

# COMMUNICABLE DISEASES SURVEILLANCE BULLETIN

NOVEMBER 2007



## FOREWORD

In this month's bulletin we highlight outbreaks of infectious diseases in South Africa. The main focus of the edition is a number of brief reports describing recent outbreaks which have occurred in South Africa. The outbreaks described have been chosen to represent the broad spectrum of outbreaks encountered locally. It is important to systematically document these outbreaks and the lessons learned from them so that we may build up a repository of knowledge which may lead to improved responses in future.

Documentation of outbreaks also assists in prioritizing diseases for control and the development of guidelines for disease prevention.

We have also included two theoretical articles on the role of the laboratory in outbreak investigation and the steps in an outbreak investigation and hope these may serve as a useful reference. We hope to include regular short reports describing local outbreaks in future editions of the bulletin and invite submissions from interested parties.

Cheryl Cohen  
Editor

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## THE ROLE OF THE LABORATORY IN OUTBREAKS OF COMMUNICABLE DISEASES

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### Introduction

The role of the laboratory in the diagnosis of infectious disease in the clinic is well established. It has been shown that 60 - 70% of important clinical decisions such as definitive diagnosis and choice of medication, admission and discharge decisions are based on laboratory results<sup>1</sup>. The laboratory's importance in public health decision making has been less certain and well defined. However, this is changing: over the past decade and especially with the increasing recognition of potential for bio-warfare and emerging infectious diseases<sup>2</sup>, attention is increasingly focusing on the role of the laboratory in public health emergencies and decision making. This article will discuss

the role the laboratory plays in outbreaks of communicable diseases specifically but will also place the laboratory in the broader context of public health. I shall attempt to show that the laboratory is crucial. This is in line with many recently published international and local regulations. However, in keeping with many of these regulations I shall focus not only on the capacities used in the analytic phase of the testing cycle (which has traditionally been the focus of attention<sup>1</sup>), but also on the importance of the pre- and post-analytic phases. As will be seen, just as these phases of laboratory testing cycle are often neglected in the

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diagnostic laboratory<sup>1,3</sup> such neglect cannot go unchecked where communities' health is concerned, especially in emergencies where timeliness, accuracy and communication are of the utmost importance.

### International and Local Regulations and Standards

The overarching instrument in international health law regarding global control of communicable disease outbreaks is the International Health Regulations (IHR)<sup>4</sup>, now in effect since June 2007. The overall purpose and scope are well known "To prevent, protect against, control and provide a public health response to the international spread of disease in ways that are commensurate with and restricted to public health risks, and which avoid unnecessary interference with international traffic and trade." The regulations regarding surveillance (Article 5), notification (Article 6) and other communications and verifications are laid out in 66 Articles. Of more practical concern though is the information to be found in the annexes. Annex One, Section A outlines the "Core Capacity Requirements for Surveillance and Response" of member states (of which South Africa is part). Of particular note is that the IHR consider laboratory results as "essential information" required "to implement preliminary control measures immediately" [Number 4, paragraphs (b) and (c) respectively]. Such sentiments are echoed in the National Health Laboratory Service Act of 2000, where by definition the NHLS is required "to promote co-operation between the Republic and other countries with regard to the epidemiological surveillance and management of diseases through the monitoring of laboratory results<sup>5</sup>" as well as in the National Institute for Communicable Diseases' mission statement<sup>6</sup>. All these documents reflect a trend in recognition towards integral involvement of the laboratory in public health decision making and action which to the best of the author's knowledge and despite the existence of 'public health laboratories' both locally and internationally for many years, were first systematically laid out in a White Paper of the Association of Public Health Laboratories (APHL), entitled "Core functions and Capabilities of state Public Health Laboratories"<sup>2,7</sup>. Although these guidelines were published for state laboratories in the United States, the core functions can be applied globally. The guidelines also acknowledge that pre- as well as post- analytical variables are part of the core functions, which are defined as follows (in no particular order of importance)<sup>7</sup>

- Disease prevention control and surveillance
- Integrated data management
- Reference and specialized testing
- Environmental health and protection
- Food safety
- Laboratory improvement and regulation
- Policy development
- Emergency response
- Public health related research
- Training and education

- Partnership and communication

### Laboratory support for Outbreak Detection and Investigation

All of the abovementioned APHL core functions apply to the role of the laboratory in outbreaks. This discussion will focus on a few of the functions in more detail, bearing in mind the steps followed in an outbreak investigation and into which phase of the testing cycle these fall. The testing cycle is also a good tool for monitoring laboratory quality systems, which in an emergency situation require special attention in order to achieve the goal of early and effective control.

### Surveillance

Surveillance is the foundation of a good outbreak detection system<sup>8</sup>. For many communicable diseases, surveillance is achieved through legally sanctioned notification systems. Although notification, of necessity for the sake of rapidity, is usually clinically or syndromically based, laboratory surveillance may strengthen the system and thus the public health response. For example laboratory-based surveillance may provide information on the most prevalent serogroups of *Neisseria meningitidis* in a given area and population over a given time. Should an outbreak occur, a public health agency could choose vaccine type with a certain degree of confidence. Similarly laboratory surveillance systems for antimicrobial susceptibility patterns in certain epidemic prone organisms known for their capacity to develop resistance may be very useful in choosing empiric therapy.

### Deciding whether this is an outbreak?

The laboratory may be of assistance in this first and very necessary step of outbreak investigation. Commonly, as laboratories are often 'central repositories' of clinical specimens for a large geographical area, a laboratory may be the first to notice an unusual increase in specimen numbers. Conversely, a laboratory may be able to rule out an outbreak, as an increase in positive results may simply be due to the introduction of a new diagnostic test.

### Confirming the Diagnosis and Establishing a Case Definition

Knowing the causative organism(s) naturally is of great importance in outbreak control: the transmission between the host, environment and pathogen can be interrupted with certainty and the laboratory can provide correct biosafety and decontamination advice<sup>10</sup>. A diagnosis also aids with increasing the specificity of the case definition and case-finding. However, a cautionary note must be sounded as 46 – 68%<sup>1</sup> of analytic errors in the clinical setting are due to pre-analytical errors such as incorrect and unsafe specimen selection, collection, labeling, storage and transport. In the field one could expect the error rate too be far greater. To mitigate against this local<sup>11</sup> and international<sup>12</sup> guidelines as well as references<sup>13</sup> are available to guide the investigator. No guidelines however, should be used in lieu of thorough planning and communication with the nearest or best placed laboratory or reference centre. This is a core part of the planning

process before the investigator proceeds to the field.

Outbreaks of previously unknown organisms may also occur, such as was the case with SARS. This creates difficulties for the laboratory, less from a scientific point of view as expert reference laboratories are usually involved, but more as regulations regarding local and international biosafety may pose problems: these concern not only transport of specimens and what level of laboratories may be utilized, but also whether novel, previously unvalidated diagnostic methods may be used. Such burdens may frustrate laboratories and hamper the public health response. However, in some countries regulations are in place to accommodate such eventualities<sup>9</sup>.

### The Descriptive and Analytical Epidemiology of an Outbreak investigation

These are several steps of an outbreak investigation, the individual components of which are described in another article in this Bulletin<sup>14</sup>. The laboratory apart from being of aid in developing hypotheses as to transmission and therefore persons at risk, may aid further analytical epidemiological studies by reinforcing epidemiological linkages using various typing techniques and molecular epidemiology. Even at a provincial/district laboratory level this may be conducted as matching antibiograms from the suspected cases may suggest relatedness of the outbreak organism. A full discussion of molecular epidemiology which is naturally laboratory based, is beyond the scope of this article.

### Public Health Action and Documentation

These final steps of the outbreak investigation involve the laboratory by its reporting and interpretation of laboratory results. The APHL refers to this function as the partnerships and communications<sup>2</sup>. It stresses the implementation and maintenance of strong communicating networks to all stakeholders as "a result is only as good as its interpreter" (Dr G de Jong, NICD). This refers to the quality of the post-analytical phase as not only is the lab responsible for getting a result out to all the necessary stakeholders, but in some cases may be responsible for ensuring understandable reporting and hence

interpretation of results. For correct action, one needs correct information.

### Conclusion

This article has highlighted the important role of the laboratory in the control of communicable disease outbreaks. Outbreaks must be rapidly contained to minimize morbidity, mortality, economic and social disruption<sup>9</sup>.

The good public health laboratory certainly helps realize this important goal.

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## STEPS IN AN OUTBREAK INVESTIGATION

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### Introduction

Infectious diseases present the most important acute problems in all countries and a major disease burden in developing countries.<sup>1</sup> Infectious diseases were the leading cause of death in South Africa (accounting for 24%) in 2004.<sup>2</sup>

In epidemiology, infectious disease causation is believed to be a result of an interaction between the agent, the host and the environment (the epidemiologic triad).<sup>3</sup> The agent

is a micro-organism or its toxic product; the host could be human, animal or inanimate object that provides a suitable place for the infectious agent to grow and multiply under natural conditions; the environment influences the agent, host, and the route of transmission of the agent from source to host.<sup>1,3</sup> The modes of disease transmission are divided into two broad categories – direct (contact, airborne, etc) and indirect (vector borne, vehicle borne, etc). Detailed understanding of the epidemiologic triad for

*(Continued on page 4)*

infectious diseases and their natural history is of importance to the control and management of these diseases.

The appropriate control and management for a particular disease in a population, depends on the burden of that disease in the population. The levels of disease occurrence in a population are described as endemic, sporadic, epidemic or outbreak, or pandemic. An endemic disease is present in a specified geographic area or population group at a constant, baseline, prevalence or incidence rate that is higher in comparison to other areas or population groups.<sup>1,3,4</sup> For example, Lassa fever is endemic in West Africa, with 300 000 to 500 000 cases and 5000 deaths occurring yearly.<sup>5</sup> A sporadic disease is an irregular occurrence of a disease at irregular intervals.<sup>3</sup> An epidemic or outbreak refers to an increase of a disease occurrence above the expected endemic rate for that area or population.<sup>6</sup> Though malaria is endemic in many countries in the Southern African region, epidemic malaria is also experienced in countries within the region such as South Africa.<sup>7</sup> A pandemic is an epidemic that has spread over several countries or continent.<sup>3</sup> The influenza virus has accounted for a few pandemics in the twentieth century.<sup>8</sup> Examples of recent outbreaks include the outbreaks of Marburg hemorrhagic fever and *Shigella dysenteriae* at the Democratic Republic of the Congo.<sup>9</sup>

When an outbreak has occurred or is suspected, identification of the casual agent, management of the outbreak and prevention of further cases are the primary goals of an outbreak investigation.<sup>10</sup> This requires a thorough understanding of the source of the causative agent. Outbreaks may be: common source, when a group of persons are exposed to an agent from the same source; propagated source, which results from transmission of an agent from one person to another; and mixed source, which has features of both the common and propagated source outbreaks.<sup>3,4</sup> Food-borne and measles outbreaks are examples of common and propagated sources outbreaks respectively.<sup>11,12</sup>

The efficient use of time is critical in outbreak investigations; in order to minimize the severity and public health impact of the outbreak investigation.<sup>13</sup> This is best achieved through team work and a stepwise approach to field investigation (Table 1). In practise, however, the different steps may run concurrently or overlap. The emphasis put on individual steps depends on the extent of existing knowledge about the causative agent or exposure.<sup>14</sup> This stepwise approach is a framework that follows the format of collect, analyse, interpret, and act.<sup>3,15</sup>

### Steps in an outbreak investigation

- Prepare for field work
- Establish the existence of an outbreak
- Confirm the diagnosis
- Define and identify cases
- Establish a case definition
- Identify and count cases

- Perform descriptive epidemiology
- Formulate a hypothesis
- Evaluate the hypothesis
- Refine the hypothesis and execute additional studies as necessary
- Implement control and preventative measure
- Communicate the findings

### The steps in detail

#### **Preparing for field work**

Preparations for field work should be done before embarking on an outbreak investigation. The field investigator must have appropriate scientific knowledge and supplies and must consult with other knowledgeable individuals and applicable literature. The investigator must also complete all the logistic preparations before departing for the investigation.<sup>3</sup>

#### **Establishing the existence of an outbreak**

An outbreak may be spurious as a result of the impressions of the observer, increased notifications, errors in diagnosis and other reasons.<sup>6,14,15</sup> It is, therefore, imperative to verify the presence of the outbreak before embarking on an investigation. Review of data from baseline surveillance systems is useful in identifying changes in the usual trends of disease occurrence in that population.

#### **Confirmation of the diagnosis**

When an outbreak is suspected or established one needs to review patients' records, have a working differential diagnosis, and use the laboratory to confirm the diagnosis. The laboratory will also assist in recommendations on appropriate specimens to take, in processing the specimens and thus confirming the diagnosis.<sup>4,6,14</sup>

#### **Define and identify cases**

A case definition is a set of standard criteria for deciding whether a person has a particular disease or health related condition.<sup>3</sup> A list of symptoms, their time of onset and duration may suggest that a person's illness forms part of the outbreak.<sup>15</sup> Defining a case requires a balance between sensitivity and specificity of the criteria. A defined case may or may not include laboratory findings and may be refined as the outbreak investigation continues.<sup>14</sup> There may be more than one case definition in an outbreak, depending on the collection of signs and symptoms observed (definite case, probable case or possible case).<sup>3,14</sup> Case finding and identification methods need to be appropriate for the setting and disease in question. These may range from active surveillance to population surveys.<sup>3</sup>

#### **Performing description epidemiology**

This step involves characterizing the outbreak according to time, place and person. The epidemic time pattern can be depicted in the form of a graph, the epidemic curve. A spot

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map is used to illustrate clusters of cases and where the cases occur. Demographic details obtained about the cases will help in identifying persons at risk.<sup>3</sup>

### Formulating a hypothesis

Developing a hypothesis will help in identifying the possible source and mode of transmission of the disease, focusing investigation efforts and in directing the immediate control measures and management of cases.<sup>15</sup>

### Evaluating the hypothesis

Analysing the data assists in verifying or disputing the hypothesis, in establishing the source of the outbreak and in redirecting the investigation and control measures.<sup>15</sup>

### Refining the hypothesis

If the previous steps are not revealing then one might need to rethink the hypothesis and the design used to investigate the outbreak.<sup>3</sup>

### Implementing control measures

Short-term measures are aimed at interrupting the chain of transmission and treating cases. Conclusions from the investigation will help in identifying weaknesses in existing surveillance systems and preventative measures as well as informing the long-term measures in preventing future outbreaks.<sup>15</sup>

### Communicating the findings

A preliminary report fulfils the immediate obligation to the requesting authority and serves as a document for action. A full report of the investigation should include the findings of the investigation and recommendation for control and preventative measures. It also serves as a reference document for assessing the quality of the investigation, for potential legal and medical issues and for epidemiological teaching purposes. Publishing of the report is advised.<sup>4,13,14</sup>

### Summary

Investigation of disease outbreaks is one of the most practical and useful applications of epidemiology. A thorough investigation that is clearly communicated and well documented contributes significantly to progress in public health delivery and clinical practise.<sup>13</sup>

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## OUTBREAK OF WIDESPREAD PHARYNGITIS WITHIN RURAL COMMUNITIES OF THE !KHEIS MUNICIPALITY, NORTHERN CAPE, SOUTH AFRICA, MARCH-MAY 2007

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### Abstract

We conducted an investigation into an outbreak of acute pharyngitis, occurring within 4 neighbouring rural communities of the Northern Cape, to determine the extent and to implement control measures. Retrospective record review and active surveillance were carried out. A total of 124 cases met the case definition. 54% of cases were children <15 years and 71% of cases were female. The pathogen was likely introduced from a point source and thereafter propagated through person-to-person transmission. *Streptococcus pyogenes* was isolated from three of 42 throat swabs collected for laboratory culture. Molecular analysis indicated that these isolates were unrelated as they were of three different *emm*-types. There were no positive viral isolations.

### Introduction

Historically outbreaks of acute pharyngitis can be caused by both bacterial and viral pathogens, including, but not limited to: adenovirus, cytomegalovirus, Epstein Barr virus, and Group A Streptococcus (GAS).<sup>1</sup> GAS pharyngitis outbreaks, with sudden onset, have primarily been associated with food contamination and can thereafter spread from person to person. Additionally these outbreaks are usually focused within institutions with high population concentrations, such as: prisons or boarding-houses.<sup>2-4</sup> In contrast, community-wide outbreaks of acute pharyngitis with rapid increase in disease incidence are seldom reported.<sup>4,5</sup> Furthermore, no such occurrences have been reported within rural communities in South Africa. In March 2007, increased incidence of acute pharyngitis was reported by rural clinics serving four neighbouring

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communities within the Northern Cape Province. Subsequently we conducted an investigation to determine the extent of the outbreak and to implement control measures.

**Methods**

A case was defined as follows: sore throat with fever ( $\geq 38^{\circ}\text{C}$ ) and/or swollen cervical lymph nodes in a resident within the !Kheis municipality, with illness onset between 1 March – 5 May 2007. Epidemiological investigation was conducted by retrospective review of clinical records and registers, and active surveillance for new cases. Thereafter we conducted interviews of selected cases. Additionally we inspected selected households and the local school to identify factors contributing to the outbreak.

Throat swabs were collected from symptomatic residents and transported under cold chain to the National Health Laboratory Service (Kimberley and Upington) diagnostic laboratories for analysis. Here bacterial swabs (dry or in Amies gel agar) were processed under optimised conditions for the culturing of GAS on 5% sheep blood agar medium. GAS isolates identified were transported to the Respiratory and Meningeal Pathogens Reference Unit at NICD, where they underwent typing by 5' *emm* variable region sequencing. Sequenced genes were screened against a database of over 100 known GAS *emm* types to identify clonality. Viral samples (in viral transport medium) were transported to the Respiratory Isolation Laboratory at NICD where they were analysed using a respiratory virus screen. Culturing was carried out by centrifugation-enhanced pooled shell vial cultures. Screened viruses include: Herpes 1 & 2 virus, respiratory syncytial virus, influenza, parainfluenza virus, and adenovirus.

**Results**

Clinical records revealed a mean of 18.7 (min 5; max 35) cases per month occurring within Wegdraai and Topline in the 7 months prior to the outbreak. In March 2007, 71 cases were reported by the same clinics, thereby indicating the presence of an outbreak (Figure 1). During the investigation a total of 124 persons met the case definition. Sore throat (100%, n=124), fever (56%, n=70), and swollen cervical lymph nodes (37%, n=46) were the most common reported symptoms (Table 1). Cases ranged in age from 4 months to 68 years with a median age of 13 years, and 71% (n=88) of cases were female (Figure 2). The female to male ratio was 1.7:1 in children < 15 years and 4.5:1 in those  $\geq 15$  years of age. Two-thirds (67%, n=84) of cases resided in Wegdraai community, and the remainder in Groblershoop (21%, n=26), Topline (10%, n=12), and Boegoeberg (2%, n=2). The epidemic curve suggested that disease occurred by mixed transmission with an initial point source followed by person-to-person spread to neighbouring communities, with an incubation period of approximately 7 days (Figure 3). Disease occurrence within Wegdraai was highly concentrated in and around the informal settlement and occurred in clusters. 29 cases (23%) formed part of 12 household clusters. The largest

cluster included 4 cases. Investigations revealed a median household occupancy rate of 7 people (min 3; max 12) for cases; with the majority of households consisting of 2 rooms of poor infrastructure, and utilised in-door wood fire cooking. Of 42 throat swabs collected GAS was isolated from three samples. Molecular analysis of the isolates showed three different *emm* types. There were no positive viral isolations.

Control measures introduced included: presumptive antimicrobial treatment of all identified cases with Penicillin-VK or Amoxicillin for 10 days and a health promotion campaign on basic hygiene targeted towards patients visiting the clinics, as well as children attending the local school. We subsequently noted a decline in clinical cases of acute upper respiratory infection to 5 cases within May 2007 within the communities (Figure 1), indicating the outbreak was successfully controlled.

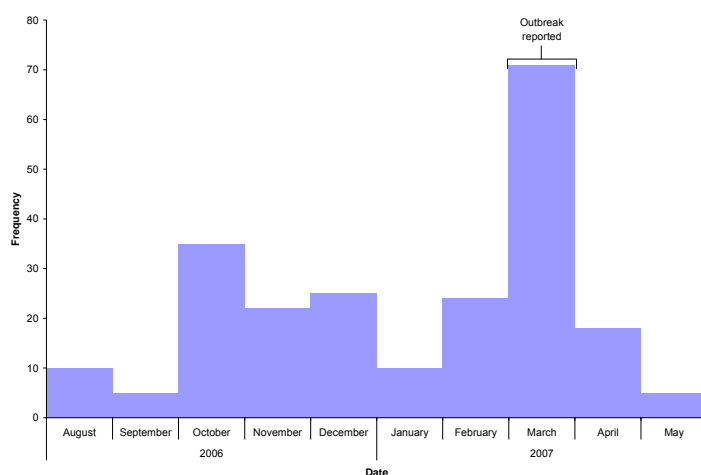


Figure 1: Frequency of upper respiratory tract infections observed at Wegdraai and Topline clinics by month of onset, !Kheis Municipality, August 2006 - May 2007

Table 1: Frequency of symptoms reported in cases meeting inclusion criteria during the outbreak of pharyngitis, !Kheis Municipality, March–May 2007 (n=124)

Signs & Symptoms	Frequency	%
Sore throat	124	100.0
Fever ( $\geq 38^{\circ}\text{C}$ )	70	56.5
Swollen cervical lymph nodes	46	37.1
Headache	40	32.3
Myalgia	27	21.8
Diarrhoea	17	13.7
Weakness/tiredness	15	12.1
Vomiting	14	11.3
Dizziness	11	8.9
Otitis media	8	6.5

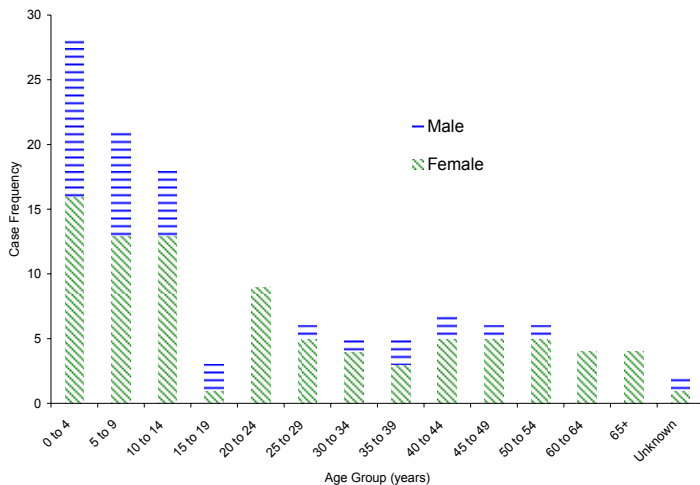


Figure 2: Age and gender distribution of pharyngitis outbreak cases, !Kheis Municipality, Northern Cape, March - May 2007

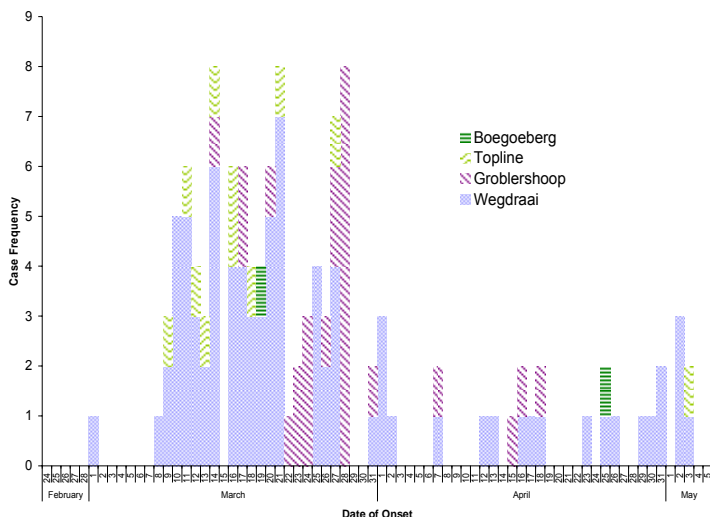


Figure 3: Epidemic curve showing distribution of pharyngitis outbreak cases by date of onset and place of residence, !Kheis Municipality, Northern Cape, March - May 2007

## Discussion

Laboratory analysis of samples showed that the 3 GAS isolates were unrelated, and we were therefore unable to identify the causative agent. Nevertheless, epidemiological investigation revealed that the outbreak spread rapidly within the community of Wegdraai, and thereafter to neighbouring rural communities. Furthermore a variety of factors suspected to contribute toward the propagation of infection were identified. Overcrowding, poor housing infrastructure, and the use of indoor wood-fire cooking may have resulted in increased susceptibility to infection. Close interactions between younger children and female caregivers may have accounted for increased infection rates within these population groups. A case control study was not conducted but may have been useful in elucidating possible risk factors for disease. In addition we were

unable to assess whether seasonal changes may have contributed to the observed increase in cases due the lack of baseline data for the same period in the preceding year.

## Conclusion

We could not identify the causative pathogen of this outbreak, primarily due to the remoteness of its location resulting in difficulties in the sample collection and transportation to the laboratory. It is therefore recommended that the relationship between field investigators and diagnostic laboratories be strengthened to address such difficulties, and that attention be given to improve the quality of laboratory specimen collection and ensure optimal processing of specimens. However, our epidemiological investigations have documented the wide spread occurrence and rapid transmission of pharyngitis within and between these rural communities. Continued vigilance and early response are needed to avert future widespread epidemics.

## Acknowledgements

Thank you to: the field investigators from Northern Cape Department of Health – Provincial Office (Kimberley) and Siyanda District Office (Upington) for their assistance during the investigation; the laboratory personnel at the National Health Laboratory Service (Kimberley & Upington) for analysis of bacterial samples; the Respiratory and Meningeal Pathogens Reference Unit (RMPRU - as part of the Group for Enteric, Respiratory and Meningeal Surveillance in South Africa) for molecular analysis of bacterial isolates; the Viral Diagnostics Unit: Respiratory and General Isolation for analysis of viral samples; and finally all expert advisors from the Epidemiology Unit, the South Africa Field Epidemiology Laboratory Training Programme (SA-FELTP), RMPRU, and the Centres for Disease Control and Prevention (Atlanta, USA) for your involvement, support and guidance during the investigation.

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## AN INSTITUTIONAL OUTBREAK OF HEPATITIS A

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**Abstract**

Outbreaks of hepatitis A in closed institutions have been previously reported in South Africa. We describe the epidemiology, clinical presentation and control measures for an institutional outbreak of Hepatitis A in Johannesburg in April 2007. Four laboratory confirmed cases of hepatitis A occurred amongst 60 mentally challenged boarding residents from April 4-5<sup>th</sup> 2007 suggesting a common source. The occurrence of the outbreak coincided with the introduction of a new catering programme involving the residents. Control measures were successfully implemented and included early identification of new cases, improved infection control and hygiene in food preparation, administration of immunoglobulin to all high risk persons and serological testing for hepatitis A IgM and IgG on suspected cases. Limited resources prevented more widespread testing of staff and residents. Hepatitis A vaccine was recommended for non-immune, individuals to prevent future infection. The early identification and reporting of hepatitis A cases is essential for timely implementation of control measures. Hepatitis A vaccine should be considered for all non-immune residents of such institutions to prevent future outbreaks.

**Introduction**

Hepatitis A is a notifiable condition in South Africa (SA). Outbreaks in closed institutions, in particular those in which individuals are unable to maintain personal hygiene, have been previously reported in SA (personal communication G de Jong) and pose a risk for spread of hepatitis A infection.<sup>1,2</sup> Person to person spread via the faecal-oral route is the most common method of transmission. However, infection may also result from exposure to a common vehicle such as contaminated food or water. The incubation period for hepatitis A virus is 15-50 days (average 28 days).<sup>3</sup> Individuals are most infectious two weeks prior to the onset of jaundice. Most individuals will remain infectious for 1-2 weeks following the onset of jaundice. In many cases, particularly in young children, infection is asymptomatic.<sup>4</sup> Currently South Africa does not administer hepatitis A vaccine routinely and post-exposure prophylaxis involves administration of pooled immunoglobulin to household contacts, and others at risk, where indicated.

**Objectives**

To describe the epidemiology, clinical presentation and control measures for an institutional outbreak of hepatitis A in Johannesburg, South Africa in April 2007.

**Methods**

Following a report of a suspected outbreak of hepatitis A in an institution caring for mentally challenged adults in

Johannesburg in April 2007, an investigation was conducted which included a site visit to identify the source and implement control measures. Inspection of the home was conducted and included assessment of levels of hygiene in the following areas: the workshop, kitchen, dining room, individual houses, bedrooms, toilets, living rooms, and grounds.

A case definition for active surveillance and identification of further cases was developed and included any person residing in the institution, presenting with one or more of the following symptoms: jaundice, nausea or vomiting, abdominal cramps, diarrhea, not eating or poor appetite, lethargy and dark urine, from the beginning of March to the end of June 2007.

A line list of all patients meeting the case definition was compiled. Serum from all suspected cases was tested for hepatitis A virus IgM antibody (anti-HAV IgM) using a chemiluminiscent microparticle immuno-assay HAVAB-M (Abbott).

**Results**

The institution had 60 mentally challenged boarding residents and 20 staff members. Six suspected cases of hepatitis A were identified in the institution over a 4 day period (4-7 April 2007), all were residents. Of these cases 4 were laboratory confirmed (anti-HAV IgM positive) and two were anti-HAV IgM negative. The confirmed cases presented from 4<sup>th</sup> to 5<sup>th</sup> April. The epidemic curve is typical of a point source outbreak with all four cases occurring over 2 days (Figure 1). The overall attack rate amongst residents was 7% (4/60).

Of the confirmed cases, two were a couple sharing a flat and two required hospital admission. There were no deaths. An additional 12 residents with non-specific symptoms were identified as part of active case finding by the attending primary health care nurse. All of these cases tested negative for anti-HAV IgM. Although anti-HAV IgG testing was requested this was not performed. Financial resources restricted more widespread testing of both staff and residents. No suspected cases were reported amongst the non-residents or staff.

Clinical presentation of cases included jaundice (n=3), dark urine (n=1) and non-specific constitutional symptoms (n=2). Confirmed cases included 3 males and 1 female with mean age, 33 years (range, 22 to 38 years).

Inspection of the home revealed that each house accommodated approximately 12 residents with one to three boarders per bedroom and each house had one to



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two separate bathrooms. The institution was generally very spacious and well maintained. The water dispenser in the workshop was visibly inspected and there was concern about the state of internal surfaces with visible green algae. It was reported that each resident used their own cups for the water. The toilets were generally clean but a common non-disposable towel was in use and the hand dryer appeared faulty. Soap dispensers were present and functioned well. A basin in the kitchen had a towel dispenser. It was noted that a new catering project had been introduced in the home in March 2007 involving the use of trained residents to prepare food.

### Recommendations for control

Advice on early identification of new cases, laboratory testing, proper clinical management of cases (including referral) and infection control measures, was given. Correct hand washing was emphasized.

Although a common source for these cases was likely, it was recommended that pooled immunoglobulin should be given as soon as possible to all remaining boarding residents, daily attendees and staff to prevent further spread of infection and attenuate disease. However, given limited resources, only high risk contacts were given pooled immunoglobulin.

A high risk contact was defined as:

- A person residing in the same house with the suspected or confirmed case.
- Any additional close contacts of cases e.g.: family members, staff and special friends

The care givers were instructed to do the following:

- Active surveillance for new cases according to the case definition and anti-HAV IgM testing on all suspected cases.
- Maintain a line list of cases to include: name, age, resident/ non resident/staff, date of onset of illness, house where resident, symptoms and outcome.
- Update the clinical management on a daily basis and refer where required.

### Discussion

The outbreak was likely from a point source involving contaminated food or water because all identified cases presented within a 4 day period. The occurrence of the outbreak coincided with the introduction of a new catering programme involving the residents which may have resulted in faecal contamination of foods due to poor personal hygiene.

Control measures were successfully implemented. The laboratory proved useful in excluding the diagnosis of hepatitis A in several suspected cases as the test is highly sensitive.<sup>1,2,3</sup> Two of the confirmed cases were admitted to hospital in keeping with the potential risk of severe disease in adults.

The early identification and reporting of hepatitis A cases is essential for timeous implementation of control measures. Hepatitis A vaccine should also be considered in South Africa for all non-immune residents of institutions particularly where personal hygiene is poor and where there is risk of severe disease.<sup>4</sup>

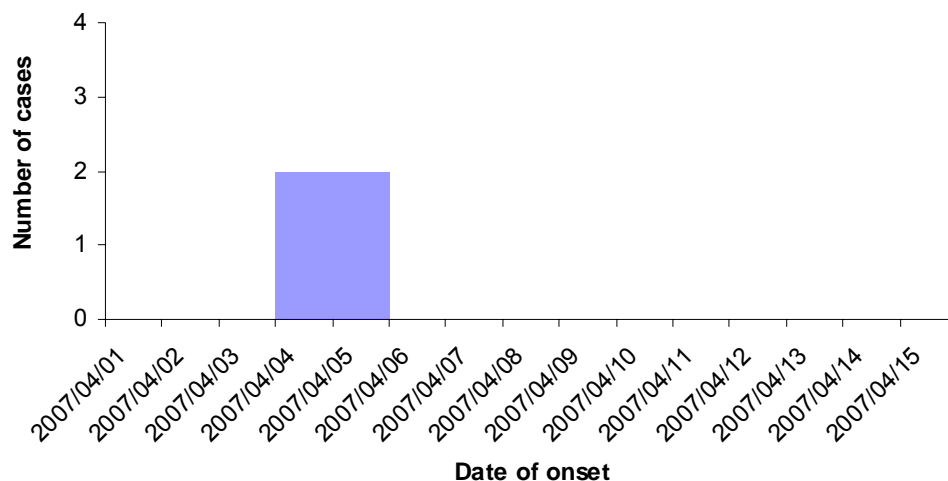


Figure 1: Epidemic curve of laboratory confirmed hepatitis A cases in an institution, Gauteng Province, April 2007.

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## A MULTI-PATHOGEN WATERBORNE COMMUNITY OUTBREAK IN THE NORTHERN CAPE PROVINCE OF SOUTH AFRICA, 2006-2007

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### Abstract

Diarrhoea outbreaks associated with faecal contamination of water sources are a major threat to human health. From September 2006 to April 2007 an outbreak of diarrhoea occurred in Hopetown (Northern Cape Province). Investigation revealed that there were 204 cases, 51 of which were part of 21 household clusters. The outbreak affected a wide area including the town and informal settlements. Most cases (n= 63, 31%) were reported from Steynville. There were 108 (53%) cases in children aged 6 months to 4 years. *Shigella flexneri* (n=13), norovirus (n=1), rotavirus (n=2) and enteropathogenic *E.coli* (n=1) were isolated from 58 stool specimens submitted. Water samples tested identified levels of coliforms in excess of the recommended limit (5cfu/100ml). Health promotion was heightened, a "boil water order" was issued and toilets were erected in the informal settlements. This outbreak highlights the need for the continuous provision of safe potable water to this community.

### Introduction

Diarrhoea is one of the priority diseases for surveillance in South Africa.<sup>1</sup> Diarrhoea may be caused by a variety of bacteria, viruses and parasitic agents<sup>2</sup> from different sources the commonest being from contaminated water and food as well as from person to person.<sup>3,4</sup> It is often accompanied by other clinical signs and symptoms including vomiting, fever, dehydration and electrolyte disturbances. In an outbreak situation, identifying the source is pivotal for control. Very little has been published on etiology of food and waterborne outbreaks in South Africa although such outbreaks occur frequently. Waterborne outbreaks associated with faecal contamination of water sources may commonly involve multiple pathogens.<sup>5</sup> Poor water quality is a threat to human health as it has been identified as the major contributor to the burden of disease attributable to diarrhoea in the developing world.<sup>6</sup>

From September 2006 to April 2007 a diarrhoeal outbreak occurred in Hopetown, Pixley Ka Seme district in the Northern Cape. Hopetown is 170 km from Kimberly along the Orange river with an estimated population of 14 000 residents.

### Methods

In September 2006, an outbreak of diarrhoeal disease was reported to the National Institute for Communicable Diseases (NICD) from Hopetown. The outbreak was suspected based on an observed increase in epidemiologically linked *Shigella flexneri* isolates from stool specimens received by the Kimberley National Health Laboratory Service (NHLS) laboratory. Preliminary investigations including visits to local clinics and the

hospital confirmed an increase in the number of cases and admissions due to diarrhoea from 26 September 2006. A comprehensive outbreak investigation was subsequently conducted.

### Establishing the existence of an outbreak

The preliminary findings raised concerns of a probable food or water source of the outbreak. The hospital confirmed that the number of diarrhoeal cases were in excess of that reported normally (personal communication N. Crisp).

### Developing a case definition

A broad case definition was developed for the investigation and included any individual of any age from Hopetown presenting with diarrhoea (2 to 3 loose stools within 24 hours) with or without vomiting, abdominal cramps or fever from September 2006-31 April 2007.

### Characterising the outbreak by person, place and time

A line list of all patients who met the case definition was recorded and included basic demographic data, clinical presentation, date of onset, date of consultation, specimen collection data and available laboratory results.

### Laboratory and field investigations

Active field investigations were conducted by the provincial Communicable Disease Control (CDC) and District Outbreak Response Team. Active surveillance for new cases was instituted at all health care facilities. An environmental assessment of the drinking water source was performed, and water samples were collected and tested.

The provincial CDC and District outbreak team also visited the affected sites to assess the level of hygiene of the residents. Health care workers were instructed to obtain stool samples (or rectal swabs where stool was not available) on all new patients meeting the case definition. All samples were processed by NHLS Kimberley Microbiology Laboratory. This included culture for *Salmonella*, *Shigella* and diarrhoeagenic *E.coli* and microscopy for stool parasites. In addition the Viral Gastroenteritis Unit Laboratory at NICD processed a portion of the stool for common enteric viruses including rotavirus, adenovirus types 40/41, norovirus and astrovirus using GastroVir-Strip (Coris Bioconcept, Belgium) for rotavirus and adenovirus types 40/41, ELISA-based RIDASCREEN Norovirus and RIDASCREEN Astrovirus (both kits from R-biopharm, Germany).

### Results

#### Descriptive epidemiology

From 26 September 2006 to 19<sup>th</sup> November 2007, there

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were 204 cases meeting the case definition. The epidemic curve (Figure 1) is typical of a persistent source outbreak with 3 waves. Most of the cases occurred from November 18<sup>th</sup> to December 4<sup>th</sup> 2006 and then there was a decrease

in cases followed by a second wave with several smaller peaks up till February 2007 when there was a 9 week period without any cases. In April, there was a resurgence of cases.

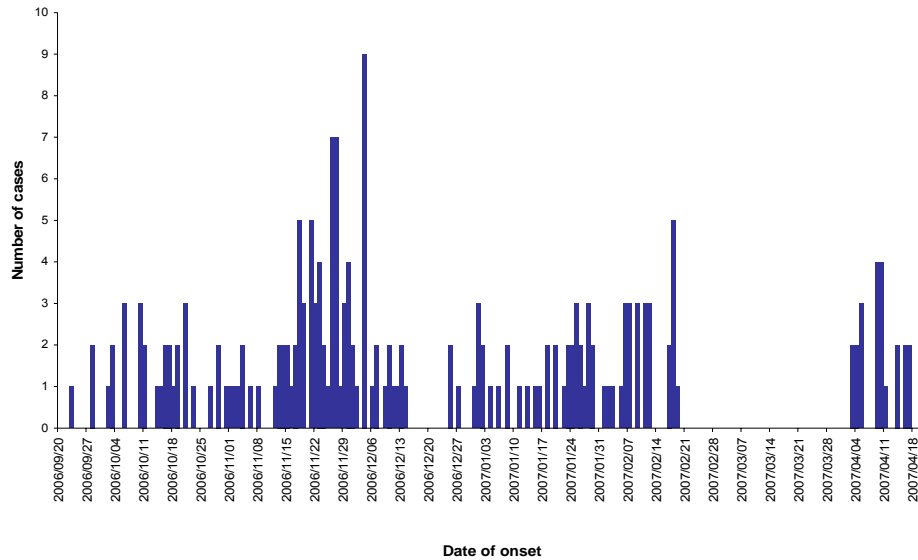


Figure 1: Epidemic curve of a diarrhoea outbreak in Hopetown, South Africa from September 2006 – April 2007

Most cases (n= 63, 31%) were from Steynville, followed by Plakkerskamp (n=48, 24%) and Vergenoeg (n=27,13%) (Figure 2). Fifty-one cases formed part of 21 household clusters. The largest cluster included 5 cases.

Most cases (n=108 (53%)) were in children aged 6 months to 4 years with a greater number in boys (62) and 55% (113) of all cases were in women. The female to male ratio was 0.9:1 in children less than 10 years and 2.4:1 in adults 10 years and older (Figure 3).

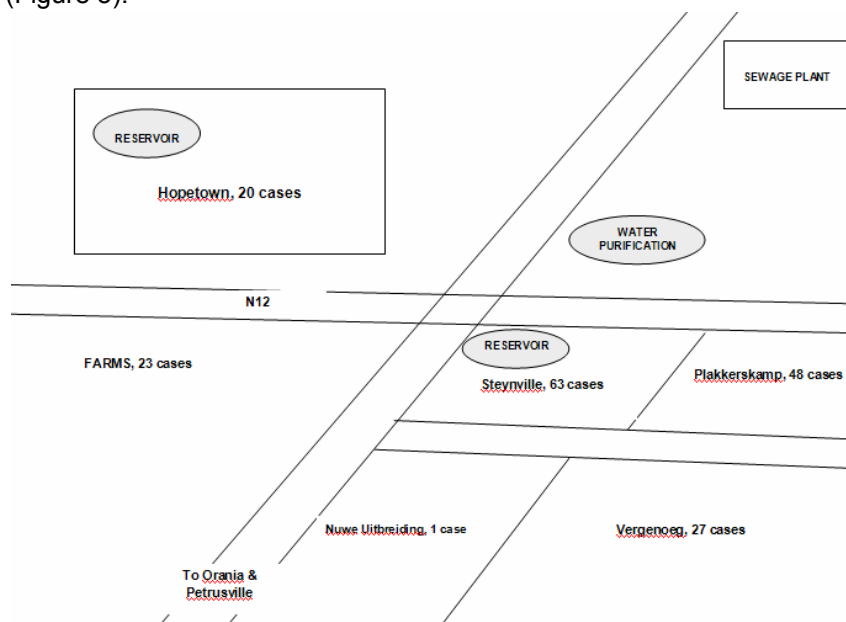


Figure 2: Map of some of the areas affected by the diarrhoea outbreak in Hopetown, South Africa from September 2006 – April 2007

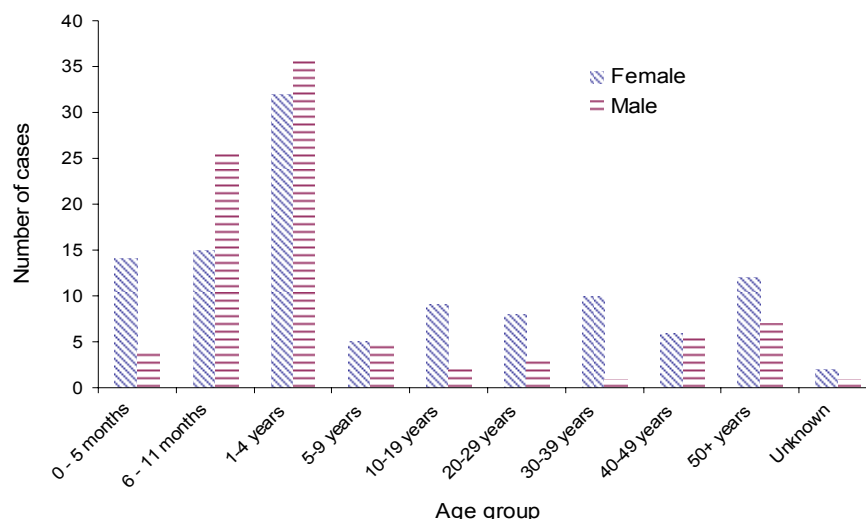


Figure 3: Age and gender distribution of diarrhoea cases in Hopetown, South Africa from September 2006 – April 2007

**Laboratory results**

**Stool Samples**

Stool samples were submitted for laboratory investigation from 28% of cases (58/204 cases) over the several months of the outbreak. A greater proportion of cases with bloody

diarrhea (69.7%; 23/33) had stool submitted then cases with no bloody diarrhea (20.5%; 35/171) ( $p < 0.0001$ ). A pathogen was isolated from 17 (29%) specimens: 13 (24%) *Shigella flexneri*, 1 norovirus, 2 rotaviruses and 1 enteropathogenic *E.coli* (Figure 4).

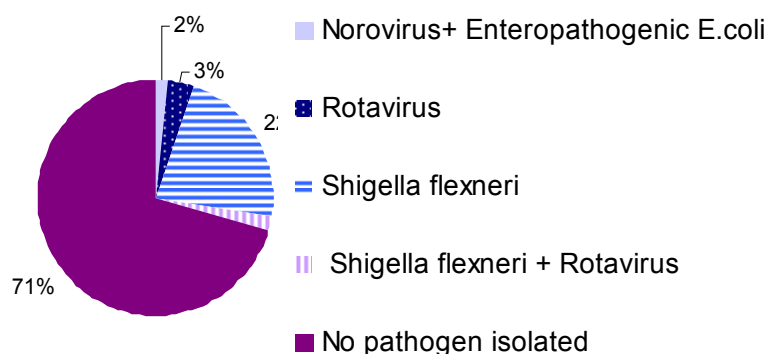


Figure 4: Relative prevalence of the pathogens identified from stool samples of diarrhoea cases in Hopetown, South Africa from September 2006 – April 2007

Table 1: Clinical presentations of cases with *Shigella* spp. and those with no isolated organisms during diarrhoea outbreak in Hopetown, South Africa from September 2006 – April 2007

Symptom*	Organism**				P-value
	<i>Shigella flexneri</i> (n=14)		No organism cultured (n=41)		
	n	%	n	%	
Bloody Stool	12	85.7	10	24.4	<0.0001
Watery Stool	7	50.0	24	58.5	0.002
Vomiting	3	21.4	17	41.5	0.374
Fever	4	28.6	6	14.6	0.192
Abdominal cramps	2	14.3	1	2.4	0.384

\* Not mutually exclusive. \*\*1 patient with norovirus and 2 with rotaviruses were excluded

The commonest symptoms were watery diarrhoea (n= 33), bloody stools (n=23) and vomiting (n=22) (Table 1). Bloody stool was more frequent among cases with *Shigella* spp. compared to those with no organism isolated (12/14 vs 10/41) (Table 1). Most *Shigella* spp. (n=6) isolated were in children 6 months to 4 years.

### Environmental samples

The drinking water source is the Orange River which goes through a purification plant into 2 reservoirs supplying the residential areas. Environmental assessment revealed that the purification plant was faulty, pipes were broken and there was animal waste draining into the river. Some of the affected sites were informal settlements with very poor levels of hygiene and inadequate toilet facilities and water supplied from standpipes. Water samples tested from several stand pipes and taps in the informal settlements as well as the town identified levels of coliforms in excess of the recommended limit (5cfu/100ml).

### Treatment of cases

Cases were managed according to clinical presentation. Treatment included rehydration and antibiotic treatment where indicated. There were no deaths.

### Outbreak Control

Based on preliminary information that water was the likely source of this outbreak, the community was immediately alerted and the water source chlorinated. Health promotion was heightened to promote hand washing and improvement in basic hygiene and a "boil water order" was issued.<sup>7</sup> In the informal settlements about 400 Ventilated Improved Pit latrine (VIP) toilets were erected.

### Discussion

The epidemic curve suggests that there was a continuous source of infection which is typical of contamination of a water source serving a community. The decrease in cases after the 1<sup>st</sup> wave may have been the result of the early interventions that were instituted which led to temporary containment of the outbreak with no further cases for a 9 week period. The 3<sup>rd</sup> wave may have arisen as a result of a recontamination of the water source. These findings point to the challenges of ensuring the sustainable delivery of potable water in communities which places an enormous constraint on health sectors in developing countries.<sup>8</sup>

Although the outbreak was widespread, some areas reflect high risk areas for person to person spread as most were informal settlements with no adequate toilet facilities. Results from the environmental assessment and the water testing suggest that contamination of the water source may have occurred prior to its distribution to the reservoir. The finding of multiple pathogens associated with diarrhoeal cases is in keeping with probable faecal contamination of the water source<sup>9</sup> and such outbreaks are common in the many South African communities affected by the challenges of access to safe, sustainable potable water and sanitation.

The predominance of *Shigella* spp. among isolated organisms may reflect selection bias where patients with bloody stools were more likely to have stool samples collected. This practice is in keeping with stool collection policies. The clinical presentations were also supportive of the *Shigella flexneri* predominance which may be waterborne and transmitted from person to person<sup>10</sup> resulting in secondary cases in households and other shared living areas. The spread of *Shigella* can be limited by the use of frequent and careful handwashing with soap and water especially in children who are not toilet trained. Children were the most affected in this outbreak but this is likely to reflect the increased detection of cases in this age group as they are more likely to have severe disease and present to health care facilities for care. This is the age group most affected by diarrhoeal diseases as reported by the South African Demographic and Health survey.<sup>11</sup>

Limitations of the current study include the fact that attack rates could not be computed because it was a community outbreak making it difficult to ascertain exposed and non exposed groups. In addition no data on controls was available so analytic epidemiologic analysis was not performed.

Obtaining an adequate number of stool samples is an ongoing challenge in diarrhoeal disease outbreaks in South Africa. Stools were submitted on only 28% of reported cases. Large distances in the Northern Cape frequently result in long delays in transport to the laboratory although clinics and hospitals are encouraged to utilize transport media.

There have been a number of previous waterborne outbreaks in the Northern Cape.<sup>12,13</sup> These recurrences clearly point to the fact that this community is in desperate need of a commitment to the provision safe potable water. It also highlights the need for continuous monitoring and treatment of the drinking water as well as health promotion and other hygiene practices which are necessary to sustain the provision of potable water.

It is therefore important that outbreaks are properly investigated to ensure appropriate lessons learnt will be useful in developing preventive measures to mitigate against future occurrences and improve water quality overall.<sup>14</sup>

### Acknowledgements

We would like to thank the staff of the National Health Laboratory Service microbiology laboratory in Kimberley and Dr Nicola Page from the National Institute for Communicable Diseases Viral Gastroenteritis Unit Laboratory for assistance with diagnostic testing of stool specimens.

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## AN OUTBREAK OF MEASLES IN THE NORTHWEST PROVINCE, SOUTH AFRICA, 2006

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### Abstract

During the widespread measles outbreak in South Africa from 2003 to 2005, the Northwest province was relatively spared. In 2006 an increase in numbers of laboratory confirmed measles cases was noted in the Central District Municipality in the Northwest Province (NWP); with 26 cases occurring between week 30 and 46. Phylogenetic analysis performed on measles virus strains from 17 cases identified two distinct genotypes. Sixteen cases occurring from week 30 to week 41 were caused by a single strain of virus of genotype D4. One case occurring in week 45 was caused by an unrelated strain of genotype B3. Seven of 16 cases with available vaccination history had received at least 1 dose of measles vaccine. No cases had a history of recent travel. Molecular epidemiologic analysis demonstrated that the strains giving rise to this outbreak were unrelated to previously circulating strains in South Africa but were similar to recently identified strains from other sub-Saharan African countries. This suggests that at least two separate importation events contributed to this outbreak.

### Introduction

Measles has been targeted for elimination in South Africa since 1995.<sup>1</sup> In that year the current measles immunization schedule which includes two doses of measles vaccine

administered to children aged 9 months and 18 months was also introduced.<sup>2</sup> National vaccination campaigns were held in 1996/7 and 2000. From 1995 to 2002 there was a > 90% reduction in measles cases in South Africa. From 2003 to 2005 widespread measles outbreaks occurred involving more than 1000 laboratory-confirmed cases from Gauteng, Western Cape, Mpumalanga, Eastern Cape and KwaZulu-Natal provinces.<sup>3,4</sup> Reasons postulated for these outbreaks included sub-optimal routine immunization coverage in specific geographical areas and the accumulation of susceptible individuals over several years and delay in implementing the mass campaign planned for 2004. The Northwest Province (NWP) was relatively spared by these outbreaks.<sup>3,4</sup>

### Methods

#### Routine measles surveillance

Laboratory surveillance and immunisation coverage data for the Northwest Province from 2003 to 2006 were reviewed. The suspected measles case definition includes fever, rash and one of the three C's (cough, coryza and conjunctivitis).<sup>5</sup> Venous blood and some urine specimens from all suspected measles cases in NWP were sent to the National Institute for Communicable Diseases (NICD). All blood specimens were tested by Enzygnost (Dade-

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Behring, Marburg, Germany) diagnostic kits for the presence of anti-measles immunoglobulin M (IgM).

Amplification of ribonucleic acid (RNA) for genotyping was attempted on all cases testing positive or equivocal for anti-measles IgM. For molecular analysis RNA was extracted directly from clinical specimens (urine if available, otherwise serum) and tested for the presence of Measles Virus by reverse transcriptase polymerase chain reaction (RT-PCR). The amplicons from positive reactions were sequenced and assigned to genotypes using phylogenetic analysis.<sup>6</sup>

Vaccine coverage was calculated as the number of vaccine doses administered in the target age group each year divided by the target population for the relevant geographic area. The dominant age group for measles 1<sup>st</sup> dose was < 12 months and for measles 2<sup>nd</sup> dose was 12-23 months, and for the mass campaign in 2004 was 0-59 months.

### Outbreak investigation

Following the identification of increased numbers of cases an outbreak investigation was conducted. An outbreak case was defined as any individual testing positive by measles IgM serology or by RT-PCR from the Central District Municipality in 2006. Cases were visited in their homes by provincial and district health care workers and data was collected on a standardized data collection form. This data included information on vaccination history, previous travel and measles contacts. The timing of cases was evaluated by date of specimen collection as date of onset of symptoms was not available for several of cases.

This paper aims to describe the epidemiology and molecular features of the outbreak.

### Results

#### Baseline burden of disease, outbreak detection and confirmation

There were <10 cases of measles reported annually from Northwest Province from 2003 to 2005. In 2006 an increase in the number of confirmed cases (Figure 1) prompted an outbreak investigation.

#### Description of the outbreak

From week 30 to 46 there were 26 laboratory confirmed measles cases from Central District Municipality peaking in week 39 and 41 with 5 cases each diagnosed (figure 2). Most cases come from a restricted geographical area (2 adjacent rural villages) of Mafikeng sub-district close to Mafikeng Hospital. Thirteen of the 23 cases were reported from Mafikeng Hospital. The mean age of reported cases was 8 years (range 6 months to 18 years) with 19/26 (73%) cases > 5 years of age and 43% (10) of 23 cases with known gender were female. Of 16 cases with available vaccination history; one was too young to be vaccinated, 7 had received at least one dose of measles vaccine and 8 had never been vaccinated.

Of 17 cases with available history, none had traveled recently outside of Mafikeng or had a history of contacts with travelers in the previous month.

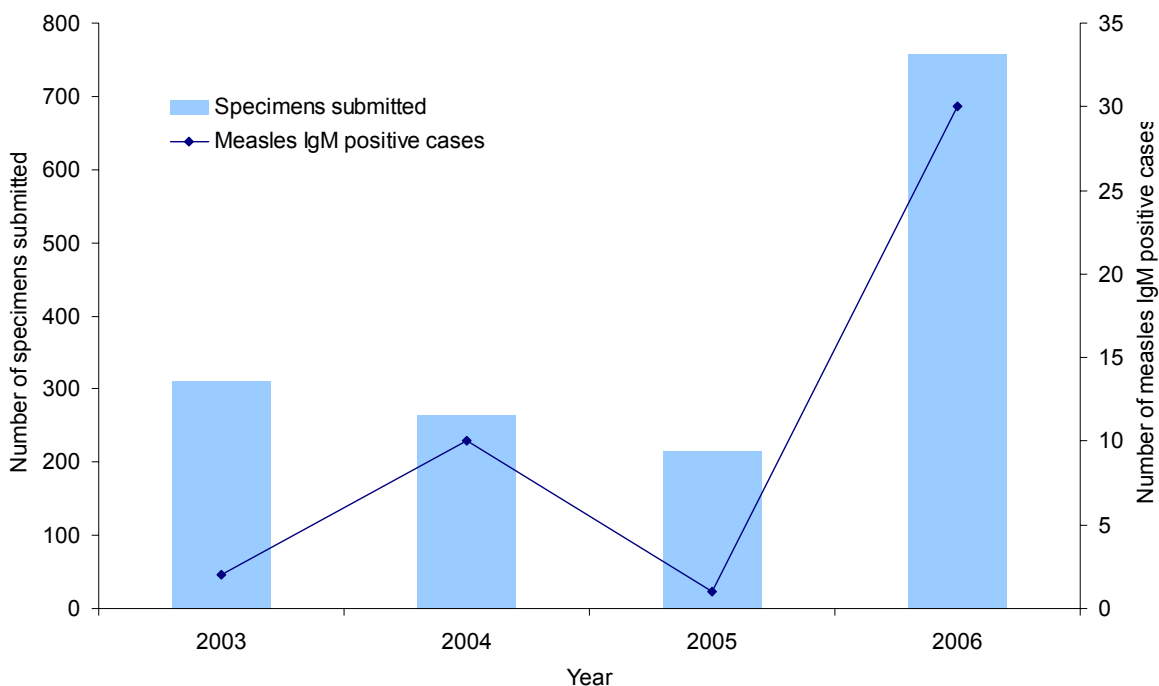


Figure 1: Number of specimens submitted and number testing positive for measles IgM from Northwest Province 2003- 2006

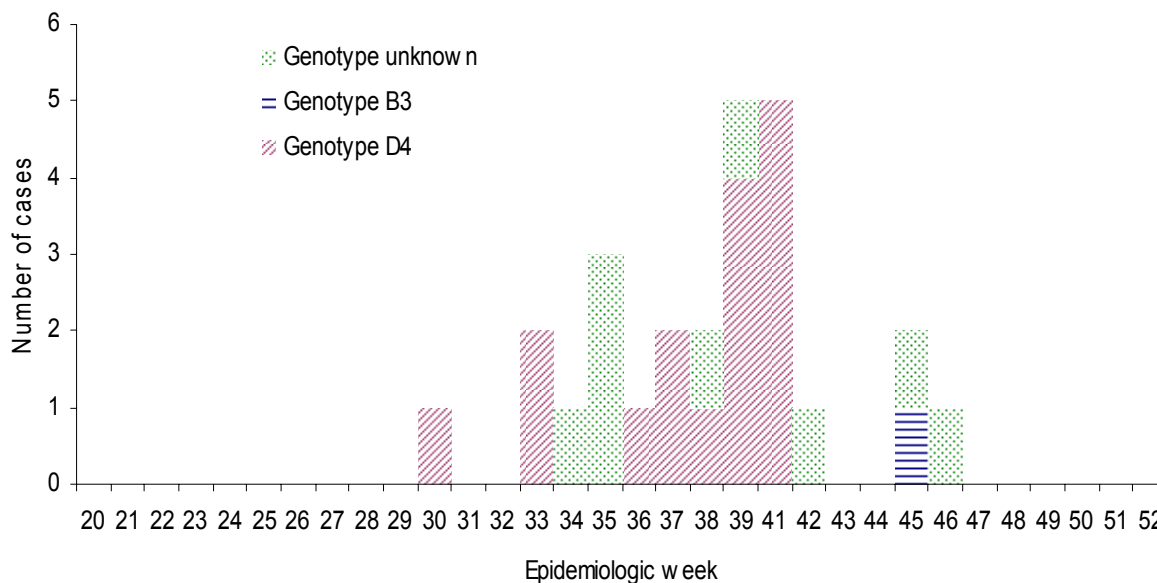


Figure 2: Epidemic curve of laboratory-confirmed measles cases by date of specimen submission and genotype of available virus isolates, Central District, Northwest Province, 2006.

### **Molecular epidemiology**

Seventeen cases were positive by RT-PCR. Molecular analysis indicated that the cases were caused by two genotypically distinct measles virus strains. Sixteen cases occurring from week 30 to week 41 were caused by a single strain of virus of genotype D4. This strain was unrelated to previous D4 isolates from South Africa during the 2003 to 2005 outbreak but identical to strains circulating in Botswana, Zimbabwe and Zambia in 2005 and 2006 (figure 3). One case occurring in week 45 was RT-PCR positive for an unrelated strain of genotype B3 which was identical to strains circulating in several other African countries in 2005 and 2006. A further case caused by this genotype was subsequently reported from the Bophirima District Municipality, NWP, in December 2006.

### **Control measures implemented**

A targeted vaccination campaign was conducted in the community; in addition children from 6 months to 15 years were vaccinated on admission to hospital. Active case finding for measles cases was strengthened.

### **Vaccine coverage**

Vaccine coverage for first dose measles vaccine in the Central District Municipality increased from 75% in 2003 to 80% in 2006. Coverage for the second dose of measles vaccine was lower increasing from 65% in 2003 to 68% in 2006. Coverage in the 2004 National Immunization Day targeting all children < 5 years of age was 94% in Central District Municipality.

### **Discussion**

Both the D4 and B3 strains identified in this outbreak had

not been previously identified in South Africa and were identical to strains circulating in other sub-Saharan African countries in recent years. This, in addition to the finding of two genotypically distinct strains suggests that at least two separate importation events contributed to this outbreak. Unfortunately genotyping data was not available for nine cases, thus we were unable to determine whether there were additional cases due to the B3 genotype.

Vaccination coverage from 2003-2006 for first dose measles vaccine in the Central District was well below the target of 95% vaccination coverage for all districts. Coverage in the mass campaign in 2004 was 94% but this campaign only included children aged < 5 years and the majority of cases in the outbreak were > 5 years of age. South Africa remains vulnerable to measles importations and it is essential to maintain a high vaccination coverage at district level to minimize the risk of spread should a case occur. In addition, effective surveillance programmes reporting at least 2 suspected measles cases per 100 000 population per district per year are necessary to allow early detection and implementation of control measures in the event of an outbreak.<sup>5</sup>

This outbreak highlights the fact that as the incidence of measles decreases molecular analysis of virus strains is of increasing importance for understanding measles epidemiology and evaluating the success of control measures. It is essential that appropriate specimens be submitted to the laboratory for RT-PCR testing (urine specimen or throat swab) within 5 days of the onset of rash, in addition to serum, in order that molecular analysis can be performed on all measles cases.



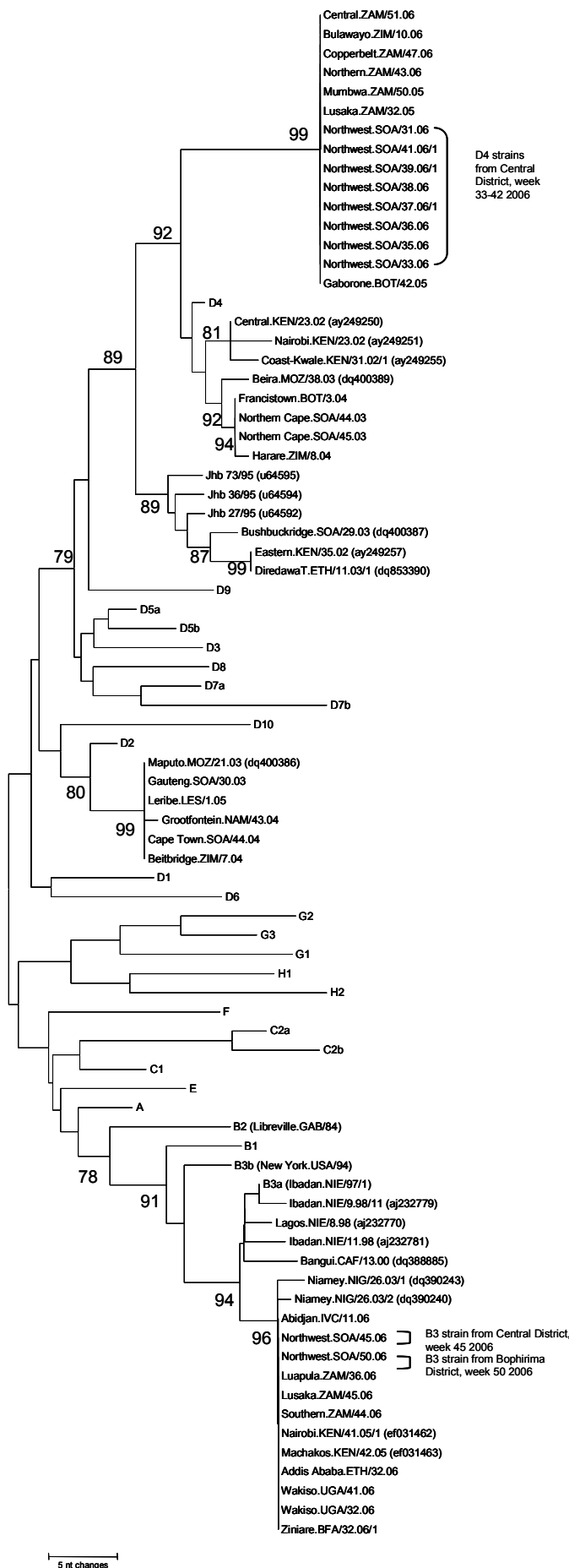


Figure 3: Phylogenetic analysis of the partially-sequenced N genes of measles virus from South Africa 2006. The sequences (450 nt) were compared to WHO reference sequences (the names of the reference strains have been deleted for clarity and have been replaced with designated genotype<sup>7</sup>) and to selected other viruses circulating in South Africa and the African region). The unrooted neighbour-joining tree was generated by bootstrap analysis (500 replicates) using MEGA3 software<sup>8</sup>; only bootstrap frequencies higher than 75% are shown. Viruses are identified by the city or province, country and date of first identification. (Key to abbreviations: BOT – Botswana, SOA – South Africa, ZAM – Zambia, KEN – Kenya, MOZ – Mozambique, ZIM – Zimbabwe, ETH – Ethiopia, LES – Lesotho, NAM – Namibia, GAB – Gabon, USA – United States, NIE – Nigeria, CAF – Central African Republic, UGA – Uganda, BFA – Burkina Faso, IVC – Côte d’Ivoire)

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Provisional listing: number of laboratory-confirmed cases in South Africa of diseases under surveillance reported to the NICD, corresponding periods 1 January - 30 September 2006/2007

Disease/ Organism	Case Definition	Subgroup	Cumulative to 30 September Year	EC	FS	GA	KZ	LP	MP	NC	NW	WC	South Africa
<b>VIRAL DISEASES</b>													
Acute Flaccid Paralysis	Cases < 15 years of age from whom specimens have been received as part of the Polio Eradication Programme		2006	48	20	55	36	44	35	7	24	29	298
			2007	33	22	47	33	36	19	8	14	21	233
Measles	Measles IgM positive cases from suspected measles cases, all ages		2006	3	0	19	2	1	9	4	21	1	60
			2007	5	1	7	1	1	5	0	1	1	22
Rubella	Rubella IgM positive cases from suspected measles cases, all ages		2006	159	37	409	194	336	137	69	139	88	1568
			2007	134	10	62	147	64	35	21	29	69	571
VHF	Laboratory-confirmed cases of CCHF (unless otherwise stated), all ages		2006	0	2	2	0	0	0	2	0	0	6
			2007	0	0	0	0	0	0	0	0	0	0
Rabies	Laboratory-confirmed human cases, all ages		2006	2	0	0	3	17	0	0	1	0	23
			2007	4	0	0	4	1	0	0	0	0	9
	Invasive disease, all ages	All serotypes	2006	17	15	125	46	1	2	8	3	36	253
			2007	8	18	127	50	1	11	1	2	43	261
		Serotype b	2006	2	4	21	8	1	1	1	0	8	46
			2007	1	2	18	9	0	1	0	2	12	45
	Invasive disease, < 5 years	Serotypes a,c,d,e,f	2006	1	1	13	2	0	0	1	0	3	21
			2007	1	0	11	2	0	0	0	0	4	18
		Non-typeable (unencapsulated)	2006	1	3	33	3	0	1	0	0	2	43
			2007	0	1	27	7	0	1	0	0	3	39
		No isolate available for serotyping	2006	7	3	21	11	0	0	1	1	5	49
			2007	0	6	22	12	1	1	1	0	12	55
	Invasive disease, all ages		2006	29	31	287	18	5	22	13	20	52	477
			2007	11	26	149	20	5	16	7	25	51	310
		Total cases	2006	219	166	1650	351	78	164	31	104	358	3121
			2007	160	201	1466	419	80	158	32	126	368	3010
		Penicillin non-susceptible isolates	2006	40	39	477	117	20	52	8	21	90	864
			2007	59	71	500	181	17	67	13	32	139	1079
		No isolate available for susceptibility testing	2006	88	11	255	33	10	23	2	11	21	454
			2007	15	21	266	82	14	11	4	17	50	480
			2006	60	57	471	119	14	38	10	22	114	905
			2007	57	62	380	150	21	41	12	29	157	909
			2006	36	19	488	96	2	26	0	15	63	725
			2007	26	33	287	70	11	14	2	17	47	507
			2006	69	28	146	155	19	37	11	52	130	647
			2007	110	22	174	87	22	72	8	19	56	570
	Confirmed cases, isolate from a non-sterile site, all ages		2006	38	1	14	13	6	7	0	0	18	97
			2007	9	1	10	7	2	8	0	2	5	44
	Confirmed cases, isolate from any specimen, all ages		2006	0	0	0	1	0	0	0	0	1	2
			2007	0	0	1	0	0	0	0	0	0	1
	Confirmed cases, isolate from any specimen, all ages	All serotypes	2006	106	36	173	163	9	29	21	14	333	884
			2007	99	48	241	93	13	31	27	11	209	772
	Confirmed cases, isolate from any specimen, all ages	All serotypes	2006	0	0	0	0	0	0	0	0	0	0
			2007	0	0	0	0	0	0	0	0	0	0
		Total cases (incl. C neoformans)	2006	1053	215	1426	1068	157	351	51	298	293	4912
			2007	378	321	1334	962	192	322	37	362	275	4183
		C. gattii	2006	3	4	30	7	16	20	3	11	7	101
			2007	0	1	26	12	14	19	0	8	3	83
<b>BACTERIAL AND FUNGAL DISEASES</b>													
Neisseria meningitidis	Invasive disease, all ages		2006	29	31	287	18	5	22	13	20	52	477
			2007	11	26	149	20	5	16	7	25	51	310
		Total cases	2006	219	166	1650	351	78	164	31	104	358	3121
			2007	160	201	1466	419	80	158	32	126	368	3010
Streptococcus pneumoniae	Invasive disease, all ages		2006	40	39	477	117	20	52	8	21	90	864
			2007	59	71	500	181	17	67	13	32	139	1079
		No isolate available for susceptibility testing	2006	88	11	255	33	10	23	2	11	21	454
			2007	15	21	266	82	14	11	4	17	50	480
Salmonella spp. (not typhi)	Invasive disease, < 5 years		2006	60	57	471	119	14	38	10	22	114	905
			2007	57	62	380	150	21	41	12	29	157	909
			2006	36	19	488	96	2	26	0	15	63	725
			2007	26	33	287	70	11	14	2	17	47	507
Salmonella typhi	Invasive disease, all ages		2006	69	28	146	155	19	37	11	52	130	647
			2007	110	22	174	87	22	72	8	19	56	570
Shigella dysenteriae 1	Confirmed cases, isolate from any specimen, all ages		2006	38	1	14	13	6	7	0	0	18	97
			2007	9	1	10	7	2	8	0	2	5	44
Shigella spp. (Non Sd1)	Confirmed cases, isolate from any specimen, all ages		2006	0	0	0	1	0	0	0	0	1	2
			2007	0	0	1	0	0	0	0	0	0	1
Vibrio cholerae O1	Confirmed cases, isolate from any specimen, all ages		2006	106	36	173	163	9	29	21	14	333	884
			2007	99	48	241	93	13	31	27	11	209	772
Cryptococcus (Cryptococcus spp.)	Invasive disease, all ages		2006	0	0	0	0	0	0	0	0	0	0
			2007	0	0	0	0	0	0	0	0	0	0

Abbreviations: VHF - Viral Haemorrhagic Fever; CCHF - Crimean-Congo Haemorrhagic Fever  
 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