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FOREWORD

South Africa's malaria affected areas include the low altitude border regions of Limpopo, Mpumamlanga and KwaZulu-Natal Provinces. Residual malaria transmission and burgeoning insecticide resistance in malaria vector populations within South Africa's borders necessitate ongoing vector surveillance. In this issue is a review of the epidemiological implications of insecticide resistance on malaria incidence in South Africa and a summary of malaria vector surveillance in South Africa during the period January 2014 to July 2015 based on specimens referred to the NICD. Analysis of these specimens shows that several known and potential malaria vector species occur in the north-eastern Lowveld regions of South Africa despite well-coordinated provincial malaria control programmes.

The 2016 winter influenza season in South Africa will again be carefully monitored by several influenza surveillance programmes coordinated at the NICD. Last year, these programmes showed that the season in South Africa was predominately influenza A(H1N1)pdm09, followed by influenza A(H3N2) and influenza B. This is the second report to combine viral pathogens with additional testing for bacterial pathogens as well as some of the atypical causes of pneumonia.

All contributors are thanked for their inputs, and we trust you will find these reports useful and interesting.

Basil Brooke, Editor

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THE EPIDEMIOLOGICAL EFFECT OF INSECTICIDE RESISTANCE ON MALARIA INCIDENCE – THE SOUTH AFRICAN EXPERIENCE

Basil Brooke

Centre for Opportunistic, Tropical & Hospital Infections, NICD

Resistance to insecticides is postulated to have a dramatic effect on the efficacy of insecticide-based malaria control interventions. This effect can usefully be measured using entomological indicators as a proxy[1], but is probably best measured in terms of epidemiological outcomes. However, natural cycles of disease transmission, bionomic factors including changes in malaria vector species composition and abundance, climatic and environmental factors, migration, changing land use patterns and other control interventions are likely to confound evaluations of the actual effect of insecticide resistance on disease incidence.

To date, the effect of insecticide resistance on malaria transmission and incidence in South Africa stands as a primary example of the epidemiological effect that insecticide resistance can exert. This is because resistance to pyrethroids was at last partially responsible for the malaria epidemic experienced in South Africa during the period 1996 to 2000. Prior to 1996, South Africa's insecticide-based indoor residual spraying (IRS) vector control programme was dependent on DDT. While this regimen was generally sufficient for control (malaria incidence seldom exceeded 4000 cases per annum), sporadic outbreaks and more severe epidemics did occur, such as the 1971-1972 epidemic followed by the 1978 epidemic both of which were congruent with widespread rains.[2] In 1995 a policy to move away from the use of DDT for IRS in favor of pyrethroids was adopted, largely because of mounting pressure against the use of DDT. Furthermore, an upsurge in cross-border migration from Mozambique coupled with good rainfall during this period coincided with a sharp rise in malaria incidence within South Africa, in which the number of cases rose from 8750 in 1995 to 27 035 in 1996 and peaked at 64 622 in 2000.[3] A primary cause of this epidemic was the resurgence of pyrethroid resistant *An. funestus* following the introduction of pyrethroids for IRS.[4] Although the link between insecticide resistance and increased malaria incidence may seem tenuous based on these events alone, the re-introduction of DDT for IRS in South Africa post 2000 and the resultant substantial decline in malaria incidence to fewer than 10 000 cases per annum during much of the subsequent period shows that pyrethroid efficacy was severely undermined by the development of pyrethroid resistance in *An. funestus* and that DDT use, in conjunction with pyrethroids, was necessary to re-establish control.[2] However, the re-introduction of DDT for IRS also coincided with a change in anti-malarial drug regimen from sulfadoxine-pyrimethamine (SP) to artemisinin-containing combination therapy (ACT) (Maharaj et al., 2013).[3] Although it is almost impossible to quantify the actual contribution of each intervention to the decrease in malaria incidence post 2000, the use of DDT dramatically decreased the abundance of *An. funestus* in South Africa to undetectable levels, leaving the less efficient vector *An. arabiensis* to maintain lower level residual transmission as a consequence of this species' behavioural plasticity and lower susceptibility to IRS.[5]

Currently, DDT is used for spraying traditional structures and pyrethroids are used for modern structures in South Africa's provincial IRS programmes, which conveniently amounts to a mosaic resistance management strategy

as described in the Global Plan for Insecticide Resistance Management (GPIRM).[6] South Africa's low incidence of malaria post 2007 has led to the adoption of a malaria elimination agenda according to which South Africa's national malaria control programme aims to eliminate malaria with the country's borders by 2018 (National Malaria Elimination Strategy for malaria 2012-2018). Part of this strategy involves the scaling up of vector control interventions including enhanced vector surveillance in transmission foci. Recent surveillance data from the Mamfene region of northern KwaZulu-Natal show that the extent of insecticide resistance in the malaria vector *An. arabiensis* is worsening[7] although the actual epidemiological implications of these data remain to be determined.

In conclusion, the data available indicate that insecticide resistance can lead to vector control failure and thereby induce an epidemiologically significant effect on malaria incidence, as witnessed in South Africa during the 1996 – 2000 epidemic. Case studies further indicate that the effect of insecticide resistance is most pronounced in an IRS control setting, as compared to programmes based on the distribution of insecticide treated nets (ITNs)[1], primarily because ITNs still offer a measure of personal protection despite insecticide resistance. Nevertheless, IRS is currently the only vector control method that allows for adequate insecticide resistance management and therefore offers the greater protection to affected communities in the longer term.

Disclaimer:

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References

1. Strode C, Donegan S, Garner P, Enayati AA, Hemingway J. 2014. The impact of pyrethroid resistance on the efficacy of insecticide-treated bed nets against African anopheline mosquitoes: systematic review and meta-analysis. *PLoS Med* 11(3):e1001619. doi: 10.1371/journal.pmed.1001619. eCollection 2014.
2. Coetzee M, Kruger P, Hunt RH, Durrheim DN, Urbach J, Hansford CF. 2013. Malaria in South Africa:110 years of learning to control the disease. *S Afr Med J* 103: No. 10 (Suppl 2): 770-778.
3. Maharaj R, Raman J, Morris N, Moonasar D, Durrheim D, Seocharan I, Kruger P, Shandukani B, Kleinschmidt I. 2013. Epidemiology of malaria in South Africa: from control to elimination. *S Afr Med J* 103: No. 10 (Suppl 2): 779-783.
4. Hargreaves K, Koekemoer LL, Brooke BD, Hunt RH, Mthembu J, Coetzee M. 2000. *Anopheles funestus* resistant to pyrethroids in South Africa. *Med Vet Entomol* 14: 181-189.
5. Hargreaves K, Hunt RH, Brooke BD, Mthembu J, Weeto MM, Awolola TS, Coetzee M. 2003. *Anopheles arabiensis* and *An. quadriannulatus* resistance to DDT in South Africa. *Med Vet Entomol* 17: 417-422.
6. WHO. *Global plan for insecticide resistance management in malaria vectors (GPIRM)*. World Health Organisation, Geneva; 2012.
7. Brooke BD, Robertson L, Kaiser ML, Raswiswi E, Munhenga G, Venter N, Wood OR, Koekemoer LL. Insecticide resistance in the malaria vector *Anopheles arabiensis* in Mamfene, KwaZulu-Natal. *S Afr J Sci* 2015; 111(11/12), Art. #2015-0261, 3 pages. http://dx.doi.org/10.17159/sajs.2015/20150261

MALARIA VECTOR SURVEILLANCE IN SOUTH AFRICA DURING THE PERIOD JANUARY 2014 TO JULY 2015

Riann Christian[1,2], Lizette Koekemoer[1,2],Eunice Agubuzo[1,2], Givemore Munhenga[1,2], Allison Gilbert[1,2], Leanne Lobb[1,2], Erica Erlank[1,2], Leonard Dandalo[1,2], Oliver Wood[1,2], Maria Kaiser[1,2], Leyya Essop[1,2], Craig Davies[1,2], Nelius Venter[1,2], Power Tshikae[1,2], Ashley Burke[1,2], Frans Mbokazi[3], Goodness Nkosi[3], Jabulani Zikhali[2], Sfisu Ngxongo[4], Maureen Coetzee[1,2], Basil Brooke[1,2]

[1]Vector Control Reference Laboratory, Centre for Opportunistic, Tropical & Hospital Infections, NICD

[2]Wits Research Institute for Malaria, Faculty of Health Sciences, University of the Witwatersrand

[3]Malaria Elimination Programme, Mpumalanga Department of Health, Ehlanzeni District

[4]Department of Health-KwaZulu-Natal, KwaZulu-Natal Provincial Government, Jozini

Introduction

South Africa's malaria affected areas include the low altitude border regions of Limpopo, Mpumamlanga and KwaZulu-Natal Provinces.[1] These regions experience active malaria transmission, especially during the peak malaria season which spans the Summer months (November to April). Each of these 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).[2]

Although IRS has proven efficacy spanning many decades[3], low-level residual malaria transmission continues and is likely caused by outdoor feeding and resting *Anopheles* vector mosquitoes that are unaffected by indoor applications of insecticide. In addition, populations of the major malaria vector species *Anopheles funestus* and *An. arabiensis* have developed resistance to insecticides, especially in northern KwaZulu-Natal.[2,4] The pyrethroid-carbamate resistance profile in *An. funestus*[5] has proved to be highly significant epidemiologically and was at least partly causative of the malaria epidemic experienced in South Africa during the period 1996 to 2000.[3,6]

Residual malaria transmission and burgeoning insecticide resistance in malaria vector populations within South Africa's borders necessitate ongoing vector surveillance. This is especially pertinent in terms of South Africa's malaria elimination agenda[7] which includes the following key objectives:

- To strengthen passive and active surveillance and monitoring and evaluation systems so that 100% of districts report promptly and routinely on key malaria indicators by 2015
- To ensure that all levels of the malaria programme have sufficient capacity to coordinate and implement malaria interventions by 2016
- To ensure 100% of the population has adequate knowledge, attitudes and practices on malaria by 2018 through appropriate IEC, social mobilization and advocacy
- To effectively prevent malaria infections and eliminate all parasite reservoirs in South Africa by 2018

Malaria vector surveillance forms an integral part of these objectives. Surveillance is routinely conducted by the entomology teams of Limpopo, Mpumalanga and KwaZulu-Natal with operational field and laboratory support from the Vector Control Reference Laboratory (VCRL) of the Centre for Opportunistic, Tropical and Hospital Infections (COTHI), NICD, and Wits Research Institute for Malaria (WRIM).

In general, the VCRL provides a service for the identification of medically important arthropods for entomologists, medical practitioners, health inspectors and health authorities. In terms of malaria vector surveillance, the VCRL conducts mosquito species identification and vector incrimination using surveillance specimens referred to the VCRL by the provincial malaria control programmes. This report summarises malaria vector surveillance in South Africa during the period January 2014 – July 2015 based on specimens referred to the VCRL.

Materials & Methods

During the period January 2014 to July 2015, *Anopheles* mosquitoes were collected by the provincial entomology teams and VCRL personnel. Adult specimens were obtained by rearing larvae obtained from routine larval collections and adults were also periodically collected using trapping techniques including exit window traps, clay pots, modified buckets, human landing catches (HLC) and CO_2 baited net traps. One or more of these collection techniques were deployed at sentinel sites in Limpopo, Mpumalanga and KwaZulu-Natal provinces (Figure 1). Collected adult *Anopheles* specimens were preserved on silica and sent to the NICD for identification to species. Identification of all mosquito specimens was based on the use of morphological keys[8,9] and PCR.[10,11]

Results & Discussion

A total of 4 746 *Anopheles* mosquitoes was collected from sentinel sites during the period under review (Figure 1). Of these, 992 (20.9%) were collected from KwaZulu-Natal, 2 592 (54.6%) from Mpumalanga, 489 (10.3%) from Limpopo and 672 (14.2%) from the northern region of the Kruger National Park. The vast majority of the anophelines collected were members of the *An. gambiae* species complex (4 557; 96%) while the remaining 4% (189) were members of the *An. funestus* species group. Subsequent PCR analysis revealed that the *An. gambiae* complex member species included *An. arabiensis*, *An. merus* and *An. quadriannulatus*. Member species of the *An. funestus* group identified included *An. rivulorum*, *An. vaneedeni* , *An. parensis* and *An. leesoni.* A summary of the species collected by relative proportion by province and species group is given in Figure 2.

Anopheles arabiensis was collected in comparatively large numbers in Mpumalanga and KwaZulu-Natal but did not appear in the Limpopo collections although this species has previously been detected there (Figure 2A,C). This species is a major malaria vector with variable feeding and resting behaviours. Outdoor feeding and resting components of South Africa's *An. arabiensis* populations are likely at least partially responsible for ongoing residual malaria transmission. This species has been directly implicated in malaria transmission in southern Mozambique.[12]

Anopheles merus was collected in the greatest relative proportion in Limpopo followed by Mpumalanga with only a small relative proportion collected in KwaZulu-Natal (Figure 2A,C,F). This species is generally listed as a minor or localised malaria vector. Currently, there is no indication of what, if any, contribution this species makes to malaria transmission in South Africa although it has also been implicated in malaria transmission in southern Mozambique.[12] 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 suggest that this species is increasing its inland range by adapting to breeding in fresh-water habitats (Mbokazi et al. - unpublished data).

Anopheles quadriannulatus is a non-vector member of the *An. gambiae* species complex that is comparatively common in the southern African region including South

Africa. This species was detected in Mpumalanga and Limpopo in comparatively large relative proportions and in a small relative proportion in KwaZulu-Natal (Figure 2A,C,F).

No *An. funestus senso strictu* were collected during the review period. In the absence of vector control, this species is the predominant malaria vector in the southern African region where it is especially prevalent in Mozambique and Zimbabwe.[13] Although the eastern Lowveld regions of South Africa form part of the natural range of this species, its absence can be attributed to intensive IRS programmes in KwaZulu-Natal, Mpumalanga and Limpopo. This is because *An. funestus* is highly endophilic (indoor-resting) and is therefore especially susceptible to IRS. Other members of the *An. funestus* species group were only detected in Mpumalanga and KwaZulu-Natal in comparatively low numbers (Figure 2B,D) although member species of this group have previously been collected in Limpopo. *Anopheles leesoni*, *An. vaneedeni* and *An. parensis* are generally considered to be non-vector species while *An. rivulorum* has been implicated as a minor malaria vector in East Africa.[14,15] The possibility of one or more of these species playing a role in residual malaria transmission in South Africa cannot be ruled out.

The occurrence of *An. arabiensis* and *An. quadriannulatus* in the northern Kruger National Park (Figure 2E) has previously been documented.[16] These species tend to occur in sympatry, especially at the Malahlapanga site. During the review period *An. quadriannulatus* predominated at Malahlapanga but previous surveys have shown a predominance of *An. arabiensis* there.[16] The change in relative densities of these two species at this site is likely linked to fluctuations in environmental conditions and weather patterns.

Conclusion

Several known and potential malaria vector species occur in the north-eastern Lowveld regions of South Africa despite well-coordinated IRS programmes that generally achieve high spray coverage rates (80% or more of targeted structures in endemic areas). It is highly likely that one or more of these species are responsible for ongoing residual transmission within South Africa's borders. It is envisaged that the vector surveillance programmes in each of the affected provinces and the scaling up of these activities in collaboration with the VCRL will clarify the role, if any, of each of these species in malaria transmission in South Africa. This information will enable an intensification of vector control activities to include methods designed to target outdoor feeding vector populations. The absence of *An. funestus sensu stricto* within South Africa's borders is indicative of continued high-level effectiveness of the provincial IRS-based vector control programmes.

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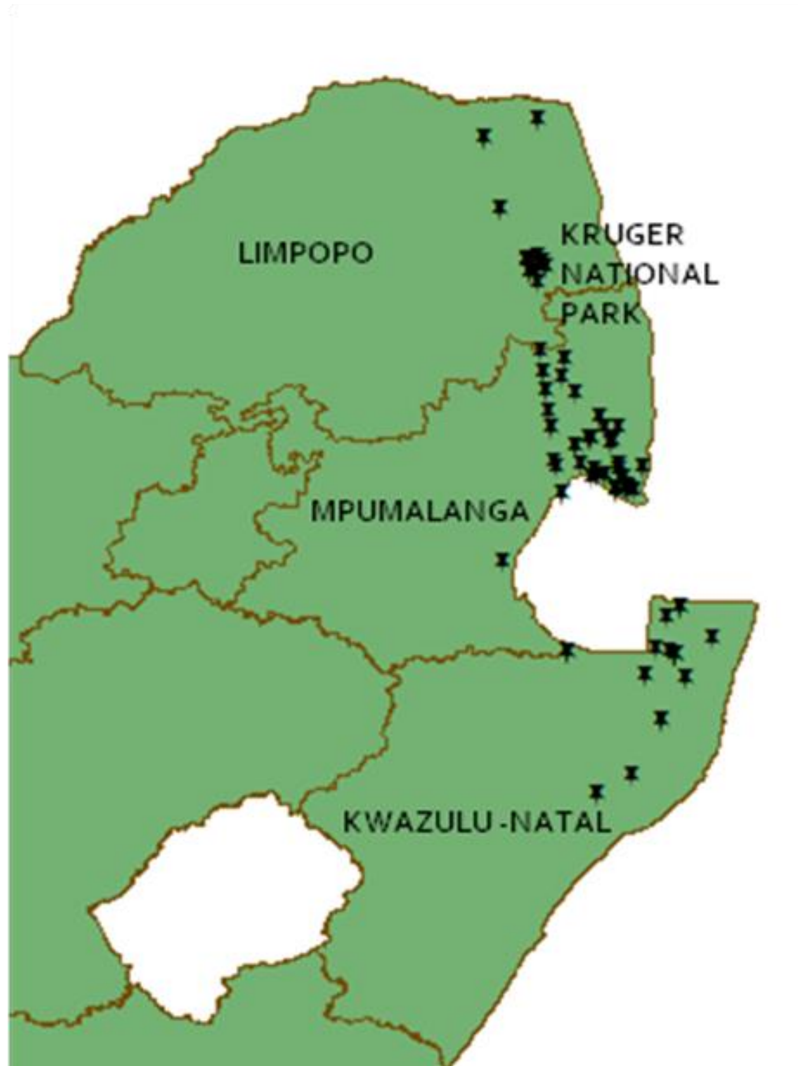


Figure 1: Sentinel sites where malaria vector surveillance was conducted in South Africa during the period January 2014 to July 2015.

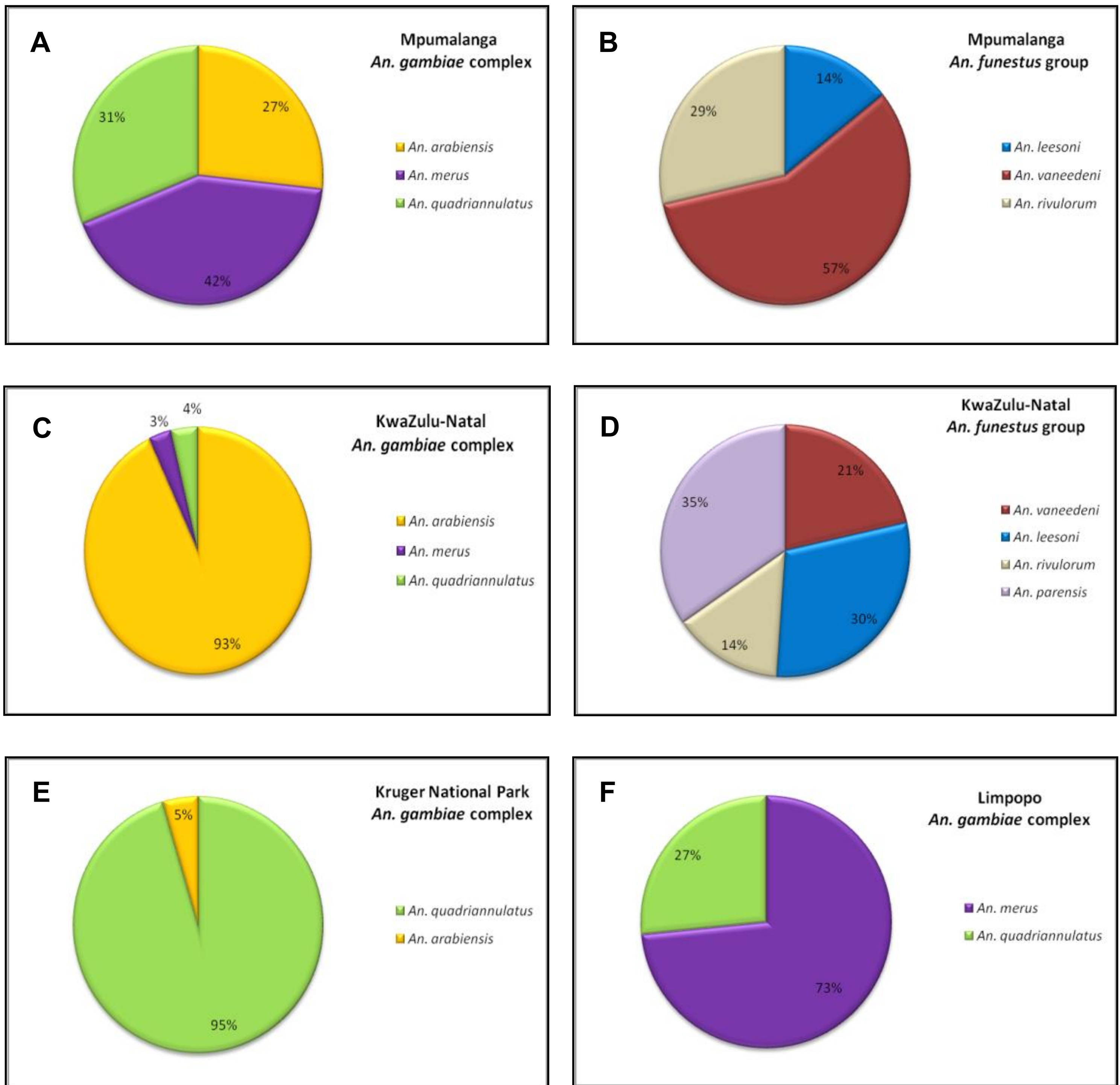


Figure 2: Relative proportions of member species of the *Anopheles gambiae* species complex and *An. funestus* species group by province/locality, South Africa. These proportions are based on *Anopheles* specimens collected during the period January 2014 to July 2015.

References

1. Morris N, Frean J, Baker L, Ukpe IS, Barnes KI, Kruger P, et al. Re-defining the extend of malaria transmission in South Africa: implications for chemoprophylaxis. *S Afr Med J* 2013, 103:861-4.
2. Brooke BD, Koekemoer LL, Kruger P, Urbach J, Misiani E, Coetzee M. Malaria Vector Control in South Africa. *S Afr Med J* 2013; 103(10 Suppl 2): 784-788.
3. Coetzee M, Kruger P, Hunt RH, Durrheim DN, Urbach J, Hansford CF. Malaria in South Africa: 110 years of learning to control the disease. *S Afr Med J* 2013, 103(10 Suppl 2):770-8.
4. Brooke BD, Robertson L, Kaiser ML, Raswiswi E, Munhenga G, Venter N, Wood OR, Koekemoer LL. Insecticide resistance in the malaria vector *Anopheles arabiensis* in Mamfene, KwaZulu-Natal. *S Afr J Sci* 2015, 111(11/12).
5. Coetzee M, Koekemoer LL. Molecular systematics and insecticide resistance in the major African malaria vector *Anopheles funestus*. *Ann Rev Entomol* 2013, 58: 393-412.
6. Maharaj R, Raman J, Morris N, Moonasar D, Durrheim DN, Seocharan I, et al. Epidemiology of malaria in South Africa: from control to elimination. *S Afr Med J* 2013,103:779-83.
7. South Africa National Department of Health, Malaria elimination strategy for South Africa 2012-2018, Pretoria, NDoH, 2012.
8. Gillies MT, De Meillon B. 1968. The Anophelinae of Africa south of the Sahara. 2nd Edition. *Publication of the South African Institute for Medical Research* 1968, Johannesburg. 54.
9. Gillies MT, Coetzee M. 1987. A supplement to the Anophelinae of Africa south of the Sahara. *Publication of the South African Institute for Medical Research* 1987, Johannesburg. 55.
10. Scott JA, Brogdon WG, Collins FH. Identification of single specimens of the *Anopheles gambiae* complex by the polymerase chain reaction. *Am J Trop Med Hyg* 1993, 49: 520-529.
11. Koekemoer LL, Kamau L, Hunt RH, Coetzee M. A cocktail polymerase chain reaction assay to identify members of the *Anopheles funestus* (Diptera: Culicidae) group. *Am J Trop Med Hyg* 2002, 66: 804-811.
12. Cuamba N, Mendis C. The role of *Anopheles merus* in malaria transmission in an area of southern Mozambique. *J Vector Borne Dis*. 2009, 46(2):157-9.
13. Sinka ME, Bangs MJ, Manguin S, Coetzee M, Mbogo CM, Hemingway J, Patil AP, Temperley WH, Gething PW, Kabaria CW, Okara RM, Van Boeckel T, Godfray HC, Harbach RE, Hay SI. The dominant Anopheles vectors of human malaria in Africa, Europe and the Middle East: occurrence data, distribution maps and bionomic précis. *Parasit Vectors*. 2010, 3:117.
14. Wilkes TJ, Matola YG, Charlwood JD. *Anopheles rivulorum*, a vector of human malaria in Africa. *Med Vet Entomol* 1996, 10: 108-110.
15. Kawada H, Dida GO, Sonye G, Njenga SM, Mwandawiro C, Minakawa N. Reconsideration of *Anopheles rivulorum* as a vector of *Plasmodium falciparum* in Western Kenya: some evidence from biting time, blood preference, sporozoite positive rate and pyrethroid resistance. *Parasit Vectors* 2012, 5:230.
16. Munhenga G, Brooke BD, Spillings BL, Essop L, Hunt RH, Midzi S, Govender D, Braack L, Koekemoer LL. Field study site selection, species abundance and monthly distribution of anopheline mosquitoes in the northern Kruger National Park, South Africa. *Malar J* 2014, 13: 27.

BURDEN OF RESPIRATORY PATHOGENS FROM INFLUENZA-LIKE ILLNESS AND PNEUMONIA SURVEILLANCE PROGRAMMES, SOUTH AFRICA, 2015

Sibongile Walaza[1], Cheryl Cohen[1], Florette Treurnicht[1] ,Nazir Ismail[3], Andries Dreyer[3], John Frean[2], Orienka Hellferscee[1],Jo Mcanerney[1], Jocelyn Moyes[1],Erika Britz[2], Bhavani Poonsamy[2], Anne von Gottberg[1], Nicole Wolter[1]

[1]Centre for Respiratory Diseases and Meningitis, NICD;

[2]Centre for Opportunistic, Tropical and Hospital Infections, NICD

[3]Centre for Tuberculosis, NICD

Introduction and methods

The National Institute for Communicable Diseases (NICD) coordinates a number of syndromic respiratory illness surveillance programmes in order to describe the epidemiology of the respiratory pathogens in South Africa. These programmes include pneumonia surveillance, influenza- like illness (ILI) (systematic ILI at public health clinics and viral watch) and the respiratory morbidity surveillance system. This report describes the findings for these programmes for the year 2015.

The pneumonia surveillance and systematic ILI surveillance programmes have previously been described.[1] 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.

Pneumonia 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 acute or chronic respiratory illness are prospectively enrolled (Table1). Dedicated staff screen and enrol patients from Monday to Friday. Clinical and epidemiological data are collected using standardized questionnaires. Information on in-hospital management and outcome are collected. Samples collected and tested vary by site and case definition (Table 2). Samples collected from all the pneumonia surveillance sites include nasopharyngeal aspirates in patients <5 years, combined oropharyngeal and nasopharyngeal swabs in patients ≥ 5 years, and blood. In addition, sputum (induced or expectorated) samples are collected from two enhanced sites, Edendale Hospital (EDH) and Klerksdorp-Tshepong Hospital Complex (KTHC) (Table 2).

Influenza like illness (ILI) surveillance

The systematic ILI surveillance programme was established in 2012 at two public health clinics serviced by the two enhanced sited (EDH and KTHC). Patients presenting at these sites meeting the ILI case definition (Table1) are enrolled prospectively. Clinical and epidemiological data are collected using standardized questionnaires and nasopharyngeal samples are collected for testing (Table 2). Dedicated staff screen and enrol patients for systematic ILI surveillance from Monday to Friday.

The Viral Watch sentinel surveillance programme, which started in 1984, was specifically designed to monitor influenza activity and has been fully described previously.[2] Participation in the programme is voluntary and is mainly composed of general practitioners who are requested to submit nasopharyngeal or oropharyngeal swabs from patients who meet the ILI case definition

(Table1). During 2015, 171 practitioners registered across South Africa submitted specimens throughout the year.

Respiratory morbidity surveillance

In order to describe the influence of the influenza season on the number of pneumonia and influenza hospitalizations, the NICD reviews anonymized data from a private hospital group. The number of hospitalizations for pneumonia and influenza during the influenza season are compared to those for the periods preceding and following the season.The start of the influenza season is defined as at least two consecutive weekly influenza detection rates of ≥10%, and the season is considered to have ended when the detection rate drops below 10% for two consecutive weeks.

In this report, findings from the pneumonia surveillance and systematic ILI surveillance are included for the following pathogens: influenza, respiratory syncytial virus (RSV), human metapneumovirus (hPMV), parainfluenza viruses 1, 2 and 3 (PIV1-3), *Streptococcus pneumoniae, Bordetella pertussis,* atypical bacterial causes of pneumonia (*Legionella species, Chlamydophila pneumoniae* and *Mycoplasma pneumoniae*), *Mycobacterium tuberculosis* and *Pneumocystis jirovecii* (PCP).

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, 2015.

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 Absence of other diagnoses	Viral watch programme and public health clinics: Jouberton and Edendale Gateway clinics
Severe acute respiratory illness (SARI)/ Acute pneumonia Patient presenting ≤ 10 days of the onset of illness	2 days - <3 months Any child hospitalised with diagnosis of suspected sepsis or physician diagnosed lower respiratory tract infection (LRTI) irrespective of signs and symptoms.	EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, Red Cross Hospital
	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, Red Cross Hospital
	≥5 years Any person hospitalised with an acute respiratory infection with fever (≥38ºC) or history of fever AND cough.	EDH, KTHC, Matikwana/Mapulaneng, RMMCH/HJH, Red Cross Hospital
Severe chronic respiratory illness (SCRI)	Any child or adult meeting the above case definitions presenting with symptoms >10 days (all sites) or any patient from EDH or KTHC with a clinical diagnosis of suspected pulmonary tuberculosis (TB) AND not meeting any of the above criteria	EDH, KTHC,Matikwana/Mapulaneng, RMMCH/HJH, Red Cross Hospital
Severe Respiratory illness (SRI)	Anyone meeting either SARI or SCRI at EDH, KTHC	EDH, KTHC

EDH = Edendale Hospital, KTHC = Klerksdorp-Tshepong Hospital Complex, RMMCH/HJH = RahimaMoosa Mother and Child Hospital/Helen Joseph Hospital

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, South Africa, 2015.

Pathogen	Programme (syndrome)	Surveillance site	Specimen collected	Test conducted
Influenza and RSV	Viral watch (ILI)	All VW sites in 9 provinces	Nasopharyngeal (NP) and oropharyngeal (OP) flocked swabs	Multiplex real-time reverse transcription polymerase chain reaction (RT-PCR)
	Systematic ILI	Edendale Gateway Clinic and Jouberton Clinic	NP and OP flocked swabs >5 years. NPA ≤5years	Multiplex RT-PCR
	Pneumonia surveillance (SARI and SCRI)	EDH, KTHC, Matikwana/ Mapulaneng, RMMCH/ HJH, Red Cross Hospital	NP and OP flocked swabs > 5 years. NPA ≤5 years	Multiplex RT-PCR
Human metapneumovirus, parainfluenza 1, 2 and 3, adenovirus, enterovirus, rhinovirus	Systematic ILI	Edendale Gateway Clinic and Jouberton Clinic	NP and OP flocked swabs > 5 years. NPA≤5 years	Multiplex RT-PCR
	Pneumonia surveillance: (SARI and SCRI)	EDH, KTHC, Matikwana/ Mapulaneng, RMMCH/ HJH, Red Cross Hospital	NP and OP flocked swabs > 5 years. NPA≤5 years	Multiplex RT-PCR
B. pertussis, M. pneumoniae, Legionella spp., C. pneumoniae	Systematic ILI	Edendale Gateway Clinic and Jouberton Clinic	NP and OP flocked swabs > 5 years. NPA≤5 years	Multiplex real-time PCR
	Pneumonia surveillance (SARI, SCRI)	Matikwana/Mapulaneng, RMMCH/HJH, Red Cross Hospital	NP and OP flocked swabs > 5 years. NPA≤5 years	Multiplex real-time PCR
	Pneumonia surveillance (SARI,SCRI)	EDH, KTHC	NP and OP flocked swabs > 5 years. NPA ≤5 years. Induced or expectorated sputum.	Multiplex real-time PCR
S. pneumoniae	Systematic ILI	Edendale Gateway Clinic and Jouberton Clinic	NP and OP flocked swabs > 5 years. NPA ≤5 years	lytA real-time PCR
	Pneumonia surveillance (SARI, SCRI)	Matikwana/Mapulaneng, RMMCH/HJH, Red Cross Hospital	NP and OP flocked swabs > 5 years. NPA ≤5 years, whole blood	lytA real-time PCR
	Pneumonia surveillance (SARI, SCRI)	EDH, KTHC	NP and OP flocked swabs > 5 years, NPA ≤5 years, induced or expectorated sputum, whole blood	lytA real-time PCR
Tuberculosis	Pneumonia surveillance (SARI, SCRI)	EDH, KTHC	Induced or expectorated sputum	GeneXpert and culture RT-PCR
Pneumocystis jirovecii	Pneumonia surveillance (SARI, SCRI)	EDH, KTHC,	Induced or expectorated sputum Oral washes, NP and OP flocked swabs > 5 years NPA ≤5 years,	Real-time PCR

ILI = influenza-like illness, SARI = severe acute respiratory illness, SCRI = severe chronic respiratory illness, EDH = Edendale Hospital, KTHC = Klerksdorp-Tshepong Hospital Complex, RMMCH/HJH = RahimaMoosa Mother and Child Hospital/Helen Joseph Hospital.

Sample collection, transport and laboratory testing for the pneumonia and ILI surveillance

Procedures for sample collection and processing for the surveillance programmes have been described previously.[1, 3-5] Upper respiratory tract samples (NP/OP and NPA) were collected in universal transport medium. Whole blood specimens were collected in EDTA containing tubes. Oral washes and sputum were collected in universal containers. Following collection, 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^{0}C at the local site laboratory before being transported to NICD on dry ice on a weekly basis. One sputum sample was tested at the surveillance site laboratory for *M. tuberculosis* using GeneXpert, and a second sputum sample was tested at the NICD for *M. tuberculosis* by culture as well as for PCP and bacterial pathogens by PCR (Table 2).

Detection of viral pathogens

Respiratory specimens were tested by multiplex real-time reverse transcriptase polymerase chain reaction (RT-PCR) assay for the following respiratory viruses: parainfluenza virus types 1, 2 and 3; human metapneumovirus, adenovirus; rhinovirus and enterovirus.[6] A commercial multiplex real-time RT-PCR assay (Fast-Track Diagnostics, Sliema, Malta) was used for detection of influenza A, influenza B and respiratory syncytial viruses. Influenza A and B positive specimens were subtyped using US Centers for Diseases Control and Prevention (CDC) real-time reverse-transcription PCR protocol and reagents (https://www.influenzareagentresource.org/).

Detection of bacterial pathogens other than tuberculosis

Induced/expectorated sputum and nasopharyngeal samples were tested for *M. pneumoniae*, *C. pneumoniae, Legionella* spp. and *B. pertussis.* DNA was extracted from the clinical specimens and tested for bacterial pathogens by real-time-PCR. A specimen was considered positive for *M. pneumoniae* if the *MP181* target was detected (Ct<45), *C. pneumoniae* if the *CP-Arg* target was detected (Ct<45) and *Legionella* spp. if the Pan-Leg target was detected (Ct<45).[7] A positive result for pertussis was obtained when a specimen was positive for *IS481* and/or *ptxS*1 genes.[8] Blood specimens were tested using quantitative real-time PCR for the presence of pneumococcal DNA (*lyt*A gene). For *lytA* testing, specimens with a *lytA* Ct-value <40 were considered positive.[9]

Detection of tuberculosis

Microbiological investigation for tuberculosis at site was performed by smear microscopy, culture and/or XpertMTB/Rif. At NICD, smear microscopy of sputum samples was performed using fluorescent auramine-O staining for acid fast bacilli (AFB). Culture was performed using liquid media with the Bactec MGIT 960 (Becton Dickinson, USA) system. Positive cultures were identified as *M. tuberculosis* complex using Ziehl-Neelsen staining and MPT64 antigen testing (Becton Dickinson, USA). Genotypic resistance to isoniazid and rifampicin in tuberculosis-positive patients was tested using the Genotype MTBDR*plus* v2 assay (Hain Life sciences, Germany).

Determination of PCP

Pneumocystis. Jirovecii was tested for one or more of the following specimens from each patient-oral wash, naso/oropharyngeal sample and sputum. DNA was extracted from the clinical specimens using an automated DNA extraction system. Fungal load was determined using a quantitative real-time PCR targeting the region coding for the mitochondrial large subunit rRNA for *P. jirovecii*.[10] All specimens with copy numbers >0 copies/µl were included as positive. These include both cases of infection and colonisation with *P. jirovecii*.

Data management

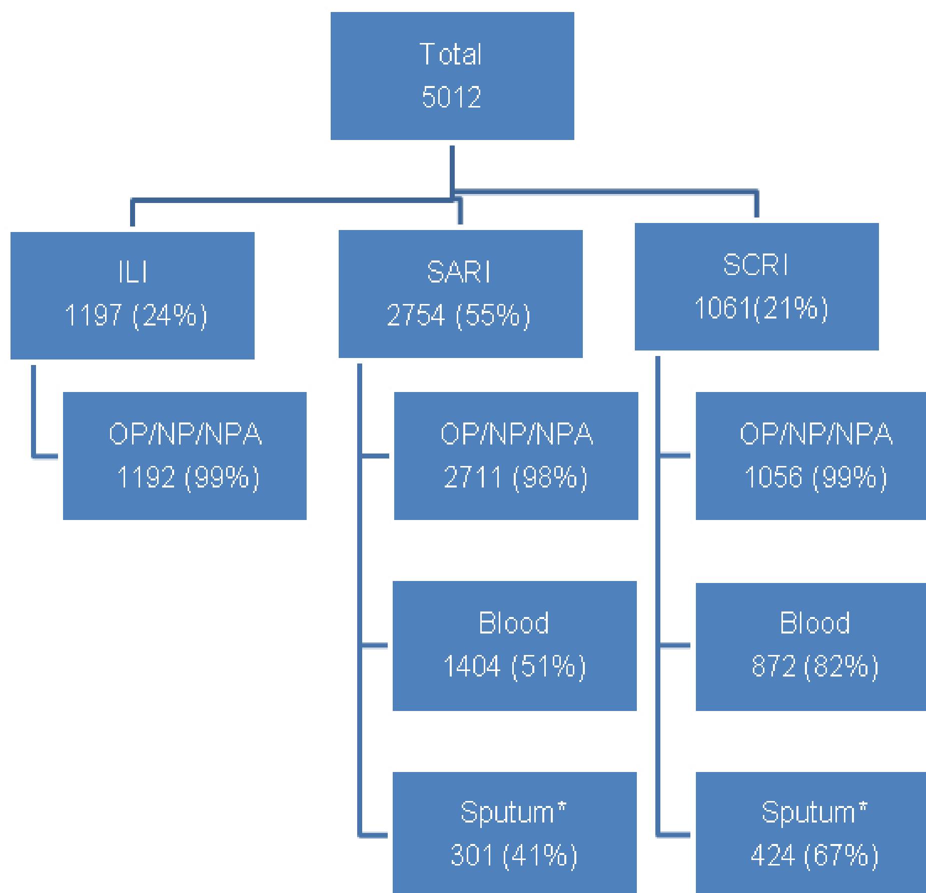
Data management was centralised at the NICD where laboratory, clinical and demographic data from enrolled patients were recorded on a Microsoft Access database.

Ethical considerations

The protocol was approved by the Research Ethics Committees of the University of the Witwatersrand, University of KwaZulu-Natal and University of Cape Town.

Results

Of the 5013 patients enrolled into the surveillance programmes in 2015, 5012 (99%) had complete data on case definition available; 1197 (24%), 2754 (55%) and 1061 (21%) met the case definition of ILI, SARI and SCRI respectively. Samples collected and tested for each of the case definitions is outlined in Figure 1. The type and number of samples collected and tested varied depending on the case definition and suitable samples available for testing. The demographic characteristics of patients enrolled in the surveillance programmes are described in Table 3.



ILI = influenza-like illness, SARI = severe acute respiratory illness, SCRI = severe chronic respiratory illness,
OP = oropharyngeal, NP = nasopharyngeal, NPA = nasopharyngeal aspirate
*Sputum collected from only two of the five sites.

Figure1: Numbers of samples collected by case definition in the systematic influenza-like illness (ILI) and pneumonia surveillance programmes (SARI and SCRI), South Africa, 2015.

Table 3: Demographic and clinical characteristics of patients with an upper respiratory sample available for testing and enrolled into the systematic influenza-like illness and pneumonia surveillance programmes, South Africa, 2015.

Characteristic	Influenza-like Illness n/N (%) N=1192	Severe Acute Respiratory Illness n/N (%) N= 2711	Severe chronic Respiratory Illness n/N (%) N=1056
Age group years			
0-4	519/1182 (44)	1993/2699 (74)	128/1050(12)
5-14	130 /1182 (11)	102/2699 (4)	18/1050 (2)
15-24	137/1182 (12)	43/2699(2)	70/1050 (7)
25-44	294 /1182(25)	329/2699 (12)	426/1050 (41)
45-64	89 /1182 (8)	164/2699 (6)	311/1050 (30)
≥ 65	13/1182 (1)	68/2699 (3)	97/1050 (9)
Female gender	733/1192 (61)	1265 /2709(47)	518/1055 (49)
Site			
Edendale Gateway clinic	865/1192 (73)	N/A	N/A
Jouberton clinic	327/1192 (27)	N/A	N/A
EDH	N/A	264/2711 (10)	296/1056 (28)
KTHC	N/A	447/2711 (16)	336/1056 (35)
Matikwana/Mapulaneng hospitals	N/A	304/2711 (11)	40/1056 (4)
RMMCH/HJH	N/A	1036/2711 (38)	373/1056 (35)
Red Cross Hospital	N/A	660/2711(24)	11/1056 (1)
Underlying illness	50/1184 (4)	321/2693 (12)	149/1049 (14)
In-hospital case fatality ratio	N/A	73/2656 (3)	75/1014 (7)

EDH = Edendale Hospital, KTHC = Klerksdorp-Tshepong Hospital Complex, RMMCH/HJH = Rahima Moosa Mother and Child Hospital/Helen Joseph Hospital

Pneumonia surveillance programme (SARI and SCRI) results

Viral pathogens

Of the 3815 patients enrolled in pneumonia surveillance, 3767 (99%) were tested for viral pathogens and 176 (5%) were positive for influenza. The influenza season started in week 20 and continued through week 25. It was predominated by influenza A(H1N1)pdm09 (80/176, 45%), followed by influenza A(H3N2) (50/176, 28%) and influenza B (45/176,26%). The peak detection rate was 23% in week 23 (Figure 2).

The overall detection rate for RSV was 13% (478/3767). The RSV season preceded the influenza season, it started in week 9 and continued through week 29. The peak detection rate of 43% was in week 16. Parainfluenza viruses 1-3 were detected in 5% (168/3767) of samples and hMPV in 2% (89/3767) of samples. There was no clear seasonality for parainfluenza viruses and hMPV (Figure 3).

The majority of cases for the different respiratory viruses were in children <5 years (influenza112/175, 64%; RSV 445/475, 94%; PIV 1-3 145/166, 87% and hMPV 82/89, 92%). The case fatality ratio was similar across the cases positive for the respiratory viruses, and ranged between 1% and 3% (Table 4).

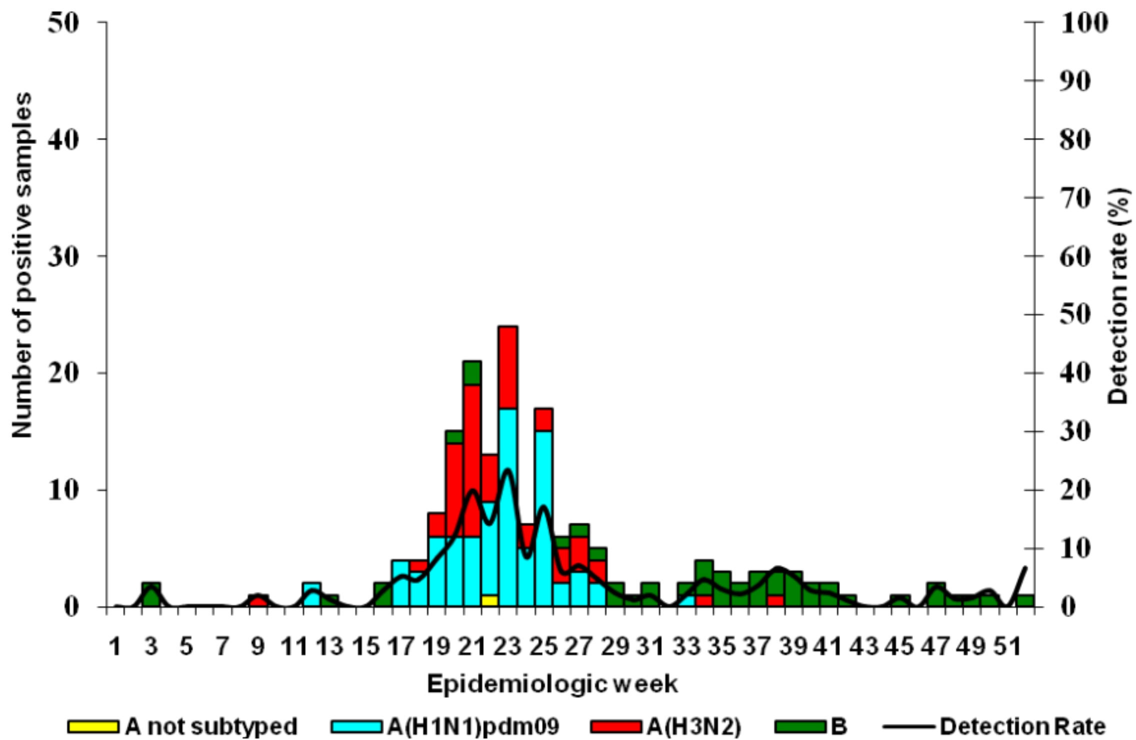


Figure 2: Numbers of samples positive for influenza and influenza detection rate, by subtype and week, in patients enrolled into the pneumonia surveillance programme and meeting the case definition of severe acute respiratory illness (SARI) or severe chronic respiratory illness (SCRI) in South Africa, 2015.

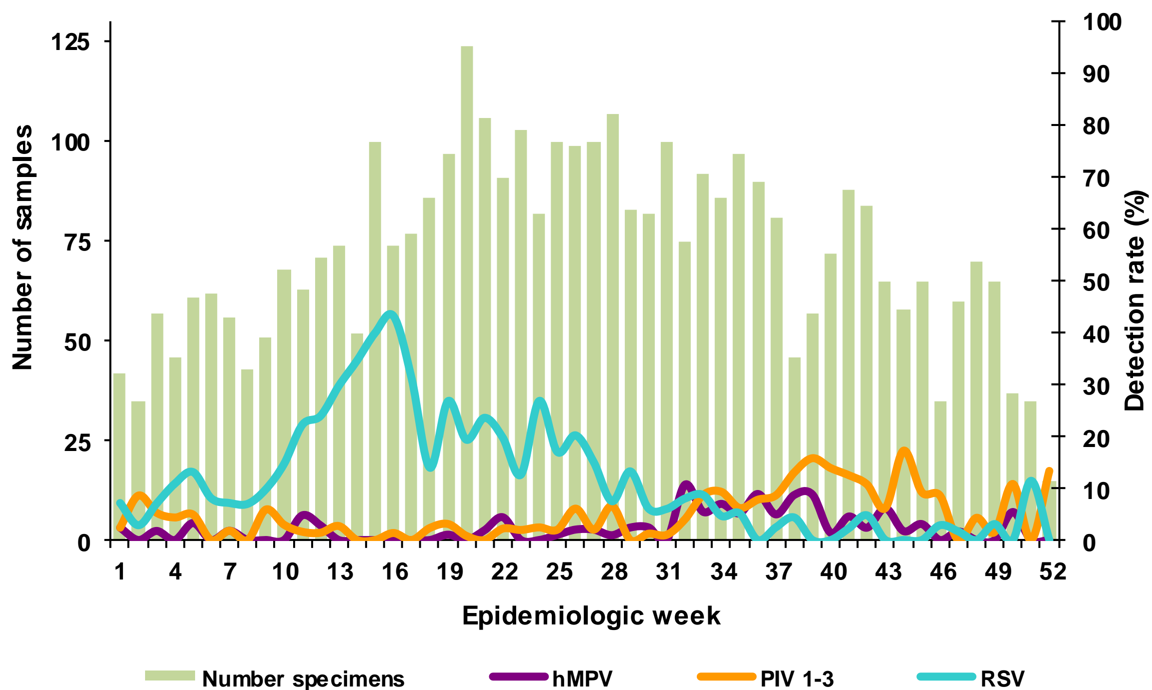


Figure 3: Numbers of samples collected and detection rates for respiratory syncytial virus (RSV), parainfluenza virus 1-3 (PIV1-3) and human metapneumovirus (hMPV), in patients meeting the case definition for severe acute respiratory illness (SARI) and severe chronic respiratory illness (SCRI), pneumonia surveillance, South Africa 2015.

Table 4: Detection rate and characteristics of patients meeting the case definition for severe respiratory illness (SARI) or severe chronic respiratory illness (SCRI) who tested positive for respiratory viruses (influenza, RSV, PIV1-3 orhMPV), pneumonia surveillance, South Africa, 2015.

	Influenza	RSV	PIV1-3	hMPV
Detection rate	176/3767 (5)	478/3767 (13)	168/3767(4)	5/3767 (2).
Age				
0-4	112/175 (64)	445/475 (94)	145/166 (87)	82/89 (92)
5-14	10//175 (6)	6/475 (1)	2/166 (1.2)	3/89(3)
15-24	2/175 (1)	1/475 (0.2)	2/166 (1.2)	0/89
25-44	27/175 (15)	10/475 (4)	13/166 (8)	3/89 (3)
45-64	17/175 (10)	9/475 (1)	2/166 (1.2)	1/89(1)
≥ 65	7/175 (4)	2/475 (0.4)	2/166 (1.2)	0/89
Female gender	81/176 (46)	216/478 (45)	83/167 (50)	50/89 (56)
Site				
EDH	31/176 (18)	63/478 (18)	20/68 (12)	8/89 (9)
KTHC	33/176 (19)	70/478 (15)	32/68 (19)	9/89 (10)
Matikwana/Mapulaneng	22/176 (12)	30/478 (6)	19/68 (11)	5/89(6)
RMMCH/HJH	63/176 (36)	164/478 (34)	49/68 (29)	21/89 (24)
Red Cross Hospital	27/176 (15)	151/478 (32)	48/68 (29)	46/89 (52)
In-hospital case fatality ration	6/174 (3)	5/468 (1)	4/167 (2)	2/89 (2)

RSV = respiratory syncytial virus, PIV = parainfluenza virus, hMPV = human metapneumovirus, RMMCH/HJH = Rahima Moosa Mother and Child Hospital/Helen Joseph Hospital, KTHC = Klerksdorp Tshepong Hospital Complex, EDH = Edendale Hospital

Bacterial pathogens

Of the 3602 patients who had respiratory samples tested for bacterial pathogens 105/3602 (3%) were positive for *B. pertussis*, 12/3591 (0.6%) for *M. pneumoniae*, 5/3590 (0.1%) for *C. pneumoniae* and 3/3591 (0.1%) for *Legionella spp*. In the same group of patients, of the 2276 blood samples tested for *S. pneumoniae,* 295 (13%) were positive (Table 5). The highest number of positive samples for the bacterial pathogens was in children <5 years, except for *Legionella spp.*, where all the cases were in the 25-44 year age group. The case fatality ratio was highest for patients testing positive for *B. pertussis* (7%, 7/101) (Table 5).The detection rate of *B. pertussis* and *S. pneumoniae* seemed to peak during the winter months (Figures 4 and 5).

Table 5: Detection rate among severe acute respiratory illness (SARI) and severe chronic respiratory illness (SCRI) cases tested, and characteristics of patients positive for *Bordetella pertussis, Mycoplasma pneumoniae, Chlamydia pneumoniae, Legionella spp.* or *Streptococcus pneumonia,* Pneumonia Surveillance Programme, South Africa 2015.

	B. pertussis* **n/N (%)**	**M. pneumoniae*** **n/N (%)**	**C. pneumoniae*** **n/N (%)**	**Legionella spp.*** **n/N (%)**	**S. pneumoniae** **n/N (%)****
Detection rate	105/3602 (3)	21/3591 (0.6)	5/3590 (0.1)	3/3591 (0.1)	295/2276 (13)
Age					
0-4	76/104 (73)	13/21 (62)	5/5(100)	0/3	111/295 (38)
5-14	6/104 (6)	2/21 (10)	0/5	0/3	16/295 (5)
15-24	1/104 (1)	2/21 (10)	0/5	0/3	14/295 (5)
25-44	10/104 (10)	4/21(19)	0/5	3/3 (100)	89/295 (30)
45-64	9/104 (9)	0/21 (0)	0/5	0/3	50/295 (17)
≥ 65	2/104 (2)	0/21 (0)	0/5	0/3	15/295 (5)
Female gender	48/104 (46)	9/21 (43)	3/5 (60)	1/3 (33.3)	156/295 (47)
Site					
EDH‡	23/105 (23)	1/21 (5)	0/5	1/3 (33)	61/295 (21)
KTHC‡	26/105 (25)	3/ 21 (14)	3/5 (60)	2/3 (67)	89/295 (30)
Matikwana/Mapulaneng#	17/105 (16)	2/21 (10)	0/5	0/3	47/295 (16)
RMMCH/HJH#	32/105 (30)	8/21 (38)	1/5 (20)	0/3	72/295 (24)
Red Cross Hospital#	7/105 (7)	7/21 (33)	1/5 (20)	0/3	26/295 (9)
In-hospital case fatality ratio	7/101 (7)	1/19 (5)	0/5	0/3	9/290 (3)

*Nasopharyngeal ± sputum samples tested; **blood samples; ‡ Nasopharyngeal, sputum and blood samples collected; # Nasopharyngeal and blood samples collected.

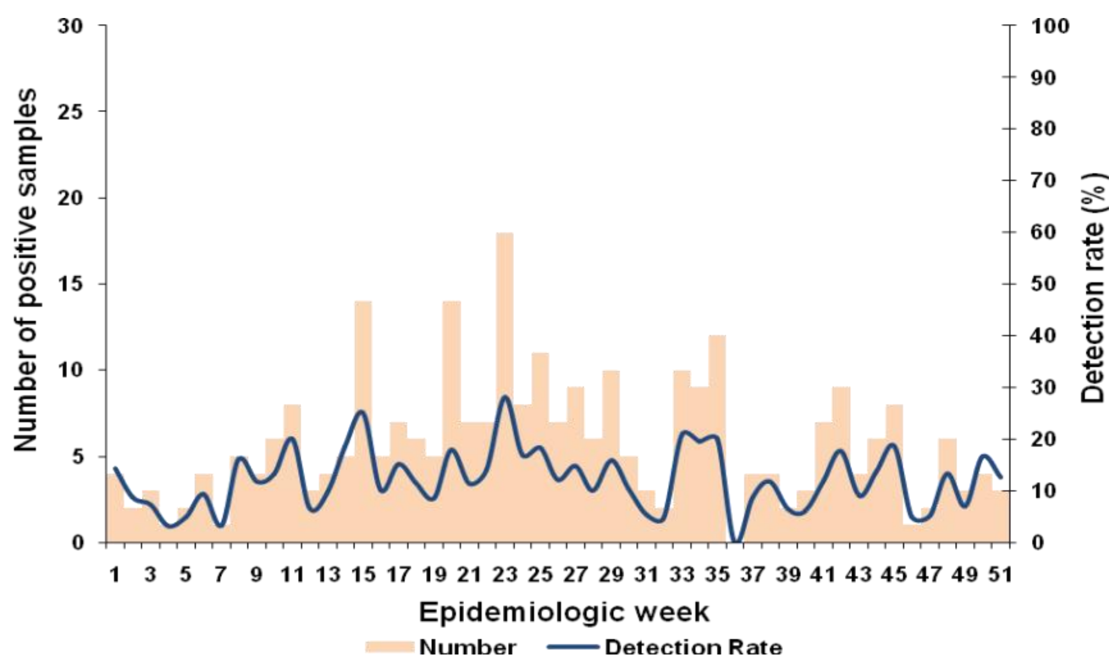


Figure 4: Numbers of positive samples and detection rate of *Streptococcus pneumoniae* from patients with severe acute respiratory illness (SARI) or severe chronic respiratory illness (SCRI) by week, Pneumonia Surveillance Programme, South Africa, 2015.

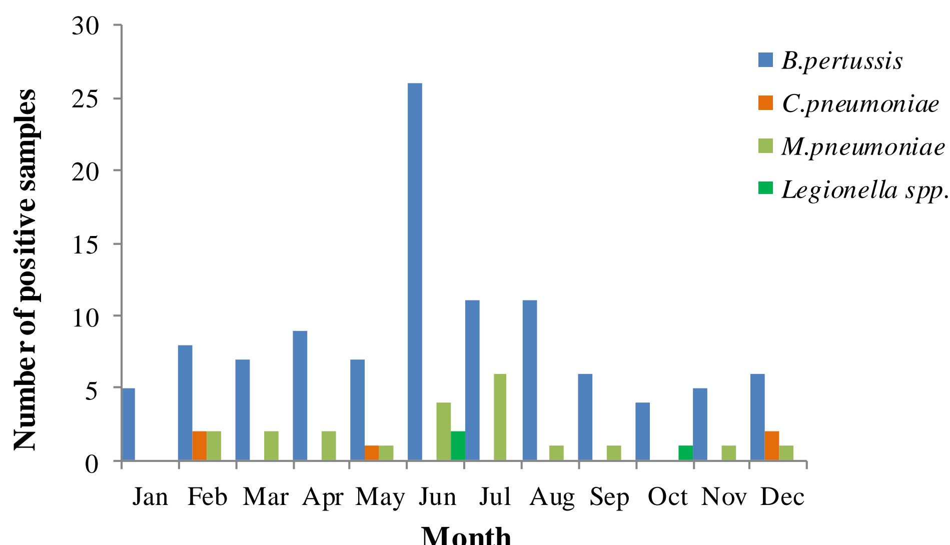


Figure 5: Numbers of positive samples of *Bordetella pertussis*, *Mycoplasma pneumoniae*, *Legionella spp.*and *Chlamydia pneumoniae* among patients with severe acute respiratory illness (SARI) or severe chronic respiratory illness (SCRI) by month, Pneumonia Surveillance Programme, South Africa, 2015.

Tuberculosis and *Pneumocystis jirovecii* pneumonia (PCP)

Of the 738 patients tested for *M. tuberculosis*, 82 (11%) were positive. Tuberculosis was detected throughout the year with no obvious seasonality (Figure 6). The majority of samples that tested positive for tuberculosis were collected at the KTHC site (57/82, 70%) and were in the 25 to 44 year age group (43/80, 54%) (Table 6).

Of the 258 (12%) samples that tested positive for PCP, 131 (51%) were from nasopharyngeal samples, 13 (5%) were from oral rinse samples and 114 (44.2%) from sputum. Similar to TB, there was no obvious seasonality (Figure 7). Most of the patients with positive samples were in the age group 25 to 44 years (87/198, 43.9%) and were female (113/201, 56.2%).

Table 6: Detection rate and characteristics of patients fitting the case definition of severe respiratory illness (SRI) enrolled into pneumonia surveillance and testing positive for tuberculosis and *Pneumocystis jirovecii.*

	Tuberculosis n/N(%)	Pneumocystis jirovecii n/N(%)
Detection rate	82/738 (11)	201/1282 (16)
Age group (years)		
0-4	2/80(2.5)	61/198 (31)
5-14	2/80 (1)	1/198 (1)
15-24	13/80 (16)	6/198 (3)
25-44	43/80 (54)	87/198 (44)
45-64	20/80 (25)	38/198 (19)
≥ 65	1/80 (1)	5/198 (2)
Female gender	41/82 (50)	113/201 (56)
Site		
EDH	25/82 (30)	84/201 (42)84/237 (35)
KTHC	57/82 (70)	117/201 (58)

EDH = Edendale Hospital, KTHC = Klerksdorp-Tshepong hospital complex

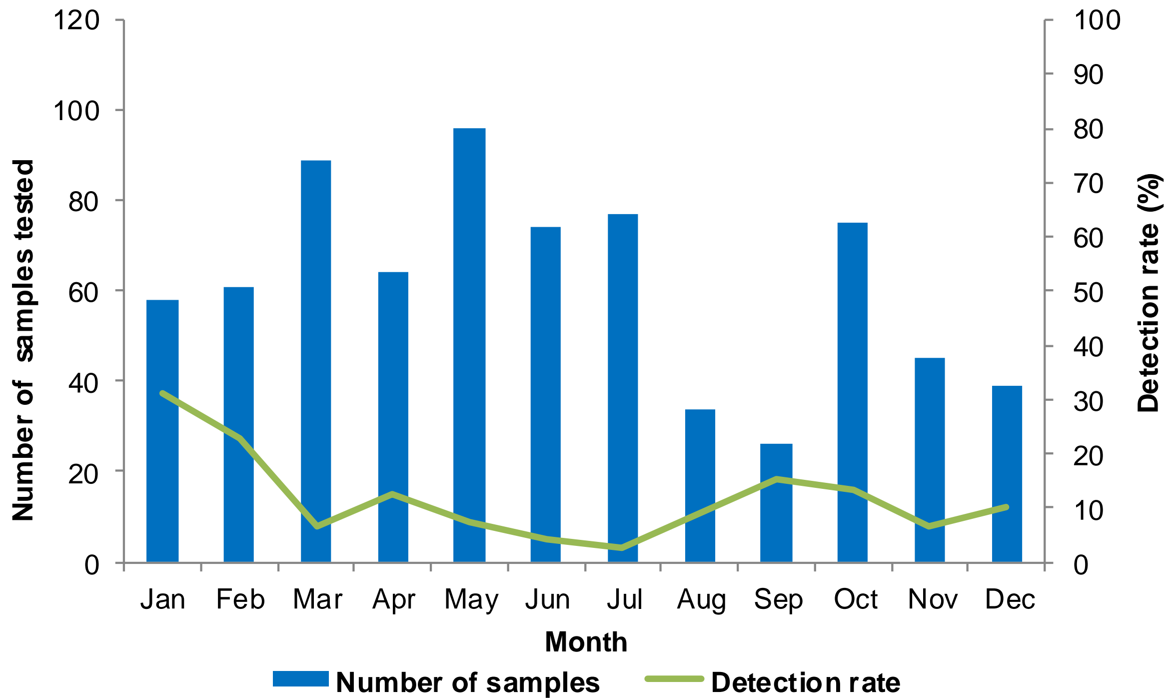


Figure 6: Numbers of samples tested for tuberculosis and detection rate among patients with severe acute respiratory illness (SARI) or severe chronic respiratory illness (SCRI) at Enhanced sites by month, Pneumonia Surveillance Programme, South Africa, 2015.

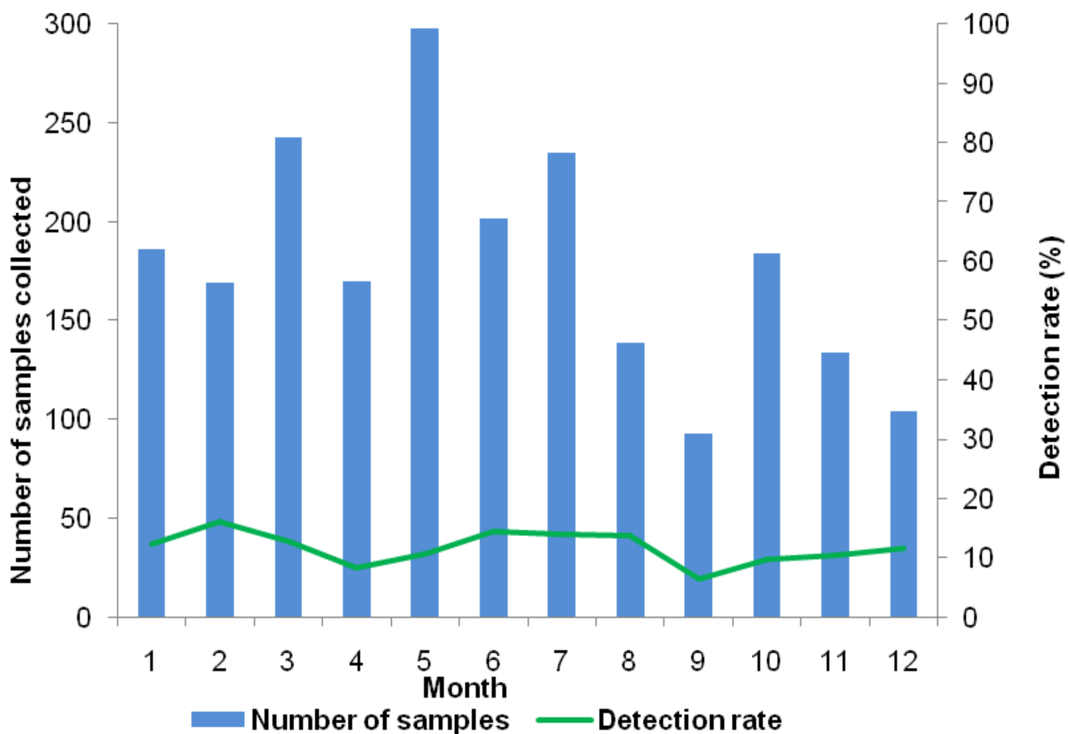


Figure 7: Numbers of samples tested for *Pneumocystis jirovecii* and detection rate for patients meeting the severe respiratory illness (SARI) or severe chronic respiratory illness (SCRI) case definition at the Enhanced sites, Pneumonia Surveillance Programme, South Africa, 2015.

Systematic ILI surveillance at primary health clinics

Respiratory viruses

During 2015, 1197 patients with ILI were enrolled at the two primary health clinics and 1192 (99%) samples were tested for respiratory pathogens. The overall detection rate of influenza was 11% (131). Of the 131 positive samples, 46 (35%), 44 (34%), 40 (31%) and 1 (<1%) were positive for influenza B, influenza A (H1N1)pdm09, influenza A(H3N2) and influenza A unsubtyped respectively (Figure 8). There were no dual infections. Influenza positive samples were detected from week 9. The detection rate reached 10% in week 17 and was sustained above 10% until week 28 when it dropped to below 10%. It rose above 10% again in week 32 and 35 (Figure 8). Of the 1192 samples tested, 50 (4%) tested positive for parainfluenza 1-3, 81 (7%) for RSV, and 11 (1%) for human metapneumovirus. RSV demonstrated a defined seasonality which preceded the influenza season. The detection rate for RSV rose above 10% in week 7 and was sustained at ≥10% until week 17 (Figure 9).

Bacterial pathogens

Of the 1139 patients enrolled with ILI and tested for bacterial pathogens, 23/1136 (2%) tested positive for *B. pertussis*, 3/1139 (0.3%) for *M. pneumoniae* and 3/1139 (0.3%) for *C. pneumonia* (Table 7). The highest number of positive samples for *B. pertussis* was in the 5 -14 age group (6/23, 26%). The highest number of positive cases was in children <5 years (2/3, 67%) and in individuals <25 years for *M. pneumoniae and C. pneumoniae respectively*. There were no positive samples for *Legionella* spp. The number of cases positive for *B. pertussis* increased during the winter months (June to August). There was no clear seasonality for the other bacterial pathogens (Figure 10).

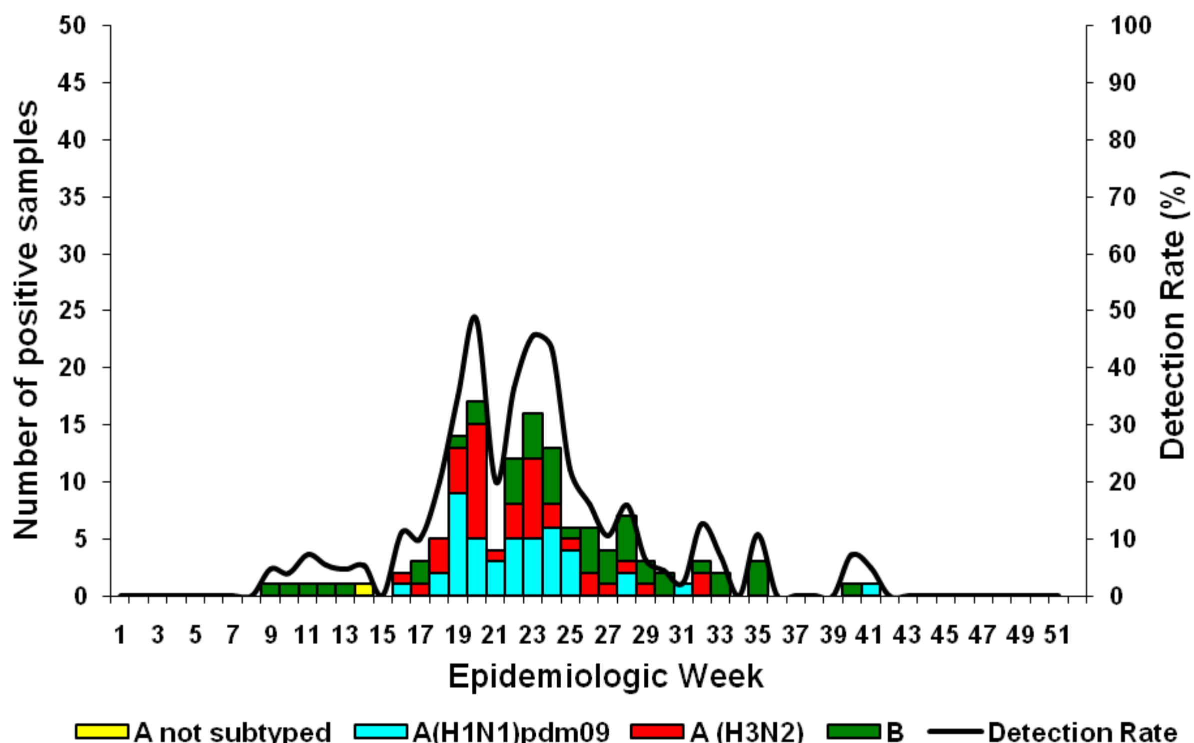


Figure 8: Influenza detection rate, by influenza subtype and week, in patients enrolled with influenza-like Illness (ILI) at the two primary healthcare clinics, South Africa, 2015.

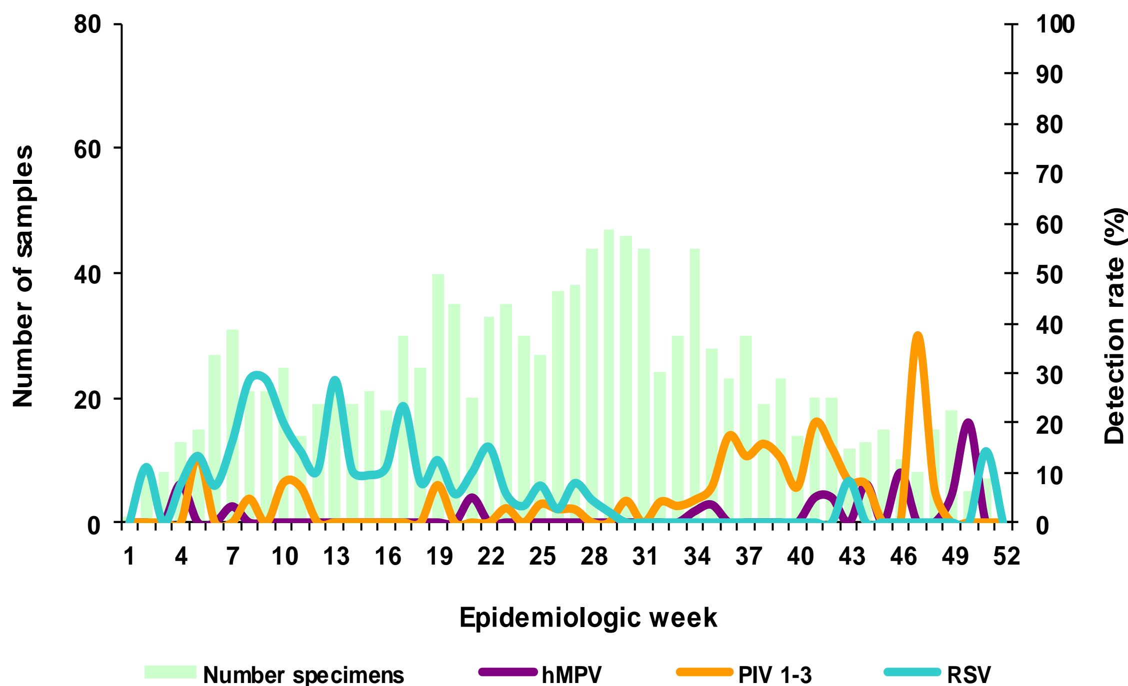


Figure 9: Detection rate of human metapneumovirus (hMPV), parainfluenza virus(PIV)1-3 and respiratory syncytial virus(RSV) by week in patients enrolled with influenza-like illness (ILI) at two primary health clinics, South Africa, 2015.

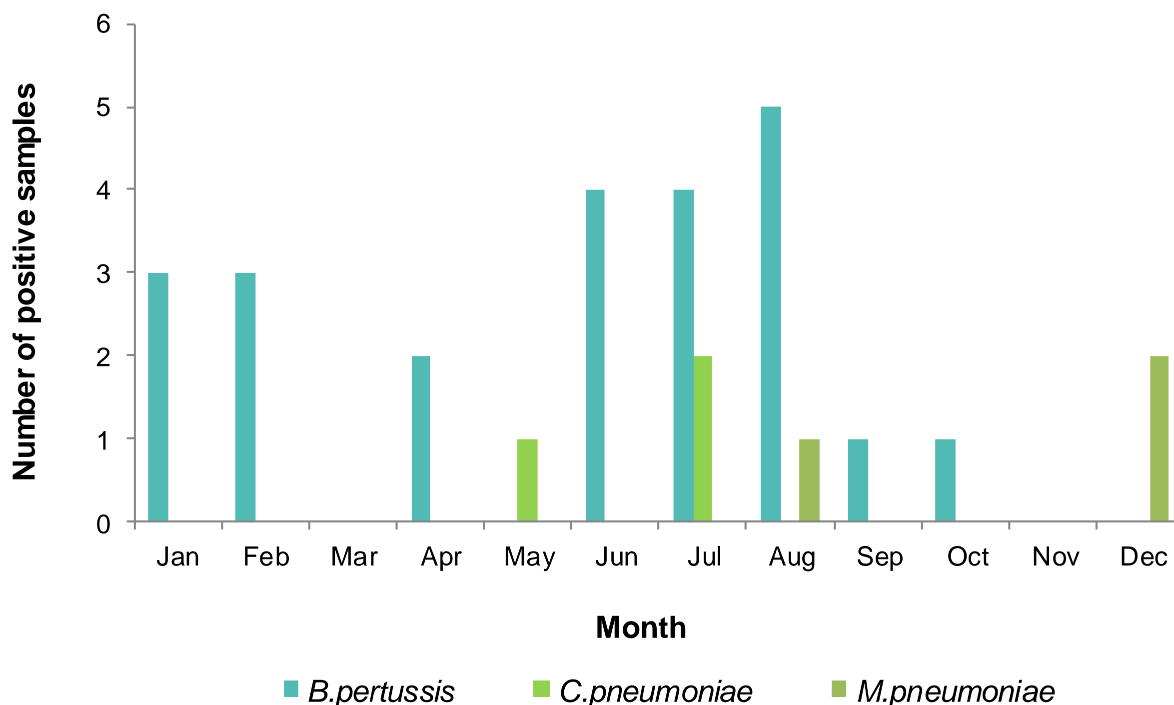


Figure 10: Numbers of positive samples for bacterial pathogens by month, in patients who met the influenza-like Illness (ILI) case definition at primary health clinics, South Africa, 2015.

Table 7: Detection rate and characteristics of patients with influenza-like illness (ILI) enrolled at public health clinics who tested positive for bacterial pathogens, South Africa, 2015.

	B. pertussis n/N(%)	M. pneumoniae n/N(%)	C .pneumoniae n/N(%)
Detection rate	23/1136 (2)	3/1139 (0.3)	3/1139(0.3)
Age group, years			
0-4	5/23(22)	2/3 (67)	1/3 (33.3)
5-14	6/23 (26)	0/3 (0)	1/3 (33.3)
15-24	4/23 (17)	0/7	1/3 (33.3)
25-44	4/23 (17)	1/3 (33)	0
45-64	4/23 (17)	0 /3	0
≥ 65	0/23 (0)	0/3 (0)	0
Female gender	16/23 (70)	2/3(67)	2/3(67)
Site			
Edendale Gateway clinic	17/23 (74)	2/3(67)	2/3(67)
Jouberton clinic	6/23 (26)	1/3(33)	1/7 (33)

Note: No samples tested positive for *Legionella spp*. in ILI patients

Additional surveillance activities

Viral watch (VW)

In 2015, 117 general practitioners across the 9 provinces participated in the VW programme. A total of 1136 samples was tested for influenza; of these 449 (40%) tested positive for influenza. The season was dominated by influenza A(H1N1)pdm09 (256/449, 57%), followed by influenza A(H3N2) (191/515,42%); and influenza B (82/449 ,18%). The season started in week 16 (ending 19 April), peaked in week 23 (ending 7 June) and ended in week 37 (ending 13 September) (Figure 11).

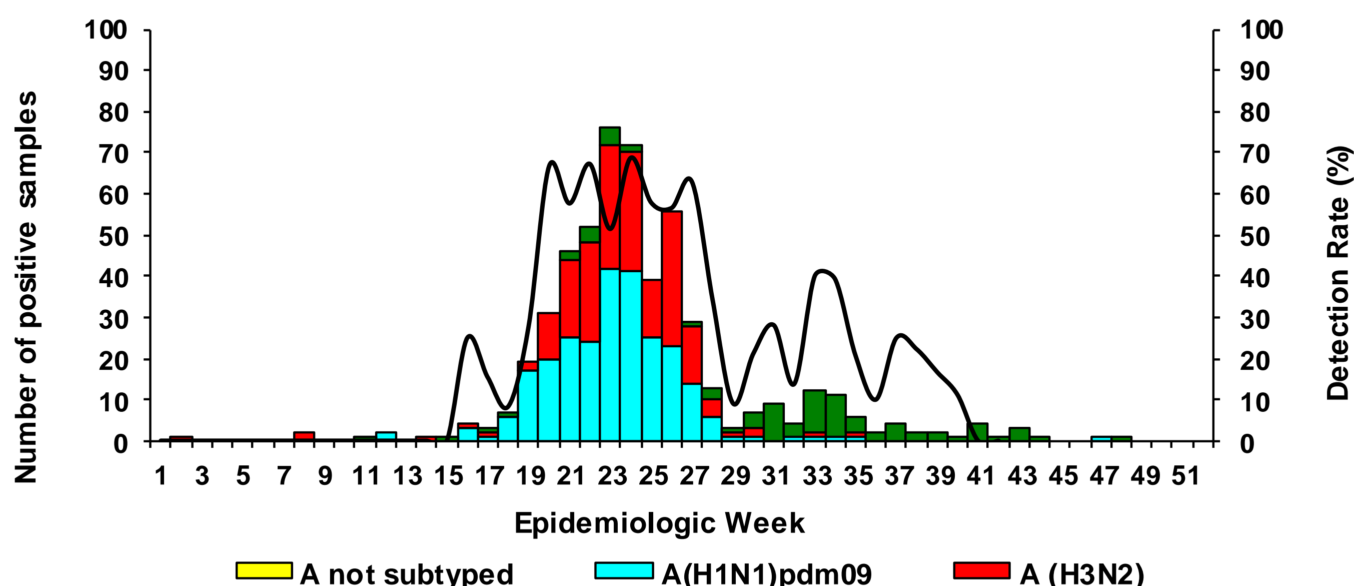


Figure 11: Numbers of samples and influenza detection rate by viral subtype and week for patients meeting the case definition of ILI, Viral Watch programme, South Africa, 2015.

Respiratory morbidity surveillance

During 2015 there were 1 169 554 consultations reported to the NICD through the respiratory morbidity data mining surveillance system. Of these, 28 655 (2%) were due to pneumonia or influenza (P&I) (International Classification of Diseases 10 codes J10-18). There were 21 401 (75%) inpatients and 7 254 (25%) 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 '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 (Figures 12 and 13, and cross reference Figure 3 - pneumonia surveillance viruses, and Figure 9 - ILI viruses).

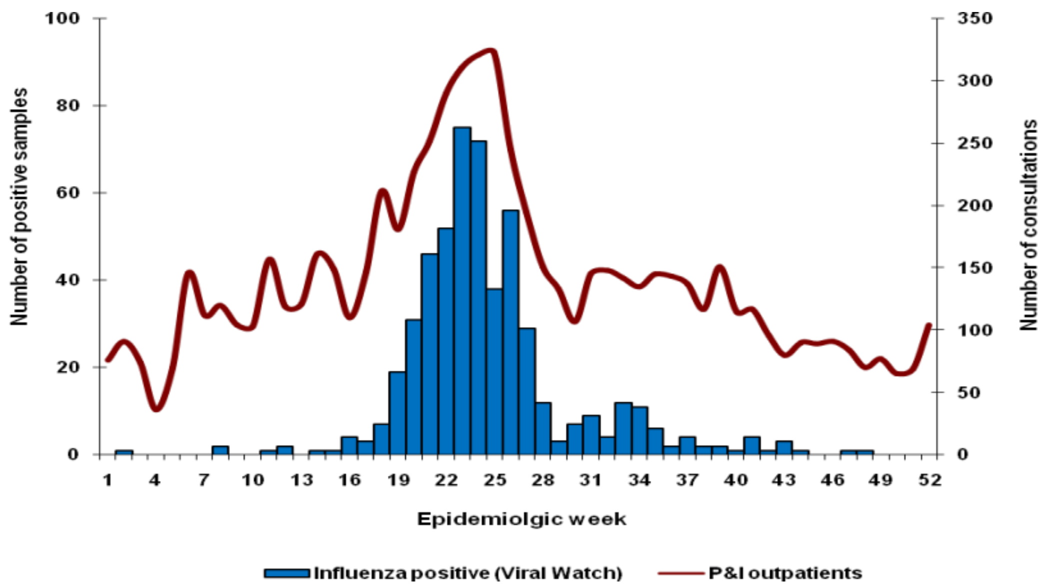


Figure 12: Numbers of private hospital outpatient consultations with a discharge diagnosis of pneumonia and influenza (P&I), and numbers of influenza positive viral isolates (Viral Watch) by week, South Africa, 2015.

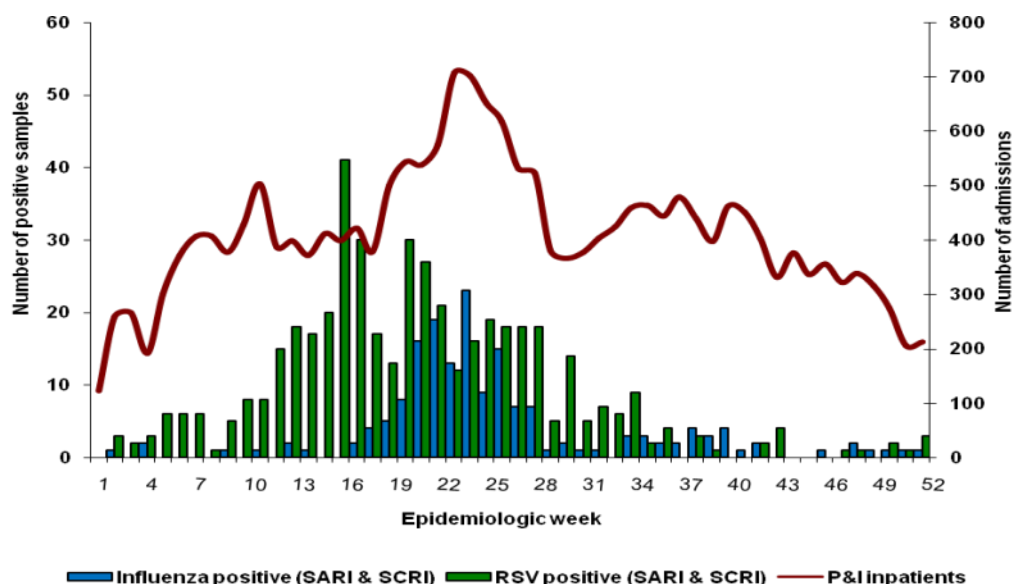


Figure 13: Numbers of private hospital admissions for pneumonia and influenza, as well as numbers of influenza positive viral isolates and respiratory syncytial virus (RSV) positive isolates (SARI and SCRI) by week, South Africa, 2015.

Discussion

The influenza season in South Africa in 2015 was predominately influenza A(H1N1)pdm09, followed by influenza A(H3N2) and influenza B. The season started in week 17 at the ILI sites but the detection rate in the pneumonia surveillance programme remained constantly above 10% from week 20. The 2015 influenza season started early compared to previous years in which the mean onset of the influenza season was week 22 (range 17-28), with an average duration of 13 weeks (range 7-25).[2] The RSV season preceded the influenza season, starting in week 7 at the ILI sites and in week 9 at the pneumonia surveillance sites. The 2015 RSV season started two weeks later than the 2014 season.[1] There was a suggestion of a winter peak for some of the bacterial pathogens including *B.pertussis and S.pneumoniae*. There was no defined seasonality for the other respiratory pathogens.

Among cases enrolled as part of pneumonia surveillance, the common pathogens detected were *S. pneumoniae* and RSV, followed by tuberculosis, PCP and influenza. All the other pathogens were detected in <5% of individuals tested. Pertussis, while relatively less common, was associated with a high case-fatality ratio of 7% (7/101). Among ILI cases the common pathogens detected were influenza followed by RSV and parainfluenza 1-3. The other respiratory pathogens were detected in ≤2% of cases.

The Centre for Respiratory Diseases & Meningitis, NICD, is working towards comprehensive surveillance for the clinical syndromes of ILI and pneumonia. This is the second report to combine the viral pathogens with the additional testing for bacterial pathogens and some of the atypical causes of pneumonia in our setting. Work is being done on the interaction between these pathogens and the risk factors for severe disease which will assist clinicians and policy makers to improve health care and implement prevention strategies such as vaccines.

Acknowledgements

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References

1. Cohen C, Frean J, Treurnicht F, Iyaloo S, Ismail N, Mcanerney J, Moyes J, Poonsamy B, von Gottberg A, Walaza S, Wolter N. Respiratory pathogens from influenza-like illness and pneumonia surveillance programmes, South Africa, 2014. *Communicable Diseases Surveillance Bulletin* 2015; 13: 10-30.
2. McAnerney JM, Cohen C, Moyes J, Besselaar TG, Buys A, Schoub BD, et al. Twenty-five years of outpatient influenza surveillance in South Africa, 1984-2008. *J InfectDis* 2012; 206 Suppl 1:S153-S8.
3. Cohen C, Moyes J, Tempia S, Groom M, Walaza S, Pretorius M, et al. Severe influenza-associated respiratory infection in a high HIV prevalence setting, South Africa, 2009-2011. *Emerg Infect Dis* 2013;19 (11):1766-74.
4. Moyes J, Cohen C, Pretorius M, Groome M, von Gottberg A, Wolter N, et al. Epidemiology of respiratory syncytial virus-associated acute lower respiratory tract infection hospitalizations among HIV-infected and HIV -uninfected South African children, 2010-2011. *J Infect Dis* 2013;208 Suppl 3:S217-S26.
5. Walaza S, Tempia S, Dawood H, Variava E, Moyes J, Cohen AL, et al., Influenza virus infection is associated with increased risk of death amongst patients hospitalised with confirmed pulmonary tuberculosis in South Africa. Options for the Control of Influenza VIII Conference; 20130 9/20130; Cape Town, South Africa 2013.
6. Pretorius MA, Madhi SA, Cohen C, Naidoo D, Groome M, Moyes J, et al. Respiratory viral coinfections identified by a 10-plex real-time reverse-transcription polymerase chain reaction assay in patients hospitalized with severe acute respiratory illness - South Africa, 2009-2010. *J Infect Dis* 2012; 206 Suppl 1:S159-65.
7. Thurman KA, Warner AK, Cowart KC, Benitez AJ, Winchell JM. Detection of *Mycoplasma pneumoniae*, *Chlamydia pneumoniae* and *Legionella spp*. in clinical specimens using a single-tube multiplex real-time PCR assay. *Diagn Microbiol Infect Dis* 2011;70(1):1-9.
8. Tatti KM, Sparks KN, Boney KO, Tondella ML. Novel multitarget real-time PCR assay for rapid detection of *Bordetella* species in clinical specimens. *J clin microbiol* 2011; 49(12):4059-66.
9. Carvalho MG, Tondella ML, McCaustland K, Weidlich L, McGee L, Mayer LW, et al. Evaluation and improvement of real-time PCR assays targeting lytA, ply, and psaA genes for detection of pneumococcal DNA. *J Clin Microbiol* 2007;45(8):2460-6.
10. Dini L, du Plessis M, Frean J, Fernandez V. High prevalence of dihydropteroate synthase mutations in *Pneumocystis jirovecii* isolated from patients with Pneumocystis pneumonia in South Africa. *J Clin Microbiol* 2010;48(6):2016-21.

Table 1: Provisional number of laboratory confirmed cases of diseases under surveillance reported to the NICD - South Africa, corresponding periods 1 January - 31 December 2014/2015*

Disease/Organism	1 Jan to 31 Dec, year	EC	FS	GA	KZ	LP	MP	NC	NW	WC	South Africa
Anthrax	2014	0	0	0	0	0	0	0	0	0	0
	2015	0	0	0	0	0	0	0	0	0	0
Botulism	2014	0	0	0	0	0	0	0	0	0	0
	2015	0	0	1	0	0	0	0	0	0	1
Cryptococcus spp.	2014	738	235	1422	1535	235	363	43	300	808	5679
	2015	673	226	1203	1336	261	332	46	385	548	5010
Haemophilus influenzae, invasive disease, all serotypes	2014	31	17	96	50	0	20	5	8	90	317
	2015	27	9	111	37	8	9	1	3	118	323
Haemophilus influenzae, invasive disease, < 5 years											
Serotype b	2014	2	2	12	3	0	0	1	0	10	30
	2015	1	1	5	1	1	0	0	1	6	16
Serotypes a,c,d,e,f	2014	1	1	6	3	0	1	1	0	5	18
	2015	0	2	5	2	1	0	0	0	10	20
Non-typeable (unencapsulated)	2014	2	1	15	6	0	1	1	0	21	47
	2015	1	0	19	2	1	1	0	0	17	41
No isolate available for serotyping	2014	3	1	24	12	0	3	0	3	1	47
	2015	2	2	22	3	2	2	0	1	8	42
Measles	2014	2	2	16	6	0	3	31	1	5	66
	2015	3	0	3	2	1	0	3	1	4	17
Neisseria meningitidis, invasive disease	2014	36	5	56	25	0	2	0	2	66	192
	2015	27	9	46	23	1	3	2	4	41	156
Novel Influenza A virus infections	2014	0	0	0	0	0	0	0	0	0	0
	2015	0	0	0	0	0	0	0	0	0	0
Plague	2014	0	0	0	0	0	0	0	0	0	0
	2015	0	0	0	0	0	0	0	0	0	0
Rabies	2014	3	0	0	0	1	0	0	1	0	5
	2015	3	1	0	1	3	0	0	0	0	8
Salmonella typhi	2014	4	4	51	18	1	10	0	0	21	109
	2015	3	1	29	9	1	12	0	1	20	76
Streptococcus pneumoniae, invasive disease, all ages	2014	228	184	987	497	35	122	41	106	532	2732
	2015	236	131	975	352	101	83	27	106	632	2643
Streptococcus pneumoniae, invasive disease, < 5 years	2014	29	19	204	84	8	15	8	18	80	465
	2015	26	12	161	53	17	15	5	26	62	377
Vibrio cholerae O1	2014	0	0	2	0	0	0	0	0	0	2
	2015	0	0	0	0	0	0	0	0	0	0
Viral Haemorrhagic Fever (VHF)											
Crimean Congo Haemorrhagic Fever (CCHF)	2014	0	2	0	0	0	0	4	0	0	6
	2015	0	1	0	0	0	0	0	0	0	1
Other VHF (not CCHF)	2014	0	0	0	0	0	0	0	0	0	0
	2015	0	0	0	0	0	0	0	0	0	0

Footnotes

*Numbers are for cases of all ages unless otherwise specified. Data presented are provisional cases reported to date and are updated from figures reported in previous bulletins.

Provinces of South Africa: EC – Eastern Cape, FS – Free State, GA – Gauteng, KZ – KwaZulu-Natal, LP – Limpopo, MP – Mpumalanga, NC – Northern Cape, NW – North West, WC – Western Cape

0 = no cases reported

Table 2: Provisional laboratory indicators for NHLS and NICD, South Africa, corresponding periods 1 January - 31 December 2014/2015*

Programme and Indicator	1 Jan to 31 Dec, year	EC	FS	GA	KZ	LP	MP	NC	NW	WC	South Africa
Acute Flaccid Paralysis Surveillance											
Cases < 15 years of age from whom specimens received	2014	59	24	85	79	47	44	26	14	41	419
	2015	86	20	113	99	71	62	17	9	33	510

Footnotes

*Numbers are for all ages unless otherwise specified. Data presented are provisional numbers reported to date and are updated from figures reported in previous bulletins.

Provinces of South Africa: EC – Eastern Cape, FS – Free State, GA – Gauteng, KZ – KwaZulu-Natal, LP – Limpopo, MP – Mpumalanga, NC – Northern Cape, NW – North West, WC – Western Cape

Monitoring for the presence of polio in a country is based on AFP (acute flaccid paralysis) surveillance – the hallmark clinical expression of paralytic poliomyelitis. The clinical case definition of AFP is an acute onset of flaccid paralysis or paresis in any child under 15 years of age. AFP is a statutory notifiable disease and requires that 2 adequate stool specimens are taken as soon as possible, 24 to 48 hours apart, but within 14 days after onset of paralysis, for isolation and characterisation of polio virus. The differential diagnosis of AFP is wide, the most common cause of which is Guillain-Barre Syndrome. The incidence of AFP in a population has been studied in a number of developing countries and WHO have determined, as a result of these studies, that the criterion for adequate surveillance of AFP is 4 cases per 100 000 population of children less than 15 years of age (it was formerly 1 per 100,000 but this was thought to be inadequately sensitive).

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