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This edition offers an informative look at the Northern Territory Notifiable Diseases System (NTNDS), the primary database for collecting notifiable disease in the Northern Territory (NT) that came into being in 2004. A structured evaluation of the NTNDS reveals that an upgrade is needed to accommodate the requirements of a contemporary disease control surveillance system.

A case series in this Bulletin reports the first reported case of Zika virus acquired in Australia, highlighting the sexual transmission that can follow from an imported case of Zika infection. The infection which most often is asymptomatic is a concern for individuals traveling to endemic areas overseas, with both vector–borne and sexual transmission posing considerable risks.

While the NT has had zero cases of measles from 2020 to 2024 – all other jurisdictions have had measles cases notified, most all overseas-acquired, during that time period. Territorians are being urged to make sure they are measles-immune before travelling. To achieve immunity 2 doses of a measles containing vaccine are required at least 1 month apart.

As always there are recent abstracts from NT authors and on NT- related issues with 13 abstracts offered this quarter.

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NORTHERN TERRITORY GOVERNMENT

Contents

An evaluation of the Northern Territory Notifiable Diseases System (NTNDS) in 2024 – the recommendation is to replace it

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ABSTRACT

The Northern Territory Notifiable Diseases System (NTNDS) is the primary surveillance database collecting information related to notifiable diseases in the Northern Territory (NT) of Australia. This web-based system has been in use since 2004 and is managed by the NT Centre for Disease Control (CDC). We aimed to evaluate the performance of the NTNDS in meeting ongoing disease surveillance requirements in 2024, against surveillance system attributes listed by the United States Centres for Disease Control and Prevention. We used quantitative and qualitative data to evaluate 9 surveillance system attributes; these were simplicity, flexibility, data quality, acceptability, sensitivity, predictive value positive, timeliness, stability and cost, as well as overall usefulness.

The evaluation revealed that the NTNDS is simple to use, stable and contains high quality data. However, the system has major limitations in terms of flexibility, timeliness, cost to implement modifications, and lacks many capabilities required in a contemporary disease surveillance system. The NTNDS is no longer suitable or fit-for-purpose when additional surveillance demands are placed on the system. We developed a list of recommendations to improve the operational efficiency of the NTNDS. However, while it is feasible to continue using and improving the NTNDS, the preference would be to replace the NTNDS with a new interoperable and contemporary surveillance system.

Keywords: *Northern Territory Notifiable Diseases System, disease surveillance, database, evaluation, Northern Territory.*

INTRODUCTION

Disease surveillance involves the continuous, systematic collection, analysis, interpretation and dissemination of public health data to inform the planning, delivery and response of health services, including treatment, prevention and policy setting.[1–3] Disease surveillance systems, including the underpinning digital technology, should be periodically evaluated to identify limitations and ensure optimal performance, cost-efficiency, and relevance to public health.[4–6]

The Northern Territory (NT) of Australia has over 100 notifiable diseases and health-related conditions[7] gazetted under the *Notifiable Diseases Act 1981* (NT).[8] The Northern Territory Notifiable Diseases System (NTNDS) is the storage database/system for notification data collected under the auspices of the *Notifiable Diseases Act 1981* (NT),[8] whereby the Northern Territory Centre for Disease Control (CDC) is obliged to maintain records of all cases of notifiable diseases in the NT.

The NTNDS was operationalised in March 2004 as an innovative (at the time), standalone, web-based system (Figure) for the processing, storage and transmission of notifiable disease data.[9] It replaced

the previous Epi-Info 6.04 system, and allowed for direct manual data entry into a central database from all regional CDC offices. This solved previous issues of non-standardised data collection across regional offices and delays in data transmission. As of September 2024, the NTNDS has been in continuous operation at the CDC for over 20 years. The system was comprehensively evaluated once in 2006.[10]

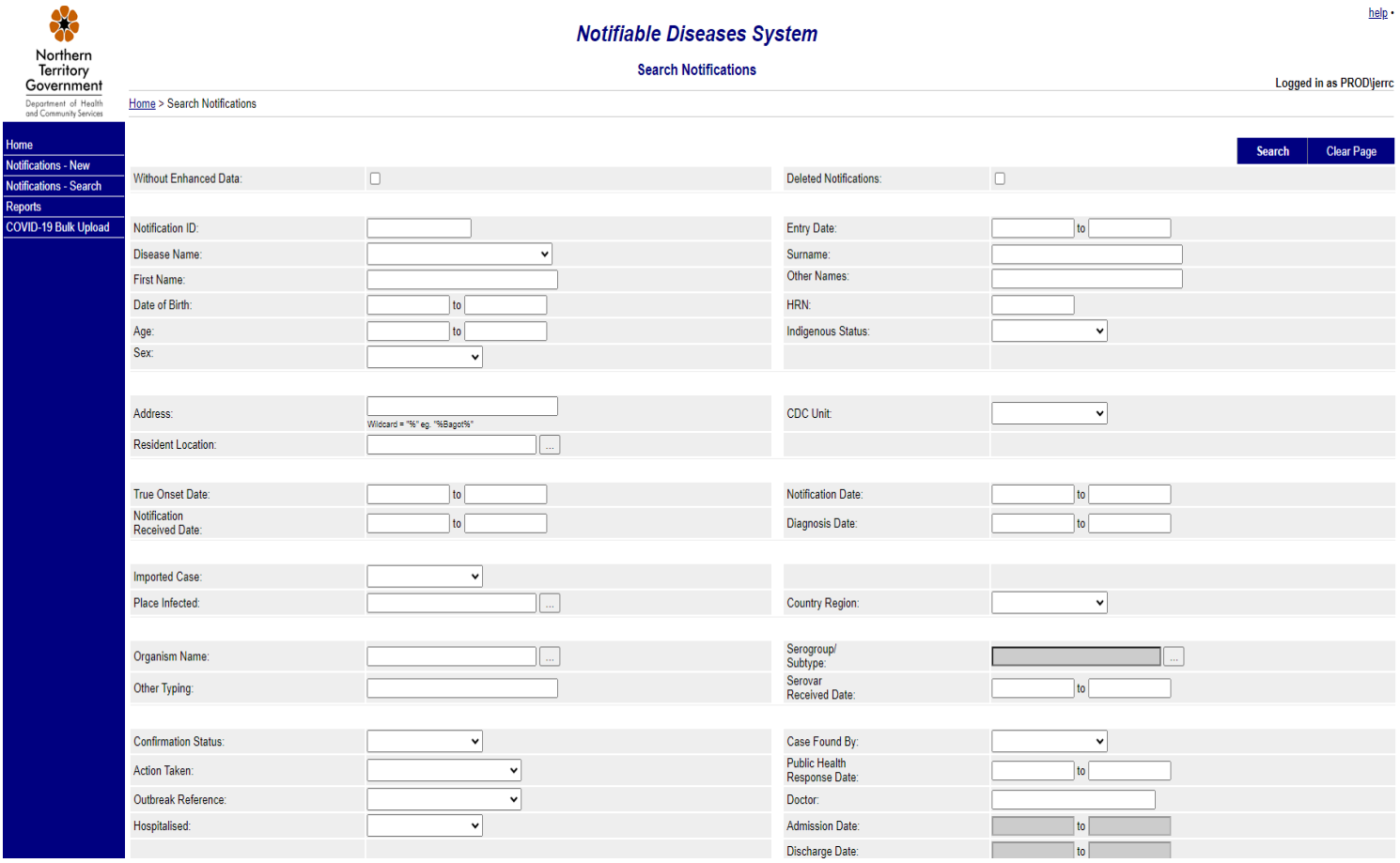
The coronavirus disease 2019 (COVID-19) pandemic during 2020-2023 rigorously tested the capability of the NTNDS. During 2022, the large volume of COVID-19 notification data overwhelmed the manual entry process of the NTNDS.

This project aimed to evaluate the performance of the NTNDS in meeting ongoing disease surveillance requirements in 2024. This project helped to answer the following question:

- Is the NTNDS a suitable surveillance system and database for ongoing surveillance requirements during baseline and surge periods (outbreaks/epidemics/pandemics)?

This paper is a condensed version of a larger evaluation of the NTNDS that is available in the investigator's Master of Philosophy (Applied Epidemiology) thesis via link (https://anulib.anu.edu.au/collections/theses).

Figure. NTNDS interface landing screen (current version 1.9.0.99; August 2024)



METHODS

We evaluated the NTNDS against a set of internationally recognised surveillance system attributes listed in 2 United States Centres for Disease Control and Prevention (USCDC) guidelines.[5,11] These attributes were simplicity, flexibility, data quality, acceptability, sensitivity, predictive value positive (PVP), timeliness, stability and cost, as well as overall usefulness. Quantitative and qualitative data were used to inform this evaluation. These included:

i) analyses of NTNDS data

ii) semi-structured interviews with key stakeholders (NT Government staff)

iii) review of relevant documentation, and

iv) observations of system capabilities by the investigator

The term 'NTNDS' used throughout this evaluation referred only to the NTNDS application interface and the database that housed NT disease notification data.

RESULTS

- **Simplicity**

The NTNDS interface is user-friendly and intuitive. The data transmission process occurs automatically. However, the NTNDS is inefficient because data must be manually entered and the system is not interoperable with other NT Department of Health (NT Health) information systems. The NTNDS is case-based instead of person-based, and cannot connect to a secure file transfer platform for sharing sensitive data.

- **Flexibility**

The NTNDS is limited in its flexibility to adapt to changing information needs. Making frontend changes requires outsourcing to a private company and the process can be time-consuming and costly. Enhanced data for certain diseases are often stored in the 'Comments' field instead of purposely built data fields. The structural integrity of the NTNDS is also fragile due to the addition of new fields and logics over time resulting in increasing complexity of its backend codes. The COVID-19 pandemic highlighted that the NTNDS is not scalable during emergencies.

- **Data quality**

The NTNDS overall contains high quality data for important core fields due to manual data entry, restricted edit rights and annual/quarterly data cleaning. Mandatory fields, inbuilt validations and conditional logics help to prevent null and invalid values. Notably, the NTNDS has high completeness of Indigenous status, hospitalisation status, death status and disease import status.

- **Acceptability**

Stakeholders accepted the NTNDS for what it was originally designed to do 20 years ago. However, stakeholders highlighted the inefficient fax notification and manual data entry processes especially in light of the growing number of notifiable conditions and with the need for additional enhanced data fields. Many found the NTNDS's limited flexibility and capacity unacceptable.

- **Sensitivity**

The estimated sensitivity of the NTNDS ranged between 92-97% for capturing laboratory confirmed diseases based on salmonellosis and shigellosis as sentinel indicators. However, sensitivity varies across different diseases and no surveillance system could achieve maximum sensitivity. The sensitivity of the NTNDS is facilitated by NT's small population and limited number of laboratories, which places less strain on the surveillance system compared to more populous Australian jurisdictions.

- **Predictive value positive (PVP)**

The estimated PVP of the NTNDS ranged between 89-99% based on selected

representative diseases from each disease category. Disease-specific variations were likely due to challenges in confirmatory serology rather than issues inherent to the NTNDS. Overall, the NTNDS demonstrated high PVP.

- **Timeliness**

The estimated time delay of the NTNDS between notification and reporting via SAP Business Objectives Business Intelligence (BI) is around 1 to 5 days, although this is likely to vary across different diseases. There is often a data entry backlog for low priority diseases which affects timely epidemiological reporting. Furthermore, system modifications delays can hinder CDC's ability to quickly respond to emergencies and changing information needs.

- **Stability**

The NTNDS interface (frontend) is stable and reliable with rare occurrences of outages. While there have been 'glitches' related to data entry, extraction and transmission in the past due to its complex backend codes, many have been resolved.

- **Cost**

The minimum annual personnel costs of NTNDS data entry for common disease notification types (respiratory diseases and sexually transmitted infections) was estimated to be $23,431. Past major system modifications have costs up to $60,000 for each modification depending on the task complexity. The fragility of the NTNDS may increase the cost of future modifications.

- **Usefulness**

The NTNDS is useful for recording core data to inform communicable disease prevention and control at a basic level, but not useful when additional surveillance demands are placed on the system, or during surge periods when there is a dramatic increase in data entry requirements.

DISCUSSION

Overall assessment of the surveillance system attributes evaluated shows the NTNDS is no longer suitable or fit-for-purpose for ongoing disease surveillance requirements at the CDC during baseline and surge periods. The information needs of notifiable diseases are constantly changing as pathogens evolve and migrate, new research findings are published, and contact tracing and treatment guidelines are updated. This means the CDC needs to continuously collect new data (for both routinely notified and emerging diseases) to meet reporting demands of decision-makers at local and national levels. The NTNDS is neither flexible nor timely enough in terms of system capacity and available resources to keep up with these demands. This often leads to many of the CDC's core functions being compromised, especially during emergencies when there are more demands for critical data to lead policies and future directions.

The evolving nature of communicable disease control presents new challenges beyond what was initially envisioned for the NTNDS. However, advancements in technology and informatics offer new tools to address these challenges and meet business demands. Continuing with incremental upgrades to the NTNDS may be less beneficial in the long-term than seeking a new interoperable and contemporary surveillance system.

RECOMMENDATIONS

The recommendations of this evaluation can be broadly summarised into 2 themes:

A) Replace the NTNDS (preferred)

B) Continue to use but improve the NTNDS

While it may be feasible to continue using and improving the NTNDS, the preference would be for theme A) to replace the NTNDS with a new interoperable and contemporary surveillance

system to meet the current and future business demands of the CDC. Recommendations in theme B) are further organised into different priority levels based on the urgency, complexity and cost involved. Those recommendations with no or minimal cost can be implemented in the interim (to improve immediate system utility) while sourcing the replacement of the NTNDS.

A) Replace the NTNDS with a new surveillance system (preferred)

Given the overall limited flexibility of the NTNDS, which also affects its simplicity, data quality, acceptability, sensitivity, timeliness, stability and cost, the CDC will likely benefit more from replacing the NTNDS with a new disease surveillance system. The ideal system should possess the following capabilities beyond what the NTNDS can currently deliver:

- Be interoperable with existing NT Health information systems
- Receive real-time direct electronic notifications from pathology providers via HL7* (Health Level Seven) or similar, followed by a triage process and tracked assignment of new notifications to different CDC program areas. It should show whether the notification met surveillance case definition, or was eventually discarded by the action officer

  **HL7 is a set of international standards for the transfer of electronic health information between different IT applications and healthcare providers*[12]
- Transmit real-time data to the data warehouse and BI
- Be a person-based data model

And have:

- Case investigation/contact tracing/public health response function
- Customisable data import function for all diseases and fields (including record overwrite with administrator permission)
- Fully customisable data fields and instruments (restricted privileges to balance the trade-off between flexibility and data quality)
- Application programming interface (API) access
- Connectivity with a secure file transfer platform
- Suggestive search results
- Customisable report building function and panel freeze
- Customisable validations (error/warning messages) and conditional logics
- Downloadable data dictionaries
- Document upload and storage function
- Detailed audit log and data change history

The ideal system should have frontend control of most system capabilities by an internal CDC administrator, who is adept in both information technology (IT) and disease surveillance, instead of a private company making iterative changes from the backend. It should be flexible in terms of data management, while at the same time preserving data quality and in compliance with relevant security and privacy laws.

Interoperability with other NT Health information systems should initially focus on core fields such as Hospital Registration Number (HRN) and Aboriginal and Torres Strait Islander status.

All notification-related data (case investigation, contact tracing, public health response, and recording of core and enhanced data) should be displayed and manipulated on a single application interface with customisable user privileges, streamlining workflow across different areas of responsibility.

A new surveillance system may require a different approach to data entry and quality assurance. The role of data entry staff will likely evolve into a data assurance role, who will be responsible for conducting routine and frequent checks on the quality of imported and automatically linked data. This includes searching for and filling in fields with missing data from external sources, and correcting any errors identified. A comprehensive cost-benefit analysis needs to be performed for each option, comparing the initial establishment cost of implementing a new surveillance system against the cumulative fixed and variable costs of operating the NTNDS over a specified period; taking into account the potential benefits the new surveillance system could offer CDC compared to the NTNDS.

B) Continue to use but improve the operational efficiency of the NTNDS

High priority

Data quality

- Provide more examples of how to enter complex notifications during fortnightly surveillance meetings. In addition, establish regular or ad-hoc data training sessions with staff in regional offices to freely discuss issues unable to be discussed over fortnightly surveillance meetings.
- Ensure all data staff have copies of and frequently refer to the NT Notifiable Diseases Public Health Management Guide,13 the NT Immunisation Schedule,14 the NTNDS Manual and Business Rules,15 and the NTNDS core data dictionary16 when entering notifications.
- Data errors in date fields identified should be immediately cleaned to improve data quality. A comprehensive analysis of date fields for all diseases should be conducted using statistical packages to identify anomalies.

Sensitivity

- Determine the cause of missing Salmonellosis, Shigellosis and invasive Pneumococcal disease notifications with pathology providers; whether the fax transmission failed, was misdirected or the faxed paper was misplaced.

Stability

- There exists a 'Data check' report in BI that shows the date and time NTNDS data were loaded into the data warehouse in the past 7 days. Ensure this report is using data from the new 'Notifiable Diseases universe' (connected to the Microsoft® SQL [Structured Query Language] server), and schedule this report on a daily or bi-weekly basis to the Head of Surveillance or delegate to check for potential data transmission failures.

Medium priority

Simplicity

- Update the NTNDS manual and business rules and core data dictionary to reflect system upgrades and changes to the data entry process since the documents' last revision.
- Place the latest versions of NTNDS manual and business rules and core data dictionary in a central location (e.g. CDC SharePoint site) easily accessible by all data staff. Advise staff to create access shortcuts on their desktop or bookmarks in their browser.
- Review and update enhanced data dictionaries for diseases with enhanced data screens if necessary; gather and place in a central location for ease of access.

Data quality

- Incorporate additional data items during annual/quarterly data cleaning including but not limited to:
    - Ensuring middle names are entered into 'Other Names' and not 'First Name'
    - Missing hospitalisation and death status
    - Missing 'Admission Date' where 'Hospitalised' is selected as 'Yes'
    - Missing 'Discharge Date' where the 'Admission Date' is not missing and it has been more than 3 months since the case was admitted to hospital (BI reports can also be created for the last three items)
- Group NTNDS records by HRN (excluding those without a valid HRN) and check for possible duplicate records created for the same disease with the same 'Notification Date' or 'Notification Received Date' because of aliases.
- Check 'Organism Name' against 'Disease Name' and look for anomalies; where a 'Disease Name' was corrected but the 'Organism Name' was not.
- Group all data cleaning reports on BI into a single folder and schedule regular automated updates to Head of Surveillance for delegation to review anomalies and clean.

Acceptability

- Increase data entry staffing capacity and arrange skills development opportunities for data staff.

Sensitivity

- Perform a comprehensive sensitivity analysis to estimate the proportion of missed notifications for all laboratory confirmed diseases; comparing positive results authorised by pathology providers with NTNDS data.

Timeliness

- Add validation to the field 'Notification Received Date' so that it cannot be later than the 'Entry Date'.
- Pre-plan additional data entry support for when there are significant backlogs, during COVID-19 or influenza seasons, or when key staff go on leave.

Stability

- Depending on the cost, engage with the system builder to identify and rectify the technical issue preventing the transmission of records to the NNDSS that were previously deleted or had their disease name changed.

Usefulness

- Review, update and expand the objectives of a notifiable disease surveillance system for the NT in the context of future health threats and the establishment of the Australian Centre for Disease Control.

Low priority

Simplicity

- The 'Notification Date' field should be made mandatory for diseases where a specimen is required to be collected and tested to confirm case definition.
- A warning message should appear advising users to add vaccination data if none have been entered for vaccine-preventable diseases (including no vaccine given).

Data quality

- Perform data linkage with external sources such as Australian Immunisation Register (AIR), NT Health Client Master Index, and inpatient data to review and verify the validity of NTNDS data.
- Update the former names of remote communities to their current names in 'Resident Location', in accordance with BushTel (NT Government's central website for information related to remote communities).17 Alternatively, have former community names linked to current community names when selected.
- Create a master list/database documenting all data entry errors identified by data entry and surveillance staff. Review, analyse and communicate this list once every six months or yearly via internal meetings.

PVP

- The NTNDS's 'lookback' function can be improved by changing the mechanism to be based on HRN (or a combination of HRN and 'Surname'), rather than the current mechanism of solely using 'Surname'.

Timeliness

- If required during weekend outbreak situations, assign a dedicated staff member to liaise with the Department of Corporate and Digital Development (DCDD) to schedule the data transmission process for a particular weekend.

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The first case of sexually transmitted Zika virus infection notified in the Northern Territory, Australia, 2024; local transmission following an imported case

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ABSTRACT

While the Zika virus (ZIKV) is not endemic in Australia, it continues to be prevalent in many neighbouring countries in the Indo-Pacific region. It poses significant public health concerns due to its association with severe outcomes, including Guillain-Barré syndrome and congenital malformations such as microcephaly. While primarily considered a vector-borne disease, documented sexual transmission of ZIKV raises concern of unrecognised and underreported infections. This report details 2 cases of ZIKV infection diagnosed in the Northern Territory of Australia. The first case is a male traveller who contracted the virus in Timor-Leste and the second, his female partner in Australia. This represents the first reported incidence of ZIKV infection acquired in Australia.

The investigation emphasizes the importance of obtaining detailed patient histories, including sexual histories, to improve detection and understanding of ZIKV transmission. It also highlights the challenges of diagnosing ZIKV due to its nonspecific symptoms and emphasises the importance of public health education regarding ZIKV transmission and prevention strategies. Clinicians need to be aware of the symptoms, geographic distribution and transmission modes of infectious diseases like ZIKV in returned travellers, as well as the potential implications for their contacts. Heightened awareness is important to ensure early detection, appropriate management and counselling, to prevent transmission.

Key words: Zika virus, public health, Northern Territory, Timor-Leste, contact tracing, mosquito-borne virus, flavivirus, sexually transmitted, travel health

INTRODUCTION

Zika virus is a flavivirus primarily transmitted by the *Aedes aegypti* mosquito which is also the vector for the dengue (DENV) and chikungunya (CHIKV) viruses.[1,2] The Zika virus (ZIKV) was named after the Zika Forest in Uganda, where it was first identified. Prior to 2007, only sporadic cases of ZIKV infection had been reported. However, in 2007 outbreaks occurred in the Pacific, firstly on the island of Yap in the Federated States of Micronesia,[3] followed by another in French Polynesia in 2013-14.[4] A notable outbreak occurred in Brazil in 2015[5] prior to the 2016 summer Olympic games.

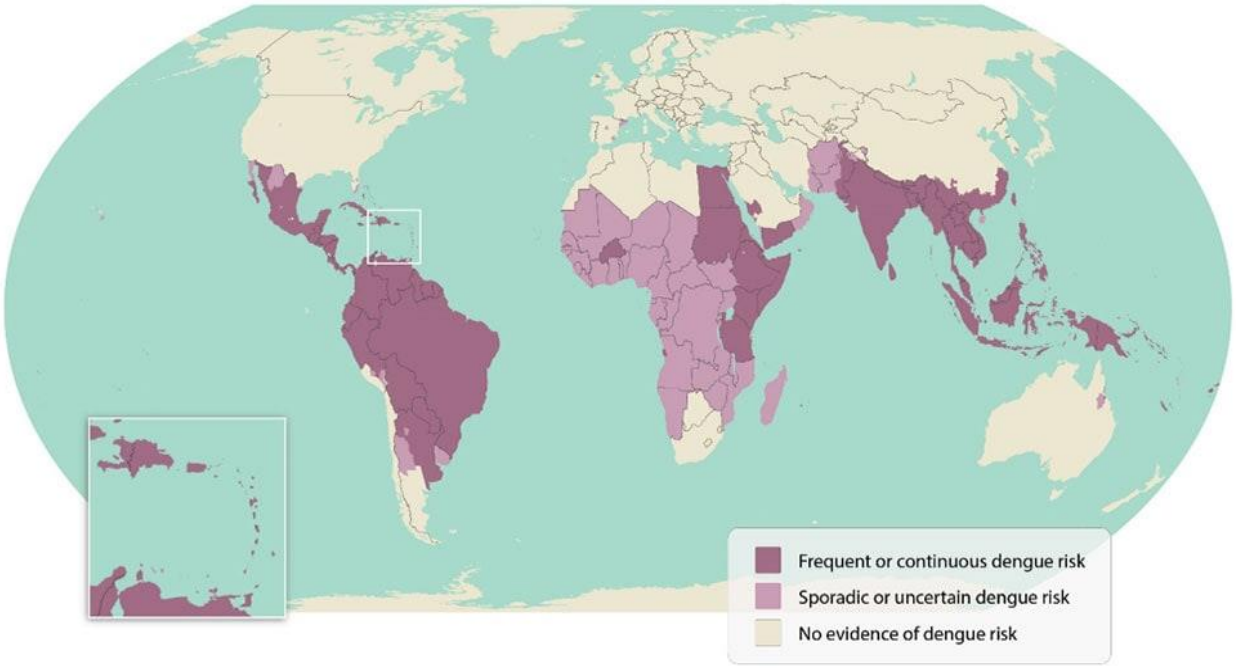
While the infection is most often asymptomatic, it may present clinically (in approximately 20% of infections) with fever, rash, pruritis, conjunctivitis, arthralgia, myalgia, fatigue and headache.[1] ZIKV infection has been associated with Guillain-Barre syndrome[6] and causal links have also been established between infection during pregnancy

and microcephaly, as well as other congenital malformations.[7] Maternal-fetal (vertical) transmission of ZIKV has been well documented.[1,5] For these reasons, ZIKV infection was declared as a Public Health Emergency of International Concern (PHEIC) in 2016.[8] In the following 6 to 7 years, up to 58 countries reported outbreaks.[2]

Although vector-borne transmission is the primary mode of ZIKV spread, sexual transmission has also been documented with ZIKV transmissible by an infected person to their partner, regardless of gender.[9] The exact incubation period for ZIKV transmission following the bite of an infected vector is not certain but case reports and observational experience indicate it is likely to be 3 - 14 days. There is some suggestion that for sexual transmission, the incubation period may be longer but this is not confirmed.[1,7] Most reported sexually transmitted cases involve symptomatic men, with persistence of ZIKV in their semen,[10] but transmission from asymptomatic men, as well as female-to-male and male-to-male transmission, has also been documented. Sexual transmission can occur before, during, or after the onset of symptoms.[11] While most flavivirus infections confer lifelong immunity following recovery, this is yet to be confirmed for ZIKV. There is a recent study from Brazil suggesting evidence of ZIKV reinfection events.[12]

ZIKV infection is a notifiable condition in the Northern Territory (NT) and in Australia.[13] Cases are being diagnosed in travellers returning from regions where *Aedes* spp mosquitos capable of transmitting dengue and ZIKV are endemic, mainly countries close to the equator (Figure 1). In the NT between 2013 and 2023 there were 3 cases of ZIKV notified in travellers returning from Indonesia, Fiji and Thailand.[14] Up until 2023, there was only 1 case of ZIKV infection with the place of acquisition reported as Timor-Leste notified to Australia's National Notifiable Diseases Surveillance System (NNDSS).[15] In 2024 Timor-Leste reported diagnosing its first locally detected case of ZIKV infection.[16]

Figure. Map showing areas of dengue risk in the world (i.e. areas where *Aedes* spp. mosquitos capable of transmitting dengue are endemic and potentially also pose a risk for Zika virus transmission)[17]



In Australia, the *Aedes aegypti* mosquito is endemic in parts of North Queensland[18] and there have been sporadic detections with short term establishment followed by successful eradication of *Ae. aegypti* in Tennant Creek in the NT. Currently there is an ongoing eradication program being conducted in the town.[19]

In the NT, each notification of ZIKV infection is investigated in order to determine the source/location of infection.[11] Cases are provided with public health education and advised not to travel to ZIKV-receptive areas of Australia (i.e. North Queensland or Tennant Creek, NT) for at least the first week after onset of symptoms in order to minimise the possible risk of transmission or introduction of circulating disease. Male cases notified with the ZIKV are advised to abstain from unprotected sex during the infectious period and for at least 6 months after their diagnosis, to prevent partner transmission.[11]

In May 2024, the NT Centre for Disease Control (CDC) was notified of 2 cases of ZIKV infection.

CASE 1

On 5 May 2024, Territory Pathology notified NT CDC of a case of ZIKV infection that was detected via blood and urine samples using the AusDiagnostics Mosquito-Borne Panel, a polymerase chain reaction (PCR) panel. Public health investigations on that day confirmed that the individual, an adult male, had travelled to Timor-Leste on 18 April, where he recalled being bitten by multiple mosquitoes. On 24 April, 7 days after arriving in Timor-Leste, he developed symptoms, including fever, arthralgia, myalgia, headache and a pruritic erythematous macular rash that began behind the ears and progressed down the body.

He returned to Darwin on 1 May and consulted his general practitioner on 3 May who ordered serum and urine diagnostic testing to be performed via AusDiagnostics Mosquito-Borne PCR Panel by Territory Pathology. On the day of notification and case interview, 5 May, the individual's symptoms had resolved. Of note, testing was negative for DENV, CHIKV, Ross River Virus, Barmah Forest virus, West Nile virus, Murray Valley encephalitis virus, Japanese encephalitis virus, Kunjin virus and malaria using the AusDiagnostics Mosquito-Borne Panel PCR.

Given the typical ZIKV incubation period of 3-14 days,[1,2] it was determined that the case acquired his ZIKV infection during his recent travels to Timor-Leste.

The case interview further revealed that he had no known sick co-travellers or contacts while in Timor-Leste and had not visited areas in Australia where *Aedes aegypti* mosquitoes had been detected in the previous 6 months. His only sexual partner, who was not a co-traveller, was well and not pregnant. The case and his partner were educated about the virus causing the ZIKV disease and that it was transmitted by mosquitos present in Timor-Leste but not in Darwin and that there was potential for sexual transmission of ZIKV for up to 6 months. It was explained that there were risks to a pregnancy in the form of potential for congenital malformations with advice to avoid unprotected sex and to use contraception for 6 months from the time of diagnosis.

On 6 May medical entomology was notified as per protocol.[11,13] As a week had passed since the onset of the case's illness, advice against travelling to any ZIKV mosquito receptive area in Australia was not required.

CASE 2

On 15 May 2024, NT CDC was again notified by Territory Pathology of a ZIKV infection that was detected in blood and urine samples using the AusDiagnostics Mosquito-Borne PCR Panel. The following day, 16 May, a case interview was carried out by NT CDC.

On 14 May, Case 2, the partner of Case 1, an adult woman, presented to the Emergency Department

(ED) at Palmerston Regional Hospital (PRH) with a 7-day history of flu-like symptoms, including myalgia, which progressively included headache, fever and a maculopapular rash. She also experienced arthralgia affecting the small joints of her fingers and pain in her knees and ankles. She had presented to her GP with these symptoms on 10 May and informed the GP of her partner's diagnosis of ZIKV infection. The patient was sent for arboviral serology on that day which later returned Zika IgG EIA and Zika IgM EIA with the interpretation as not detected. After visiting her GP, Case 2 contacted the CDC physician who had spoken with her partner 11 days prior regarding his diagnosis of ZIKV infection, and had provided education on the virus, its modes of transmission, and recommended actions. The CDC physician advised Case 2 to seek care at the ED if her symptoms worsened and to advise the ED staff also of her partner's recent ZIKV diagnosis. Given her symptoms and identification as a sexual contact of a confirmed ZIKV case, the ED physician also suspected an arboviral infection and the blood and urine samples collected detected ZIKV ribonucleic acid (RNA) on both via the AusDiagnostics Mosquito-Borne PCR Panel. Testing was negative for DENV, CHIKV, Ross River Virus, Barmah Forest virus, West Nile virus, Murray Valley encephalitis virus, Japanese encephalitis virus, Kunjin virus and malaria. The full blood count (FBC) revealed a white cell count of 4.0 $x10^9$/L (reference range 4.0-11.0 $x10^9$/L) and a platelet count of 226 $x10^9$/L (reference range 150-450 $x10^9$/L).

At the case interview it was confirmed that Case 2 had not travelled outside of greater Darwin recently and was not pregnant. The likely mode of transmission for acquisition of ZIKV infection was identified as unprotected sexual contact with her partner, Case 1, prior to his diagnosis and awareness of the risks of sexual transmission with ZIKV infection. Both were educated again about disease and the ongoing risks of potential sexual transmission for up to 6 months.

To minimise the risk of sexually transmitting the virus Case 2 was advised to avoid unprotected sex for at least 8 weeks after her diagnosis. She was also advised to refrain from traveling to ZIKV-receptive areas such as Tennant Creek and Northern Queensland until at least a week after her illness onset or the laboratory confirmation date, i.e. 15 May, of her infection. She and her partner were to defer donating blood for 4 months after symptoms had dissappeared.[7] Case 2 was also counselled to avoid unprotected sex with her partner for 6 months, due to the uncertainty around the potential for reinfection[11] and his ongoing infectiousness.

Medical entomology was notified as per protocol.[11,13]

This case series represents both the first reported case of ZIKV acquired in Australia and first reported incidence of sexually transmitted ZIKV infection in Australia.[15]

DISCUSSION

This public health investigation highlights key considerations for healthcare providers managing suspected or confirmed ZIKV infections, particularly in patients returning from ZIKV endemic countries and their sexual partners. ZIKV can be transmitted sexually before individuals are tested or even aware they may be infected. In addition, ZIKV infection often presents with nonspecific symptoms such as flu-like illness, fever, rash, and myalgia, making accurate diagnosis challenging without a thorough travel history, contact tracing and timely testing.

The potential for sexual transmission of ZIKV by both symptomatic and asymptomatic cases raises concern about the likelihood of unrecognised and underreported infections. This emphasises the necessity of obtaining detailed patient histories, including thorough sexual histories in addition to travel histories of patients and their close contacts to enhance detection and understanding of ZIKV transmission.

Testing and educating patients about mosquito protection is crucial for preventing ZIKV infection. Healthcare providers should advise individuals travelling to or living in ZIKV endemic areas to take protective measures, including using DEET (diethyltoluamide), picaridin or oil of lemon eucalyptus (p-menthane-3,8-diol - PMD) containing insect repellent, and wearing light-coloured, long-sleeved clothing, including during the day when the *Ae. aegypti* mosquitoes are most active.

Though ZIKV is primarily transmitted by the *Ae. aegypti related* mosquito, sexual transmission can also occur from both symptomatic and asymptomatic individuals, before, during, and after symptom onset. This highlights the need for clinicians to provide guidance on preventive measures, especially in cases where pregnant individuals or those planning pregnancy are involved, given the link to severe congenital defects.

Men diagnosed with ZIKV infection should avoid unprotected sex however the duration of communicability is uncertain. Current Australian guidelines recommend avoiding unprotected sex for at least 6 months after diagnosis. Infected women should avoid unprotected sex for at least 8 weeks after diagnosis.[11]

Perinatal transmission (vertical transmission), blood transfusion and laboratory exposure are also known to occur.[1] Although ZIKV RNA has been detected in breast milk, there have been no reported cases of ZIKV transmission to infants through breastfeeding.[20] The World Health Organization (WHO) advises that breastfeeding should continue, as the benefits for both the infant and mother outweigh any potential risk of transmission via breast milk.[20]

CONCLUSION

ZIKV remains a concern for individuals traveling to endemic areas, with both vector-borne and sexual transmission posing considerable risks. Clinicians should include ZIKV infection as a differential diagnosis in people returning from areas where the ZIKV vector mosquitos are endemic. Clinicians also need to provide clear guidance on mosquito protection and safe sex practices to people prior to travelling to these countries and offer tailored counselling to pregnant individuals or those planning pregnancy to minimize the risk of ZIKV-related complications.

It is also important that clinicians take a detailed case history when suspecting an arboviral infection, including that of sexual partners and their travel history.

ACKNOWLEDGMENTS

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Hard rubbish collection in the fight against the dengue mosquito in Tennant Creek

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The NT Health's dengue mosquito elimination efforts are continuing since the mosquito was detected in Tennant Creek in February 2021. In previous *NT Disease Control Bulletins*, we reported on the detection[1] and provided an update on the dengue elimination program progress. Our last report noted no detections of *Aedes aegypti* during round 14 of property inspections and treatments (20 May to 26 July 2024).[2] However, between 29 July and 24 December 2024, *Aedes aegypti* larvae were found at 1 property and adults collected from three traps, indicating that drought resistant eggs might still be present in the town.

To assist *Ae. aegypti* elimination by reduction of potential mosquito breeding containers from Tennant Creek, Medical Entomology, NT Health liaised with the Barkly Regional Council prior to their annual hard rubbish collection on 18 December 2024. A social media post, was issued by NT Health (Figure 1) supported with message from Barkly Regional Council (Figure 2, encouraging Tennant Creek residents to dispose of any unwanted water-holding items, on the hard rubbish collection day). The call for action was successful, with many residents participating (Figures 3 and 4), and all items disposed of and buried at the local waste transfer station.

Figure 1. NT Health social post, requesting Tennant Creek residents to participate in the Barkly Regional Council hard rubbish collection in December 2024.

Figure 2. Barkly Regional Council message, encouraging Tennant Creek residents to reduce mosquito breeding

Figure 3. Hard rubbish placed on the road verge in Tennant Creek for collection by the Barkly Regional Council on 18 December 2024

Figure 4. Old tyres placed on the road verge in Tennant Creek for collection by the Barkly Regional Council on 18 December 2024

Acknowledgements

We would like to thank the Barkly Regional Council for assisting NT Health in the fight against the dengue mosquito in Tennant Creek.

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Measles in the Territory –'ZERO' cases from 2020 to 2024

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Background: Measles is a highly infectious viral illness, that can spread rapidly and cause serious disease. In Australia today, the disease most often originates from people who have travelled and acquired the disease internationally, who can then spread the infection to non-immune individuals during travel and on return to Australia.

Current Situation: During the COVID-19 pandemic years (2020 – 2023), Australia saw very few measles cases, with no cases notified in 2021 due to strong public health measures such as closures of interstate and international borders, restrictions on gatherings, hand hygiene and the use of face masks. With the reopening of borders and increased travel, measles notifications in Australia have been on the rise.

Globally, there has been an interruption in childhood vaccination programs due to the COVID-19 pandemic and consequently an increase in cases and deaths due to measles. In 2023, 57 countries experienced a large or disruptive measles outbreak. [1]

Childhood measles mumps rubella (MMR) immunisation coverage for the 2 year old cohort sits at 92.55% nationally and 92.88% in the NT as of June 2024,[2] both below the World Health Organization's target rate of 95%. To achieve herd immunity for measles, Australia needs a vaccination coverage rate of about 92 – 94%.[3]

The Northern Territory (NT) had its last outbreak of measles in 2019 with 31 confirmed cases. In the last 5 years (2020 - 2024), there have been no measles notifications in the NT (see Table). The NT Centre for Disease Control (CDC) has been on the forefront, disseminating up-to-date measles information and training its staff to respond to measles outbreaks by conducting simulation sessions over the past year.

Table: Measles notifications received by jurisdiction (2019 – 2024)[4]

State	2019	2020	2021	2022	2023	2024
ACT	2	0	0	0	1	1
NSW	62	11	0	1	6	18
NT	31	0	0	0	0	0
QLD	74	6	0	0	5	8
SA	4	0	0	0	3	6
TAS	1	0	0	0	1	0
VIC	58	4	0	6	4	17
WA	52	4	0	0	6	6
Total	**284**	**25**	**0**	**7**	**26**	**56**

Vaccination: Measles is a vaccine preventable disease and the best protection against it is to be immunised with a measles-containing vaccine such as the measles, mumps, rubella (MMR) vaccine.[5] To achieve immunity, 2 doses of the vaccine are required, at least 1 month apart.

- The MMR vaccines are free, safe and very effective. This is a reminder to check that people are up to date with their vaccines and protected against measles.
- Children receive their 1st dose of MMR vaccine at 12 months and 2nd dose (measles, mumps, rubella plus varicella vaccine, (MMRV) at 18 months.
- People born during or after 1966, who do not have documentation of having received 2 doses of measles-containing vaccine, should be offered free MMR vaccine. Those individuals who are unsure of their vaccination history should also be vaccinated. There is no need to check measles serology prior to vaccination.
- Anyone planning overseas travel should make sure they have received appropriate travel vaccinations, which includes documentation of 2 measles-containing vaccines (e.g. MMR) to make sure they are not at risk of measles.
- Children travelling overseas to high risk areas before 12 months of age can have a MMR vaccine from 6 months of age onward to cover the 6 to 12 month vulnerable age period but then require 2 age-appropriate measles containing vaccines.

Testing: The best test for measles is a PCR on a throat swab, nasal swab and a urine sample. CDC will expedite measles testing so ensure you contact your regional NT CDC. A person with suspected measles should not be sent to a pathology collection centre as this may expose others who are non-immune.

Practices should ensure all staff members have received 2 doses of MMR vaccine or have proof of immunity.

Case management: Symptoms usually begin 7- 21 days (most commonly 10 -12 days) after exposure to the virus, which may start with runny nose, fever, cough, red and watery eyes, or Koplik spots (white spots inside the mouth). A prominent rash begins on average 2 to 4 days after these symptoms, usually starting at the hairline, face and upper neck and spreading over the body, eventually to the hands and feet.[5,6]

Anyone with a presentation consistent with measles should be treated as a suspect case, avoid the waiting room and be directed immediately to an isolated room that can be closed off for at least 30 minutes following the suspect case leaving the room. The suspect case should isolate at home until the results of testing for measles are known. If the results are positive, the patient needs to isolate for at least 4 days after the onset of the rash, at which time the case is no longer considered infectious.

Public health management: CDC will organize the public health response to identify contacts of measles cases and offer vaccination for susceptible contacts and advise about exclusion periods as necessary.

It is through continued public health measures including timely testing, robust surveillance, education and high levels (≥95%) of immunisation coverage that we can strive to keep measles cases in the NT at 'ZERO'.

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Media and health alerts issued October to December 2024

Public health alerts were issued on Gonorrhoea, Whooping cough (Pertussis), Box Jellyfish, Syphilis, Mpox, Melioidosis, COVID-19, Influenza and Respiratory Syncytial Virus (RSV) by the NT Centre for Disease Control (CDC) from October to December 2024. Below are excerpts from these alerts, noting some may no longer be active at the time of publishing this issue. The full Whooping cough (Pertussis) alert is available on the following page. Current and previous health alerts can be viewed at the NT Health website.

Gonorrhoea

Since January 2023 the remote Northern Territory (NT) has seen an increase in cases of penicillinase-producing *Neisseria gonorrhoeae* (PPNG) and an outbreak was declared. Cases and their sexual contacts have been indentified across the NT.

All cases of suspected or confirmed uncomplicated genital and anorectal gonorrhoea should be treated with: Ceftriaxone 500mg in 1.8mL 1% lignocaine IM single dose and Azithromycin 1g oral single dose

Read the full alert issued 1 October 2024

Whooping Cough (Pertussis)

National pertussis notifications continue to increase in 2024, with the highest number of cases reported in any year-to-date. The increase is driven by New South Wales, Queensland and Victoria with the highest proportion of notifications in school-aged children (5-14 years). The current situation may be due to several factors such as decreased vaccination coverage, waning immunity and overall population having reduced exposure to pertussis in recent years. The NT has seen an increase in cases since June 2024 and this is likely to continue as per national trends. Children need to be up-to-date with their pertussis vaccines. Healthcare workers and adults taking care of children need pertussis-containing vaccines every 10 years. All pregnant women need to be vaccinated from 20 weeks in each and every pregnancy to protect their infant at birth.

Read the full alert issued 2 October 2024

Box Jellyfish

It is now stinger season in the Northern Territory (NT). Jellyfish are an active part of the NT ocean environment. *Chironex fleckeri* is a sea animal, also known as the major box jellyfish. It has the most rapidly acting venom known to science and is capable of killing a person in under 5 minutes.

Venomous box jellyfish are more likely to be in the water from October up until the end of May.

Issued 10 October 2024 for more information visit Box jellyfish | NT Health.

Syphilis

An infectious syphilis outbreak has been ongoing in the NT since 2013, with 2,287 cases notified as at 22 October 2024.

Read the full alert issued 28 October 2024

Mpox

There were 3 cases of mpox detected in the NT in October 2024 with 1 case likely acquired in the NT and 2 cases were acquired interstate. All cases were clade IIb. There has been no known onward transmission reported from these cases. There have been 1,073 cases of mpox in 2024 in Australia, most occurring in NSW, Victoria and QLD. All cases which were typed were clade IIb.

Mpox has been declared as a Public Health Emergency of International Concern (PHEIC) by the World Health Organization on 14 August. This is in response to an upsurge in cases of mpox and emergence of clade Ib mpox in the Democratic Republic of the Congo (DRC), which then spread to neighbouring countries including the Central African Republic (CAR), Burundi, Uganda, Rwanda and Kenya.

Single cases of clade Ib mpox have been detected in Sweden, Thailand, India and Germany in travellers returning from central Africa. No cases of clade Ib mpox have been detected in Australia to-date.

The National Rapid Assessment Team (RAT) has determined the risk in Australia is currently low to moderate for mpox.

Vaccines are available across the NT to help protect against mpox and are recommended for those at increased risk.

Read the full alert issued 30 October 2024

Melioidosis

Melioidosis is a serious disease caused by bacteria that live in tropical soils and water. Heavy rainfall brings them up into surface water and soil, where they can be picked up by the wind and spread in the air. In the NT, there is a higher chance of getting sick with melioidosis during the wet season from October to April.

People most at risk are those with diabetes mellitus, with liver, lung and kidney disease, those who are immunosuppressed and those with heavy alcohol intake.

Melioidosis requires urgent medical attention as it can be fatal if not treated with the right antibiotics.

Issued 22 November 2024 for more information visit Melioidosis | NT Health.

Covid-19, Influenza and RSV

COVID-19, influenza, and RSV notifications have all increased in December 2024 in the NT, presenting a challenge to healthcare systems across the holiday season.

Since 1 December, 162 cases of COVID-19 have been notified in the NT, a 35% increase compared to the previous 3 weeks with cases now increasing across Central Australia.

Since mid-late November, a steady increase in RSV cases has been seen, mostly in the Top End, particularly in Darwin. RSV infection in communities is often a prelude to influenza outbreaks.

Since early December the Top End has seen an increase in influenza case that is expected to continue to rise. Notably, 34% of cases have been influenza B, which is a concern as earlier outbreaks of influenza this year have been almost exclusively influenza A and current community immunity to influenza B is likely to be low. The 2024 influenza vaccine is still available and effective.

Cases of COVID-19 and influenza (particularly influenza B) have also been increasing across Australia.

Read the full alert issued 28 October 2024

NORTHERN TERRITORY GOVERNMENT

Centre for Disease Control

NT HEALTH

⚠ Public Health Alert

Issued: 2 October 2024
Issued by: NT Centre for Disease Control
Issued to: Health Practitioners

Increase in Pertussis

Summary

- Increased pertussis cases are occurring across Australia especially in school-aged children in New South Wales, Queensland and Victoria.
- NT has seen increasing pertussis numbers since June 2024, which is likely to continue.
- Early diagnosis, isolation and antibiotics can reduce further transmission and protect vulnerable infants.
- *Bordetella pertussis* PCR on a nasopharyngeal (preferred) or throat swab is the best test. Serology (IgA) is not useful to detect early infection and only recommended after a cough of 4 weeks duration.
- Vaccination remains key to protecting the community. Ensure infants and children are vaccinated on time at 6 weeks, 4 months, 6 months, 18 months and 4 years. And for adolescents vaccinate from 12 years (Year 7) with catch up until 19 years. NIP funded.
- All pregnant women need to be vaccinated from 20 weeks in each and every pregnancy to provide protection against pertussis for infants from birth.
- Health care workers should receive pertussis containing vaccine every 10 years.

Current situation

- National pertussis notifications continue to increase in 2024, with the highest number of cases reported in any year to date. The increase is driven by New South Wales, Queensland and Victoria with the highest proportion of notifications in school-aged children (aged 5-14 years). The current situation may be due to several factors such as decreased vaccination coverage, waning immunity and overall population having reduced exposure to pertussis in recent years.
- NT has seen an increase in cases since June 2024 and this is likely to continue as per national trends.

Testing

- Patients with a cough illness lasting 14 days or more without an apparent cause plus one of the following: (a) paroxysms of coughing; (b) inspiratory 'whoop'; (c) post-tussive vomiting should be tested.
- *Bordetella pertussis* PCR on a nasopharyngeal (preferred) or throat swab. Pertussis PCR may be included in respiratory multiplex PCR panels.
- Serology is not recommended for detecting infection unless the presentation is delayed until after 4 weeks from any cough onset.

Centre for Disease Control
Public Health Division
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CDCSurveillance.DARWIN@nt.gov.au

Treatment

- Early treatment with antibiotics stops transmission and may reduce the duration of symptoms.
- For recommended treatment please see the latest edition of *Therapeutic Guidelines: Antibiotic*.

Vaccination

- Vaccination remains the most effective means of preventing pertussis and spread to vulnerable people such as babies and pregnant women.
- Rates of all vaccinations have dropped in the NT over recent years and the risk of hospitalisations from pertussis infection is highest in infants under 3 months of age.
- All pregnant women need to be vaccinated from 20 weeks in each and every pregnancy (funded) to protect infants from birth with passive antibodies until the infant can receive their own vaccination at 6 weeks.
- Vaccines given in pregnancy offer neonates 90% protection against confirmed disease and 97% against death in infants under 3 months of age prior to their first vaccinations.
- Vaccination against pertussis are part of the routine childhood immunisation schedule (at 6 weeks, 4 months, 6 months, 18 months, 4 years and 12 years.
- Health care workers should receive pertussis containing vaccine every 10 years.
- All people caring for young children are encouraged to be vaccinated every 10 years e.g. family members, childcare and any others who wish to be vaccinated. Privately funded vaccine is available from GP's or Pharmacies who offer vaccination services
- See Australian Immunisation handbook Pertussis (whooping cough) | The Australian Immunisation Handbook (health.gov.au).

Preventing Spread

- People diagnosed with pertussis are no longer infectious (even if the PCR result is still positive) from:
    - 21 days after the onset of any cough, or
    - 14 days after onset of paroxysmal cough (if the onset is known), or
    - when they have completed 5 days of a course of an appropriate antibiotic
- Ask your patient not to attend school, childcare or any place with infants or pregnant women until they have completed at least 5 days of antibiotics or it is 21 days after the onset of their cough.

Further information

- Whooping cough (pertussis) | NT Health
- Contact the NT CDC for any questions

Scan QR Code for more on Public Health Alerts

Darwin	(08) 8922 8044	**Katherine**	(08) 8973 9041	**Nhulunbuy**	(08) 8987 0357
Tennant Creek	(08) 8932 4259	**Alice Springs**	(08) 8951 7540		

Issued by: Vicki Krause, Director, Centre for Disease Control, Public Health Division, NT Health

Centre for Disease Control
Public Health Division
(08) 8922 8044 or 1800 008 002
CDCSurveillance.DARWIN@nt.gov.au

Northern Territory disease notifications by onset date and district – 1 July to 30 September, 3rd quarter, (2023 vs. 2024)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023
Acute Post Strep GN	0	3	0	2	5	5	1	0	1	3	7	13
Adv Vacc Reaction	0	1	0	1	2	0	1	0	0	1	3	3
AIDS	0	0	0	0	0	0	0	0	0	0	0	0
Amoebiasis	0	0	0	0	0	0	0	0	0	0	0	0
Anthrax	0	0	0	0	0	0	0	0	0	0	0	0
Arbovirus NOS	0	0	0	0	0	0	0	0	0	0	0	0
Aust Bat Lyssavirus	0	0	0	0	0	0	0	0	0	0	0	0
Avian influenza	0	0	0	0	0	0	0	0	0	0	0	0
Barmah Forest	0	0	0	0	1	0	0	0	0	0	1	0
Botulism	0	0	0	0	0	0	0	0	0	0	0	0
Brucellosis	0	0	0	0	0	0	0	0	0	0	0	0
Campylobacteriosis	7	12	1	3	52	66	1	3	4	4	65	88
Chancroid	0	0	0	0	0	0	0	0	0	0	0	0
Chickenpox	1	1	0	0	11	15	0	0	1	8	13	24
Chikungunya	0	0	0	0	0	0	0	0	0	0	0	0
Chlamydia	289	240	30	33	351	381	22	60	77	101	769	815
Chlamydial conj	0	0	0	0	1	0	0	0	0	1	1	1
Cholera	0	0	0	0	0	0	0	0	0	0	0	0
Ciguatera	0	0	0	0	0	0	0	0	0	0	0	0
CJD	0	1	0	0	0	0	0	0	0	0	0	1
Congenital Rubella	0	0	0	0	0	0	0	0	0	0	0	0
COVID-19	69	68	14	3	377	246	21	32	38	11	519	360
Crusted scabies	4	2	2	2	12	10	6	2	6	3	30	19
Cryptosporidiosis	2	2	0	2	4	27	1	0	0	0	7	31
Dengue	1	2	0	0	10	3	0	0	1	0	12	5
Diphtheria	0	0	0	0	0	1	0	0	0	0	0	1
Donovanosis	0	0	0	0	0	0	0	0	0	0	0	0
Food/water borne dis	0	0	0	0	0	0	0	0	0	0	0	0
Gastro - related cases	0	0	0	0	0	0	0	0	0	0	0	0
Gonococcal conj	0	0	0	1	0	1	0	0	0	0	0	2
Gonococcal infection	330	259	20	35	187	216	18	44	76	87	631	641
Gonococcal neon ophth	1	0	0	1	0	0	0	0	0	0	1	1
Group A strep invasive	4	5	6	3	23	18	3	0	4	7	40	33
Hendra virus	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis A	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis - acute viral	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis B - chronic	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis B - new	0	0	0	0	0	1	0	0	0	1	0	2
Hepatitis B - unspec	2	6	0	0	20	17	0	0	0	1	22	24
Hepatitis C - chronic	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis C - new	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis C - unspec	0	8	0	1	7	16	0	2	0	0	7	27

(Table continued next page)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023
Hepatitis D	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis E	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis NOS	0	0	0	0	0	0	0	0	0	0	0	0
H Influenzae b	0	0	0	1	0	1	0	0	0	0	0	2
H Influenzae non-b	2	2	1	0	4	1	0	1	0	1	7	5
HIV	2	1	0	0	2	3	0	0	0	0	4	4
HTLV1 adult TCL	0	0	0	0	0	1	0	0	0	0	0	1
HTLV1 asyptom/unspec	11	33	0	1	0	2	0	0	1	2	12	38
HTLV1 TSP	0	0	0	0	0	0	0	0	0	0	0	0
HUS	0	0	0	0	0	0	0	0	0	0	0	0
Hydatid	0	0	0	0	0	0	0	0	0	0	0	0
Influenza	340	157	73	34	660	160	45	8	70	19	1,188	378
Japanese Encephalitis	0	0	0	0	0	0	0	0	0	0	0	0
Kunjin Virus	0	0	0	0	0	0	0	0	0	0	0	0
Lead - elevated	1	0	0	1	4	35	0	1	1	4	6	41
Legionellosis	0	0	0	0	1	0	0	0	0	0	1	0
Leprosy	0	0	0	0	0	0	0	0	0	0	0	0
Leptospirosis	0	0	0	0	0	1	0	0	0	0	0	1
LGV	0	0	0	0	1	0	0	0	0	0	1	0
Listeriosis	0	0	0	0	0	0	0	0	0	0	0	0
Lyssavirus NOS	0	0	0	0	0	0	0	0	0	0	0	0
Malaria	0	0	1	0	0	2	0	0	0	0	1	2
Measles	0	0	0	0	0	0	0	0	0	0	0	0
Melioidosis	0	0	0	0	3	3	0	0	0	0	3	3
Meningococcal infection	0	0	0	0	1	1	0	0	0	0	1	1
MERS	0	0	0	0	0	0	0	0	0	0	0	0
Mpox virus infection	0	0	0	0	2	0	0	0	0	0	2	0
Mumps	0	0	0	0	0	0	0	0	0	0	0	0
MVE	0	0	0	0	0	0	0	0	0	0	0	0
Non TB Mycobacteria	0	0	0	0	2	6	0	0	0	0	2	6
Ornithosis	0	0	0	0	0	0	0	0	0	0	0	0
Paratyphoid	0	0	0	0	0	0	0	0	0	0	0	0
Pertussis	6	0	2	0	10	0	0	0	3	0	21	0
Plague	0	0	0	0	0	0	0	0	0	0	0	0
Pneumococcal disease	12	12	3	8	12	12	0	0	5	0	32	32
Poliomyelitis	0	0	0	0	0	0	0	0	0	0	0	0
Q Fever	0	0	0	0	0	1	0	0	0	0	0	1
Rabies	0	0	0	0	0	0	0	0	0	0	0	0
Rheumatic Fever	17	24	4	5	15	13	8	4	6	10	50	56
Rheumatic heart disease	8	4	3	0	10	6	5	4	0	5	26	19
Ross River Virus	0	0	0	1	6	14	0	1	0	3	6	19
Rotavirus	2	51	1	17	14	66	1	12	4	7	22	153
RSV infection	134	94	9	2	76	52	0	7	7	8	226	163
Rubella	0	0	0	0	0	0	0	0	0	0	0	0
Salmonellosis	7	6	7	5	64	47	2	8	6	9	86	75

(Table continued next page)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023	2024	2023
SARS	0	0	0	0	0	0	0	0	0	0	0	0
Shigellosis	6	8	1	6	10	17	5	5	0	5	22	41
Smallpox	0	0	0	0	0	0	0	0	0	0	0	0
STEC/VTEC	0	0	0	1	0	0	0	0	0	0	0	1
Strongyloidiasis extra-int	0	0	0	0	0	0	0	0	0	0	0	0
Syphilis	0	0	0	0	0	0	0	0	0	0	0	0
Syphilis < 2y duration	24	34	2	3	30	10	5	1	20	10	81	58
Syphilis > 2y or unk duration	4	7	0	0	10	2	0	3	3	2	17	14
Syphilis congenital	0	1	0	0	0	0	0	0	0	0	0	1
Tetanus	0	0	0	0	0	0	0	0	0	0	0	0
Trichomoniasis	290	217	44	43	240	310	77	104	85	134	736	808
TTP	0	0	0	0	0	0	0	0	0	0	0	0
Tuberculosis	0	0	0	0	3	8	0	0	0	2	3	10
Tularaemia	0	0	0	0	0	0	0	0	0	0	0	0
Typhoid	0	0	0	0	2	0	0	0	0	0	2	0
Typhus	0	0	0	0	0	1	0	0	0	0	0	1
Varicella - unspec	0	9	1	0	5	12	1	4	0	2	7	27
Vibrio food poisoning	0	0	0	0	1	0	0	0	0	0	1	0
Vibrio invasive	0	0	0	0	0	0	0	0	0	0	0	0
Viral Haemorrhagic Fevers	0	0	0	0	0	0	0	0	0	0	0	0
Yellow Fever	0	0	0	0	0	0	0	0	0	0	0	0
Yersiniosis	0	3	0	0	8	7	0	0	0	0	8	10
Zika	0	0	0	0	0	0	0	0	0	0	0	0
Zoster	16	13	4	4	103	90	2	4	5	4	130	115
Sum:	**1,592**	**1,286**	**229**	**219**	**2,362**	**1,907**	**225**	**310**	**424**	**455**	**4,832**	**4,177**

Dengue notifications for July to September 2024– overseas acquired

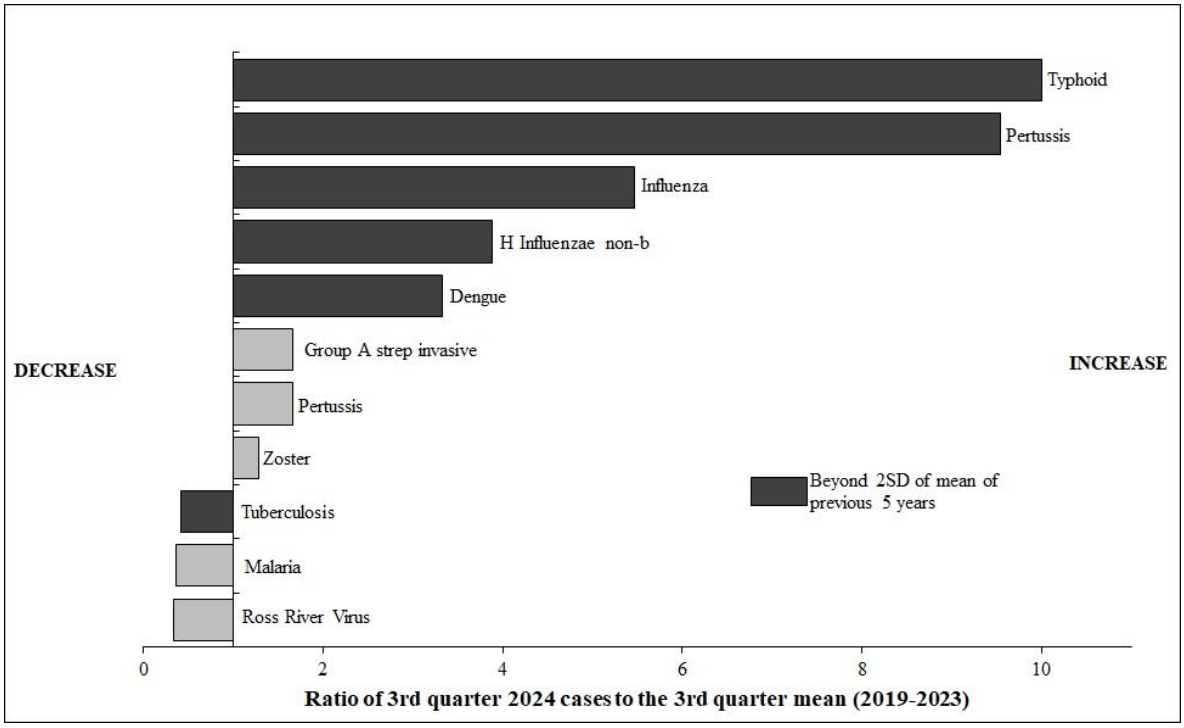
Number of cases	Origin of infection	NT Region notified (number of cases)
6	Indonesia	Darwin (4), Katherine (1), Alice Springs (1)
4	Philippines	Darwin (4)
1	Nepal	Darwin (1)
1	Thailand	Darwin (1)

Malaria notifications for July to September 2024 – overseas acquired

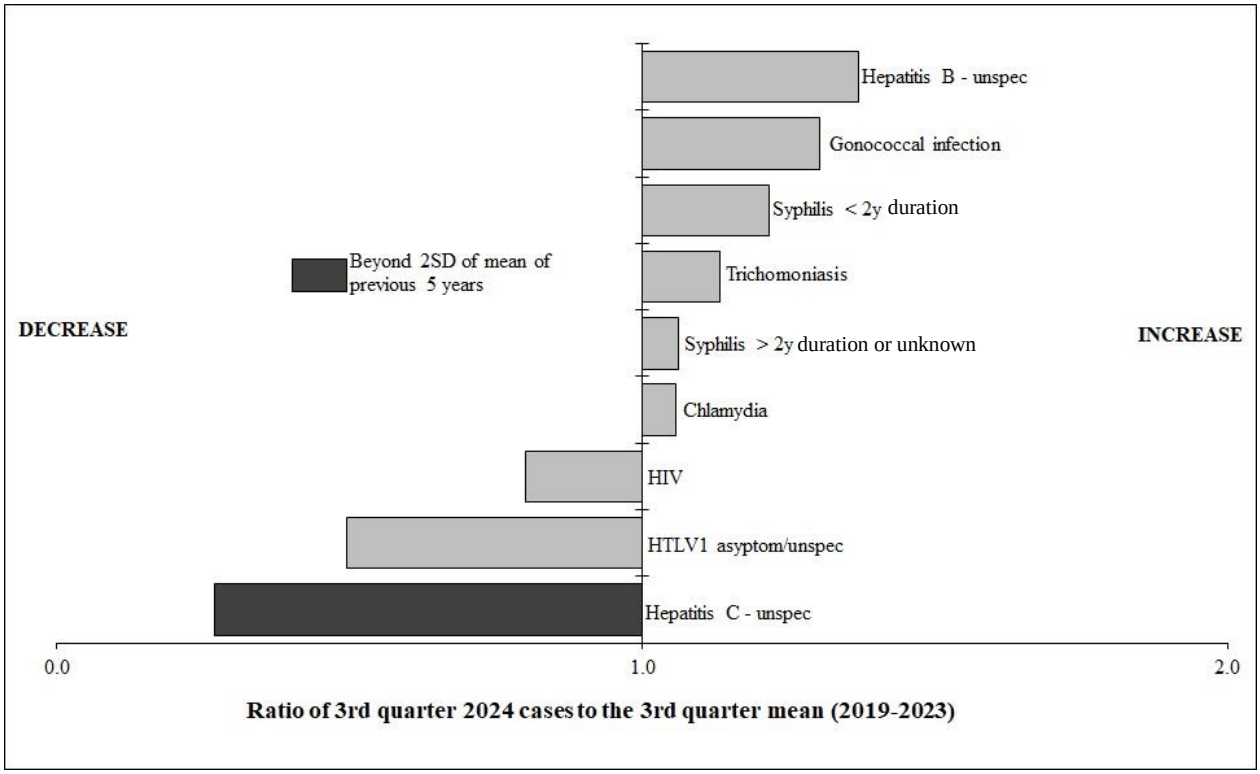
Number of cases	Origin of infection	Agent	Chemoprophylaxis	NT Region
1	Uganda	*Plasmodium malariae*	None	Barkly

Graphs of selected diseases and STIs – Q3 2024

Ratio of the number of notifications in 3rd quarter of 2024 to the 3rd quarter mean (2019 – 2023): Selected diseases



Ratio of the number of notifications in 3rd quarter of 2024 to the 3rd quarter mean (2019 – 2023): Sexually transmitted infections



Comments on selected disease notifications

Mpox (formerly Monkeypox)

There were 2 notifications of mpox in the NT in the 3rd quarter of 2024. There have now been 3 cases notified in the NT since the global outbreak began in May 2022. One case acquired their infection locally and 1 interstate. There was no onward spread.

Dengue

There were 12 notifications of dengue virus infection in the 3rd quarter of 2024, a marked increase compared to a 5 year 3rd quarter mean of 3.6 cases. In the pre-pandemic period between 2015 to 2019, the 5 year 3rd quarter mean was 7 notifications. All cases acquired their infection overseas (dengue virus infection is not endemic in the NT although the vector, *Aedes aegypti*, has been detected in Tennant Creek where there is an active mosquito eradication program in place). Of the 12 cases of dengue, 6 acquired their infection in Indonesia, 5 in Bali, 2 in the Philippines, 1 in Thailand, and 1 in Nepal.

***Haemophilus influenzae* non-b**

There were 7 notifications of *Haemophilus influenzae* non-b infection in the 3rd quarter of 2024 compared to a 5 year 3rd quarter mean of 1.8 notifications. In the pre-pandemic period between 2015 to 2019, the 5 year 3rd quarter mean was 1 notification.

Influenza

There were 1,188 notifications of influenza in the 3rd quarter of 2024, showing a marked increase compared to a 5 year 3rd quarter mean of 217 notifications. In the pre-pandemic period between 2015 to 2019, the 5 year 3rd quarter mean was 407 notifications. The overwhelming majority (99.1%) of the 3rd quarter 2024 cases were influenza A.

Pertussis

There were 21 notifications of pertussis in the 3rd quarter of 2024 in the NT compared to a 5 year 3rd quarter mean of 2.2 notifications. Other jurisdictions in Australia saw a massive increase in pertussis notifications during this quarter. By the end of the 3rd quarter 2024 there have been well over 30,000 pertussis notifications nationally.

Typhoid

There were 2 notifications of typhoid in the 3rd quarter of 2024 in the NT compared to a 5 year 3rd quarter mean of 0.2 notifications. One person acquired their infection in India and the other in Bangladesh.

Tuberculosis

There were 3 notifications of tuberculosis in the 3rd quarter of 2024 in the NT compared to a 5 year 3rd quarter mean of 7.2 notifications.

Hepatitis C – unspecified

There were 7 notifications of hepatitis C – 'unspecified' in the 3rd quarter of 2024 in the NT compared to a 5 year 3rd quarter mean of 27 notifications. This was due to adjustments in surveillance practices leading to more accurate classification of cases.

Lymphogranuloma venereum

There was a single case of lymphogranuloma venereum (LGV) notified in the 3rd quarter of 2024 in the NT. This person acquired their infection in Indonesia. There were 2 cases of LGA notified in the 2nd quarter of 2024. The last case of this disease in the NT before 2024 was notified in 2021.

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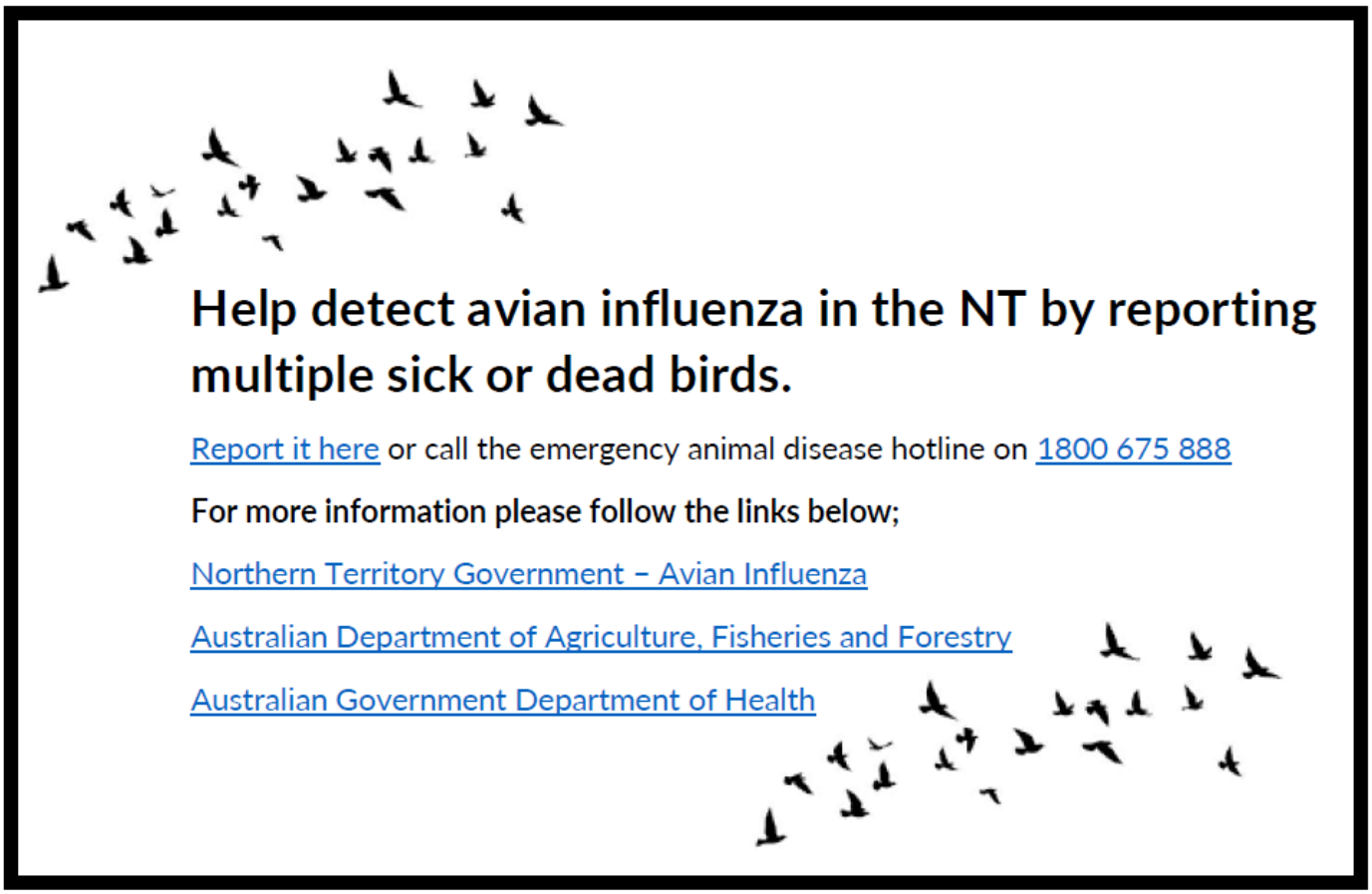
Immunisation coverage in the Northern Territory

Northern Territory (NT) immunisation data is accessible from the Australian Government website. The following link provides tables of the latest annualised quarterly report on childhood immunisation coverage from the Australian Government Department of Health and Aged Care, which combines the December, March, June and September quarters for NT and Australia.

The data show the proportion of children fully immunised at 1, 2 and 5 years of age according to the National Immunisation Program Schedule.



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NT Health Fact sheet

Melioidosis- Wet Season Factsheet for Health Professionals

Background

Melioidosis is a serious disease caused by bacteria called *Burkholderia pseudomallei*, which live in tropical soils and water worldwide, particularly in Southeast Asia and northern Australia. Melioidosis mostly occurs in the wet season (October to April), but cases also occur in the dry season. Heavy rainfall brings the bacteria into surface water and soil, where they can be picked up by the wind and spread in the air.

Melioidosis bacteria can infect a person through penetrating injuries, skin cuts and sores exposed to soil and water, breathing in dust or droplets (especially during storms or spray from high-pressure hoses), and rarely by drinking unchlorinated water that contains the bacteria. It can also infect some domestic and farm animals and animals in zoos. Melioidosis does not usually spread from one person to another or from animals to humans.

The people with the following conditions are most at risk of melioidosis:

- Diabetes mellitus
- Kidney disease
- Lung disease
- Cancer
- Transplant recipients
- Treatment with immunosuppressive therapy, including steroids
- Heavy alcohol consumption (more than 20 standard drinks a week, or binge drinking)

High risk oncology, rheumatology and all haemodialysis patients should commence prophylactic trimethoprim-sulfamethoxazole during the wet season.

Up to 20% of cases occur in healthy people without any of the above risk factors, but who have been exposed to the bacteria in soil or water, usually through skin exposure.

Healthy children are much less likely to get melioidosis than adults. However, children with chronic diseases or a weakened immune system can become sick with melioidosis.

Clinical features

- Around half of melioidosis cases present with pneumonia.
- Other presentations range from skin lesions without systemic illness, to overwhelming sepsis with abscesses disseminated in multiple internal organs.
- Genitourinary disease with prostatic abscesses is especially common in the Top End.
- Bone, joint and neurological infections are all well documented.

Testing

The likelihood of diagnosing melioidosis is maximized if the diagnosis is considered in at-risk subjects and appropriate clinical samples from a variety of sites are sent to the microbiology laboratory for microscopy and culture.

Culture is the mainstay of diagnosis. Blood cultures are positive in over 50% of all patients. Diagnosis of melioidosis (i.e. active disease) is NOT made based on a positive serology (IHA) result, although melioidosis serology should be ordered if melioidosis is suspected. Serologic testing alone is not a reliable method of diagnosis and culture confirmation should always be vigorously sought in patients with suspected melioidosis.

All patients with suspected melioidosis should have the following samples, if available, taken for culture:

- Blood cultures
- Sputum
- Urine
- Abscess fluid or pus
- Swab of an ulcer or skin lesion; placed into Ashdown's selective medium (purple bottle)* to enhance recovery of the organism
- Throat swab; placed into Ashdown's selective medium*
- Rectal swab; placed into Ashdown's selective medium*

*In remote clinics where Ashdown's media is not available, do not do throat and rectal swabs. But for skin sores collect standard swabs and place in bacterial transport medium tubes. For these AND for sputum and urine samples, please add to the laboratory request form 'Melioidosis culture also please".

Chest X-ray should be performed in all suspected cases.

Treatment

All confirmed cases of melioidosis and any suspected cases without confirmation despite appropriate diagnostic work up (as above) should be referred to the RDH Infectious Diseases team or ASH Infectious Diseases team. Melioidosis is a laboratory-notifiable disease in the NT.

Public health management

There is no way to eradicate melioidosis from tropical soils and there is no vaccine against melioidosis. People who have previously had melioidosis can get infected again. For key preventive measures see Melioidosis (nt.gov.au)

For more information call your nearest Centre for Disease Control.

Location	Phone
Darwin (Top End Region)	(08) 8922 8044, 1800 008 002
Katherine (Big Rivers Region)	(08) 8973 9049
Tennant Creek (Central Australia Region)	(08) 8962 4259
Alice Springs (Central Australia Region)	(08) 8951 7540
Nhulunbuy (East Arnhem Region)	(08) 8987 0357

Abstracts from peer reviewed published articles related to the Northern Territory

Osteomyelitis and Septic Arthritis in the Darwin Prospective Melioidosis Study

Campbell S, Hicks D, Shetty RP, Currie BJ

Open Forum Infect Dis .2024 Dec 19;12(1):ofae741. doi: https://doi.org/10.1093/ofid/ofae741

Background: Melioidosis is a multisystem infectious disease caused by the environmental bacterium *Burkholderia pseudomallei*. Osteomyelitis (OM) and septic arthritis (SA) are uncommon primary presentations for melioidosis but important secondary foci, often requiring prolonged therapy and multiple surgeries. We characterized the epidemiology, presentation, treatment, and outcomes of patients from 24 years of the Darwin Prospective Melioidosis Study (DPMS).

Methods: DPMS patients from October 1, 1999, until September 30, 2023, were included if they had a primary or secondary diagnosis of OM or SA. Epidemiological, risk factor, clinical, and outcome data were retrieved from the DPMS database. Antibiotic and surgical data were collated from patient records.

Results: From 1129 consecutive patients with culture-confirmed melioidosis, 122 (10.8%) had OM and/or SA, with 115 evaluable. Ninety-four of 1129 (8.3%) had OM, and 62/1129 (5.5%) had SA, with 41/115 (35.7%) of these having both OM and SA. Many combined infections involved contiguous bone and joints or soft tissue. Fifty-nine (51.3%) were male, and only 4.3% were ≤16 years old. Diabetes mellitus was present in 69.6%, and only 12.2% had no identifiable clinical risk factor. There were 8 deaths (7.0%) and 20 (17.4%) recurrent infections. Seventy-one (61.7%) had operative management, with combined infection associated with more procedures and longer length of stay.

Conclusions: The current paradigm of care for osteoarticular melioidosis involves prolonged intravenous antibiotics in conjunction with timely and complete operative management, and in our setting where these are available, outcomes are good. In many melioidosis-endemic regions these resources are limited, and mortality remains high.

Keywords: *Burkholderia pseudomallei*; bone and joint infection; melioidosis; osteomyelitis; septic arthritis

The heart of the matter: a re-iteration of the role of the social determinants of health in addressing health inequity in Central Australia

Naughton W, Baumann A. A, Neal K, Wilson D, Johnson R and Holwell A

Intern Med J. 2024 Oct 26 PMID: 39460656 DOI: 10.1111/imj.16548

The persisting life-expectancy 'gap' between First Nations and non-First Nations Australians is fundamentally driven by the social determinants of health. These include income and social protection, access to adequate housing and food security, among others. These factors are particularly prominent in Central Australia. Inadequate housing has led to some of the highest rates of *Streptococcus pyogenes* infection in the world, which in turn drives an extremely high prevalence of rheumatic heart disease. Food insecurity and inadequate social protection manifesting as energy insecurity result in

inadequate nutrition and have resulted in a huge burden of diabetes in Central Australia. These factors, combined with social exclusion, racism and the pervasive effect of colonisation, also drive a high rate of alcohol misuse. Only by prioritising equity in these 'social determinants' and emphasising the importance of First Nations leadership in formulating and implementing solutions will health inequity be addressed

Keywords: alcohol use disorders; diabetes; rheumatic heart disease; skin infections; social determinants.

Global impact of ten-valent and 13-valent pneumococcal conjugate vaccines on invasive pneumococcal disease in all ages (the PSERENADE project): a global surveillance analysis

Bennett JC, Knoll MD, Kagucia EW, Garcia Quesada M, Zeger SL, Marissa K Hetrich MK, Yang Y, Herbert C, Ogyu A, Cohen AL, Yildirim I, Winje Ba, von Gottberg a, Viriot D, van der Linden M, Valentiner-Branth P, Suga S, Steens A, Skoczynska A, Sinkovec Zorko N, J Scott A, Savulescu C, Savrasova L, Carlos Sanz J, Russell F, Ricketson LJ, Puentes R, Nuorti JP, Mereckiene J, McMahon K, McGeer A, Mad'arová L, Mackenzie GA, MacDonald L, Lepp T, Ladhani SN, Kristinsson KG, Kozakova J, Klein NP, Jayasinghe S, Ho PL, Hilty M, Heyderman RS, Hasanuzzaman Md, Hammitt LL, Guevara M, Grgic-Vitek M, Gierke R, Georgakopoulou T, Galloway Y, Diawara I, Desmet S, De Wals P, Dagan R, Colzani E, Cohen C, Ciruela P, Chuluunbat U, Chan G, Camilli R, Bruce MG, Brandileone MCC, Bigogo G, Ampofo K, O'Brien KL, Feikin DR, Hayford K, the PSERENADE Team

Lancet Infect Dis 2024; published online Dec 17. *https://doi.org/10.1016/S1473-3099(24)00665-0*

Background

Pneumococcal conjugate vaccines (PCVs) that are ten-valent (PCV10) and 13-valent (PCV13) became available in 2010. We evaluated their global impact on invasive pneumococcal disease (IPD) incidence in all ages.

Methods

Serotype-specific IPD cases and population denominators were obtained directly from surveillance sites using PCV10 or PCV13 in their national immunisation programmes and with a primary series uptake of at least 50%. Annual incidence rate ratios (IRRs) were estimated comparing the incidence before any PCV with each year post-PCV10 or post-PCV13 introduction using Bayesian multi-level, mixed-effects Poisson regressions, by site and age group. All site-weighted average IRRs were estimated using linear mixed-effects regression, stratified by product and previous seven-valent PCV (PCV7) effect (none, moderate, or substantial).

Findings

Analyses included 32 PCV13 sites (488 758 cases) and 15 PCV10 sites (46 386 cases) in 30 countries, primarily high income (39 sites), using booster dose schedules (41 sites). By 6 years after PCV10 or PCV13 introduction, IPD due to PCV10-type serotypes and PCV10-related serotype 6A declined substantially for both products (age <5 years: 83–99% decline; ≥65 years: 54–96% decline). PCV7-related serotype 19A increases before PCV10 or PCV13 introduction were reversed at PCV13 sites (age <5 years: 61–79% decline relative to before any PCV; age ≥65 years: 7–26% decline) but increased at PCV10 sites (age <5 years: 1·6–2·3-fold; age ≥65 years: 3·6–4·9-fold). Serotype 3 IRRs had no consistent trends for either product or age group. Non-PCV13-type IPD increased similarly for both products (age <5 years: 2·3–3·3-fold; age ≥65 years: 1·7–2·3-fold). Despite different serotype 19A trends, all-serotype IPD declined similarly between products among children younger than 5 years (58–74%); among adults aged 65 years or older, declines

were greater at PCV13 (25–29%) than PCV10 (4–14%) sites, but other differences between sites precluded attribution to product.

Interpretation

Long-term use of PCV10 or PCV13 reduced IPD substantially in young children and more moderately in older ages. Non-vaccine-type serotypes increased approximately two-fold to three-fold by 6 years after introduction of PCV10 or PCV13. Continuing serotype 19A increases at PCV10 sites and declines at PCV13 sites suggest that PCV13 use would further reduce IPD at PCV10 sites.

First detection of Culex tritaeniorhynchus in Western Australia using molecular diagnostics and morphological identification

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Background

Culex tritaeniorhynchus has long been considered the primary vector of Japanese encephalitis virus (JEV), but until recently, it was considered exotic to Australia. When the species was detected in the country's Northern Territory (NT) for the first time, the Western Australia (WA) Department of Health was cognisant of the risk it posed to the State because of the shared border and continuous mosquito habitat adjoining the two jurisdictions. The aim of this study was to undertake intensive mosquito surveillance in the Kimberley region to ascertain whether *Cx. tritaeniorhynchus* was present in WA, define the extent of its distribution and undertake phylogenetic analysis of select specimens to support hypothesized routes of entry into the state.

Methods

Carbon dioxide (CO2)-baited encephalitis virus surveillance (EVS) mosquito traps were deployed at various sites throughout the Kimberley region by surveillance officers within the Medical Entomology unit of the Western Australia (WA) Department of Health. Mosquitoes were then morphologically identified, and a subset of four specimens were confirmed as *Cx. tritaeniorhynchus* by molecular identification using Cytochrome Oxidase I (COI) DNA data and phylogenetic analysis.

Results

From 31 March 2021 to 30 May 2024, a total of 211 female *Cx. tritaeniorhynchus* specimens were collected from 21 unique trap sites in the Kimberley's Shire of Wyndham-East Kimberley (SWEK). Four COI DNA barcode regions were amplified and successfully sequenced for analysis. These sequences fell within a clade recognised as *Cx. tritaeniorhynchus* and specifically all sequences were in a clade with other specimens from the NT and Timor-Leste.

Conclusions

This study represents the first detection of *Cx. tritaeniorhynchus* in WA. Given the widespread nature of trap sites that yielded the species and consecutive seasons over which it was observed, the authors surmise that *Cx. tritaeniorhynchus* is now established within the northeast Kimberley region. The findings are significant given the detection of the species coincides with the first significant outbreak of JEV activity on mainland Australia involving an estimated 45 human cases of Japanese encephalitis, 80 impacted commercial piggeries and widespread feral pig activity. Although the role that *Cx. tritaeniorhynchus* may play in JEV transmission into the future is not yet understood, it presents a potential risk to public health in the region.

Temporal and Geographic Strain Dynamics of Invasive *Streptococcus pyogenes* in Australia: A Multi-Centre Clinical and Genomic Epidemiology Study 2011-2023

Xie Ouli, Chisholm R H, Featherstone L, Nguyen A, Hayes AJ, Jespersen Magnus, Zachreson C, Tellioglu N, Tonkin-Hill G, Dotel R, Spring S, Liu A, Rofe A, Duchene S, Sherry N, Baird R, Krause V, Holt D C, Coin L, Joshi Rai N, O'Sullivan M V, Bond K, Corander J, Howden B, Korman Tony, Currie BJ, Tong S Y.C, Davies MR

http://dx.doi.org/10.2139/ssrn.4799123

Background: Invasive *Streptococcus pyogenes* (Group A Streptococcus) disease disproportionately affects socioeconomically disadvantaged communities including Aboriginal and Torres Strait Islander Australians. Elucidating temporal dynamics and differences between hyperendemic and lower incidence regions is crucial to understanding drivers of pathogen diversity and informing preventative measures. We examined clinical and temporal lineage dynamics across different disease settings in Australia with the aim to understand drivers of pathogen diversity.

Methods: Cases of invasive *S. pyogenes* (n=995) were retrospectively identified across five hospital networks representing lower incidence regions in temperate southeast (SE) Australia and the hyperendemic tropical Top End of the Northern Territory (January 2011–February 2023). Available isolates (n=642) were assigned lineages at whole-genome resolution. A multi-strain transmission model was used to examine the relationship between population-specific parameters and observed lineage dynamics.

Findings: Incidence in the Top End was six times higher than SE Australia and disproportionately affected Aboriginal and Torres Strait Islander people. Circulating lineages and longitudinal *S. pyogenes* strain patterns were markedly different between the regions. The Top End was characterised by waves of lineage replacement compared to endemic maintenance of lineages in SE Australia. The transmission model reproduced a similar pattern of strain replacement when using a high transmission rate, small population size, and high human movement, akin to communities in the Top End suggesting these population parameters may contribute to observed lineage dynamics. Despite distinct circulating lineages, the frequency of non-core genes in the bacterial population was maintained across geography and temporal periods.

Interpretation: In a hyperendemic setting, lineage replacement occurred in waves and may be linked to the disproportionate burden of disease and sparse human population, with maintenance of bacterial gene frequency consistent with multilocus selection. These findings suggest that interventions such as vaccines-in-development without broad cross-protection may lead to lineage replacement.

Keywords: *Streptococcus pyogenes*, group A streptococcus, invasive disease, iGAS, genomic epidemiology, population genomics, surveillance, evolutionary biology, modelling.

Scrub Typhus Outbreak among Soldiers in Coastal Training Area, Australia, 2022

Suhr R, Belonogoff S, McCallum F, Smith J, Shanks GD

Emerg Infect Dis. 2024 Nov;30(14):41-46.

DOI: 10.3201/eid3014.240056

A scrub typhus outbreak occurred among 24 soldiers from 2 Australian Defence Force infantry units following separate training events conducted in the same coastal location in tropical North

Queensland, Australia, in June 2022. Seven soldiers visited a hospital, 5 requiring admission. Outbreak recognition was hampered by the geographic dispersion of soldiers after the exercise and delayed case identification resulting from such factors as prolonged incubation, cross-reactive serologic responses to other pathogens, the nonspecific symptoms of scrub typhus, and the illness's non-notifiable status in the state of Queensland. Our investigation focused on personal protective measures in a subanalysis of 41 soldiers, revealing an association between scrub typhus infection and the use of doxycycline chemoprophylaxis and permethrin uniform dipping.

Keywords: Australia; Leptotrombidium; Orientia tsutsugamushi; Rickettsia; Scrub typhus; bacteria; chigger; infection; outbreak; soldiers.

Systematic review of the evidence for treatment and management of common skin conditions in resource-limited settings: An update

Amgarth-Duff I, Thomas H, Ricciardo BM, Anderson L, Stephens M, Currie BJ, Steer AC, Tong SYC, Crooks K, Hempenstall A, Tatian A, Foster R, Kavalam G, Pallegedara T, Walls K, Bowen A

Trop Med Int Health. 2024 Nov;29(11):923-950. DOI: 10.1111/tmi.14047

Introduction: The skin is the largest and most visible organ of the human body. As such, skin infections can have a significant impact on overall health, social wellbeing and self-image. In 2019, we published a systematic review of the treatment, prevention and public health control of skin infections including impetigo, scabies, crusted scabies and tinea in resource-limited settings where skin infections are endemic. This current review serves as an update to assess the evidence for treatment of these conditions as well as atopic dermatitis, molluscum contagiosum and head lice in endemic settings. The data from this systematic review have supported an update to the Australian National Healthy Skin guidelines.

Methods: A systematic review was conducted using two separate searches in MEDLINE, PubMed, Embase, CINAHL, Cochrane and Web of Science. The first search was an update of the 2018 systematic review using the same search strategy for the same skin conditions to identify emerging literature from 2018 to 2022. The second search strategy used the same key terms but with the addition of atopic dermatitis, head lice and molluscum contagiosum from 1960 to 2022.

Eligible studies included Indigenous peoples and populations in resource-limited settings with a diagnosis of impetigo, scabies, crusted scabies, tinea capitis, atopic dermatitis, molluscum contagiosum or who presented with head lice. Studies conducted in high-income countries were excluded. Articles were screened for inclusion independently by one author with a second group of reviewers independently double screening. Data extraction and an in-depth quality assessment conducted by one author and checked by two others.

Results: Of 1466 original articles identified, 68 studies were included and key findings outlined for impetigo, scabies, crusted scabies, atopic dermatitis, head lice and molluscum contagiosum. Recommendations for each condition based on the available evidence are provided.

Conclusion: The importance of assessing literature relevant to the populations with heavy burden of skin infections is outlined in this systematic review. We have summarised updates to this literature, which may benefit in developing guidelines for skin infection management similar to the National Healthy Skin Guidelines for Australia.

Keywords: atopic dermatitis; crusted scabies; head lice; impetigo; management; molluscum contagiosum; scabies; systematic review; treatment.

Invasive *Streptococcus dysgalactiae* Subsp. Equisimilis in Australia and the Emergence of a Globally Disseminated stG62647 Lineage: A Comparative Clinical and Genomic Epidemiology Study with *Streptococcus pyogenes*

Xie, Ouli and Featherstone, Leo and Nguyen, An and Hayes, Andrew J. and Pitt, Miranda E. and Spring, Stephanie and Liu, Alice and Tonkin-Hill, Gerry and Dotel, Ravindra and Joshi Rai, Neela and Rofe, Alexander and Duchene, Sebastian and Holt, Deborah C. and Judd, Louise and Coin, Lachlan and Krause, Vicki and O'Sullivan, Matthew V. and Baird, Robert and Bond, Katherine and Howden, Benjamin and Korman, Tony M. and Currie, Bart J. and Davies, Mark R. and Tong, Steven,

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http://dx.doi.org/10.2139/ssrn.5011562

Background: *Streptococcus dysgalactiae* subsp. equisimilis (SDSE) is closely related to *Streptococcus pyogenes* with overlapping disease manifestations. We compared the clinical and genomic epidemiology of invasive SDSE to invasive *S. pyogenes* across different settings in Australia and contextualised within global SDSE genomes.

Methods: Cases of invasive SDSE (January 2011-Feburary 2023) were retrospectively identified and sequenced across five hospital networks in temperate south-east (SE) Australia and the tropical Top End of the Northern Territory. Clinical details and longitudinal lineage dynamics were compared to co-collected invasive *S. pyogenes* cases and also 1,166 global SDSE genomes. Related genomic clusters inferred as recent community transmission networks were defined using single nucleotide variant thresholds from transmission studies (SDSE ≤7, *S. pyogenes* ≤5).

Findings: There were 693 invasive SDSE cases, almost exclusively in adults. The overall invasive SDSE incidence in SE Australia was comparable to invasive *S. pyogenes*. Unlike *S. pyogenes*, SDSE incidence did not decline during COVID-19 non-pharmaceutical interventions (NPIs), 2020-2021, and lineages remained stable. In the Top End, SDSE incidence was lower than *S. pyogenes* (incidence rate ratio [IRR] 0·25, 95% CI 0·20-0·30). However, crude incidence remained higher than SE Australia (IRR 1·24, 95% CI 1·07-1·42) and disproportionately affected First Nations Australians (IRR 3·46, 95% CI 2·30-4·91). In well-sampled lineages (≥5 isolates), only 6% (24/384) of SDSE cases were assigned genomic transmission clusters compared to 52% (271/524) for *S. pyogenes*. A stG62647-lineage encompassed 26% (113/436) of sequenced SDSE isolates. Global analysis inferred near-simultaneous expansion of the stG62647-lineage in Australia, Western Europe, and North America between 1990-2005.

Interpretation: There is a substantial burden of invasive SDSE driven by the emergent stG62647-lineage. SDSE genomic infection patterns and incidence during COVID-19 NPIs indicate fundamental transmission and pathogen population differences compared to *S. pyogenes* and has implications for disease control measures.

Keywords: *Streptococcus dysgalactiae* subspecies *equisimilis*, group C/G Streptococcus, *Streptococcus pyogenes*, group A Streptococcus, invasive disease, iGAS, genomic epidemiology, surveillance

Alcohol-related injury hospitalisations in relation to alcohol policy changes, Northern Territory, Australia, 2007–2022: A joinpoint regression analysis

Chen J L J, Zhang X, Draper A DK, Kaur G, Field E, Boffa J, Liddle LM, Burgess P, Wright A

Australasian Professional Society on Alcohol and other Drugs (APSAD) Drug Alcohol Rev. 2024;1–12. published: 10 December 2024
https://doi.org/10.1111/dar.13976

Introduction: The Northern Territory (NT) of Australia has the highest rates of alcohol consumption and injury in the country. We aimed to: (i) describe the epidemiology of alcohol-related injury (ARI) hospitalisations in the NT; (ii) estimate the proportion of alcohol involvement in injury hospitalisations; and (iii) consider the influence of alcohol policies on ARI hospitalisation trends.

Methods: We conducted a retrospective time-series study using coded hospitalisation data from NT public hospitals between 2007 and 2022. ARI hospitalisation was defined combining indicators for injury and acute alcohol use. We undertook descriptive analyses and calculated alcohol involvement against all injury hospitalisations. Annual percent changes (APC) were computed using joinpoint regression to examine the influence of alcohol policies on ARI hospitalisation trends by NT geographical regions (Central Australia and Top End).

Results: Alcohol use was associated with 22.6% of all injury hospitalisations. The most common cause of ARI hospitalisations was assault (46%). In Central Australia, a significant trend decline (APC 12.2; p = 0.011) was observed after 2017 following alcohol policies implemented between 2017 and 2018 (Banned Drinkers Register v2; Minimum Unit Price; and Police Auxiliary Liquor Inspectors). Consecutive years with the greatest decrease in Central Australia were 2013–2014 (APC 25.8) and 2018–2019 (APC 35.1); likely influenced by alcohol policies in effect at the time. In the Top End, a non-significant trend decline (APC 26.1; p = 0.186) was observed after 2020.

Discussion and Conclusions: Alcohol policies implemented between 2017 and 2018 were associated with reduced ARI hospitalisations in Central Australia. Alcohol policies that demonstrated reduced harm should be sustained.

KEYWORDS

Alcohol, alcohol-related injury, hospitalisation, Northern Territory, policy.

Insights gained from sequencing Australian non-invasive and invasive *Streptococcus pyogenes* isolates

Butler T AJ, Story C, Green E, Williamson K M, Newton P, Jenkins F, Varadhan H, van Hal S

Microb Genom. 2024 Jan 10;10(1):001152.doi: 10.1099/mgen.0.001152

Abstract

Epidemiological data have indicated that invasive infections caused by the Gram-positive cocci *Streptococcus pyogenes* (group A streptococcus, GAS) have increased in many Australian states over the past two decades. In July 2022, invasive GAS (iGAS) infections became nationally notifiable in Australia via public-health agencies. Surveillance for *S. pyogenes* infections has been sporadic within the state of New South Wales (NSW). This has led to a lack of genetic data on GAS strains in circulation, particularly for non-invasive infections, which are the leading cause of GAS's burden on the Australian healthcare system. To address this gap, we used whole-genome sequencing to analyse the genomes of

318 *S. pyogenes* isolates collected within two geographical regions of NSW. Invasive isolates were collected in 2007–2017, whilst non-invasive isolates were collected in 2019–2021. We found that at least 66 different *emm*-types were associated with clinical disease within NSW. There was no evidence of any Australian-specific clones in circulation. The $M1_{UK}$ variant of the *emm1* global pandemic clone ($M1_{global}$) has been detected in our isolates from 2013 onwards. We detected antimicrobial-resistance genes

(mainly *tetM*, *ermA* or *ermB* genes) in less than 10% of our 318 isolates, which were more commonly associated with non-invasive infections. Superantigen virulence gene carriage was reasonably proportionate between non-invasive and invasive infection isolates. Our study adds rich data on the genetic makeup of historical *S. pyogenes* infections within Australia. Ongoing surveillance of invasive and non-invasive GAS infections within NSW by whole-genome sequencing is warranted to inform on outbreaks, antimicrobial resistance and vaccine coverage.

Keywords: group A streptococcus

Vibrio parahaemolyticus Foodborne Illness Associated with Oysters, Australia, 2021–2022

Fearnley E, Leong LEX, Centofanti A, Dowsett P, Combs BG, Draper ADK, Hocking H, Howden B, Horan K, Wilmot M, Levy A, Cooley LA, Kennedy KJ, Wang Q, Arnott A, Graham RMA, Sinchenko V, Jennison AV, Kane S, and Wright R

Emerging Infectious Diseases, *30*(11), 2271-2278. https://doi.org/10.3201/eid3011.240172.

The bacterium *Vibrio parahaemolyticus* is ubiquitous in tropical and temperate waters throughout the world and causes infections in humans resulting from water exposure and from ingestion of contaminated raw or undercooked seafood, such as oysters. We describe a nationwide outbreak of enteric infections caused by Vibrio parahaemolyticus in Australia during September 2021–January 2022. A total of 268 persons were linked with the outbreak, 97% of whom reported consuming Australia-grown oysters. Cases were reported from all states and territories of Australia. The outbreak comprised 2 distinct strains of *V. parahaemolyticus*, sequence types 417 and 50. We traced oysters with V. parahaemolyticus proliferation back to a common growing region within the state of South Australia. The outbreak prompted a national recall of oysters and subsequent improvements in postharvest processing of the shellfish.

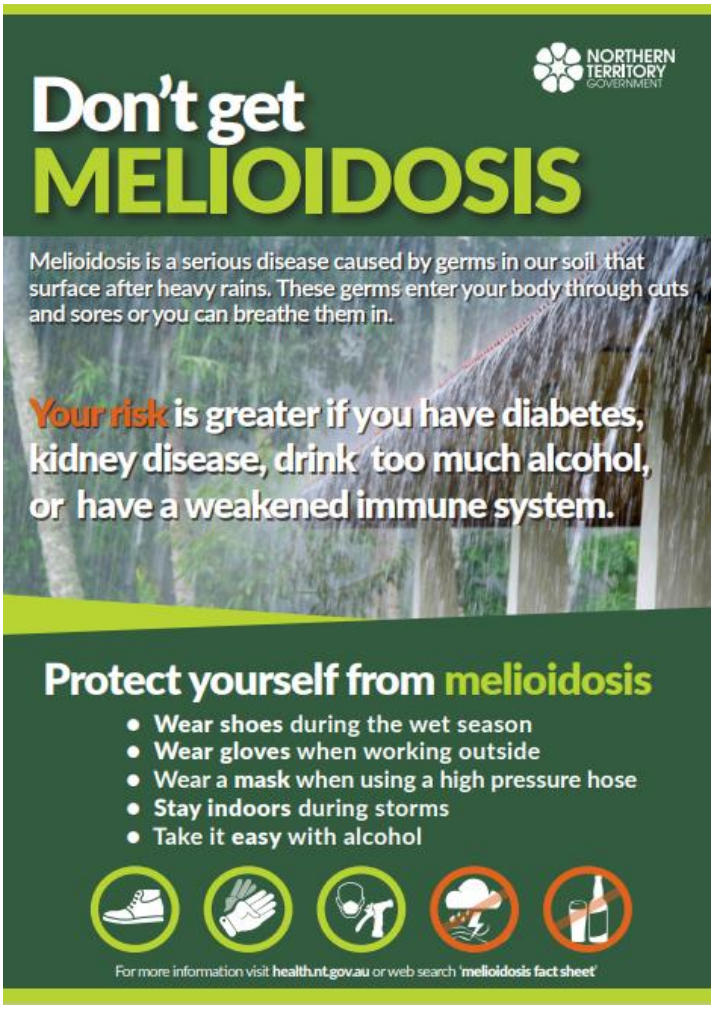
Adverse reactions to trimethoprim/sulfamethoxazole for melioidosis eradication therapy: An evaluation of frequency and risk factors

Martin GE, Bramwell J, Gadil E, Woerle C, Ewin T, Davies J, Janson S, Currie BJ

Int J Infect Dis. 2025 Jan:150:107283. Epub 2024 Nov 8 DOI: 10.1016/j.ijid.2024.107283

Trimethoprim/sulfamethoxazole is the first-line agent for oral eradication therapy for melioidosis but has been associated with toxicity in this context. This study aimed to quantify adverse drug reactions (ADRs) to trimethoprim/sulfamethoxazole when used for treatment of melioidosis, and assess risk factors for ADR development. A retrospective review of antimicrobial associated ADRs was performed in all patients treated for melioidosis in the Northern Territory of Australia from January 2017-September 2022. Over this time, 268 treatment episodes from 256 individuals were included. The frequency of clinician- attributed ADRs to trimethoprim/sulfamethoxazole (51% of exposed)

was higher than for other antimi- crobials used (ceftazidime 12%, meropenem 8%, and doxycycline 12% of those exposed; P < 0.0 0 01). 44% of those treated with trimethoprim/sulfamethoxazole required drug cessation or dose reduction and 5 individuals (2%) had a severe cutaneous adverse reaction, with one fatality. Acute kidney injury was the most frequent ADR (25% of those exposed), with age and pre-existing renal disease indepen- dently associated with its development. Here we report very high rates of ADRs attributed to trimetho-prim/sulfamethoxazole resulting in frequent discontinuation of this drug as part of oral eradication ther- apy for melioidosis. Further work is needed to balance the necessity and toxicity of this drug in this clinical context.



Is Respiratory Viral Infection an Inciting Event in the Development of Melioidosis? A Systematic Evaluation of Co-infection with Burkholderia pseudomallei and SARS-CoV-2 or Influenza

Martin GE, Chen J LJ, Woerle C, Hinchcliff A, Baird RW, Davies J, Currie BJ

Open Forum Infect Dis. 2024 Dec 4;11(12):ofae700.

DOI: 10.1093/ofid/ofae700

Respiratory viral infection may increase infection with *Burkholderia pseudomallei* progressing to clinical disease (melioidosis). This data linkage study evaluated associations between melioidosis and SARS-CoV-2 or influenza. Among 160 melioidosis cases, there was no difference in risk factors, vaccine status, or disease severity between 17 with viral co-infection and 143 without.

Keywords: SARS-CoV-2; influenza; melioidosis