateway EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, RCH/MPH Pneumonia surveillance

EDH=Edendale Hospital (KwaZulu-Natal), KTHC=Klerksdorp-Tshepong Hospital Complex (North-West Province), RMMCH/HJH= Rahima Moosa Mother and Child Hospital/Helen Joseph Hospital (Gauteng), RCH/MPH=Red Cross War Memorial Children's Hospital/ Mitchell's Plain Hospital (Western Cape), LRTI= Lower respiratory tract infection

Table 2: Pathogens tested for by clinical syndrome/programme, surveillance site, type of specimen collected and tests conducted, influenza-like illness (ILI) and pneumonia surveillance programmes, South Africa, 2018.

Pathogen	Programme (syndrome)	Surveillance site	Specimens collected	Tests conducted
Influenza and RSV	Viral Watch (ILI)	All Viral Watch sites in 8 provinces	Nasopharyngeal (NP) and oropharyngeal (OP) flocked swabs in universal transport medium (UTM)	Multiplex real-time reverse transcription polymerase chain reaction (PCR)
	Systematic ILI	Edendale Gateway Clinic, Jouberton Clinic	NP and OP flocked swabs from individuals aged ≥1years and NPA from children aged <1years in UTM	
	Pneumonia surveillance (SRI)	RMMCH/HJH, RCH/MPH	NP and OP flocked swabs (all age groups) in UTM	
		EDH, KTHC and Matikwana/ Mapulaneng	NP and OP flocked swabs from individuals aged ≥1years and NPA from children aged <1years in UTM	
Bordetella pertussis	Systematic ILI	Edendale Gateway Clinic and Jouberton Clinic	NP and OP flocked swabs in UTM	Multiplex real time PCR
			NP in Regan Lowe medium	Culture
	Pneumonia surveillance (SRI)	RMMCH/HJH, RCH/MPH	NP and OP flocked swabs in UTM	Multiplex real time PCR
			NP in Regan Lowe medium	Culture
		EDH, KTHC and Matikwana/ Mapulaneng	NP and OP flocked swabs from individuals aged ≥1years and NPA from children aged <1years in UTM	Multiplex real time PCR
			Sputum (induced/expectorated)	Culture
			NPS in Regan Lowe medium	

ILI= influenza-like illness, SRI=severe respiratory illness, EDH= Edendale Hospital, KTHC=Klerksdorp-Tshepong Hospital Complex, RMMCH/HJH= Rahima Moosa Mother and Child Hospital/Helen Joseph Hospital, RCH/MPH=Red Cross War Memorial Children's Hospital/Mitchell's Plain. NPA= nasopharyngeal aspirate, NPS=nasopharyngeal swab

Sample collection and laboratory testing for pneumonia and ILI surveillance

Upper respiratory tract samples (NP/OP and NPA) were collected and placed into universal transport medium. Upper respiratory samples and blood were stored at 4°C at the local site laboratory, and were transported to NICD on ice within 72 hours of collection. Sputum samples were stored separately at -20˚C at the local site laboratory before being transported to NICD on dry ice on a weekly basis.

Detection of RSV and influenza

A commercial multiplex real-time reverse transcriptase PCR assay (Fast-Track Diagnostics, Luxembourg) was used for detection of influenza A virus, influenza B virus and RSV. Influenza A and B positive specimens were subtyped using US Centers for Diseases Control and Prevention (CDC) real-time RT PCR protocol and reagents (https://www.influenzareagentresource.org/).

Detection of Bordetella pertussis

Induced/expectorated sputum and nasopharyngeal samples were tested for *B. pertussis.* A specimen was considered positive for pertussis if it tested positive (on at least 2 out of 3 repeats) for *IS481* and/or *ptxS*1 genes with a Ct<45. A positive case of *B. pertussis* is defined as having either or both specimens testing positive by real-time PCR.

Data management and analysis

Data management is centralised at the NICD where laboratory, clinical and demographic data from enrolled patients are recorded on a Microsoft Access database with double data entry. Data included in this report are preliminary and may change as data cleaning is finalised.

Results

Pneumonia and systematic ILI surveillance

In 2018, 5386 patients were enrolled into the systematic ILI and pneumonia surveillance programmes. Nasopharyngeal (NP) and oropharyngeal (OP) swabs were collected from 5350 (99%) participants. Of these 13% (720) were enrolled in the ILI programme and 87% (4930) were hospitalized individuals (Figure 1). Those aged <15 years made up the majority of both ILI and SRI cases (60% 428/720 and 63% 2901/4930 respectively). The majority of individuals hospitalized with SRI aged <15 years had acute illness (94%; 2715/2901), while among individuals aged ≥15 years 50% (861/1729) had acute illness. The HIV prevalence varied by age group and case definition (Figure 2). HIV prevalence was highest in cases with SCRI (55%; 553/986) and similar in ILI and SARI (17%;

117/704 and 16%; 542/3353) cases respectively. HIV prevalence was highest in the 25-44 year age group for SARI and SCRI cases (76%; 285/375 and 83%;345/414 respectively) but highest in the 45-64 year age group (54%;43/79) year age group for ILI.

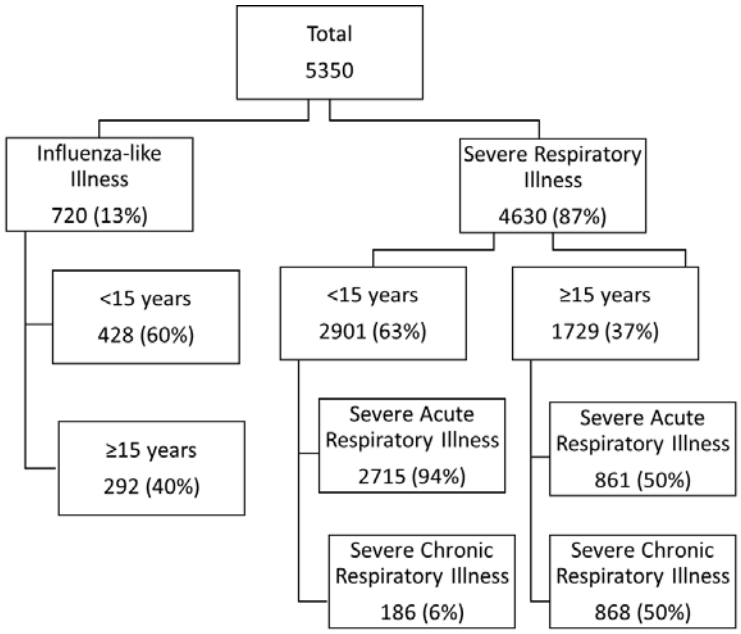

Figure 1: Individuals who had a nasopharyngeal (NP) sample collected by case definition in the systematic influenza-like illness (ILI) and pneumonia surveillance programmes (SRI), South Africa, 2018.

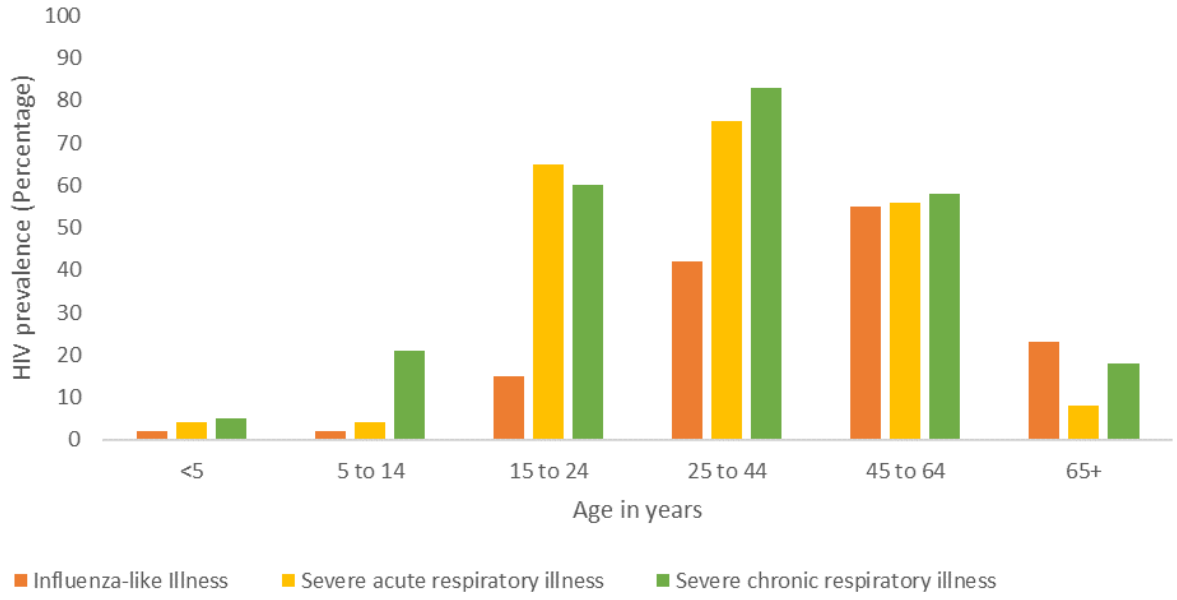

Figure 2: HIV prevalence by age group for individuals meeting case definitions of influenza-like illness (ILI=111/679, 16%), severe acute respiratory illness (SARI=534/3280, 16%) and severe chronic respiratory illness (SCRI=551/1004, 54%), among patients enrolled in pneumonia surveillance and influenza-like illness surveillance, 2018.

Influenza, RSV and pertussis in individuals aged <15 years enrolled into the systematic ILI programme

Nearly a third of the 428 individuals enrolled into the ILI systematic surveillance were aged 2-4 years (28%; 118/428). A similar proportion of those who tested positive for influenza were in the 2-4 year age group (44%; 32/73). This was different for those who tested positive for RSV, where 29% (12/42) were in the 6-11 month age group. Of the 11 pertussis cases 36% (4/11) were in very young infants aged 0-2 months. Vaccine coverage (vaccine up to date for age) was high with 90% of enrolled individuals having pneumococcal conjugate vaccine (PCV) up to date and 91% having *Haemophilus influenza* type B (HIB) vaccine up to date. Vaccine coverage was lower for those who tested positive for pertussis with 62% and 75% coverage for PCV and HIB respectively (Table 3a). A similar proportion of cases was enrolled across the sites, with the highest proportion of pertussis cases presenting at the Klerksdorp site (82%; 9/11).

Influenza, RSV and pertussis in individuals aged ≥15 years enrolled into the systematic ILI programme

Of individuals aged ≥15 years who met the case definition for ILI, 48% (140/292) were in the age group 25-44 years. The highest proportion of influenza and RSV cases were in the same age group, 25-44 years (influenza 50%; 14/28, RSV 63%; 5/8). Of the pertussis cases 2/5 (40%) were in the age groups 15-24 and 24-44 years respectively. Four of five pertussis cases were from Klerksdorp (Table 3b).

Table 3a: Demographic and clinical characteristics of patients aged <5 years enrolled into the systematic influenza-like illness surveillance programmes, South Africa, 2018.

	Overall n/N (%)	Influenza positive n/N (%)	RSV positive n/N (%)	*Bordetella pertussis* positive n/N (%)
Age group				
0 – 2 months	36/428 (8)	1/73 (1)	7/42 (17)	4/11 (36)
3 – 5 months	40/428 (9)	2/73 (3)	5/42 (12)	1/11 (9)
6 – 11 months	69/428 (16)	6/73 (8)	12/42 (29)	1/11 (9)
12 –23 months	61/428 (14)	8/73 (11)	2/42 (5)	0/11 (0)
2-4 years	118/428 (28)	32/73 (44)	11/42 (26)	2/11 (18)
5–14 years	105/428 (25)	24/73 (33)	5/42 (12)	3/11 (27)
Sex (Female)	216/428 (50)	34/73 (47)	21/42 (50)	6/11 (55)
Race (Black)	428/428 (100)	73/73 (100)	42/42 (100)	11/11 (100)
Site				
Edendale Gateway Clinic	202/428 (47)	39/73 (53)	20/42 (48)	2/11 (18)
Jouberton Clinic	229/428 (53)	34/73 (47)	22/42 (52)	9 (82)
HIV exposure (< 1 year)				
HIV-unexposed uninfected	89/140 (64)	3/8 (37)	12/24 (50)	3/6 (50)
HIV-exposed uninfected	48/140 (32)	5/8 (63)	12/24 (50)	3/6(50)
HIV infected	3/140 (2)	0	0	0
HIV-infected	6/424 (1)	1/72 (1)	0	0
Weight for age <–2 z scores	24/327 (7)	4/49 (8)	2/37 (5)	1/8 (13)
Premature	15/326 (5)	1/49 (2)	1/37 (3)	0/8 (0)
Other underlying illness[1]	1 (<1)	0	0	0
Up to date vaccination for age for PCV	275/306 (90)	41/46 (89)	31/35 (89)	5/8 (63)
Up to date vaccination for age for HIB	283/310 (91)	45/46 (98)	32/36 (89)	6/8 (75)

PCV= Pneumococcal conjugate vaccine HIB=*Haemophilus influenza* B

[1]Underlying conditions included any of the following: Asthma, other chronic lung disease, chronic heart disease (valvular heart disease, coronary artery disease, or heart failure excluding hypertension), seizures, liver disease (cirrhosis or liver failure), renal disease (nephrotic syndrome, chronic renal failure), immunocompromising conditions excluding HIV infection (organ transplant, immunosuppressive therapy, immunoglobulin deficiency, malignancy), neurological disease (cerebrovascular accident, spinal cord injury, seizures, neuromuscular conditions).

Table 3b: Demographic and clinical characteristics of patients aged ≥15 years enrolled into the systematic influenza like illness surveillance programme, South Africa, 2018.

	Overall n/N (%)	Influenza positive n/N (%)	RSV positive n/N (%)	*Bordetella pertussis* n/N (%)
Age group (years)				
15-24	60/292 (21)	10/28 (36)	1/8 (13)	2/5 (40)
25-44	139/292 (48)	14/28 (50)	5/8 (62)	2/5 (40)
45-64	79/292 (27)	3/28 (11)	2/8 (25)	1/5 (20)
≥65+	14/292 (5)	1/28 (4)	0	0
Sex (Female)	175/292 (60)	14/28 (50)	4/8 (50)	2/5 (40)
Race (Black)	292/292 (100)	28/28 (100)	8/8 (100)	5/5 (100)
Site				
Edendale Gateway Clinic	141/292 (48)	15/28 (54)	7/8 (88)	1/5 (20)
Jouberton Clinic	151/292 (52)	13/28 (46)	1/8 (13)	4/5 (80)
HIV-infected	111/279 (40)	13/27 (48)	4/8 (50)	3/5 (60)
Other underlying illness[1]	22/292 (8)	2/28 (7)	0/8 (0)	1/5 (20)

[1]Underlying conditions included any of the following: Asthma, other chronic lung disease, chronic heart disease (valvular heart disease, coronary artery disease, or heart failure excluding hypertension), seizures, liver disease (cirrhosis or liver failure), renal disease (nephrotic syndrome, chronic renal failure), immunocompromising conditions excluding HIV infection (organ transplant, immunosuppressive therapy, immunoglobulin deficiency, malignancy), neurological disease (cerebrovascular accident, spinal cord injury, seizures, neuromuscular conditions) or pregnancy.

Influenza, RSV and pertussis in individuals aged <15 years enrolled into the pneumonia surveillance programme

Of the 2901 individuals aged <15 years enrolled into the surveillance programme, 35% (1006/2901) were less than 3 months of age and 60% (1722/2901) were enrolled at the RCH/MPH sites. The majority presented with a symptom duration of less than 10 days (93%; 2696/2901) and spent less than 5 days in hospital (77%; 211/2901). The highest proportion of cases of RSV (42%; 333/792) and pertussis (68%; 55/81) were in very young infants (<3 months). The highest proportion of influenza cases were in the older infants (6-11 months 29%; 60/206). More than half of the pertussis cases were enrolled at the RCH/MPH sites (Table 4a). Overall 90% (275/306) of children were up to date for age for PCV and 91% (283/310) were up to date for age for HIB vaccine. However, vaccine

coverage in pertussis cases was lower, with only 75% (6/8) and 63% (5/8) of pertussis cases being up to date for age for PCV and HIB respectively.

Influenza, RSV and pertussis in individuals aged ≥15 years enrolled into the pneumonia surveillance programme

Of the 1729 individuals aged ≥ 15 years meeting the SRI case definition, the highest proportion were in the age group 25-44 years (49%;847/1729). Of these individuals, half had symptoms for ≤10 days (50%; 864/1729) and two thirds were HIV infected (65%; 1022/1606). The length of hospital stay was greater than in younger individuals (<15 years), with 64% (1078/1697) spending ≥5 days in hospital. In-hospital mortality was also higher than in the <15 year age group, with 7% (128/1729) dying in hospital. The HIV prevalence was highest in individuals who tested positive for pertussis (82%; 14/17) as compared to influenza (60%; 59/99) and RSV (71%; 20/28). Nearly half the pertussis cases were enrolled at the Klerksdorp site (47% 8/17) (Table 4b).

Table 4a: Demographic and clinical characteristics of patients aged <15 years enrolled into the pneumonia surveillance programme, South Africa, 2018.

	Overall n/N(%)	Influenza positive n/N(%)	RSV positive n/N(%)	*Bordetella pertussis* positive n/N(%)
Age group months				
0 – 2 months	1006/2901 (35)	17/206 (8)	333/792 (42)	55/81 (68)
3 – 5 months	443/2901 (15)	19/206 (9)	182/792 (23)	5/81 (6)
6 – 11 months	540/2901 (19)	60/206 (29)	152/792 (19)	9/81 (11)
12 –23 months	434/2901 (15)	47/206 (23)	82/792 (10)	2/81 (2)
2-4 years	362/2901 (12)	50/206 (24)	38/792 (5)	7/81 (9)
5 –14 years	116/2901 (4)	13/206 (6)	5/792 (1)	3/81 (4)
Sex (female)	1233/2901 (42)	88/206 (43)	336/792 (42)	48/81 (59)
Race (Black)	2050/2901 (71)	151/2901 (73)	551/792 (70)	55/81 (68)
Site				
Mapulaneng/Matikwana	164/2901 (6)	23/206 (11)	46/792 (6)	5/81 (6)
Edendale Hospital	326/2901 (11)	19/206 (1)	76/792 (10)	4/81 (5)
KTHC	211/2901 (7)	17/206 (8)	34/792 (4)	12/81 (15)
RMMCH/HJH	480/2901 (16)	34/206 (16)	156/792 (20)	12/81 (21)
RCH/MPH	1720/2901 (60)	113/206 (55)	480/792 (61)	43/81 (53)
Symptoms ≤10 days	2696/2901 (93)	21/206 (10)	28/792 (95)	68/81 (84)
HIV exposure (<1 year)				
HIV-unexposed uninfected	1412/1871 (75)	59/91 (65)	521/649 (50)	50/64 (78)
HIV-exposed uninfected	425/1871 (23)	31/91 (34)	126/649 (19)	14/64 (23)
HIV- infected	34/1871 (2)	1/91 (1)	2/649 (<1)	0/64 (0)
Weight for age <–2 z scores[1]	493/2794 (18)	32/192 (17)	98/786 (12)	13/78 (17)
Premature	539/2795 (19)	32/193 (17)	155/787 (20)	14/78 (18)
Other underlying illness[1]	40/2901 (1)	7/206 (3)	3/792 (<1)	1/81 (1)
Up to date vaccination for age for PCV	1940/2170 (89)	172/185 (93)	571/622 (92)	34/50 (68)
Up to date vaccination for age for HIB	1983/2671 (74)	177/188 (94)	577/766 (75)	36/72 (50)
Duration of hospitalization <5 days	2211/2875 (77)	165/201 (82)	597/790 (76)	54/80 (68)
ICU admission	72/2901 (2)	4/206 (2)	25/792 (3)	4/81 (5)
In-hospital mortality	25/2901 (1)	2/206 (1)	2/792 (<1)	2/81 (2)

RMMCH/HJH=Rahima Moosa Mother and Child Hospital/Helen Joseph Hospital, KTHC=Klerksdorp Tshepong Hospital Complex, EDH=Edendale Hospital, RCH/MPH =Red Cross Hospital/Mitchell's Plain Hospital PCV= Pneumococcal conjugate vaccine HIB=*Haemophilus influenza* B

[1]Underlying conditions included any of the following: Asthma, other chronic lung disease, chronic heart disease (valvular heart disease, coronary artery disease, or heart failure excluding hypertension), liver disease (cirrhosis or liver failure), renal disease (nephrotic syndrome, chronic renal failure), prematurity, malnutrition, seizures, immunocompromising conditions excluding HIV infection (organ transplant, immunosuppressive therapy, immunoglobulin deficiency, malignancy), neurological disease (cerebrovascular accident, spinal cord injury, seizures, neuromuscular conditions)

Table 4b: Demographic and clinical characteristics of patients aged ≥15 years enrolled into the pneumonia surveillance programme, South Africa, 2018.

	Overall n/N (%)	Influenza positive n/N (%)	RSV positive n/N (%)	*Bordetella pertussis* positive n/N (%)
Age group years				
15-24	134/1729 (8)	9/103 (9)	5/28 (18)	3/17 (18)
25-44	844/1729 (49)	45/103 (44)	10/28 (35)	10/17 (59)
45-64	545/1729 (32)	36/103 (35)	11/28 (39)	4/17 (24)
≥65	206/1729 (12)	13/103 (13)	2/28 (7)	0/17 (0)
Sex (female)	880/1729 (51)	60/103 (58)	17/28 (61)	13/17 (76)
Race (Black)	1531/1729 (89)	89/103 (86)	22/28 (79)	15/17 (88)
Site				
Mapulaneng/Matikwana	145/1729 (8)	19/103 (19)	0/28 (0)	0/17 (0)
Edendale Hospital	372/1729 (22)	19/103 (19)	6/28 (22)	4/17 (24)
KTHC	480/1729 (28)	21/103 (20)	9/28 (32)	8/17 (47)
HJH	542/1729 (32)	35/103 (34)	6/28 (21)	2/17 (12)
MPH	190/1729 (11)	9/103 (9)	7/28 (25)	3/17 (18)
Symptoms ≤10 days	864/1729 (50)	66/103 (64)	18/28 (64)	8/17 (47)
HIV-infected	1022/1606 (65)	59/99 (60)	20/28 (71)	14/17 (82)
Other underlying illness[1]	338/1732 (20)	30/103 (29)	5/28 (18)	5/17 (29)
Duration of hospitalization <5 days	619/1697 (36)	52/102 (51)	10/28 (36)	9/17 (53)
ICU admission	10/1726 (1)	2/102 (2)	0/28 (0)	0/17 (0)
In-hospital mortality	128/1729 (7)	6/103 (6)	5/28 (18)	1/17 (6)

HJH=/Helen Joseph Hospital, KTHC=Klerksdorp Tshepong Hospital Complex, EDH=Edendale Hospital, MPH = Mitchell's Plain Hospital.

[1]Underlying conditions included any of the following: Asthma, other chronic lung disease, chronic heart disease (valvular heart disease, coronary artery disease, or heart failure excluding hypertension), liver disease (cirrhosis or liver failure), renal disease (nephrotic syndrome, chronic renal failure), prematurity, malnutrition, seizures, immunocompromising conditions excluding HIV infection (organ transplant, immunosuppressive therapy, immunoglobulin deficiency, malignancy), neurological disease (cerebrovascular accident, spinal cord injury, seizures, neuromuscular conditions).

The 2018 influenza season

Viral Watch Programme

The influenza season started in week 18 (first week of May) when the detection rate for influenza in the Viral Watch Programme rose above the seasonal threshold. The season ended in week 41 (second week of October). The Viral Watch Programme received 1459 specimens, from which influenza was detected in 689 of them - 388 (56%) influenza A(H1N1)pdm09, 278 (40%) influenza B and 20 (3%) influenza A (H3N2). Three influenza A samples were not subtyped due to a low viral load in the specimen (Figure 3).

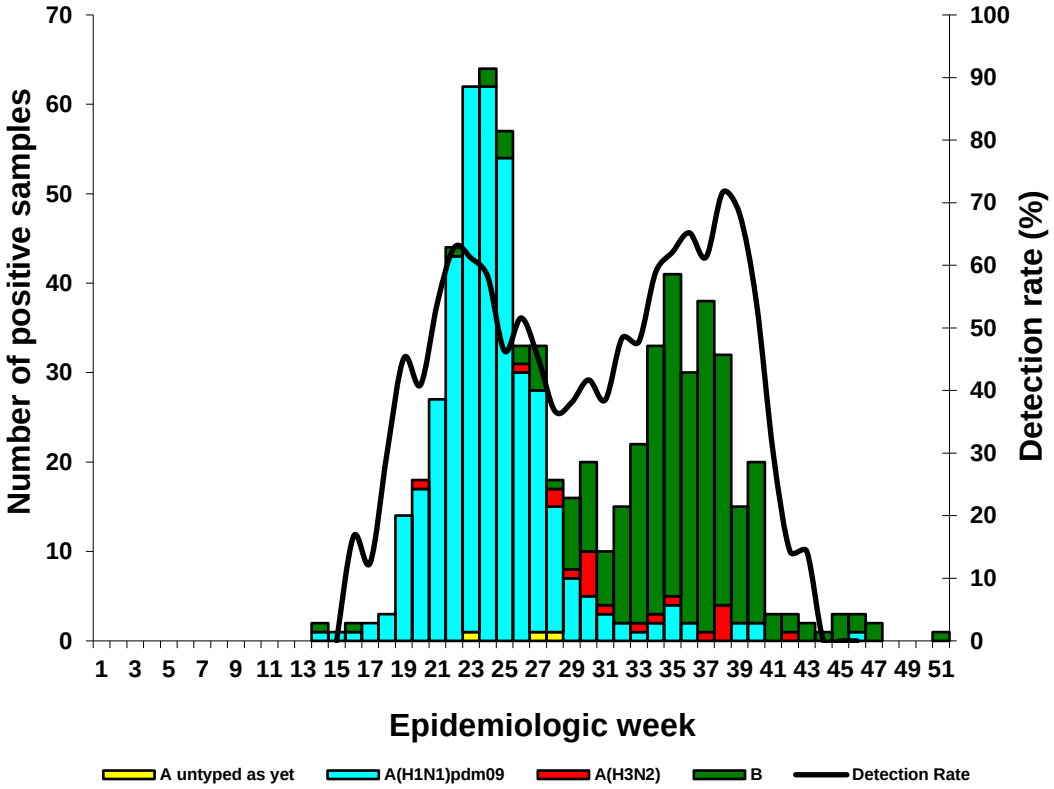

Figure 3: Numbers of samples and influenza detection rate by viral type, subtype and week for patients meeting the case definition of influenza-like illness (ILI), Viral Watch programme, South Africa, 2018.

The transmissibility of influenza was estimated by applying the MEM method to plot the 2018 Viral Watch detection rate against thresholds set by data collected from Viral Watch between 2009 and 2017 (Figure 4). For the 2018 influenza season, the transmissibility of influenza was mostly moderate. In the week of the highest detection rate for influenza B, the transmissibility crossed to the high range.

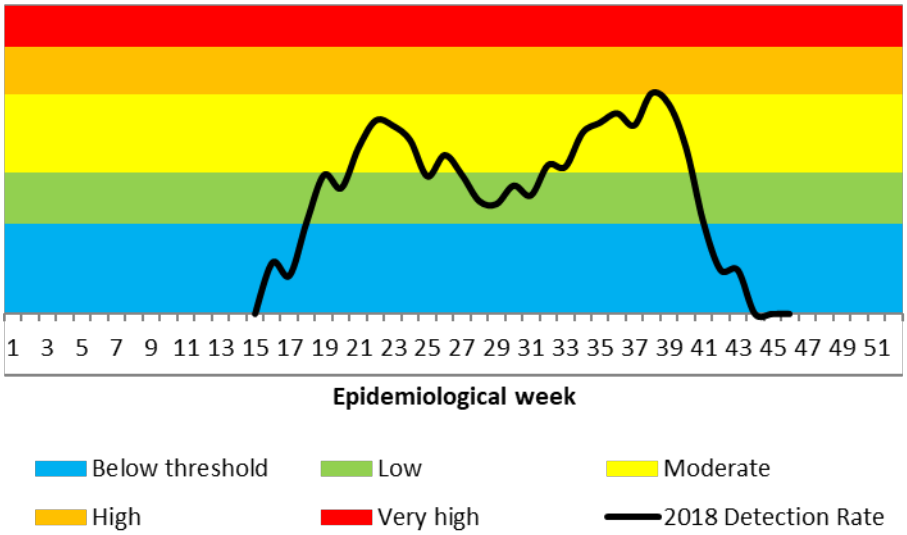

Figure 4: Viral Watch 2018 influenza transmissibility thresholds based on 2007-2017 data (excluding the pandemic year: 2009), South Africa, 2018.

Influenza season systematic ILI programme

In the systemic ILI programme, of the 720 specimens tested, 14% (101) were positive for influenza. Influenza A (H1N1)pdm09 accounted for 66% (n=67) of the samples and these were collected between week 15 and week 31. The remaining 33% (33) of specimens tested positive for influenza B and were collected between week 34 and week 40 (Figure 5).

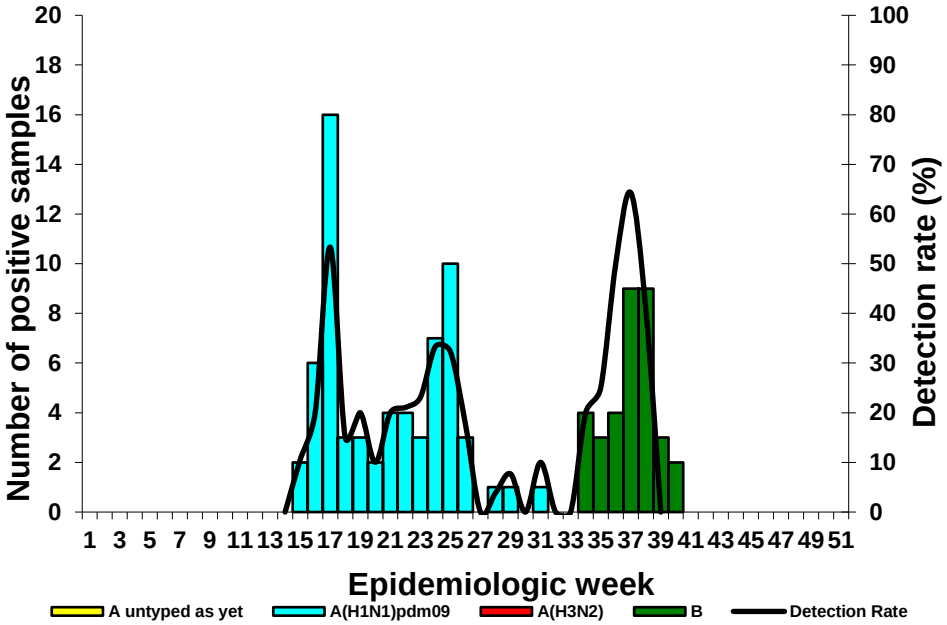

Figure 5: Influenza detection rate, by influenza type, subtype and week, in patients enrolled with influenza-like Illness (ILI) at the two primary healthcare clinics, South Africa, 2018.

The national syndromic pneumonia surveillance programme

In the pneumonia surveillance programme 309/4630 (7%) influenza cases were detected, most of which were influenza A (H1N1)pdm09 173/309 (56%). Influenza B accounted for 133/309 (43%) cases. A single influenza A (H3N2) was detected. Two influenza A were not subtyped due to low viral load. In the Viral Watch Programme the first part of the season was predominately influenza A(H1N1)pdm09 and the second part was predominately influenza B (Figure 6). The impact of the 2018 influenza season was moderate (Figure 7).

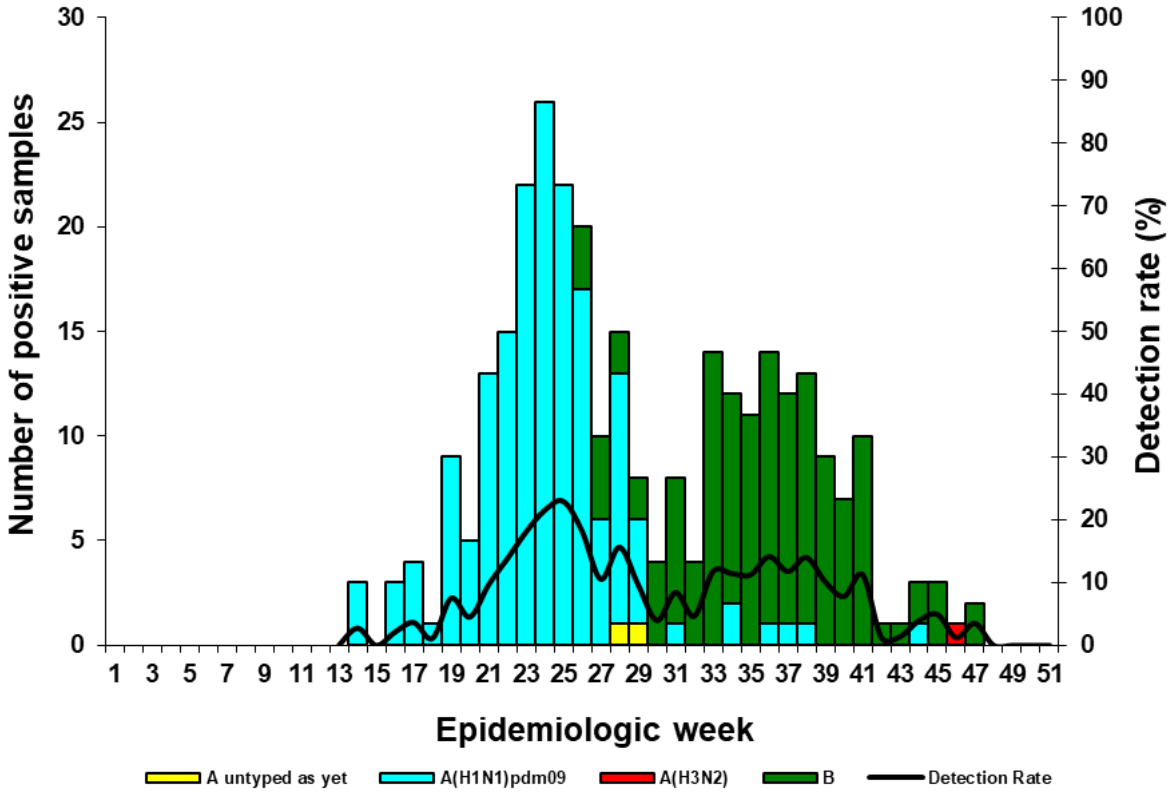

Figure 6: Numbers of samples positive for influenza and influenza detection rate, by type, subtype and week, in patients enrolled into the pneumonia surveillance programme and meeting the case definition of severe respiratory illness (SRI) in South Africa, 2018.

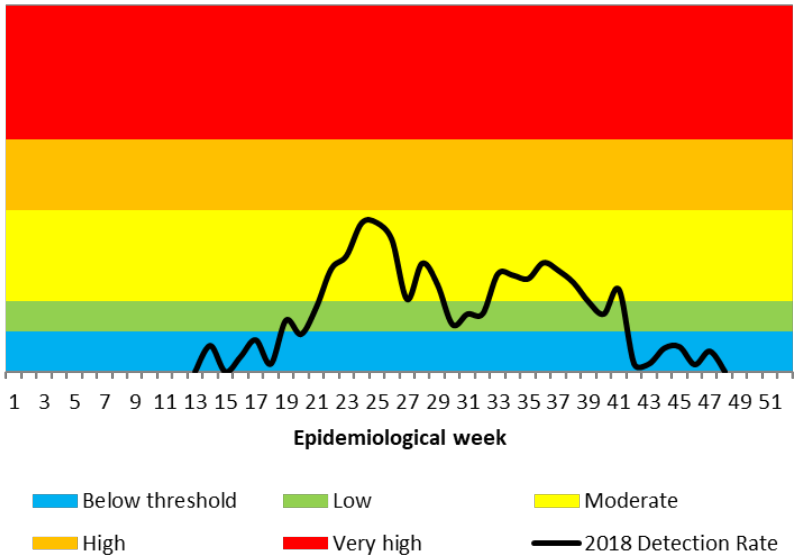

Figure 7: The impact of influenza based on the pneumonia surveillance programme influenza detection rate, South Africa, 2018. Thresholds are based on 2010 – 2017 data.

Respiratory syncytial virus

Systematic ILI programme

RSV circulation in the systematic ILI programme started in week 2 with the season threshold being reached by week 6. The overall detection rate was 7% (50/720), with a peak detection rate of 36% (3/8) in week 7. No positive samples were collected after week 25 (Figure 8).

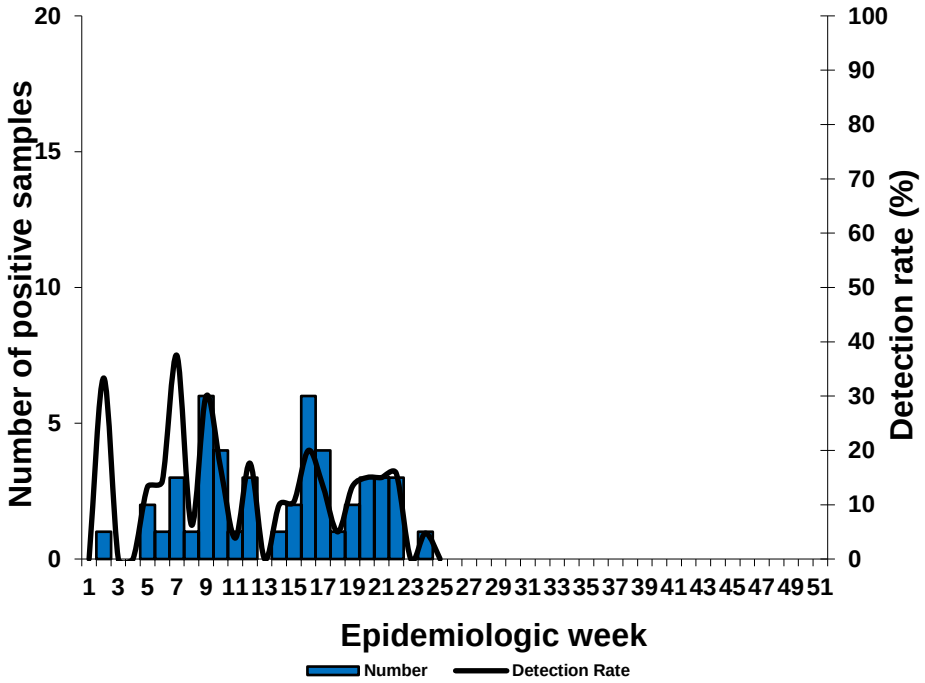

Figure 8: Detection rate of respiratory syncytial virus (RSV) by week in patients enrolled with influenza-like illness (ILI) at two primary health clinics, South Africa, 2018.

The pneumonia surveillance programme

RSV was detected from week one in the pneumonia surveillance programme. The overall detection rate was 18% (820/4630). The seasonal threshold was detected in week 7; the highest detection rate of 52% (51/98) was in week 18. The season ended in week 29 although RSV was detected throughout the year (Figure 9).

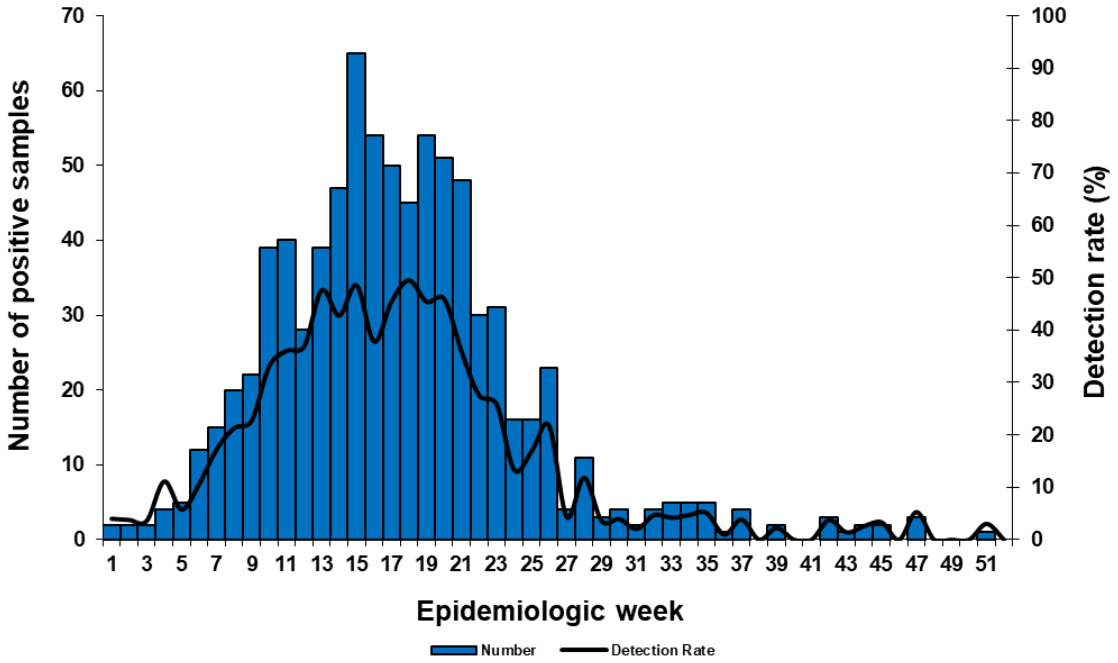

Figure 9: Numbers of samples collected and detection rates for respiratory syncytial virus (RSV), in patients meeting the case definition for severe respiratory illness (SRI), pneumonia surveillance, South Africa, 2018.

Bordetella pertussis

Systematic ILI programme

Pertussis cases were detected throughout the year in the ILI surveillance programme with the highest detection rate being 8% (5/59) in August 2018. Over 80% (81%; 13/16) of cases were detected at the Klerksdorp site (Jouberton Clinic) (Figure 10).

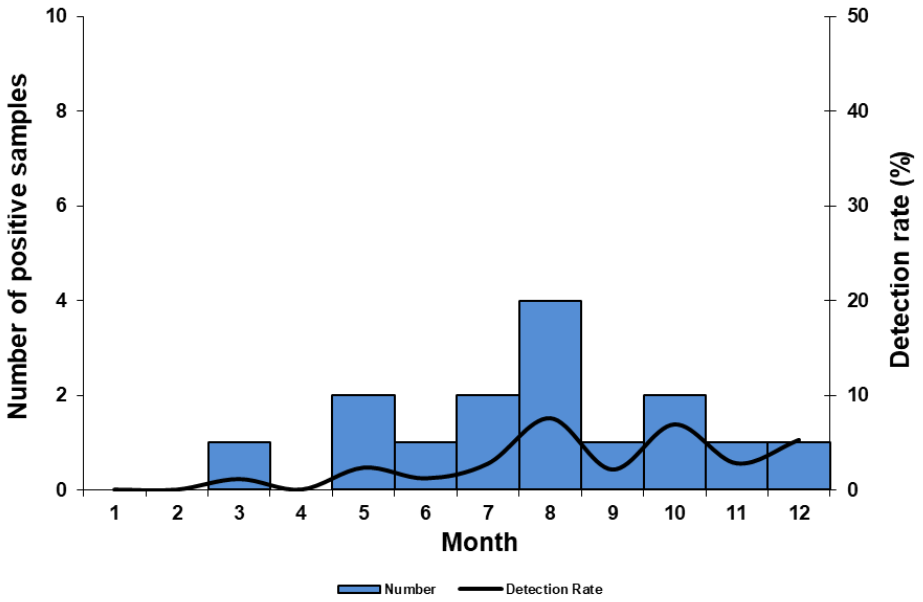

Figure 10: Numbers of positive samples for *Bordetella pertussis* among patients enrolled with influenza-like illness (ILI) at two primary health clinics, South Africa, 2018.

Pneumonia surveillance

The detection rate for pertussis in SRI cases was 2% (98/4630), and cases were detected all year. The peak detection rate was in July at 5% (20/420). Nearly half the cases (40%; 46/114) were identified at the RCH/MPH (Figure 11). Pertussis detection was more widespread in 2018 compared to 2017. This increase in pertussis detection was reported on the NICD webpage in August 2018. http://www.nicd.ac.za/wp-content/uploads/2018/08/PertussisAlert_2018-08-08.pdf

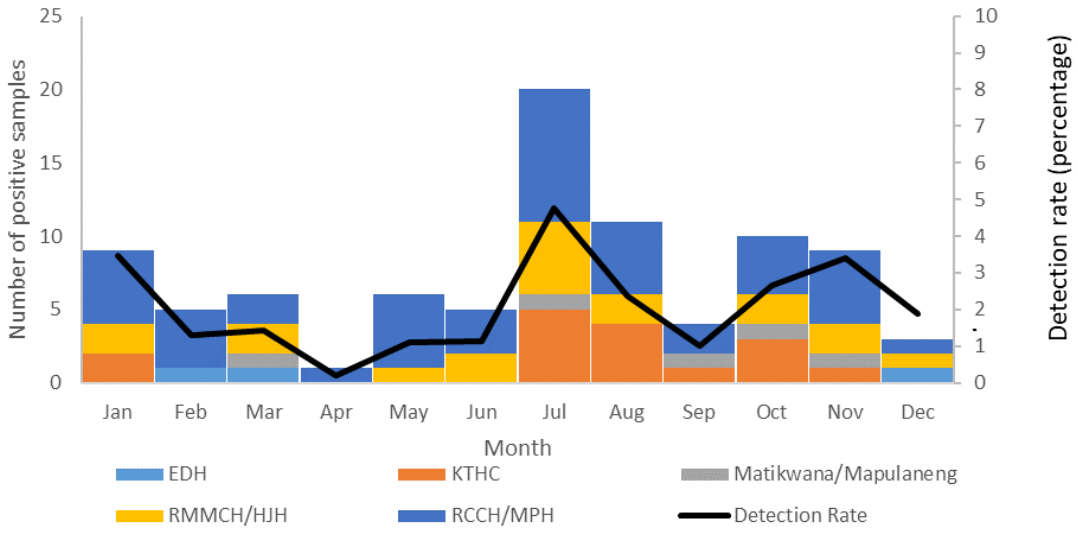

Figure 11: Detection rate and number of samples positive for *Bordetella pertussis* by site and month, among patients with severe respiratory illness (SRI), pneumonia surveillance programme, South Africa, 2018.

Respiratory morbidity surveillance

During 2018 there were 1 149 399 consultations reported to the NICD through the respiratory morbidity data mining surveillance system. Of these, 25 545 (2%) were due to pneumonia or influenza (P&I) (International Classification of Diseases 10 codes J10-18). There were 18 508 (72%) inpatients and 7 037 (28%) outpatients with P&I discharge data. An increase in P&I consultations and admissions was observed during the period with a higher number of seasonal influenza virus isolations reported to the viral watch and pneumonia surveillance programmes respectively (Figures 12 and 13). A second lower peak preceded the influenza season, corresponding to the circulation of respiratory syncytial virus.

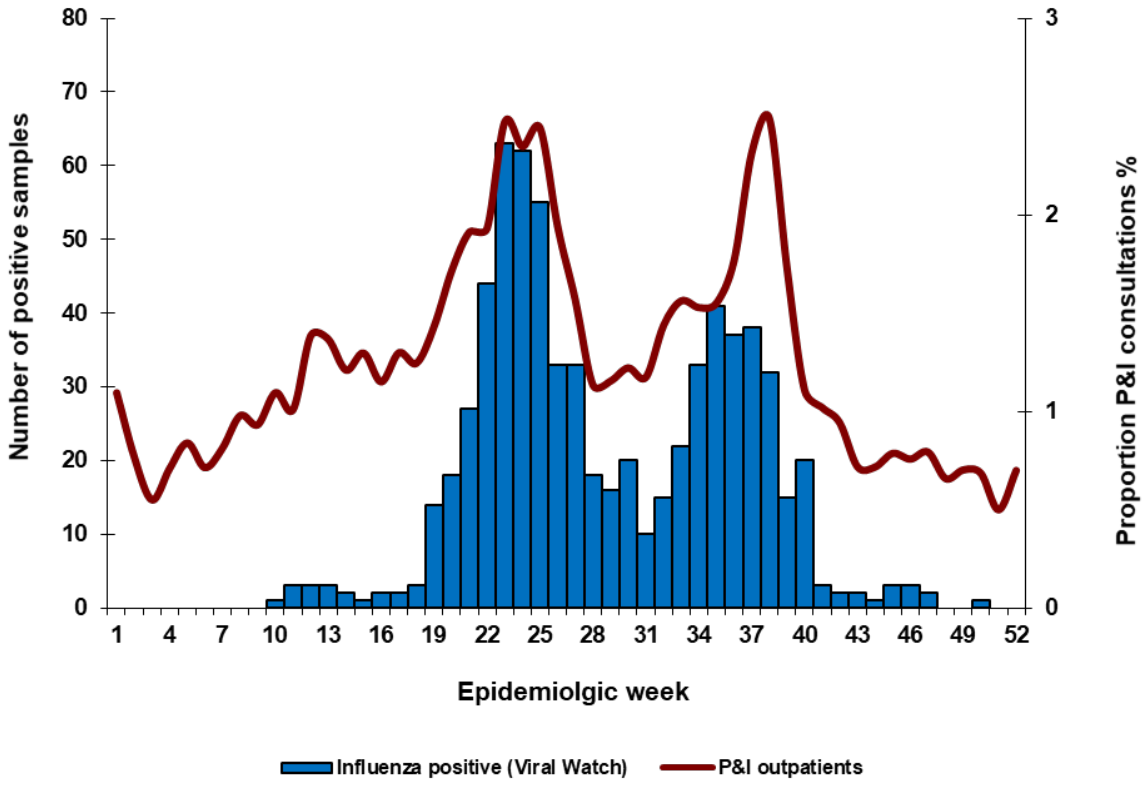

Figure 12: Numbers of private hospital outpatient consultations with a discharge diagnosis of pneumonia and influenza (P&I), and numbers of influenza positive viral isolates (Viral Watch) by week, South Africa, 2018.

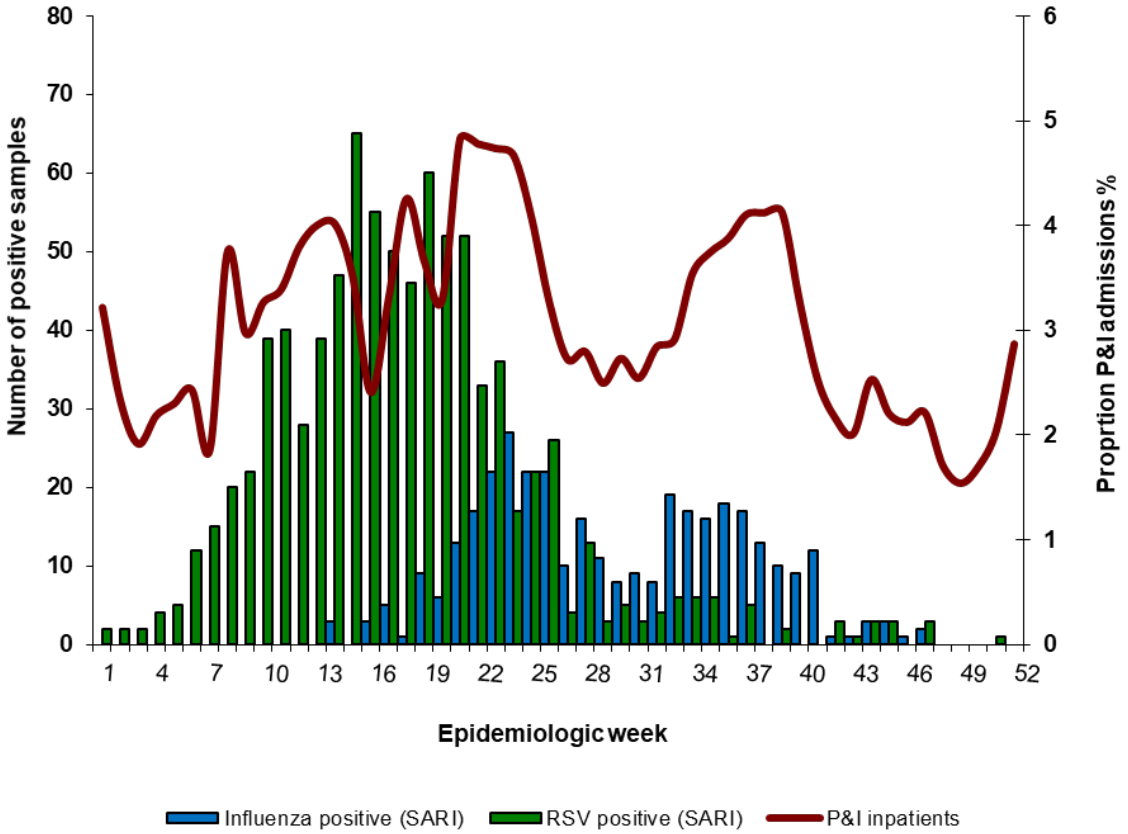

Figure 13: Numbers of private hospital admissions for pneumonia and influenza, as well as numbers of influenza positive viral isolates and respiratory syncytial virus (RSV) positive isolates by week, South Africa, 2018.

Virology of circulating influenza viruses and vaccine effectiveness (VE), 2018 influenza season

In all three surveillance programs influenza A(H1N1)pdm09 viruses were detected as the dominant circulating strain. Both influenza B/Victoria and B/Yamagata lineage viruses circulated and were detected at frequencies of 68% (313/460) and 21% (95/460), respectively. The influenza B lineage could not be determined in 11% (52/460) cases. Cell culture-derived influenza virus isolates were obtained with a 75% (157/208) success rate. Influenza A(H1N1)pdmo9 viruses (99%, 124/125) were typed as A/Michigan/45/2015-like with normal reactivity. A two-fold or greater reduction in hemagglutination inhibition titre against relevant vaccine strain antisera was observed at frequencies of 19% (3/16) for B/Yamagata virus isolates and 100% (6/6) for B/Victoria virus isolates.

Of the 1 465 individuals enrolled in viral watch and tested during the influenza season, 1 186 (81%) were eligible for the vaccine effectiveness (VE) analysis. The influenza detection rate was 54% (642/1186) amongst individuals included. The majority of influenza detections were A(H1N1)pdm09

which accounted for 365/642 (57%) of the total number of subtypes. These were followed by influenza B which accounted for 256 (40%) of detections with the remainder being influenza A(H3N2). The influenza vaccine coverage was 4.7% (30/642) in cases and 8.6% (47/544) in controls. Coverage in patients with underlying conditions was 12.4% (11/89) in cases and 20.7% (22/106) in controls, and in those aged ≥65 years was 25% (5/20) in cases and 33% (10/30) in controls. The overall VE estimate, adjusted for age and seasonality, was 51.3% (95% CI: 10.5% to 73.5%) against any influenza virus type. Against influenza A(H1N1)pdm09 it was 56.9% (95% CI 18.7% - 77.2%) in all patients, and 70.6% (95% CI 33.2% - 87.0%) in adults aged between 18 and 64 years (adjusted for seasonality only). Vaccine effectiveness against influenza B, adjusted for age and seasonality, was 14.3%
(95% CI: -120.1% - 66.6%).

Discussion

The 2018 influenza season in South Africa was predominated by influenza A(H1N1)pdm09 with co-circulation of influenza B (influenza B/Victoria and B/Yamagata) and sporadic influenza A(H3N2) cases. In all the surveillance programmes, circulation in the initial period of the season was almost exclusively influenza A(H1N1)pdm09 with influenza B predominating during the last weeks of the season. The season onset was within the average onset period compared to previous years in which the mean onset was week 22 (range 17-28)[1]. The 2018 season as measured by the Viral Watch Programme was 24 weeks long, and within the range described over the last 30 years (range 7-25). The influenza vaccine was effective in South Africa against influenza A(H1N1)pdm09 in 2018. Additional information from this surveillance programme including information on the risk groups for severe illness[2,3], annual estimates of influenza vaccine effectiveness [4-6], and details of virus characterisation are presented in different reports and complement the information presented here.

The RSV season preceded the influenza season, starting in week 7 at the ILI sites and in week 8 at the pneumonia surveillance sites. There was no obvious seasonality identified for *B. pertussis*. The surveillance programme identified an increase in pertussis cases from all sites, prompting alerts to be circulated to all sentinel sites nationally. These alerts urged clinicians to adopt a high index of suspicion for pertussis and initiate early treatment and public health action.

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MALARIA VECTOR SURVEILLANCE REPORT, SOUTH AFRICA, JANUARY – DECEMBER 2018

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Executive summary

Malaria in South Africa is seasonal and primarily occurs in the Limpopo, Mpumalanga and KwaZulu-Natal provinces. The control of malaria vector mosquito species is based on indoor spraying of residual insecticides (IRS) and limited larval source management. Malaria incidence in 2018 was comparatively high with 18 638 confirmed malaria cases and 120 confirmed deaths. Vector surveillance in collaboration with the National Institute for Communicable Diseases (NICD) during 2018 revealed the presence of three malaria vector species - *Anopheles arabiensis* (n=775, 36%), *An. merus* (n=219, 10%) and *An. vaneedeni* (n=129, 6%) – which have previously been shown to contribute to ongoing residual malaria transmission in South Africa. In addition to these, *An. parensis* (n=231, 11%) has recently been incriminated as a minor vector in South Africa. Several closely related non-vector *Anopheles* species were also collected. Most of the specimens analysed were collected from KwaZulu-Natal (61%, n= 1 324) followed by Limpopo (23%, n=491) and Mpumalanga (16%, n = 366) provinces. The surveillance information by province and municipality shows that IRS based vector control needs to be maintained at a high rate of coverage and that spraying should ideally be completed before the onset of each malaria season. Given that all sporozoite positive (and therefore malaria infective) adult *Anopheles* females recently collected were found resting outdoors, and given that there are no large-scale vector control tools targeting

outdoor-resting mosquitoes, larviciding, including the treatment of winter breeding sites, should be used as a complimentary method to enhance the effect of IRS in high incidence areas.

Introduction

South Africa's malaria affected areas include the low altitude border regions of Limpopo, Mpumalanga and KwaZulu-Natal Provinces. These regions typically experience active malaria transmission, especially during the peak malaria season that spans the summer months of November to April. Malaria incidence in 2018 (18 638 cases) decreased by approximately half of that recorded in 2017 (+/- 31 000 cases) but was still substantially higher than that of 2016 (9 478 cases). Limpopo and Mpumalanga provinces were most affected, especially the Vhembe, Mopani (Limpopo) and Ehlanzeni (Mpumalanga) districts.[1]

Each of South Africa's malaria endemic provinces have developed well-coordinated malaria control operations including routine vector control which is primarily based on the application of indoor residual insecticide spraying (IRS) and, to a lesser extent, larval source management.[2] Although IRS has proven efficacy spanning many decades, residual malaria transmission continues and is likely caused by outdoor feeding and resting *Anopheles* vector mosquitoes that are unaffected by indoor applications of insecticide.[3,4] In addition, populations of the major malaria vector species, *Anopheles funestus* and *An. arabiensis*, have developed resistance to insecticides, especially in northern KwaZulu-Natal.[2,5] The pyrethroid resistance phenotype in *An. arabiensis* in this region is however of low intensity currently and is not considered to be operationally significant at this stage, unlike the pyrethroid-carbamate resistance profile in *An. funestus* which is of high intensity, is highly significant epidemiologically and was at least partly causative of the malaria epidemic experienced in South Africa during the period 1996 to 2000.[6]

Residual malaria transmission, comparatively high incidence and burgeoning insecticide resistance in malaria vector populations within South Africa's borders necessitate ongoing and enhanced vector surveillance. This is especially pertinent in terms of South Africa's malaria elimination agenda.[7] Currently, surveillance is routinely conducted by the entomology teams of Limpopo, Mpumalanga and KwaZulu-Natal provinces with support from partner institutions including the National Institute for Communicable Diseases (NICD), the Wits Research Institute for Malaria (WRIM), University of the Witwatersrand, the Institute for Sustainable Malaria Control, University

of Pretoria, the South African Medical Research Council and the Clinton Health Access Initiative. This report summarises malaria vector surveillance in South Africa in 2018 based on specimens referred to the Vector Control Reference Laboratory (VCRL) of the Centre for Emerging Zoonotic and Parasitic Diseases (CEZPD), NICD.

Methods

Anopheles mosquitoes were collected from sentinel sites in KwaZulu-Natal, Limpopo and Mpumalanga provinces (Figure 1). These specimens were either collected by VCRL personnel or were referred to the VCRL by partner institutions and provincial malaria control programme entomology teams during the period January to December 2018.

Adult *Anopheles* mosquitoes were collected by baited net traps (goat and cow baited), silver bullet traps (UV LED, white light and no light), CO_2 traps, resting in tyres, outdoor placed clay pots and modified buckets, and by human landing catches. Other specimens were collected as larvae and were reared to adults for subsequent analysis. One or more of these collection techniques were deployed at each sentinel site (Figure 1). Adult specimens were preserved on silica gel in 1.5ml tubes and were identified as far as possible using external morphological characters by VCRL, partner institution and/or provincial malaria control programme personnel. Specimens identified as members of the *An. gambiae* complex or *An. funestus* group were subsequently identified to species using standard polymerase chain reaction (PCR) assays. Quality assurance based on the ISO 17025 standard was used to ensure the quality of results.

Results

A total of 2 181 *Anopheles* mosquitoes was collected from sentinel sites in the Umkhanyakude region in KwaZulu-Natal Province, the Vhembe region of Limpopo Province and the Ehlanzeni region of Mpumalanga Province (Figure 1).

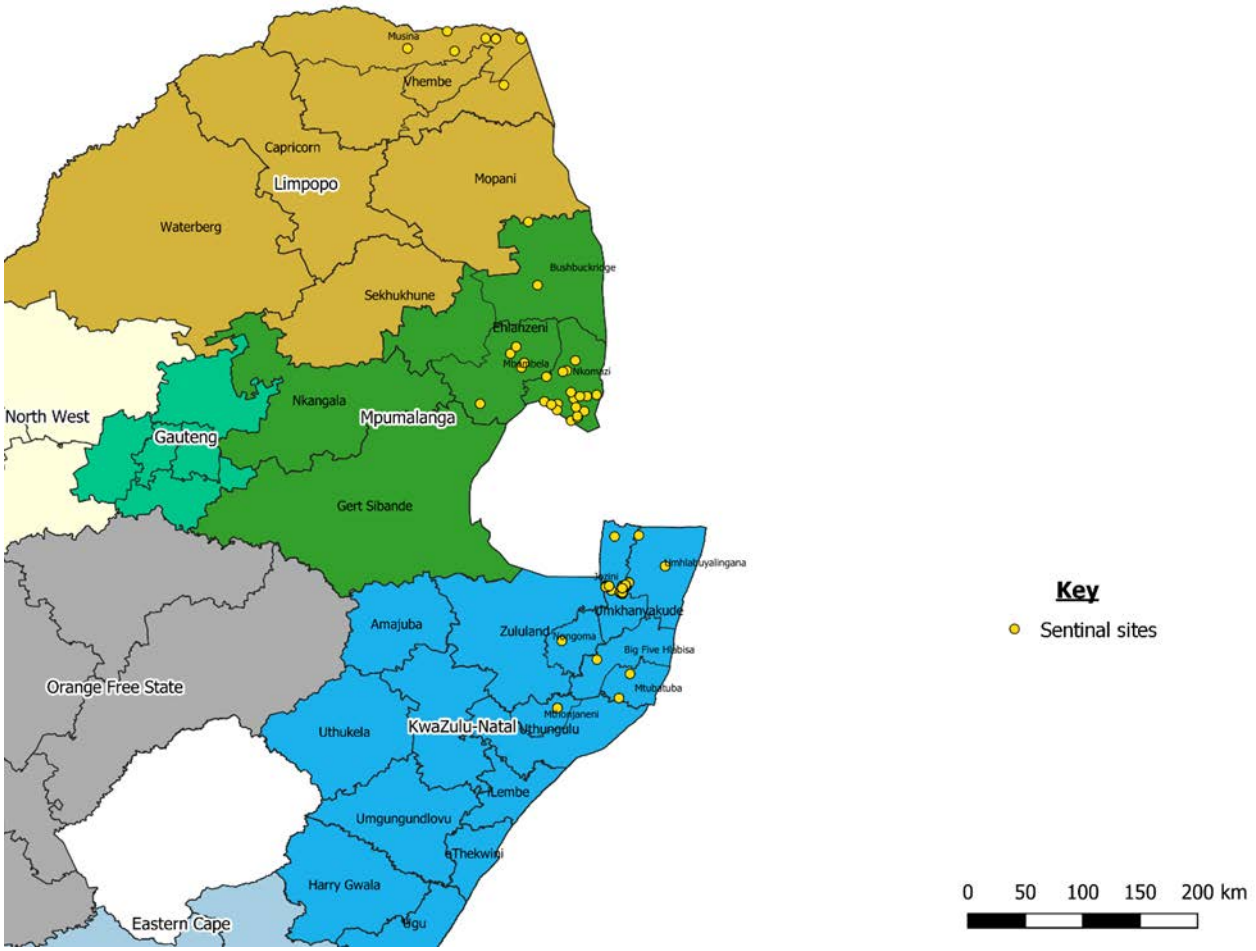

Figure 1: Sentinel *Anopheles* collection sites in KwaZulu-Natal, Limpopo and Mpumalanga provinces, South Africa, 2018.

Most of the specimens were collected from KwaZulu-Natal (61%, n=1 324) followed by Limpopo (23%, n=491) and Mpumalanga (16%, n=366) provinces (Table 1, Figure 2). These were subsequently identified as members of the *An. gambiae* complex (60%, n=1 312), *An. funestus* group (30%, n=658) or other *Anopheles* species (10%, n=211). *Anopheles arabiensis* predominated the collections (36%, n=775) although substantial numbers of *An. merus*, *An. quadriannulatus*, *An. parensis*, *An. vaneedeni* and *An. rivulorum* were also obtained (Table 1, Figure 2).

Table 1: Numbers of *Anopheles* specimens collected by species and province, South Africa, 2018.

***Anopheles* species complex, group or other**	***Anopheles* species**	**KwaZulu-Natal**	**Limpopo**	**Mpumalanga**	**Total**
***An. gambiae* complex**	*An. arabiensis*	614	49	112	775
	An. merus	66	9	144	219
	An. quadriannulatus	63	150	105	318
***An. funestus* group**	*An. leesoni*	27	19	0	46
	An. parensis	229	2	0	231
	An. rivulorum	100	133	1	234
	An. rivulorum-like	0	18	0	18
	An. vaneedeni	81	46	2	129
Other *Anopheles* species	*An. coustani*	11	3	0	14
	An. demeilloni	0	1	0	1
	An. listeri	0	15	0	15
	An. marshallii	96	0	0	96
	An. pharoensis	5	0	0	5
	An. pretoriensis	28	15	0	43
	An. rhodesiensis	0	1	0	1
	An. rufipes	1	16	0	17
	An. squamosus	3	2	2	7
	An. tenebrosus	0	12	0	12
Total		1324	491	366	2181

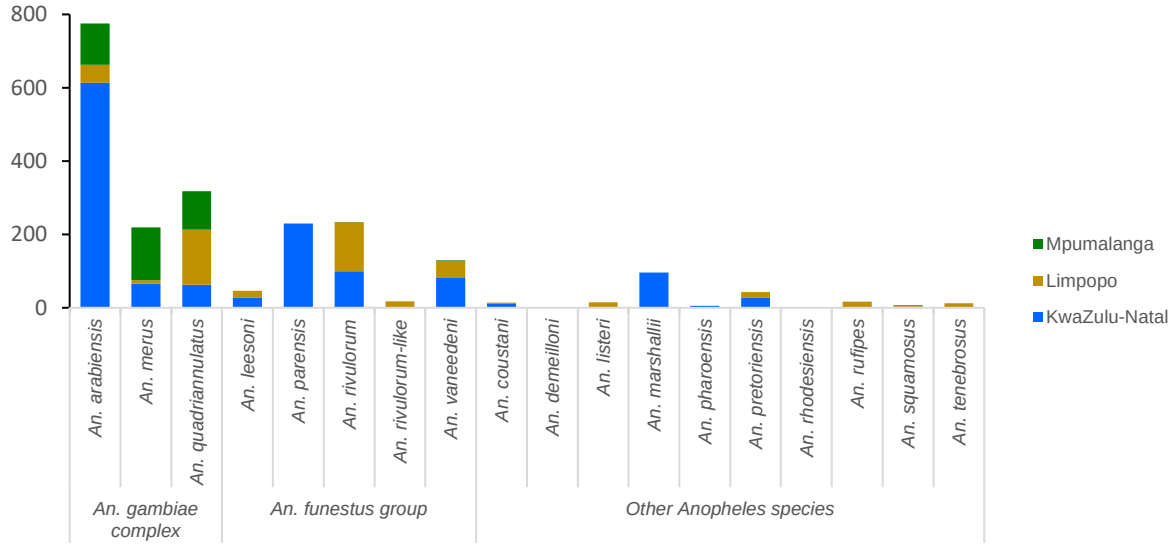

Figure 2: Proportional distribution (in absolute numbers) of *Anopheles* specimens collected by species and province, South Africa, 2018.

The malaria vectors *An. arabiensis* and *An. merus* (members of the *An. gambiae* species complex) were collected from sentinel sites in all three endemic provinces (Table 1, Figure 3). In KwaZulu-Natal Province, populations of these species were found in Jozini, Umhlabuyalingana and Mtubatuba municipalities of the Umkhanyakude District. In Limpopo Province, populations of these species were found in Musina and Collins Chabane of the Vhembe District. In Mpumalanga Province's Ehlanzeni District, these species were found in Nkomazi, Bushbuckridge and Mbombela.

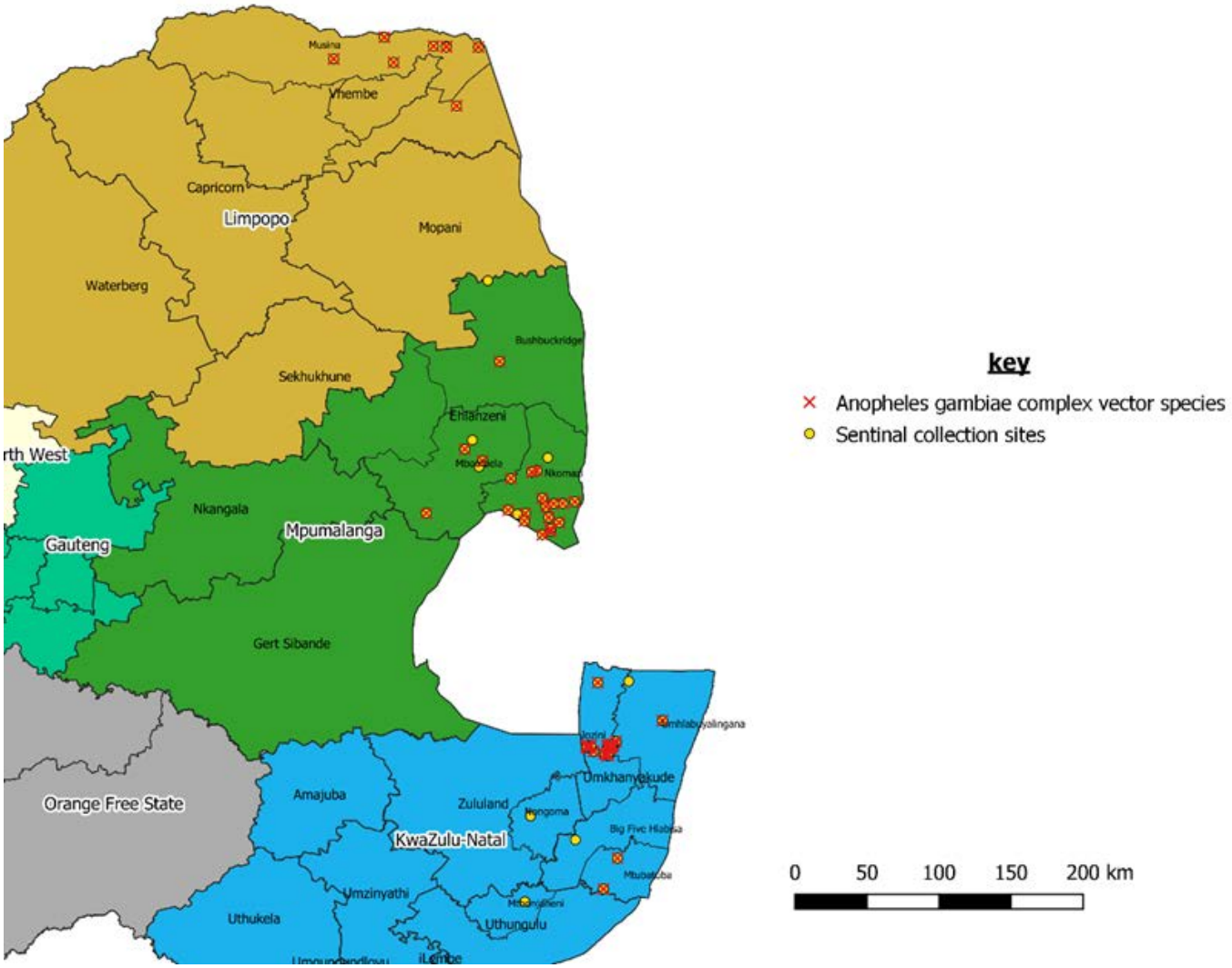

Figure 3: Sentinel sites in KwaZulu-Natal, Limpopo and Mpumalanga provinces from which samples of the malaria vectors *Anopheles arabiensis* and *An. merus* were collected, South Africa, 2018.

The secondary malaria vector species *An. vaneedeni* was collected from sentinel sites in all three endemic provinces while *An. parensis*, also a secondary vector, was collected in KwaZulu-Natal and Limpopo provinces (Table 1). Other potential malaria vector species within the *An. funestus* group that were collected from the provincial sentinel sites include *An. leesoni* and *An. rivulorum*. *Anopheles rivulorum* was collected in all three endemic provinces while *An. leesoni* was collected in KwaZulu-Natal and Limpopo provinces (Table 1).

The distribution of all known and suspected vector species within the *An. funestus* group is shown in Figure 4. Specimens of these species were collected in Jozini, Umhlabuyalingana and Mtubatuba

in the Umkhanyakude District of KwaZulu-Natal Province, in Musina of the Vhembe District in Limpopo Province, and in Nkomazi of the Ehlanzeni district of Mpumalanga Province.

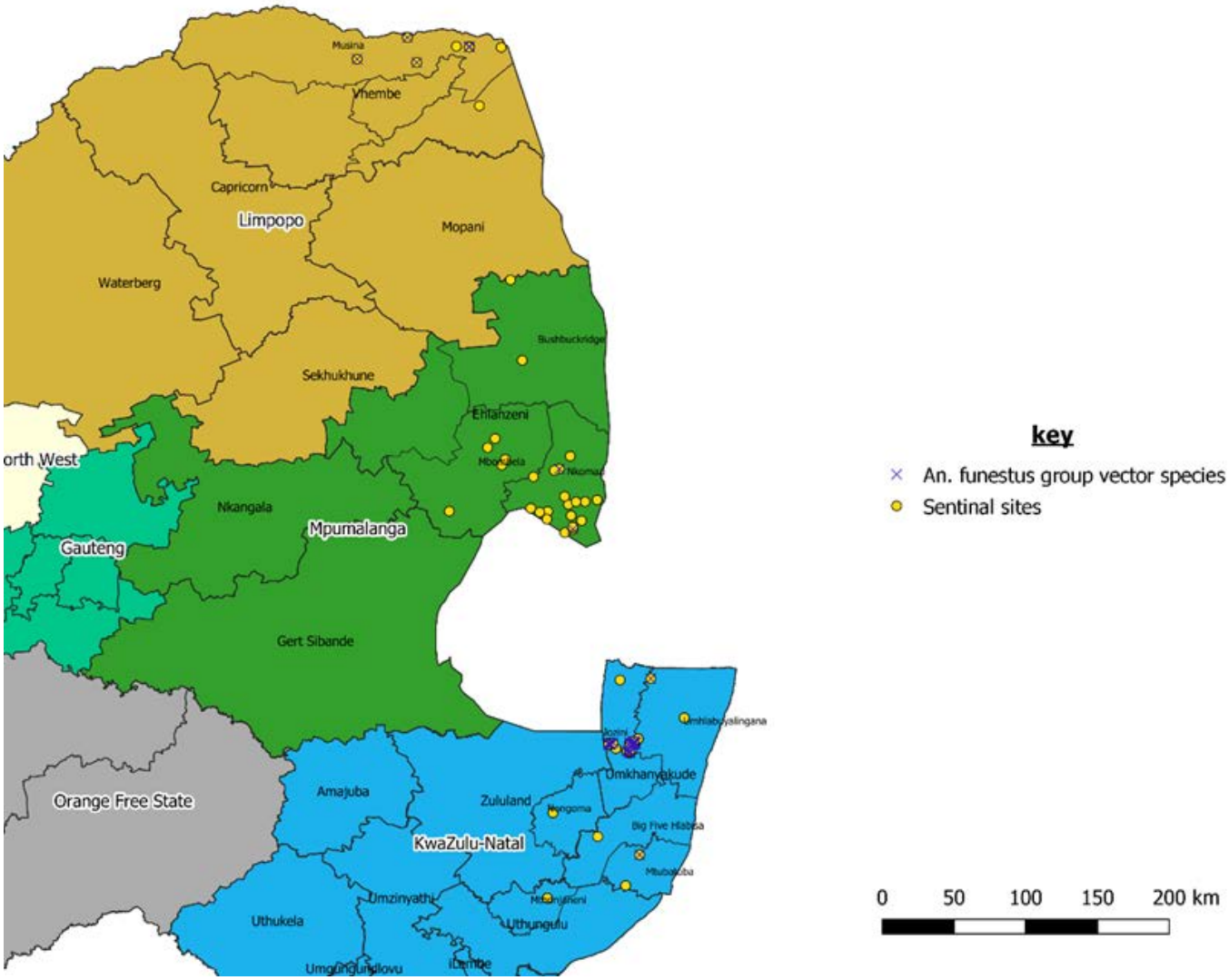

Figure 4: Sentinel sites in KwaZulu-Natal, Limpopo and Mpumalanga provinces from which samples of the known and potential secondary malaria vectors *Anopheles vaneedeni*, *An. parensis*, *An. rivulorum* and *An. leesoni* were collected, South Africa, 2018.

Anopheles coustani, *An. demeilloni*, *An. marshallii*, *An. pharoensis*, *An. rufipes* and *An. squamosus* have been incriminated as malaria vectors in other regions of Africa[8,9,10] but not in South Africa. *Anopheles coustani* was collected in KwaZulu-Natal and Limpopo provinces, *An. demeilloni* was collected in Limpopo Province, *An. marshallii* and *An. pharoensis* were collected in KwaZulu-Natal Province, *An. rufipes* was collected in KwaZulu-Natal and Limpopo provinces and *An. squamosus* was collected in all three endemic provinces (Table 1, Figure 2).

The number of anophelines collected by species and locality was highly variable across seasons. For example, *An. arabiensis* was most prevalent during late summer in KwaZulu-Natal Province while *An. merus* was most prevalent during spring and early summer in Mpumalanga Province (Figure 5). *Anopheles vaneedeni* and *An. parensis* predominated in late summer in Limpopo and KwaZulu-Natal provinces, respectively (Figure 6).

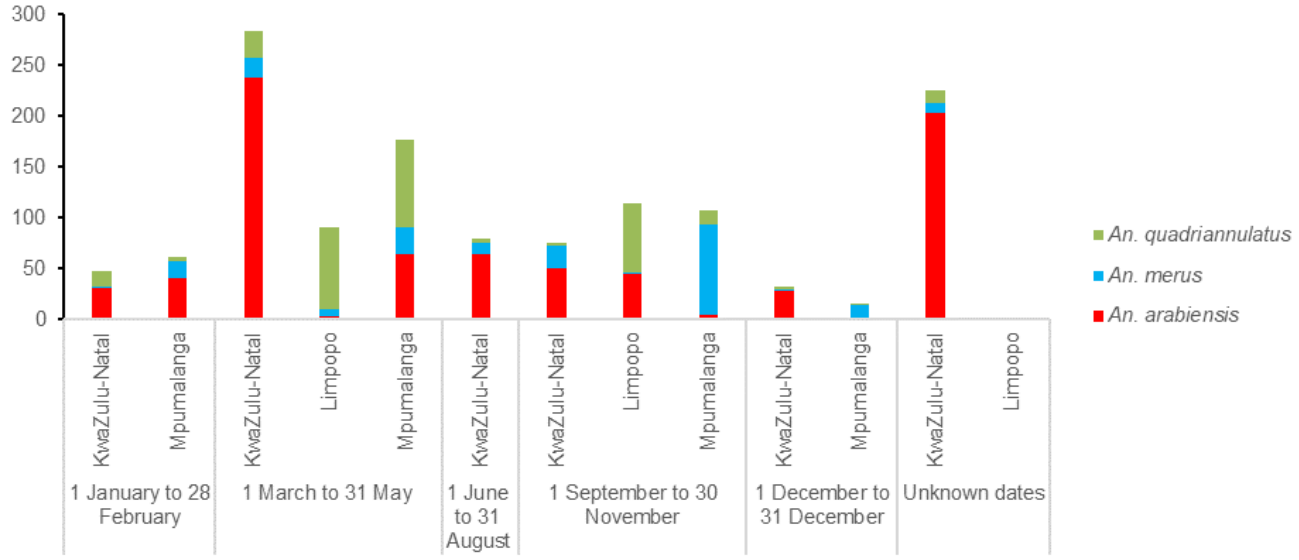

Figure 5: Proportional distribution (in absolute numbers) of *Anopheles gambiae* complex specimens collected by species, province and season, South Africa, 2018.

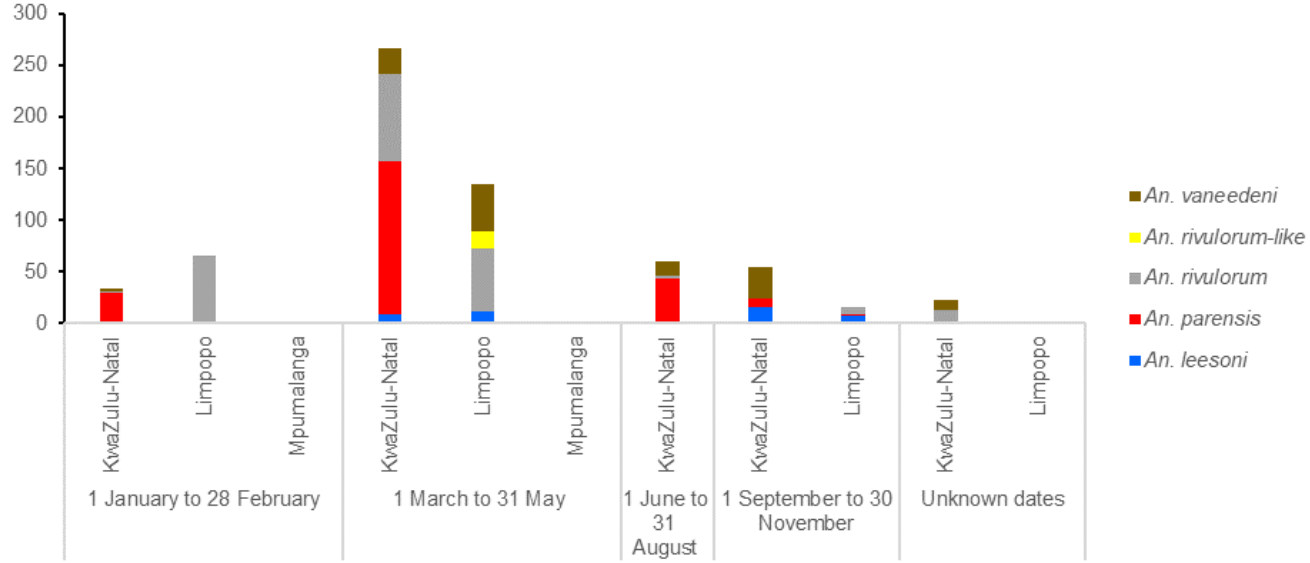

Figure 6: Proportional distribution (in absolute numbers) of *Anopheles funestus* group specimens collected by species, province and season, South Africa, 2018.

Discussion

In 2018, malaria vector surveillance revealed 18 *Anopheles* species across South Africa's three endemic provinces. These included species incriminated as vectors within South Africa as well as suspected vector species that have been incriminated in other African localities.

Anopheles arabiensis is a major malaria vector in South Africa[4] with variable feeding and resting behaviours. Outdoor feeding and resting components of *An. arabiensis* populations are at least partially responsible for ongoing residual malaria transmission.

Anopheles merus is likely an important secondary malaria vector in South Africa[2] and has also been implicated in transmission in southern Mozambique. Interestingly, this species is traditionally described as a salt-water coastal breeder but the larval collections from which most of these specimens accrued were found in fresh-water breeding sites. Recent data from Mpumalanga Province suggest that this species is increasing its inland range and abundance by adapting to breeding in fresh-water habitats.[11]

Anopheles vaneedeni tends to rest outdoors and will readily feed on humans. It has been implicated as a secondary malaria vector in Mpumalanga and KwaZulu-Natal provinces[3] and likely plays an important role in residual transmission in South Africa.

Anopheles parensis has only recently been incriminated as a malaria vector.[12] Its contribution to residual malaria transmission in South Africa is likely to be minimal at best owing to its strong tendency to feed on livestock animals. This species will nevertheless feed on humans as well and will rest indoors and outdoors.

No *An. funestus* were collected during 2018. In the absence of vector control, this species is the predominant malaria vector in the southern African region where it is especially prevalent in neighbouring Mozambique and Zimbabwe.[2] Although the eastern Lowveld regions of South Africa form part of the natural range of this species, its absence is likely attributable to intensive IRS programmes in KwaZulu-Natal, Mpumalanga and Limpopo provinces.[2] However, the possibility of transmission by this species in the border regions of Limpopo cannot be ruled out. Other members

of the *An. funestus* group detected during 2018 include *An. leesoni*, *An. rivulorum* and *An. rivulorum*-like. Of these, only *An. rivulorum* has been implicated as a minor malaria vector in East Africa.

Other species that occur in South Africa and that have been incriminated as malaria vectors in various African localities include *An. marshallii*, *An. coustani*, *An. demeilloni*, *An. pharoensis*, *An. rufipes* and *An. squamosus*.[8,9,10] It is possible that one or more of these species plays a role in residual malaria transmission in South Africa.

Relative *Anopheles* population densities tend to fluctuate between seasons and are generally highest during the summer months congruent with increased rainfall.[4] These increased densities coincide with South Africa's summer malaria season because greater numbers of vector mosquitoes invariably translate into higher rates of transmission assuming there are adequate parasite populations.

Conclusion & recommendations

Several anophelines, including malaria vector species, occur in the north-eastern Lowveld regions of South Africa, with their relative abundances varying considerably by season. Despite coordinated provincial IRS programmes that usually achieve high spray coverage rates (80% or more of targeted structures in endemic areas), populations of these species persist and at least four of them - *An. arabiensis*, *An. merus*, *An. vaneedeni* and *An. parensis* – have previously been implicated in ongoing residual transmission in South Africa (tentative in the cases of *An. merus* and *An. parensis*). The reasons for this are multiple and certainly include outdoor-biting and outdoor-resting components of these species.

Based on this information it is recommended that:

- IRS based vector control be maintained at a high rate of coverage in endemic districts
- IRS activities should ideally be completed before the onset of each malaria season
- Larval source management[13], including the treatment of winter breeding sites, be implemented and maintained so as to enhance the effect of IRS in high incidence areas
- Insecticide resistance management practices be maintained and periodically revised based on surveillance information

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