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Editor's note:

In this June 2025 issue of the NT Disease Control Bulletin we learn about the mosquito surveillance carried out on the Tiwi Islands from 2021 to 2024 following the first case of Japanese encephalitis to be diagnosed as acquired in the Northern Territory in early 2021. The individual was resident on the Tiwi Islands during the time of acquisition. Knowing the levels of mosquito vector species and host animals and presence of mosquito breeding areas in the place of acquisition will help the understanding of epizootic transmission potential.

The newly updated, 2025 Tropical Health Orientation Manual (THOM), published by the Menzies School of Health Research with support from the Northern Territory Primary Health Network (NT PHN), is highlighted here with a web link for access. There is an invitation to provide feedback on the content and suggestions for improvement of the 2025 THOM, to inform a revised pdf version later in 2025 and for a print run to be prepared as in the 2 previous editions.

The NT Health Fact Sheet for this issue is reporting on 'Mortality in the Northern Territory, 1967-2020' and is produced by colleagues in the Health Statistics and Informatics Branch of the Public Health Division, NT Health. The findings report that the majority of deaths (69%) are from non-communicable diseases. When looking at deaths from the main disease groups by age group, however, communicable diseases were the major cause of death in the age group 0-4 years.

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Contents

Mosquito surveillance in the Tiwi Islands, following the first Northern Territory Japanese encephalitis virus case

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ABSTRACT

The first case of Japanese encephalitis (JE) in the Northern Territory occurred during 2021 in Wurrumiyanga, Bathurst Island, in the Tiwi Islands at the northwestern edge of the NT. Wet season mosquito surveillance commenced in response to the JE case, which comprised of adult mosquito trapping and larval mosquito surveys. The program was carried out from 2021 to 2024. Generally low mosquito numbers were collected, and there was an absence of large wetlands in Wurrumiyanga. However, several known Japanese encephalitis virus (JEV) vector species were detected, with Culex annulirostris the most abundant vector collected during the mosquito surveillance program.

Potential JEV host animals such as pigs and waterbirds were also present in and nearby to Wurrumiyanga. Despite the low vector abundance, the presence of known vector mosquitoes and host animals suggested there was the possibility for local epizootic transmission. However, there were no further JE cases from Wurrumiyanga. Lack of major mosquito breeding sites may have contributed to there being no further JE cases in Wurrumiyanga. The NT JEV vaccination program, community awareness, source reduction via drain maintenance and methoprene 30-day residual insecticide treatments may also have played a role in the absence of further cases.

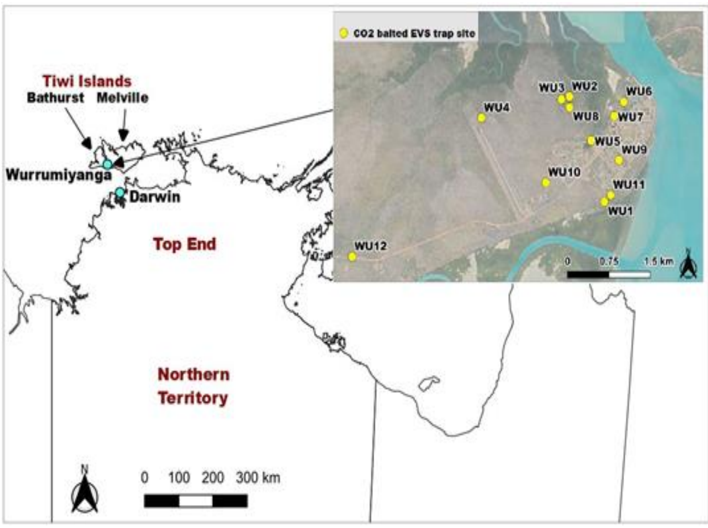
Key words. *Japanese encephalitis virus, vector, mosquito surveillance, abundance*

INTRODUCTION

In February 2021, a fatal case of Japanese encephalitis (JE) occurred, which was later confirmed via complete Japanese encephalitis virus (JEV) genome sequence.[1] This was the first locally acquired case of JEV in the Northern Territory (NT). In response to the case, wet season adult mosquito trapping and larval mosquito surveys were carried out in and around Wurrumiyanga, the resident town of the fatal case, each wet season from April 2021 to May 2024. The aim was to identify mosquito abundance and species diversity during the case month and other wet season months, and important larval habitats. The Wurrumiyanga investigation was part of a broader NT-wide JE response investigating potential vector mosquiotes.[2]

Wurrumiyanga is located 70km north of Darwin on Bathurst Island, the smaller of the 2 Tiwi Islands (Figure 1). At its closest point, the Tiwi Islands are located 25km from the nearest point on the NT mainland. Wurrumiyanga has a small population, with 1,209 people counted in the 2021 census.[3]

Figure 1. Location of Wurrumiyanga and adult mosquito trapping sites



METHODS

Adult mosquito trapping

Overnight carbon dioxide (CO2) baited Encephalitis Virus Surveillance (EVS) traps (Rohe and Fall 1979) were used between April 2021 and May 2024, with traps set predominantly during the wet season months. The mosquito trapping sites are shown in Figure 1. Traps were set adjacent to potential mosquito breeding sites within about 1.5km of Wurrumiyanga, with the exception of trap site WU12, which was set adjacent to a wetland 3.5km west of Wurrumiyanga.

Two (2) to 5 EVS traps were set around Wurrumiyanga in the afternoon and collected the following morning, with the CO2 source provided by food grade gas cylinders or dry ice. A 250ml/minute flowrate was set for the traps when using the gas bottles. Medical Entomology (ME) Officers and Tiwi Resources Rangers conducted the initial trapping each wet season, with subsequent trapping conducted by the Rangers. The majority of the mosquitoes collected in the EVS traps, except for a few damaged specimens, were identified to species level using standard taxonomic keys.

Larval mosquito surveillance

Larval mosquito surveys targeted localised drains, pig ruts, borrow pits, sewage ponds, the wet season temporary landfill site and small wetlands located within 1.6km of Wurrumiyanga. Container habitats were also inspected in residential and commercial yards. Larval mosquito surveys were conducted by ME officers in liaison with the Tiwi Resources Rangers. Mosquito larvae were identified to species when possible, except for the very small instars. Mosquito larvae progress through four development stages (instars), with first instar larvae lacking key distinguishing features. Second and third instar larvae from many mosquito species also lack some key distinguishing features but can still be identified by experienced technicians.

RESULTS

Adult mosquito trapping (CO2 baited EVS traps)

There were 26 mosquito species collected in the overnight EVS traps, accounting for a total of 1124 adult female specimens (Table 1).

Aedes vigilax was the most common mosquito, accounting for 43% of all mosquitoes collected, followed by *Aedes notoscriptus* (17%), *Culex annulirostris* (10%), *Aedes kochi* (9%) and *Verrallina reesi* (7%) (Table 1). Mosquito catches were mostly low, except in December 2021, with catches averaging 114 and 70 on 15 and 16 December respectively, with *Ae. vigilax* the dominant species (Table 1). February was the second most productive month for mosquitoes, and the most productive month for *Cx. annulirostris. Ae. notoscriptus* and *Ae. kochi* were most common from December to February, and *Ve. reesi* were most common in February and March.

Figure 2 shows the spatial abundance of the 5 most common species collected during the trapping program, noting that some trap sites were used more than others. *Cx. annulirostris* was collected in most trap sites surrounding the residential area, with *Ae. notoscriptus* and *Ae. vigilax* also widespread around the community.

Larval mosquito surveys

The results of the larval mosquito surveys are provided in Table 2, with site locations positive for mosquito larvae shown in Figure 3.

Table 1. Wurrumiyanga overnight CO_2 baited EVS mosquito trapping results April 2021 to May 2024. Total female mosquitoes

Species	14/04 /21	15/04 /21	15/12 /21	16/12 /21	13/01 /22	15/02 /22	18/03 /22	16/02 /23	16/03 /23	22/03 /23	2/02 /24	24/05 /24	Total	%
Aedes alboscutellatus	0	0	0	0	2	0	0	1	0	0	0	0	**3**	**0.27**
Aedes kochi	1	0	26	14	19	17	3	2	2	1	19	0	**104**	**9.25**
Aedes notoscriptus	6	5	35	7	19	33	1	20	2	5	64	0	**197**	**17.53**
Aedes alternans	0	0	3	0	0	0	0	0	0	0	0	0	**3**	**0.27**
Aedes normanensis	0	0	0	0	0	0	1	0	0	0	0	0	**1**	**0.09**
Aedes phaecasiatus	0	0	0	0	0	0	0	0	0	0	17	0	**17**	**1.51**
Aedes vigilax	0	0	211	203	39	1	0	0	0	0	27	1	**482**	**42.88**
Aedes daliensis	0	0	0	0	0	1	0	0	0	0	2	0	**3**	**0.27**
Aedes species	0	0	0	0	0	1	0	0	0	0	0	0	**1**	**0.09**
Anopheles bancroftii	0	1	0	0	0	1	0	0	0	0	0	0	**2**	**0.18**
Anopheles farauti s.l.	0	1	0	1	3	7	0	4	0	0	2	0	**18**	**1.60**
Anopheles hilli	0	0	0	0	1	0	0	0	0	0	0	0	**1**	**0.09**
Anopheles meraukensis	1	2	0	0	0	15	9	0	0	0	1	0	**28**	**2.49**
Anopheles species	0	0	0	0	0	0	0	0	0	1	0	0	**1**	**0.09**
Coquillettidia xanthogaster	0	0	0	1	1	0	0	6	1	0	1	6	**16**	**1.42**
Culex pullus	0	0	0	0	0	2	0	0	0	0	0	0	**2**	**0.18**
Culex annulirostris	3	4	3	3	4	47	0	25	1	1	23	0	**114**	**10.14**
Culex gelidus	1	0	0	0	1	0	0	2	0	0	0	0	**4**	**0.36**
Culex palpalis	0	0	0	0	0	0	0	0	0	0	0	1	**1**	**0.09**
Culex sitiens	0	0	3	0	1	1	0	0	0	0	0	0	**5**	**0.44**
Culex Marks *species 32*	0	0	0	0	0	2	1	0	0	0	0	0	**3**	**0.27**
Culex bitaeniorhynchus	0	0	0	0	0	1	0	0	0	0	1	0	**2**	**0.18**
Culex squamosus	0	0	0	0	0	0	0	0	0	0	1	0	**1**	**0.09**
Mansonia uniformis	0	0	0	0	0	1	3	1	0	0	0	0	**5**	**0.44**
Mosquitoes damaged	0	0	0	0	0	1	0	0	0	0	0	0	**1**	**0.09**
Uranotaenia diagonalis	0	0	0	0	0	0	1	0	0	0	0	0	**1**	**0.09**
Uranotaenia albescens	0	0	0	0	0	0	0	1	0	0	0	0	**1**	**0.09**
Verrallina funerea	0	0	1	0	2	2	0	0	0	0	15	0	**20**	**1.78**
Verrallina reesi	0	0	0	0	0	7	37	6	9	7	21	0	**87**	**7.74**
Total	**12**	**13**	**282**	**229**	**92**	**140**	**56**	**68**	**15**	**15**	**194**	**8**	**1124**	**100**
No. traps set	**2**	**2**	**4**	**2**	**4**	**4**	**3**	**4**	**2**	**3**	**5**	**4**	**39**	
Ave. per trap	**6**	**7**	**71**	**115**	**23**	**35**	**19**	**17**	**8**	**5**	**39**	**2**	**29**	

Figure 2. Spatial distribution of the 5 most common adult mosquitoes collected in Wurrumiyanga

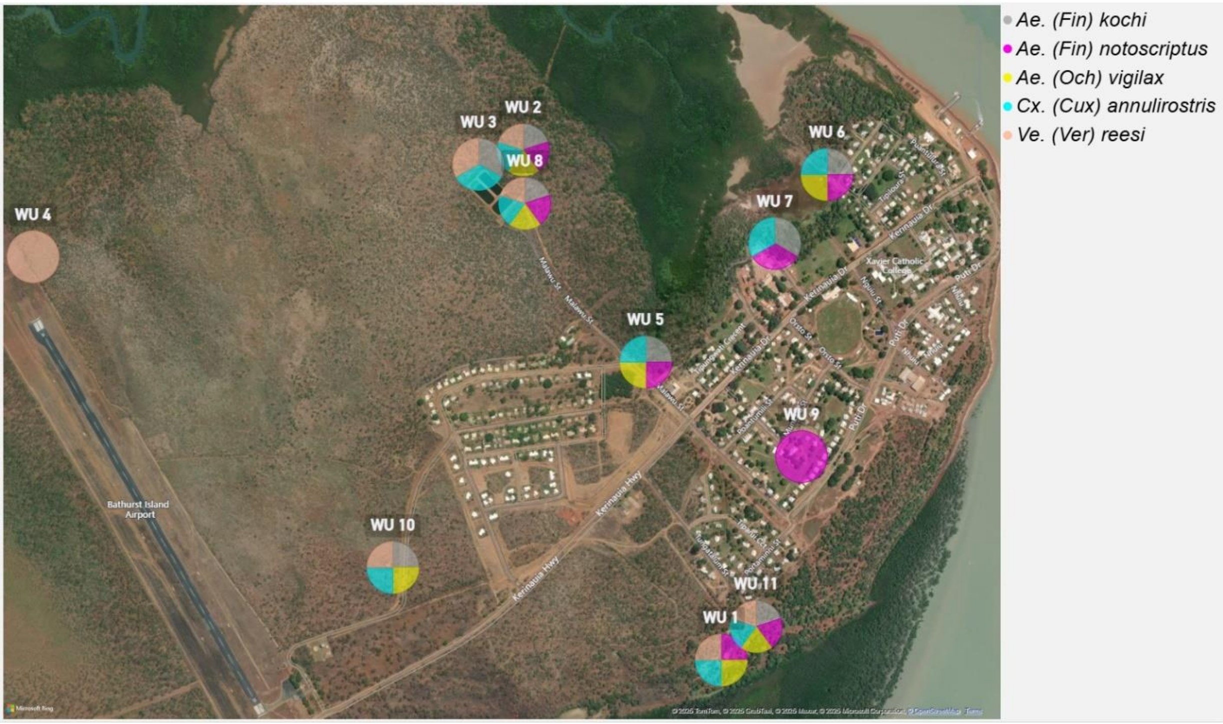


Figure 3. Larval mosquito species detection locations 2021-2024

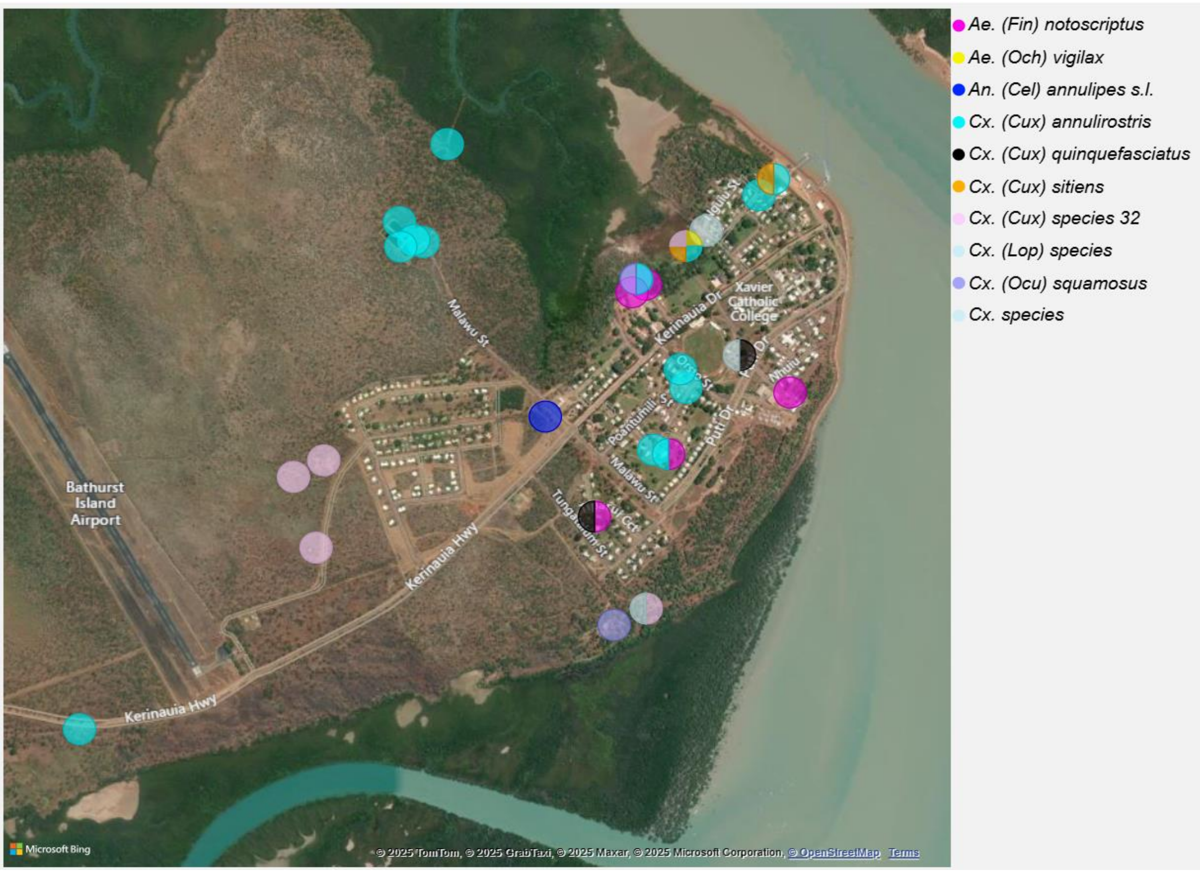


Table 2. Larval mosquito survey results by location (natural and artificial habitats), species collected and average number of larvae per ladle dip

Survey location	*Aedes alboscutellatus*	*Aedes notoscriptus*	*Aedes vigilax*	*Anopheles annulipes s.l.*	*Culex annulirostris*	*Culex quinquefasciatus*	*Culex sitiens*	*Culex* Marks species 32	*Culex species*	*Culex squamosus*
Brackish water *Eleocharis* reed swamp, north edge of town	0	0	5	0	0.1	0	95	0.1	0	0
Bucket (mop)	0	0	0	0	0	0	0	0	5	0
Depression in front of house in Munkara St (water pipe leak)	0	0	0	0	10	0	0	0	0	0
Drain at corner of Ullungura St and Kelantumana St	0	0	0	0	0	0	0	0	0.2	0
End point of open drain from Puautjimi Road	0	0	0	0	0	0	0	0	0	0.5
Fridge (disused)	0	0	0	0	1	0	0	0	0	0
Frying pan	0	5	0	0	0	0	0	0	0	0
Ground pool near the car graveyard	0.2	0	0	0	0	0	0	0	0	0
Munkara St, depression in house access track	0	0	0	0	1	0	0	0	0	0
Old gravel pits near old cemetery	0	0	0	0	0	0	0	1	1	0
Old laydown area between airport and houses	0	0	0	0	0	0	0	0.5	0	0
Old laydown area between airport and houses, south edge	0	0	0	0	0.2	0	0	0	0	0
Open stormwater drain alongside Malawu street near shop	0	0	0	0.2	0	0	0	0	0	0
Paperbark swamp swimming hole west edge of houses	0	0	0	0	0	0	0	0.3	0	0
Puantulura St, roadside drain adjacent to house	0	0	0	0	5	0	0	0	0	0
Roadside depression adjacent to house in Punguatji Close	0	0	0	0	0.2	0	0	0	0	0
Roadside depression adjacent to house in Forestry suburb	0	0	0	0	0.1	0	0	0	0	0
Roadside drain adjacent to house in Orsto St	0	0	0	0	1	0	0	0	0	0
Roadside drain adjacent to house in Tipuamantimirri Street	0	0	0	0	1	0	0	0	0	0
Sewage overflow area from primary sewage pond	0	0	0	0	2	0	0	0	0	0
Sewerage overflow area adjacent to tertiary pond	0	0	0	0	10	0	0	0	0	0
Swimming hole depression between airport and houses	0	0	0	0	0	0	0	0.5	0	0
Tarpaulin	0	5	0	0	0	0	0	0	0	0
Tertiary wastewater pond overflow area	0	0	0	0	5	0	0	0	0	0
Tidally affected open drain from Puti Drive to mangroves	0	0	0	0	1	0	1	0	0	0
Tub (plastic)	0	0	0	0	0	5	0	0	0	0
Tyre (car)	0	5	0	0	0	5	0	0	0	0
Temporary wet season landfill site, 1.3km west of town	0	0	0	0	2	0	0	0	0	0
Wheel ruts in sewage ponds overflow pipe access track	0	0	0	0	0.1	0	0	0	0	0
Wheel ruts near end point of Puatjimi Road open drain	0	0	0	0	2	0	0	0	0	2
Wheel ruts opposite the fish trap	0	0	0	0	0	0	0	0.1	0	0
Borrow pit area at south end of town near mangrove margin	0	0	0	0	0	0	0	0	0	0.2
Primary sewerage pond, amongst sludge	0	0	0	0	2	0	0	0	0	0
Secondary sewerage pond, amongst sludge.	0	0	0	0	50	0	0	0	0	0

Cx. annulirostris was the most common mosquito larvae collected in Wurrumiyanga and was found in a range of larval habitats. The largest larval habitat was the tidally influenced *Eleocharis* reed swamp at the northern edge of Wurrumiyanga, although only low densities of *Cx. annulirostris* larvae were found at this site. *Eleocharis* is a genus of flowering plants in the Cyperaceae family that are know as sledges. They have a cosmopolitan distribution and are concentrated more in tropical zones. The reed swamp was about 2ha in size and bordered a freshwater grassland swamp of about 0.5-1ha in size. *Cilex sitiens* and *Ae. vigilax* larvae were collected in the *Eleocharis* reed swamp during the early wet season, when it was still saline, albeit in a small depression in the floor of the swamp. *Cx. sitiens* larvae were also found in a tidally influenced open drain.

The most productive sites for *Cx. annulirostris* larvae were amongst algal mats along the margins of the secondary sewerage pond, followed by the effluent overflow area, although predominantly small instar larvae were collected at these sites. A small roadside depression was found to be a productive site for *Cx. annulirostris* larvae, with *Cx. annulirostris* larvae were also found in several open unlined drains and a discarded fridge.

Culex quinquefasciatus and Ae. notoscriptus larvae were only collected in container habitats, with *Anopheles annulipes s.l.* larvae found in low densities in a stormwater drain.

Overall, productive mosquito breeding habitats within 1.6km of Wurrumiyanga were very small, whilst the larger areas of ponding, such as the *Eleocharis* reed swamp and old borrow pits, were not productive. The larval mosquito survey results concurred with the low adult mosquito abundance.

DISCUSSION

Adult mosquito trapping has previously been carried out in Wurrumiyanga during the months of October[4], November[5] and December.[6] While low numbers of *Cx. annulirostris* were recorded during those surveys, it needs to be noted that trapping was not carried out during the peak *Cx. annulirostris* months, which is typically January to August in the Top End of the NT. Trapping in October 1981 recorded high *Ae. vigilax* numbers around the community, with 908 collected in a single trap.[4] Moderate to high *Ae. vigilax* numbers were also collected in November 1991.[5] It appears that peak season *Ae. vigilax* numbers in Wurrumiyanga were identified by the past surveys, while the 2021-2024 trapping program adds to the previous knowledge by providing information on mid to late wet season mosquito diversity and abundance.

Generally, low adult mosquito numbers were collected in EVS traps during the recent trapping program. While adult mosquito trapping was probably not frequent enough to identify the peak season abundance of most species in Wurrumiyanga, several known JEV vector species were collected, with those species discussed further.

Cx. annulirostris was the most common *Culex* species collected during the adult mosquito trapping program, and the most common and widespread larvae collected. This species was most abundant during February, the month the JE case occurred. *Cx. annulirostris* has generally been implicated as an important JEV vector species in Australia[7,8,9], and qPCR testing has recently identified JEV in *Cx. annulirostris* samples from Darwin and Tennant Creek.[2] This suggests *Cx. annulirostris* is likely to be the most important JEV vector species in Wurrumiyanga.

Cx. sitiens, *Culex gelidus*, and *Cx. quinquefasciatus* have also been described as potential JEV vectors in Australia[7] and overseas[10], with *Culex bitaeniorhynchus* considered a JEV vector overseas.[10,11] *Cx. sitiens*, *Cx. gelidus* and *Cx. bitaeniorhynchus* were collected in very low numbers during the Wurrumiyanga adult mosquito trapping, while *Cx. quinquefasciatus* was only recorded during larval mosquito surveys. Of these 4 species, only *Cx. gelidus* has yielded positive qPCR samples in the Darwin region.[2] *Cx. sitiens* and *Cx. quinquefasciatus* have occasionally been implicated in pest mosquito complaints in the Darwin region, while *Cx. gelidus* and *Cx. bitaeniorhynchus* have not. While all 4 of these *Culex* species could potentially play some role in JEV transmission in Wurrumiyanga, they might be of lesser importance compared to *Cx. annulirostris* due to lower abundance.

Ae. vigilax was the most abundant adult mosquito collected during the trapping program and was also collected during the month of February in 2022 and 2024. While JEV has been isolated from field caught specimens[13], *Ae. vigilax* has been found to be an inefficient JEV vector under laboratory conditions[7], suggesting *Ae. vigilax* might be of lower importance as a JEV vector in Wurrumiyanga compared to *Culex* species.

Cx. tritaeniorhynchus was first identified from NT mosquito samples in 2020[14], with this species collected every year in the Darwin region since the initial detection. *Cx. tritaeniorhynchus* is considered the principal vector of JEV in Asia.[10,15] *Cx. tritaeniorhynchus* was not collected during mosquito surveillance in Wurrumiyanga. Wet season adult mosquito trapping in other areas of Bathurst Island and neighbouring Melville Island also did not detect this species.[13] While more extensive and consistent adult mosquito trapping is required to determine its presence or absence on the Tiwi Islands, presently, *Cx. tritaeniorhynchus* does not appear to be a mosquito species of concern in Wurrumiyanga.

Pigs can act as amplifying host animals for JEV[16,17] and are prevalent on Bathurst Island as feral animals, with a small population of semi-domesticated pigs living in Wurrumiyanga. Migratory ardeid waterbirds, referring to wading birds that include herons, egrets and bitterns, are considered the main wildlife reservoir for JEV.[18,19] Egrets were observed during site visits at the wastewater ponds and tidal flats near the community. Therefore, JEV host and amplifying animals are present in Wurrumiyanga, and along with the presence of several potential mosquito vector species, conditions could have been suitable for local epizootic JEV transmission in 2021.

There were no further clinical cases of JEV during the study period in Wurrumiyanga, and all mosquitoes tested negative for JEV.[2] The lack of further human cases was probably due to low vector abundance. However, the NT JE vaccination program, community awareness, source reduction via drain maintenance and methoprene 30-day residual insecticide treatments may have also played a role in the absence of further human cases.

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Tropical Health Orientation Manual 2025 – for health staff working in central and northern Australia

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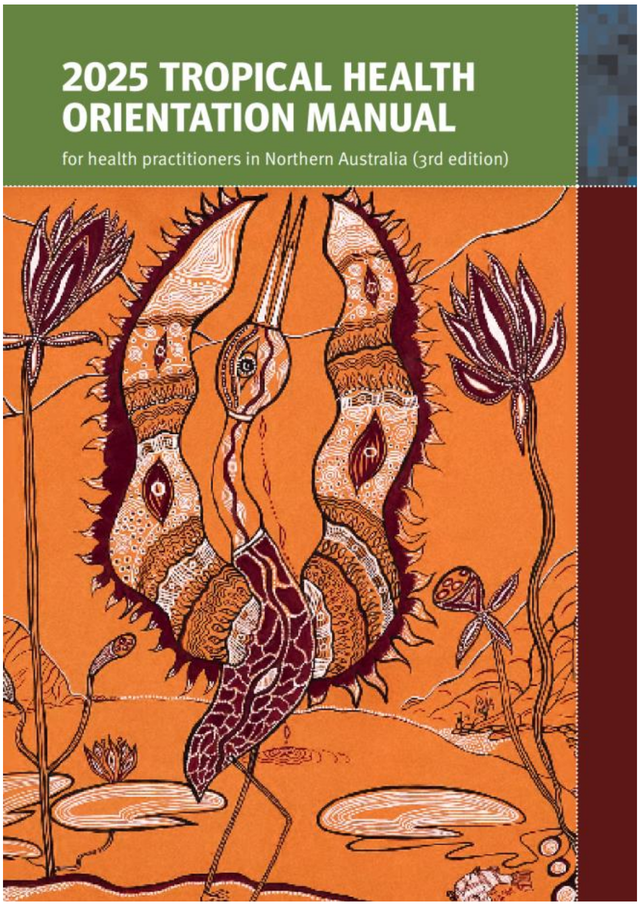
The 2025 Tropical Health Orientation Manual (THOM) provides an introductory overview of clinically important conditions encountered by health staff in tropical and Central Australia. It aims to complement existing management guidelines and includes links to important resources for further guidance.

The THOM can be accessed at and downloaded from **Tropical Health Orientation Manual (THOM) 2025 - Menzies**

BACKGROUND

The first edition of what was initially called the Tropical Health in the Top End was developed and published by the Northern Territory Top End Division of General Practice in 2003, is now in its third edition and called the 2025 Tropical Health Orientation Manual (THOM). The second edition, with the name slightly changed to Tropical Health Orientation Manual (THOM), was published in 2020 by the Centre for Remote Health. This second edition included an update of existing topics and was also broadened to be helpful for clinicians working in Western Australia and Queensland by using some of those jurisdictions' links and resources. This broadening was done in response to requests from clinicians and practitioners across northern Australia. The second edition was also aligned with and complemented the Remote Primary Health Care Manuals such as the CARPA manual, which continued to be developed by health practitioners, for health practitioners working in rural and remote locations.



2025 UPDATE

The third edition of the THOM, the 2025 Tropical Health Orientation Manual, is published by the Menzies School of Health Research with support from the Northern Territory Primary Health Network (NT PHN). As with the prior editions, many clinical colleagues generously gave of their own time to update topics and provide new content. Resources now focus back to the NT and several new sections have been added. A valuable archive of clinical photographs and radiology images accompany the text. New, overarching topics including Cultural safety in health care, Antimicrobial resistance, and Medication supply issues in the Northern Territory have been added as well as several new topics across the broad headings of:

- Bacterial infections and post-streptococcal syndromes
- Viruses, spirochetes, chlamydial and vector borne diseases
- Infestations, parasitic and fungal infections
- Sexually transmitted infections
- Toxins
- Other conditions

Hyperlinks provide access with 1 click to open-source documents and relevant guidelines and resources, especially CARPA, Therapeutic Guidelines and NT HealthPathways. While resources are Northern Territory-focussed, the topics and content remain relevant for colleagues working across northern Australia.

NEXT STEPS

Feedback is welcome on content and suggestions for improvement.

Please direct feedback to globalhealthadmin@menzies.edu.au. This will be incorporated into a revised pdf version later in 2025.

Funding is being sought for a print run of the revised pdf version (as for the prior 2 editions) to make hard copies available for students and health staff and for all remote health clinics.

The THOM will also be available to colleagues in Queensland and Western Australia, with the plan to facilitate incorporating the relevant links to their own jurisdictional resources where appropriate.

For more information contact sara.noonan@menzies.edu.au

Northern Territory Centre for Disease Control presentations at the 2025 Public Health Association of Australia, Communicable Disease and Immunisation Conference, Adelaide, South Australia, 9-12 June 2025

The theme of the conference was "Future directions for immunisation and communicable disease control: embracing ideas, innovations and improvements". There were 4 presentations given by 3 Northern Territory Centre for Disease Control (NT CDC) staff at the conference. The abstract or summary of their presentations follow.

First case of sexually transmitted Zika virus infection, Northern Territory, 2024

Thalia Hewitt, NT CDC, NT Health

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-Barre syndrome and congenital malformations such as microcephaly. Although vector-borne transmission is the primary route, sexual transmission has been documented, raising the possibility of unrecognised and underreported infections.

We report the details of 2 cases of ZIKV infection diagnosed in the Northern Territory of Australia in May 2024. The first case was a male traveller who contracted the virus in Timor-Leste and the second, his female partner in Australia. We believe this represents the first reported incidence of sexually transmitted 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 the necessity 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.

This presentation is also published as an article in [*The Northern Territory Disease Control Bulletin*, Vol 31, No. 4, December 2024](#)

Effective Measles Outbreak Response: Vaccine Efficacy and REDCap's Role in Contact Tracing

Sarah Sim, Master of Applied Epidemiology Scholar (ANU), Health Statistics and Informatics and NT CDC, NT Health

Measles is a highly contagious viral, airborne disease which typically presents with high fever, cough, conjunctivitis and a maculopular rash. While no longer endemic in Australia, imported cases do occur. A single case of measles is a public health emergency requiring rapid contact tracing to prevent further cases. In January 2025 a returned traveller with measles was notified to the Centre for Disease Control (CDC) in Darwin, Northern Territory (NT); the first case in NT since 2019.

A weekend outbreak team was formed to follow national public health response guidelines. We interviewed the case to determine travel history, infectious period and potential contacts and provided isolation advice.

A Research Electronic Data Capture (REDCap) database recorded contact details, vaccination status and past infection history. Telstra Integrated Messaging was used to send text messages to contacts, asking them to telephone CDC. A REDCap questionnaire was administered to determine susceptibility to infection, identify further contacts and determine appropriate public health action. Eligible contacts were given either measles-mumps-rubella (MMR) vaccine or normal human immunoglobulin (NHIG) to prevent measles infection. Staff overtime hours and cost were calculated.

We identified 164 contacts; 155 (94%) were successfully contacted; 9 (5%) were lost to follow up but fully vaccinated. Five contacts (3%) received the MMR vaccine, one person received NHIG. Two contacts were symptomatic and tested for measles - both tested negative. The contact tracing was completed by 8 staff over 12 hours on a weekend. We calculated the human resource cost for this outbreak response to be approximately $7,200.

This outbreak response highlighted vaccine effectiveness and that a rapid, co-ordinated response was critical in preventing transmission. The use of REDCap as a contact tracing database allowed for an effective and cost-efficient public health response.

This presentation is also published as an article in *The Northern Territory Disease Control Bulletin, Vol 32, No. 1, March 2025*.

An outbreak of salmonellosis after consuming wild hunted kangaroo, Northern Territory 2024

Anthony Draper, NT CDC, NT Health

An outbreak of salmonellosis occurred in August 2024 after consuming wild hunted kangaroo in a remote area of the Northern Territory (NT), Australia.

We conducted an outbreak investigation via telephone and face-to-face interviews, using a standardised questionnaire that recorded

symptoms and exposures to foods and activities prior to onset of symptoms. A confirmed outbreak case was defined as anyone with laboratory confirmed *Salmonella* Muenchen infection who was part of a group of people who shared meals on 25–26 August 2024. A probable outbreak case was defined as anyone who was part of a group of people who shared meals on 25–26 August 2024 and subsequently experienced diarrhoea, in the absence of a laboratory test.

Of the 7 members of the group who shared meals, all became ill (attack rate 100%); 3 were confirmed cases and 4 were probable cases. The median age was 32 years (range 23–65 years); 6 (86%) were male. The median incubation period was 24 hours (range 6–30 hours). The most commonly reported symptoms were diarrhoea (100%, 7/7) and abdominal pain (86%, 6/7). Two cases were admitted to hospital, both for an overnight stay; all recovered.

All 7 cases consumed the same meal – a single, locally hunted and butchered kangaroo. Contamination likely occurred due to unsafe butchering, storage, transportation and insufficient cooking of the meat. This outbreak highlights the risks of contamination of game meat (in this case kangaroo) with Salmonella. Those preparing hunted meat should wash hands and knives regularly while butchering an animal to avoid contamination; should store butchered meat below 5 °C to avoid bacterial growth and cook foods thoroughly to kill microbes. We estimate that the cost to society of this outbreak was 9,810 Australian dollars.

This presentation is also published in [*Communicable Diseases Intelligence, 2025; 49*].

The epidemiology of amoebiasis in the Northern Territory of Australia (2005-2024)

Anthony Draper, NT CDC, NT Health on behalf of Bhavya Balasubramanya, NT CDC Darwin.

Summary: The Northern Territory (NT) is the only jurisdiction in Australia where amoebiasis is notifiable. A retrospective study was undertaken to describe the epidemiology of amoebiasis in the NT from January 2005 to June 2024.

The results of the study highlight that amoebiasis in the NT is both endemic and overseas acquired, and that clinicians should consider this differential diagnosis in anyone presenting with abdominal pain, fever and/or diarrhoea and initiate timely testing and appropriate treatment. A national surveillance system for amoebiasis, could show the incidence of disease across Australia and encouraging clinicians to maintain an index of suspicion for this condition.

A manuscript on this study is currently being submitted for publication in a peer reviewed journal.

Media and health alerts

Public health alerts were issued on HIV, Nitazenes, Measles and Gonorrhoea by the NT Centre for Disease Control (CDC) in the time period April to June 2025. Below are excerpts from these alerts, noting some may no longer be active at the time of publishing this issue. The full Influenza alert is available on the following page. Current and previous health alerts can be viewed at the NT Health website.

HIV

There is a noted increase in newly diagnosed HIV cases in the NT with 4 cases notified year-to-date in 2025, compared to 1 case notified in the same period in 2024.

This is in the setting of a current supply shortage of HIV pre-exposure prophylaxis (PrEP) in Australia.

Patients using HIV PrEP medications or those at risk of HIV infection may report difficulty in obtaining an adequate supply of PrEP. HIV PrEP prescribers need to advise patients about the shortage and discuss alternative sourcing or dosing options during this period.

Read the full alert issued 14 April 2025

Nitazenes

Nitazenes are synthetic opioids that are stronger and may be longer acting than many other opioids. They are up to 500 times more potent than heroin.

Drugs seized in the NT have been found to contain Nitazenes. This is the first detection of this substance in the NT.

Read the full alert issued 17 April 2025

Gonorrhoea

A case of extensively drug-resistant (XDR) gonorrhoea has been detected in the Top End. This is the first ever case of XDR gonorrhoea detected in the NT. The case was acquired locally, with an unknown source of infection.

XDR gonorrhoea is characterised by resistance to both ceftriaxone and azithromycin, which are routinely used to treat gonococcal infections.

There have been almost 700 notifications of gonococcal infection in the NT in 2025 todate. Cases have been increasing over time - the highest number of annual recorded cases occurred in 2023, with 2,493 notifications received that year.

Read the full alert issued 5 June 2025

NORTHERN TERRITORY GOVERNMENT

Centre for Disease Control

NT HEALTH

⚠ Public Health Alert

Issued: 30/4/2025
Issued to: NT healthcare providers

Measles Alert - Be alert for cases of measles

Summary

- Measles cases have been increasing across Australia this year to-date, with 67 cases notified since 1 January, including 1 case notified in the NT who had travelled overseas.
- Measles outbreaks continue in multiple countries across the world, with cases in Australia linked to travel from Vietnam, Indonesia, the Philippines, and Pakistan.
- An increasing number of measles cases have recently been **acquired in Australia**, with local outbreaks reported in Western Australia and Victoria (Melbourne suburbs) following cases in returned overseas travellers.
- Clinicians in the NT are strongly encouraged to consider measles in their differential diagnosis for anyone presenting with fever and rash, particularly if they have travelled internationally **or interstate**.
- Measles is a highly infectious viral illness, which is spread by breathing in air droplets. Symptoms include fever, conjunctivitis, cough, coryza, and a maculopapular rash which begins on the face and neck, and spreads over the rest of the body. It can take up to 18 days to develop symptoms.
- **Immunity to measles requires either having had measles, or being completely vaccinated. Those born before 1966 are considered immune – those born on or after 1966 must have had 2 measles-containing vaccines after 12 months of age, or have had measles to be immune.** Encourage all patients and staff to check their vaccination status, and ensure they are immune to measles. Offer or recommend measles vaccination if non-immune, or immunity is unknown.

Action

- Please consider measles in anyone presenting with fever and rash. Isolate the person and test with 3 samples:
  - 1 urine sample (PCR measles)
  - 1 throat swab (PCR measles)
  - 1 nose swab up both nostrils (PCR measles)

Samples should be forwarded to Royal Darwin Hospital (or nearest public hospital) following discussion with Centre for Disease Control (CDC) on (08) 8922 8044. The CDC can help you to get the test completed as quickly as possible.

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

Transmission

- Measles is highly contagious and is spread by brief casual contact. Contacts are defined as having shared the same air space in enclosed areas as a case for any length of time.
- Measles virus may remain in environments up to 30 minutes after the case has left.
- It may take up to 18 days for symptoms to develop. Cases are considered infectious from 24 hours before the onset of first symptoms, or from 4 days prior to the rash developing if no prodromal symptoms, until 4 days after the rash has developed.
- Contacts of asymptomatic contacts are not currently considered to be at risk of infection.

Clinical Management

Importantly:

- Notify the CDC immediately of any suspected cases on (08) 8922 8044.
- Do not send patients with suspected measles to pathology collection centres.
- Do not sit suspected measles patients in the general waiting areas. See them in a separate room (the room should not be used for susceptible patients/staff for 30 minutes following the consultation with the suspected case).
- Ensure that all your staff are immune, i.e. they have either had measles or have had 2 doses of measles-containing vaccine at least 4 weeks apart.
- Anyone with confirmed measles should be excluded from work, school, and other places where susceptible people may be, until at least 4 days after the onset of their rash.
- **MMR vaccinations are available for free in NT for people born after 1966 who have no evidence of 2 previous measles vaccines**. GP's, Aboriginal Community Controlled Health Services, other health care clinics and vaccinating pharmacies can provide MMR vaccination.

For more information about measles, including information for contacts of measles, the public, and healthcare providers, visit this link: Measles | NT Health

Contact & advice

View all CDC units NT wide at the NT Health website.

See here for more on Public Health Alerts Health alerts | NT Health

Issued on behalf of the 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 January to 31 March, 1st quarter (2024 vs. 2025)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024
Acute Post Strep GN	3	0	0	0	1	4	1	0	0	2	5	6
Adv Vacc Reaction	3	0	0	0	5	1	0	0	1	0	9	1
AIDS	0	0	0	0	0	0	0	0	0	0	0	0
Amoebiasis	0	0	0	0	1	2	0	0	0	1	1	3
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	1	0	0	0	0	0	0	0	0	1	1	1
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	2	19	3	4	32	59	0	1	3	5	40	88
Chancroid	0	0	0	0	0	0	0	0	0	0	0	0
Chickenpox	4	0	0	0	10	11	1	6	0	1	15	18
Chikungunya	0	0	0	0	0	4	0	0	0	1	0	5
Chlamydia	320	273	28	42	318	348	22	37	34	57	722	757
Chlamydial conj	0	0	0	0	0	2	0	0	0	0	0	2
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	0	0	0	0	1	0	0	0	0	0	1
Congenital Rubella	0	0	0	0	0	0	0	0	0	0	0	0
COVID-19	74	195	34	32	316	397	39	60	40	52	503	736
Crusted scabies	2	1	4	1	5	7	7	6	1	1	19	16
Cryptosporidiosis	2	14	2	3	32	7	3	3	1	0	40	27
Dengue	0	0	0	0	7	13	0	1	1	0	8	14
Diphtheria	0	0	0	0	0	0	0	0	0	0	0	0
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	0	0	1	0	0	0	0	0	1
Gonococcal infection	289	314	42	38	138	188	23	25	25	71	517	636
Gonococcal neon ophth	0	0	0	0	0	0	0	0	0	0	0	0
Group A strep invasive	1	5	2	2	6	9	1	2	4	2	14	20
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	0	0	0	0	0	0	0
Hepatitis B - unspec	3	1	0	1	23	22	1	1	2	1	29	26
Hepatitis C - chronic	0	0	0	0	0	0	0	0	0	0	0	0
Hepatitis C - new	1	1	0	0	0	0	0	0	0	0	1	1
Hepatitis C - unspec	2	3	1	1	13	15	0	2	2	3	18	24

(Table continued next page)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024
Hepatitis D	0	0	0	0	1	1	0	0	0	0	1	1
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	0	0	0	0	0	0	0	0	0
H Influenzae non-b	0	0	0	0	0	1	0	0	0	1	0	2
HIV	1	4	0	0	3	5	0	0	0	0	4	9
HTLV1 adult TCL	0	0	0	0	0	0	0	0	0	0	0	0
HTLV1 asyptom/unspec	12	11	1	1	3	1	0	0	0	0	16	13
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	26	31	2	1	760	170	87	65	38	11	913	278
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	0	0	2	0	3	69	6	2	3	1	14	72
Legionellosis	0	0	0	0	4	0	0	2	1	0	5	2
Leprosy	0	0	0	0	0	0	0	0	0	0	0	0
Leptospirosis	0	0	0	0	2	4	0	0	0	1	2	5
LGV	0	0	0	0	0	0	0	0	0	0	0	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	1	0	0	0	2	1	0	1	0	0	3	2
Measles	0	0	0	0	1	0	0	0	0	0	1	0
Melioidosis	0	1	0	1	24	37	1	2	6	4	31	45
Meningococcal infection	0	0	0	0	0	0	0	0	0	0	0	0
MERS	0	0	0	0	0	0	0	0	0	0	0	0
Mpox virus infection	0	0	0	0	0	1	0	0	0	0	0	1
Mumps	1	0	0	0	0	0	0	0	0	0	1	0
MVE	0	0	0	0	0	0	0	0	0	0	0	0
Non TB Mycobacteria	0	0	0	0	6	4	0	0	0	0	6	4
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	13	0	4	0	15	5	0	0	4	0	36	5
Plague	0	0	0	0	0	0	0	0	0	0	0	0
Pneumococcal disease	3	5	2	2	5	1	2	0	3	1	15	9
Poliomyelitis	0	0	0	0	0	0	0	0	0	0	0	0
Q Fever	0	0	0	0	0	0	0	0	0	0	0	0
Rabies	0	0	0	0	0	0	0	0	0	0	0	0
Rheumatic Fever	23	13	7	8	10	14	5	5	8	6	53	46
Rheumatic heart disease	14	19	1	3	11	11	6	2	7	1	39	36
Ross River Virus	0	2	0	0	26	24	1	1	2	4	29	31
Rotavirus	18	13	8	4	47	17	4	9	6	1	83	44
RSV infection	2	84	1	56	177	235	3	117	13	126	196	618
Rubella	0	0	0	0	0	0	0	0	0	0	0	0
Salmonellosis	12	15	5	12	75	101	3	5	14	11	109	144
SARS	0	0	0	0	0	0	0	0	0	0	0	0

(Table continued next page)

	Alice Springs		Barkly		Darwin		East Arnhem		Katherine		N T	
	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024	2025	2024
Shigellosis	6	13	1	6	5	14	1	3	0	2	13	38
Smallpox	0	0	0	0	0	0	0	0	0	0	0	0
STEC/VTEC	0	0	1	0	0	0	0	0	0	0	1	0
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	22	23	4	6	42	17	19	7	24	7	111	60
Syphilis > 2y or unknown duration	1	2	1	0	20	6	0	1	2	3	24	12
Syphilis congenital	0	0	0	0	0	0	0	0	0	0	0	0
Tetanus	0	0	0	0	0	0	0	0	0	0	0	0
Trichomoniasis	234	241	70	57	322	356	116	79	43	85	785	818
TTP	0	0	0	0	0	0	0	0	0	0	0	0
Tuberculosis	0	1	0	0	1	6	0	0	0	1	1	8
Tularaemia	0	0	0	0	0	0	0	0	0	0	0	0
Typhoid	0	0	0	0	0	0	0	0	0	0	0	0
Typhus	0	0	0	0	0	0	0	1	0	0	0	1
Varicella - unspec	2	6	0	0	32	15	0	4	1	0	35	25
Vibrio food poisoning	0	0	0	0	0	0	0	0	0	0	0	0
Vibrio invasive	0	0	0	0	0	0	0	0	0	0	0	0
Vibrio parahaemolyticus infection	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	1	0	0	3	7	0	0	0	1	3	9
Zika	0	0	0	0	0	0	0	0	0	0	0	0
Zoster	12	16	0	0	49	78	3	13	2	6	66	113
Sum:	**1,110**	**1,327**	**226**	**281**	**2,556**	**2,292**	**355**	**463**	**291**	**471**	**4,538**	**4,834**

Dengue notifications for January to March 2025

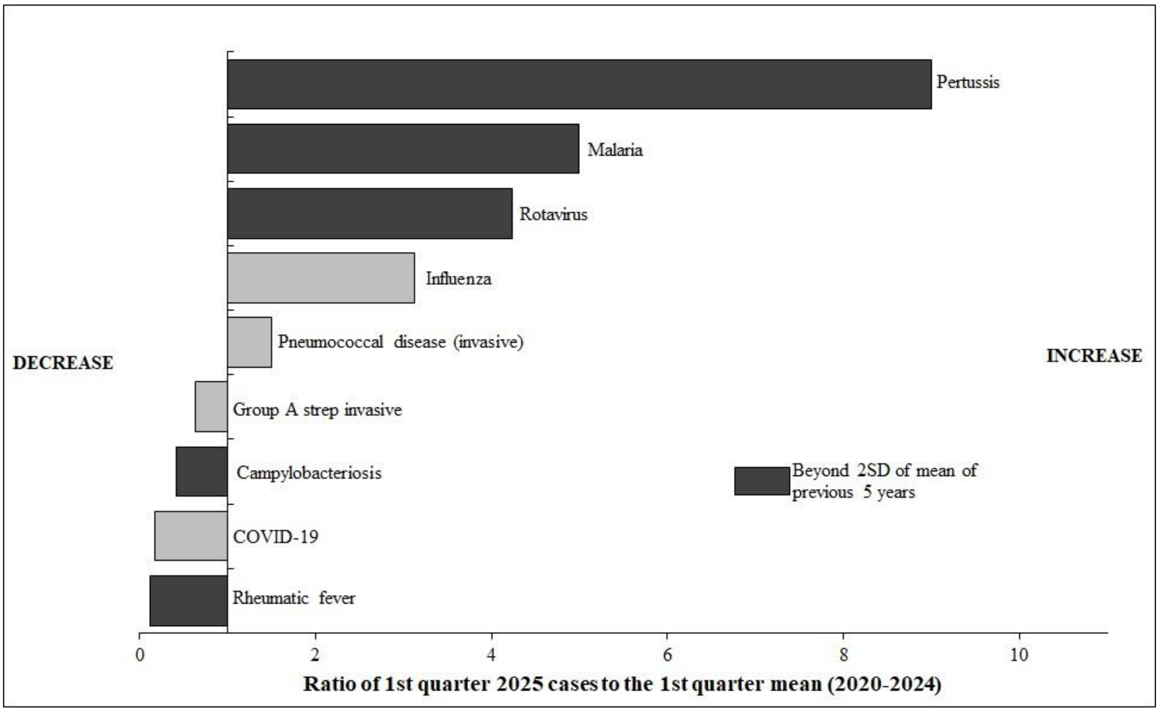
Number of cases	Origin of infection	NT Region notified
7	Indonesia (6), Thailand (1)	Darwin
1	Solomon Islands (1)	Katherine

Malaria notifications for January to March 2025

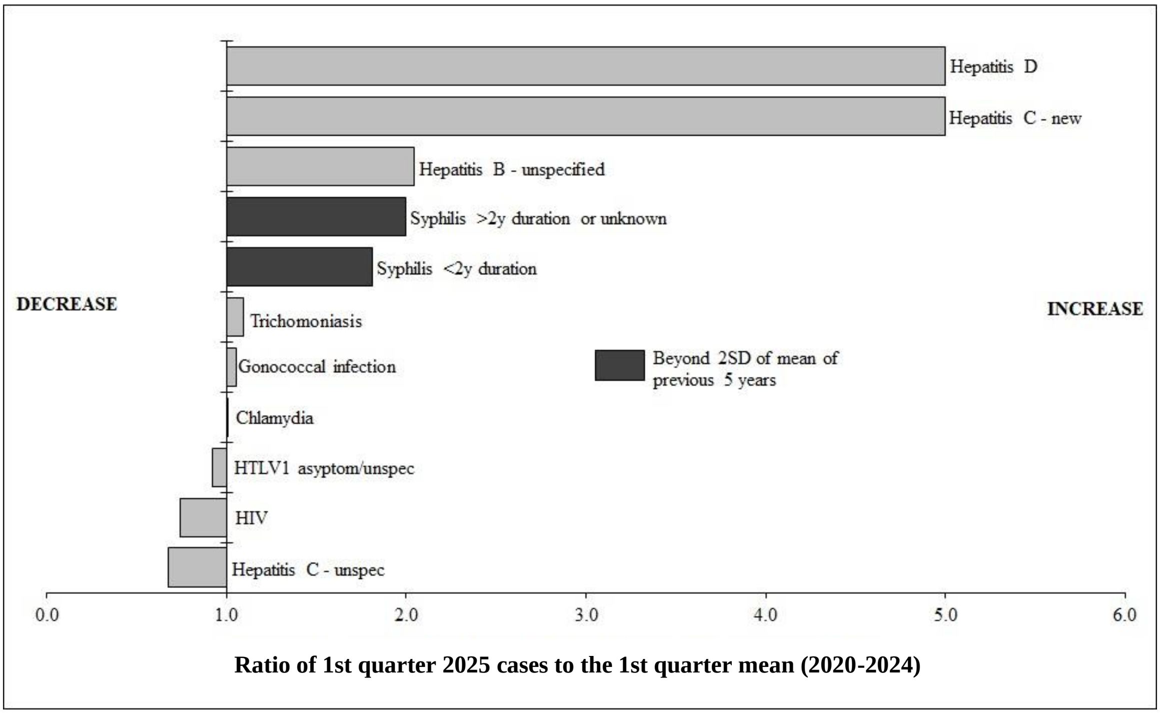
Number of cases	Origin of infection	Agent	Chemoprophylaxis	NT Region
1	Indonesia	*Plasmodium falciparum*	No	Darwin
1	Uganda	*P. falciparum*	No	Darwin
1	Uganda	*P. malariae*	No	Alice Springs

Graphs of selected diseases and STIs – Q1 2025

Ratio of the number of notifications in 1st quarter of 2025 to the 1st quarter mean (2020 – 2024): Selected diseases



Ratio of the number of notifications in 1st quarter of 2025 to the 1st quarter mean (2020 – 2024): Sexually transmitted infections



Comments on selected disease notifications

Pertussis

There were 36 notifications of pertussis in the Northern Territory (NT) in the 1st quarter of 2025 compared to a 5-year 1st quarter mean of 4 notifications. This reflects the high numbers seen nationwide in 2024, where Australia experienced its highest ever annual incidence of pertussis with over 57,000 notifications and for the NT elevated numbers are continuing.

Rotavirus

There were 83 notifications of rotavirus in the NT in the 1st quarter of 2025 compared to a 5-year 1st quarter mean of 19.6 notifications.

Syphilis <2 years duration

There were 111 notifications of syphilis (<2 years duration) in the 1st quarter of 2025 in the NT compared to a 5-year 1st quarter mean of 61.4 notifications. An incident management team (IMT) has been established in response to an increase in syphilis cases in the Top End, East Arnhem and Big Rivers regions since the 3rd quarter of 2024. Enhanced testing efforts and active case finding are currently underway across the NT, which is likely to be contributing to some of the observed increase in notifications.

Syphilis >2 years duration or unknown

There were 24 notifications of syphilis (>2 years duration or unknown) in the 1st quarter of 2025 compared to a 5-year 1st quarter mean of 12 notifications. This increase may also reflect ongoing enhanced testing and case finding across the NT.

Measles

There was 1 notification of measles in the 1st quarter of 2025 in a person who acquired their infection in Indonesia. This was the first measles notification in the Northern Territory since 2019. There was no ongoing transmission. The outbreak response to this single imported case can be read at [Northern Territory Disease Control Bulletin Vol. 32. No. 1.]

Campylobacteriosis

There were 40 notifications of campylobacteriosis in the 1st quarter of 2025 compared to a 5-year 1st quarter mean of 97.2 notifications.

Tuberculosis

There was 1 notification of tuberculosis in the 1st quarter of 2025 compared to a 5-year 1st quarter mean of 8 notifications.

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Immunisation coverage in the Northern Territory

Northern Territory 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

Mortality in the Northern Territory, 1967–2020

Key findings

From 1967–2020:

- Mortality rates have declined in the NT, by: 40% for Aboriginal males; 46% for Aboriginal females; 62% for non-Aboriginal males and 63% for non-Aboriginal females.
- Infant mortality rates decreased in the NT from 52 to 8 deaths per 1,000 live births. For Aboriginal infants, deaths per 1,000 live births dropped from 90 to 13.
- Life expectancy at birth has improved in the NT. For Aboriginal peoples, life expectancy increased from 53 to 67 years for males and from 54 to 70 years for females.
- Despite these overall improvements, the gap in mortality and life expectancy outcomes between Aboriginal and non-Aboriginal peoples remains.

During 2011–2020:

- There were 11,031 deaths amongst NT residents.
- The majority of deaths (69%) were due to non-communicable diseases.
- The mortality rate due to non-communicable diseases was 1,057 and 439 deaths per 100,000 population, for Aboriginal and non-Aboriginal peoples, respectively.
- Coronary heart disease was the leading cause of chronic disease deaths in the NT for males at 249 and 87 deaths per 100,000 population for Aboriginal males and non-Aboriginal males, respectively.
- Dementia was the leading cause of chronic disease deaths in the NT for females at 108 and 50 deaths per 100,000 population for Aboriginal females and non-Aboriginal females, respectively.
- The median age of death in the NT was 56 years for Aboriginal peoples and 71 years for non-Aboriginal peoples.

Background

Mortality and related life expectancies are important indicators of the health of populations. This factsheet provides a routine update on mortality statistics[1] in the Northern Territory (NT). We present long-term trends between 1967 and 2020 for all-cause mortality. We also report key causes of death over a 10-year period 2011–2020.

Mortality data was sourced from the Australian Bureau of Statistics (ABS) and the Australian Coordinating Registry (ACR).[2] We used the NT historical research mortality datasets for the years 1967 to 1988.[3] To calculate mortality rates, population data based on the ABS estimated resident population and live births from the ABS was used.[4, 5] Age-adjusted rates are estimated using the ABS 2001 Australian standard population.[6]

Mortality trends

Since 1967, all-cause mortality rates have markedly decreased in both the NT and Australia across all population groups (**Table 1 and 2**).

Table 1: Male mortality rates for all causes, NT and Australia, 1967–2020

Males			
Years	Northern Territory		Australia
	Aboriginal	Non-Aboriginal	
1967–1970	2538.4	1805.7	1607.8
1971–1975	2662.6	2084.3	1502.5
1976–1980	2736.9	1490.0	1331.2
1981–1985	2227.3	1320.7	1200.1
1986–1990	2468.6	1179.7	1088.9
1991–1995	2134.1	1221.5	980.4
1996–2000	2078.3	942.5	875.3
2001–2005	2049.3	808.7	761.2
2006–2010	1690.5	903.5	722.6
2011–2015	1655.3	766.9	659.9
2016–2020	1528.3	684.1	616.2
% change	39.8%	62.1%	61.7%

Note: Age-adjusted mortality rates per 100,000 population by 5-year periods.

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Table 2: Female mortality rates for all causes, NT and Australia, 1967–2020

Females			
Years	Northern Territory		Australia
	Aboriginal	Non-Aboriginal	
1967–1970	2409.2	1152.3	1017.5
1971–1975	1919.0	1200.8	944.6
1976–1980	2081.6	920.5	825.3
1981–1985	1700.6	732.8	755.8
1986–1990	1839.1	598.1	703.4
1991–1995	1635.1	739.2	647.6
1996–2000	1571.0	610.6	598.1
2001–2005	1366.4	539.9	546.7
2006–2010	1411.9	507.4	491.9
2011–2015	1421.0	464.3	462.9
2016–2020	1308.7	428.7	435.5
% change	45.7%	62.8%	57.2%

Note: Age-adjusted mortality rates per 100,000 population by 5-year periods.

In the NT, mortality rates decreased by: 40% for Aboriginal males; 46% for Aboriginal females; 62% for non-Aboriginal males and 63% for non-Aboriginal females (**Table 1 and 2**). The decline in mortality rates aligns with international trends, of which the main drivers have been identified as improvements in cardiovascular health among older adults and reductions in deaths among infants.[7] These factors were explored for the NT context in the below sections that report on causes of death and infant mortality.

Across all years, mortality rates in the NT were highest in the Aboriginal populations. For NT males in 2016–2020, the age-adjusted mortality rates were 1,528 and 684 deaths per 100,000 population for Aboriginal and non-Aboriginal males, respectively (**Table 1**). For NT females in 2016–2020, the age-adjusted mortality rates were 1,309 and 429 deaths per 100,000 population for Aboriginal and non-Aboriginal females, respectively (**Table 2**).

Aboriginal peoples in the NT had higher death rates than the national average. The Australian Institute of Health and Welfare (AIHW) for the years 2018 to 2022 reported age-adjusted rates of death at 1,109 deaths per 100,000 population for Aboriginal males and 884 deaths per 100,000 population for Aboriginal females.[8]

The interplay between population and mortality is bidirectional. Globally, improvements in the health of older adults, declines in fertility rates and reduced infant mortality have directly contributed to ageing populations.[9, 10] In the NT, the recent decrease in outbound migration of older NT residents,[11] mean the total proportion of Territorians aged 65 and older increased from 2.5% in 1986 to 6.9% in 2016.[12] In line with these changes, the proportion of deaths among older Territorians (age ≥65 years) increased from 34% in 1991–2000 (**Figure 1**) to 49% in 2011–2020 (**Figure 2**).

Figure 1: Age distribution of mortality, proportion of the number of deaths, by Aboriginal status, NT, 1991–2000

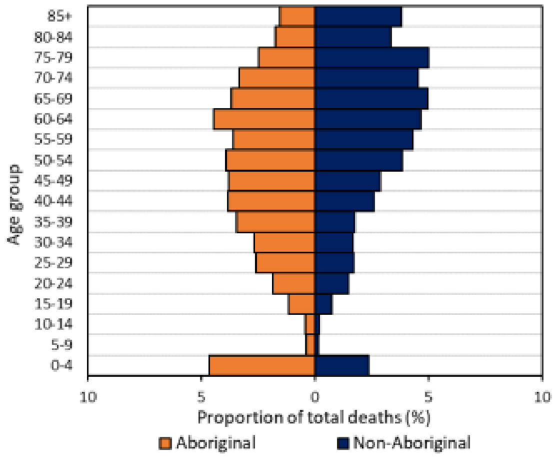
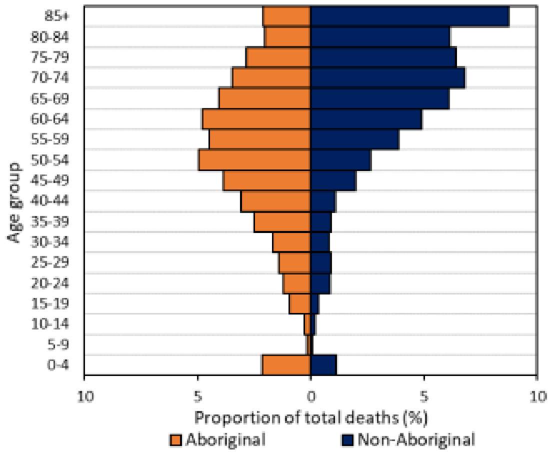


Figure 2: Age distribution of mortality, proportion of the number of deaths, by Aboriginal status, NT, 2011–2020



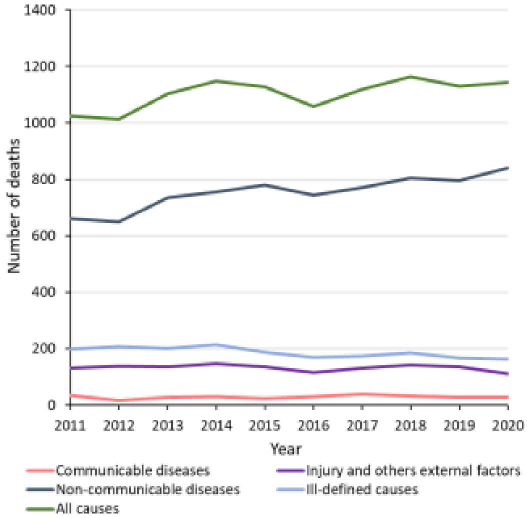
Mortality in 2011–2020

Between 2011 and 2020, there were 11,031 deaths amongst NT residents. Of these deaths, 59% were males, 46% were Aboriginal peoples, and 28% were remote residents (remote refers to all areas in the NT excluding the Darwin and Alice Springs urban districts and the towns of Katherine, Tenant Creek and Nhulunbuy).

The analysis by cause of death is based on the underlying cause of death (UCoD), coded in ICD-10-AM.[13] Following the Institute for Health Metrics and Evaluation (IHME) global burden of disease study,[14] the UCoD was classified into four broad disease groups. Note, we did not redistribute the ill-defined causes of death into the other categories of death.

From 2011 to 2020, the total number of deaths in the NT due to all causes increased by 119 from 1,025 to 1,144 deaths as seen in **Figure 3**. Non-communicable was the main cause of death in the NT, accounting for 69% of deaths. Decreases were observed in deaths due to communicable, maternal, neonatal and nutritional diseases (hereafter referred to as communicable diseases), as well as injury and other external factors, and ill-defined causes, whilst deaths due to non-communicable diseases increased by 179 from 662 to 841 deaths (**Figure 3**).

Figure 3: Number of deaths by disease group, NT, 2011–2020



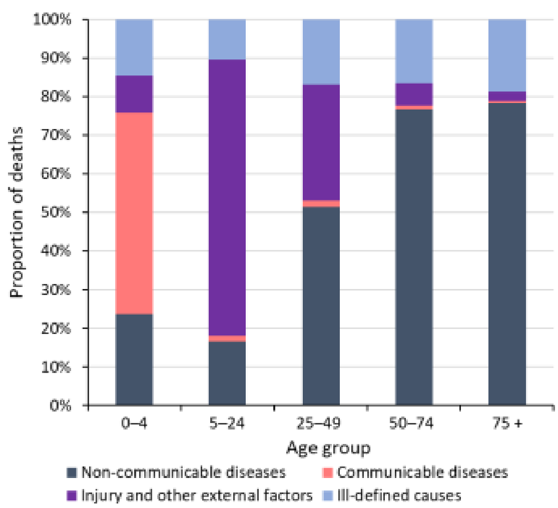
Note: Communicable diseases includes maternal, neonatal and nutritional diseases aligned with GBD classifications.[13]

There was variation in cause of death by age groups, which is in line with expected results. **Figure 4** graphs death from the main disease groups by age group, as listed in **Table 3**. Communicable diseases was the major cause of deaths in the age group 0–4 years; injury and other external factors claimed the majority of deaths in the age group 5–24 years. Unlike communicable diseases, the proportion of deaths due to injury and other external factors persisted in older age groups at 30% among 25–49 years old and 6% in the age group 50–74 years. Non-communicable diseases accounted for an increasing proportion of deaths with age, contributing to over 75% of deaths from age 50 onwards (**Figure 4**).

Table 3: Number of deaths by age group, 2011–2020

Northern Territory				
0–4	5–24	25–49	50–74	75+
364	444	2,009	5,091	3,123

Figure 4: Proportion of deaths by disease group and age group, 2011–2020



Note: Communicable diseases includes maternal, neonatal and nutritional diseases aligned with GBD classifications.[13]

The age-adjusted mortality rate due to non-communicable diseases was 559 deaths per 100,000 population for all Territorians. Whereas, the mortality rate due to injury and others external factors, and communicable diseases for all Territorians was considerably lower at 60 and 13 deaths per 100,000 population, respectively (**Table 4**).

Mortality rates were the highest among Aboriginal populations across all disease groups especially in the non-communicable diseases. For Aboriginal and non-Aboriginal peoples, the mortality rate from non-communicable diseases was 1,057 and 439 deaths per 100,000 population, respectively (**Table 4**).

Table 4: Disease group, age-adjusted mortality rates per 100,000 population, by Aboriginal status, NT and Australia, 2011–2020

Northern Territory			
Disease group	Aboriginal	Non-Aboriginal	Total
Communicable	23.5	8.4	13.1
Non-communicable	1057.0	439.1	559.3
Injury	95.1	44.2	59.6
Ill-defined causes	288.8	97.4	135.0
All causes	**1464.5**	**589.1**	**767.1**

Note: Communicable diseases includes maternal, neonatal and nutritional diseases aligned with GBD classifications.[13]

Leading causes of death

The ranking of underlying causes is based on ICD-10-AM[15] chapters. Each chapter is a group of disorders in the same physiological system or with a similar pathological nature. Between 2011 and 2020, the most common cause of death in the NT was cancer with a rate of 254 deaths (per 100,000 population) for males and 165 deaths for females, which is comparable with Australian mortality statistics **(Table 5 and 6**).

The top three most common causes of death for NT Aboriginal males and females were circulatory system diseases, cancer and endocrine disorders. Mortality rates due to circulatory system diseases were 398 and 291 deaths per 100,000 population for Aboriginal males and females, respectively (**Table 5 and 6**).

The top three causes for NT non-Aboriginal males and females were cancer, circulatory system diseases and respiratory disorders. Mortality rates due to cancer were 236 and 135 deaths per 100,000 population for non-Aboriginal males and females, respectively (**Table 5 and 6**).

For most causes, death rates were higher among males than females. However, Aboriginal females had higher death rates from endocrine and genitourinary disorders (214 and 64 per 100,000 population, respectively) than males (171 and 63 per 100,000 population, respectively) as seen in **Table 5 and 6**.

Compared to Australia, the NT had higher mortality rates in every cause of death except for nervous system disorders for both males and females. Within the NT, disparity by Aboriginality was most evident in genitourinary and endocrine disorders as Aboriginal females had an age-adjusted rate over eight times higher and Aboriginal males had an age-adjusted rate over five times higher than their non-Aboriginal counterparts (**Table 5 and 6**).

Table 5: Top ten causes of death in males, age-adjusted mortality rates per 100,000 population, by Aboriginal status, NT and Australia, 2011–2020

Males				
Cause of death	Northern Territory			Australia
	Aboriginal	Non-Aboriginal	Total	
Cancer	341.7	235.8	253.5	200.1
Circulatory	397.9	165.7	208.6	169.7
Injury	150.6	71.9	92.8	55.5
Respiratory	170.3	74.1	89.3	57.0
Endocrine	170.8	32.2	53.7	26.7
Mental	103.4	39.1	48.5	28.1
Digestive	71.0	25.5	34.2	23.0
Nervous	37.9	29.2	31.4	31.8
Genitourinary	63.3	11.1	18.9	13.1
Infectious	27.0	10.3	13.4	10.3

Note: The causes of death were classified using the ICD-10-AM disease chapters[15] and ranked in order of NT Total.

Table 6: Top ten causes of death in females, age-adjusted mortality rates per 100,000 population, by Aboriginal status, NT and Australia, 2011–2020

Females				
Cause of death	Northern Territory			Australia
	Aboriginal	Non-Aboriginal	Total	
Cancer	274.4	135.2	165.3	129.8
Circulatory	291.4	99.5	143.0	122.4
Endocrine	214.3	25.4	66.3	19.0
Respiratory	154.2	39.3	64.1	39.8
Mental	99.7	38.6	51.1	31.0
Injury	82.0	31.1	46.4	25.1
Digestive	68.6	14.6	27.8	16.9
Nervous	25.5	21.7	23.1	26.7
Genitourinary	64.1	7.5	19.7	10.6
Infectious	24.2	6.3	10.7	7.5

Note: The causes of death were classified using the ICD-10-AM disease chapters[15] and ranked in order of NT Total.

Key chronic conditions causing death

From 2011 to 2020, the five most common chronic conditions in the NT by numbers and age-adjusted rates were coronary heart disease, dementia, chronic obstructive pulmonary disease (COPD), cancer of the lung and chronic kidney disease (**Figure 5 and 6**). Males accounted for the majority of deaths due to coronary heart disease, lung cancer and COPD, whereas females accounted for the majority of deaths due to chronic kidney diseases and dementia in the NT (**Figure 5**).

Australia reported the same top five chronic conditions except had cerebrovascular disease (stroke) instead of chronic kidney disease (**Figure 6**). This difference can likely be explained by the disproportionate impact chronic kidney disease has on the Aboriginal population in the NT.[16] Chronic kidney condition was the common cause of death for Aboriginal females (175 deaths per 100,000 population) and the second most common cause of death for Aboriginal males (132 deaths per 100,000 population), significantly greater than non-Aboriginal Territorians (**Figure 6**).

Across all population groups, NT Aboriginal peoples had higher rates of chronic conditions compared to NT non-Aboriginal peoples. A pronounced difference by Aboriginal status was observed from coronary heart disease among Aboriginal males, whose death rate was nearly three times higher than non-Aboriginal males (248.7 vs 87.1 deaths per 100,000 population) (**Figure 6**).

Additionally, Aboriginal females were also the only population group to have diabetes in its top five chronic disease causes of death (94 per 100,000 population) (**Figure 6**).

Between 2011 and 2020, the median age of death in the NT was 56 years for Aboriginal peoples and 71 years for non-Aboriginal people. Across all five leading chronic conditions causing death, Aboriginal peoples had a lower median age of death than non-Aboriginal peoples (**Table 7**). The most pronounced difference was observed in coronary heart disease, where the median age of death was 55 years for Aboriginal peoples, compared to 73 years for non-Aboriginal peoples – a difference of 18 years. Whereas, dementia had the lowest difference in the median age of death between Aboriginal and non-Aboriginal peoples at 4.3 years.

Table 7: Median age of death for the most common chronic conditions, by Aboriginal status, NT, 2011–2020

Northern Territory			
Cause of Death	**Aboriginal**	**Non-Aboriginal**	**Difference in years**
Coronary heart disease	55.0	73.0	18.0
Dementia	81.7	86.0	4.3
Chronic obstructive pulmonary disorder	66.0	74.0	8.0
Lung cancer	63.0	69.0	6.0
Chronic kidney disease	63.0	79.0	16.0
All causes	**56.0**	**71.0**	**15.0**

Figure 5: Five most common chronic conditions causing death, number of deaths, by sex, NT, 2011–2020

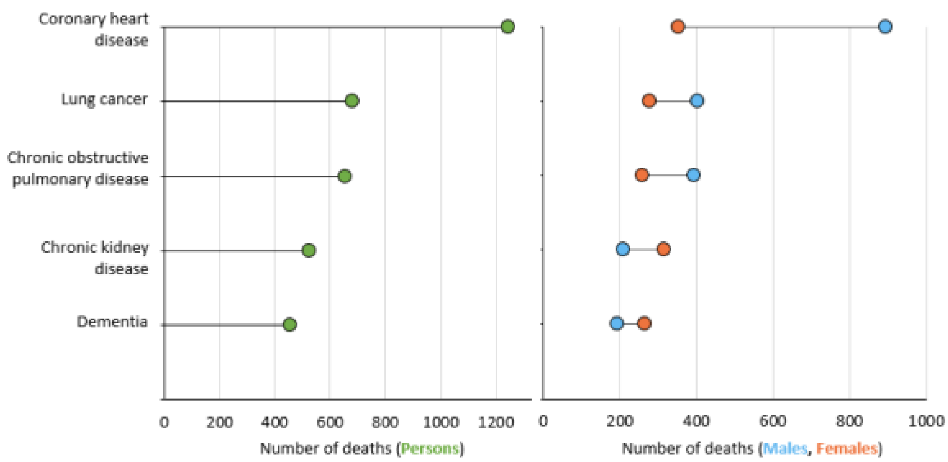


Figure 6: Five most common chronic conditions causing death, age-adjusted mortality rates, by sex and Aboriginal status, NT and Australia, 2011–2020

Rank	Males		Females		NT Total	Australia Total
	Aboriginal	Non-Aboriginal	Aboriginal	Non-Aboriginal		
1	Coronary Heart Disease (248.7)	Coronary Heart Disease (87.1)	Chronic Kidney Disease (174.5)	Dementia (50.4)	Coronary Heart Disease (86.7)	Coronary Heart Disease (64.0)
2	Chronic Kidney Disease (132.4)	COPD (54.3)	Dementia (107.6)	Coronary Heart Disease (40.0)	Dementia (59.0)	Dementia (42.1)
3	COPD (122.7)	Dementia (49.4)	Coronary Heart Disease (106.1)	Lung Cancer (32.0)	COPD (52.9)	Stroke (34.3)
4	Dementia (91.7)	Lung Cancer (47.1)	COPD (102.6)	COPD (25.4)	Lung Cancer (44.7)	Lung Cancer (29.7)
5	Lung Cancer (80.1)	Stroke (26.2)	Diabetes (93.5)	Stroke (21.4)	Chronic Kidney Disease (36.6)	COPD (23.4)

Note: All rates presented above were age-adjusted mortality rates. This analysis differed from previous mortality reporting[1] by classifying chronic diseases according to the leading conditions identified in the recent NT report[17] on the burden of disease and injury. These conditions were subsequently ranked based on their age-adjusted mortality rates.

Neonatal, post-neonatal and infant mortality

Infant mortality (age <365 days), more specifically neonatal mortality (age <28 days) and post-neonatal mortality (age 28 days to <365 days), are key indicators of the health of a population. Neonatal mortality globally serves as a measure of access to high-quality antenatal and perinatal care, highlighting a population's ability to manage complications such as prematurity, birth asphyxia, and neonatal infectious-related diseases. In contrast, post-neonatal mortality reflects the effectiveness of public health initiatives, including breastfeeding promotion, infection control, immunisation programs, and the influence of broader social and environmental conditions on child health.[18]

Since 1967, the NT has made significant progress in reducing both neonatal and post-neonatal mortality rates across all populations. Neonatal mortality rates decreased by 72% and 71% for Aboriginal and non-Aboriginal populations, respectively (**Table 8**). Post-neonatal mortality rates have also decreased in the NT by 94% and 86% for Aboriginal and non-Aboriginal populations, respectively (**Table 9**).

These improvements can largely be attributed to the increased access to antenatal care, greater number of births within hospitals, improved neonatal care, vaccination uptake among infants and mothers, and effective perinatal screening.[19, 20]

Table 8: Neonatal deaths, crude mortality rates per 1,000 live births by 5-year period, by Aboriginal status, NT and Australia, 1967–2020

Neonatal mortality (<28 days)				
Years	Northern Territory			Australia
	Aboriginal	Non-Aboriginal	Total	
1967–1970	35.6	14.4	23.6	–
1971–1975	30.5	17.0	22.1	–
1976–1980	19.0	10.8	14.2	–
1981–1985	12.5	8.2	9.8	–
1986–1990	14.6	5.8	9.0	5.1
1991–1995	13.2	6.2	8.7	4.0
1996–2000	13.8	4.1	7.8	3.6
2001–2005	9.2	3.7	6.0	3.4
2006–2010	7.8	2.2	4.5	3.0
2011–2015	8.8	2.2	4.6	2.5
2016–2020	9.9	4.2	6.3	2.3
% change	72.2	70.8	73.3	54.9

Note: – Neonatal deaths for Australia could not be calculated prior to 1986 without data of actual age in days of newborns.

Table 9: Post-neonatal deaths, crude mortality rates per 1,000 live births by 5-year period, by Aboriginal status, NT and Australia, 1967–2020

Post-neonatal mortality (>=28 days, <365 days)				
Years	Northern Territory			Australia
	Aboriginal	Non-Aboriginal	Total	
1967–1970	54.8	8.1	28.4	~
1971–1975	40.5	5.7	18.9	~
1976–1980	19.0	3.4	9.9	~
1981–1985	14.7	4.0	8.0	~
1986–1990	12.0	2.7	6.0	3.4
1991–1995	10.4	2.0	5.0	2.2
1996–2000	9.1	1.4	4.3	1.8
2001–2005	6.2	2.1	3.8	1.5
2006–2010	5.3	1.6	3.1	1.3
2011–2015	5.4	1.3	2.8	1.0
2016–2020	3.3	1.1	1.9	0.8
% change	94.0	86.4	93.3	76.5

Note: ~ Neonatal deaths for Australia could not be calculated prior to 1986 without data of actual age in days of newborns.

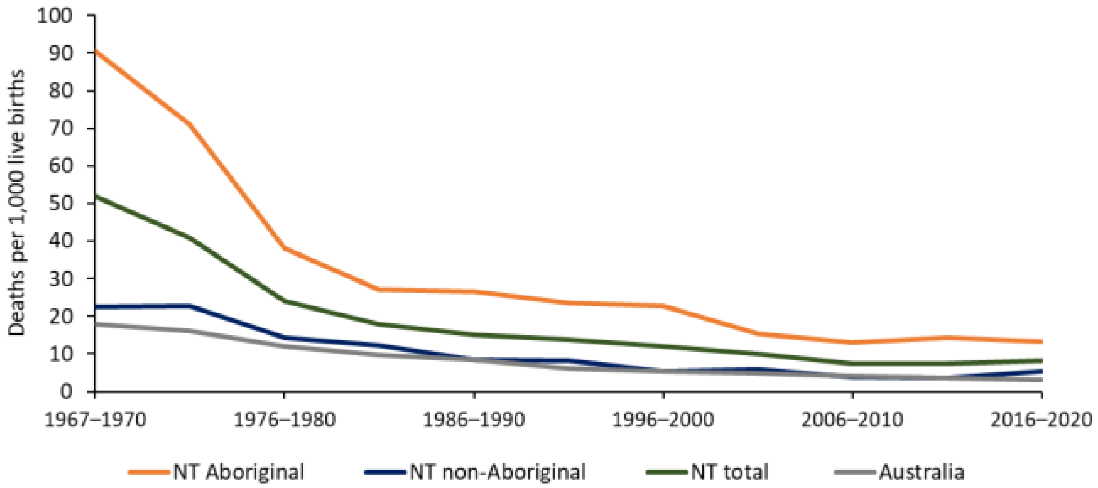
Over the years, infant mortality rates have improved for all NT infants reducing mortality by 84%. For NT Aboriginal infants, rates declined by 85% and for NT non-Aboriginal infants, rates declined by 76%. This was similar to the fall in rates for Australia at 82% (**Table 10**). The large reductions in infant mortality rates are graphed in **Figure 7.**

Despite these overall improvements, across all years, the infant death rates were higher for Aboriginal populations compared to non-Aboriginal and Australia populations (**Table 10**). Addressing these disparities requires targeted efforts to improve healthcare access, reduce socio-economic inequities, and address preventable risk factors such as smoking and alcohol consumption. Culturally appropriate programs and investments in housing, education, and infrastructure remain essential to closing the gap in infant mortality rates and achieving equitable health outcomes.[21, 22]

Table 10: Infant deaths, crude mortality rate per 1,000 live births by 5-year period, by Aboriginal status, NT and Australia, 1967–2020

Infant mortality (<365 days)				
Years	Northern Territory			Australia
	Aboriginal	Non-Aboriginal	Total	
1967–1970	90.4	22.4	51.9	18.0
1971–1975	71.1	22.7	41.0	16.2
1976–1980	38.1	14.2	24.1	12.1
1981–1985	27.2	12.2	17.9	9.8
1986–1990	26.6	8.5	15.0	8.4
1991–1995	23.6	8.1	13.7	6.2
1996–2000	22.8	5.5	12.1	5.4
2001–2005	15.4	5.8	9.9	4.9
2006–2010	13.1	3.8	7.5	4.2
2011–2015	14.2	3.5	7.4	3.5
2016–2020	13.2	5.3	8.3	3.2
% change	85.4	76.3	84.0	82.2

Figure 7: Infant mortality rate trends by 5-year period, by Aboriginal status, NT and Australia, 1967–2020



Life expectancy at birth

Life expectancy at birth is a measure of the average lifespan a newborn is expected to live and reflects the overall mortality level of a population. From 1967 to 2020, life expectancy in the NT has improved for all Territorians. Among males, life expectancy increased by 14.2 and 15.5 years for Aboriginal and non-Aboriginal peoples, respectively (**Table 9**). Among females, life expectancy increased by 16.1 and 13.3 years for Aboriginal and non-Aboriginal peoples, respectively (**Table 10**).

In 2016–2020, non-Aboriginal males and females had a life expectancy of 80.2 and 85.9 years, respectively. Whilst, Aboriginal males and females life expectancy was 66.7 and 70.0 years, respectively (**Table 11 and 12**). The gap in life expectancy between Aboriginal and non-Aboriginal peoples has persisted over time due to the complexity in addressing the underlying social determinants of health including intergenerational colonial trauma, discrimination, socioeconomic disadvantage, high-risk behaviours and accessibility to culturally safe health care services and prevention programs.[23, 24]

Examining national figures over the years, non-Aboriginal females in the NT had a similar life expectancy to Australian females. However, non-Aboriginal males in the NT generally had a slightly lower life expectancy to Australian males. Both Aboriginal males and females in the NT have a life expectancy lower than their Australian males and females (**Figure 8 and 9**).

Table 11: Male life expectancy at birth by 5-year period by Aboriginal status, NT and Australia, 1967–2020

Males			
Years	Northern Territory		Australia
	Aboriginal	Non-Aboriginal	
1967–1970	52.5	64.7	67.6
1971–1975	52.6	64.7	68.7
1976–1980	53.3	67.9	70.6
1981–1985	57.4	70.4	72.3
1986–1990	55.6	71.9	73.8
1991–1995	58.5	72.3	75.6
1996–2000	59.3	75.9	77.3
2001–2005	59.3	78.5	79.6
2006–2010	63.0	76.9	79.5
2011–2015	64.5	79.0	80.7
2016–2020	66.7	80.2	81.4

Table 12: Female life expectancy at birth by 5-year period by Aboriginal status, NT and Australia, 1967–2020

Females			
Years	Northern Territory		Australia
	Aboriginal	Non-Aboriginal	
1967–1970	53.9	72.6	74.7
1971–1975	58.5	73.3	76.0
1976–1980	60.2	76.2	78.2
1981–1985	63.2	79.9	79.7
1986–1990	62.6	84.1	80.9
1991–1995	64.2	80.2	82.3
1996–2000	65.2	83.5	83.6
2001–2005	67.9	85.3	85.2
2006–2010	68.0	84.0	84.2
2011–2015	67.7	84.7	84.9
2016–2020	70.0	85.9	85.5

Figure 8: Male life expectancy at birth, NT and Australia by Aboriginal status, 1967–2020

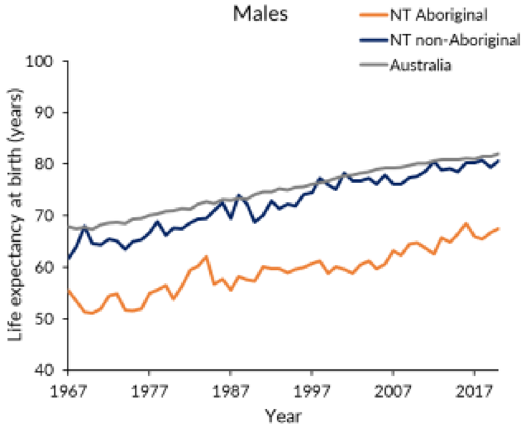
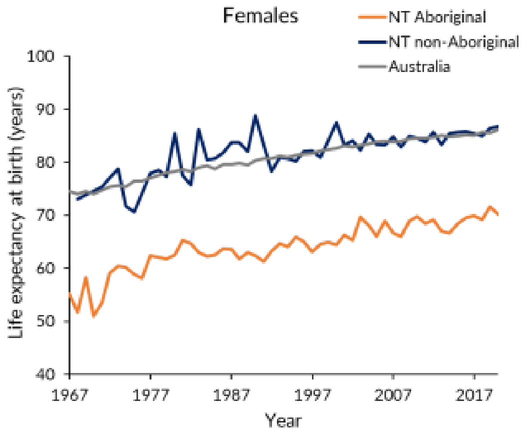


Figure 9: Female life expectancy at birth, NT and Australia by Aboriginal status, 1967–2020



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Abstracts from peer reviewed published articles related to the Northern Territory

Antimicrobial resistance in northern Australia: the HOTspots surveillance and response program annual epidemiology report 2022

Wozniak T M, Young A R, Shausan A, Legg A, Leung M J, Coulter S A, Pereira S, Baird R W, Murphy M

Commun Dis Intell (2018). 2025 May 19:49. doi:10.33321/cdi.2025.49.030

Background: The HOTspots surveillance and response program monitors antimicrobial resistance (AMR) in selected bacterial pathogens across three jurisdictions in northern Australia. In 2022, the program collected data from 164 community healthcare clinics and 50 hospitals to assess AMR trends and geographic variations.

Methods: Data on resistance rates for methicillin-resistant *Staphylococcus aureus* (MRSA) and for *Escherichia coli* (*E. coli*) were analysed. Geographic regions were compared to identify variations in AMR across the Northern Territory, northern Western Australia and northern Queensland. Resistance rates were compared between community clinics and hospitals.

Findings: In 2022, there were 56,003 clinical isolates submitted to HOTspots. Geographic variation was evident in *S. aureus* methicillin resistance, with MRSA accounting for 14.4% of *S. aureus* isolates in the east, 53.1% in central northern Australia and 46.3% in western northern Australia. Clindamycin-resistant MRSA was highest in the Northern Territory (21.7%) compared to Western Australia (16.1%) and Queensland (5.9%), limiting treatment options for community-acquired MRSA. Ceftriaxone-resistant *E. coli* also varied geographically, with resistance rates ranging from 3.9% in the east to 23.4% in central and 10.1% in the west. High rates of ceftriaxone resistance were observed in both community clinics (10.6%) and hospitals (16.3%). Nitrofurantoin-resistant *E. coli* remained low (0.2%) and stable over the past five years.

Interpretation: HOTspots data are critical for informing local antibiotic guidelines and aiding clinical decision-making. This detailed surveillance captures geographic and healthcare-setting-specific variations in AMR, which can improve regional treatment strategies across northern Australia, with a focus on the Northern Territory, which had previously lacked comprehensive surveillance.

Keywords: *antimicrobial resistance; community; northern Australia; regional; surveillance.*

Diagnostic and phylogenetic perspectives of the 2023 Murray Valley encephalitis virus outbreak in Australia: an observational study

Howard-Jones AR, Mahar J, Proudmore K, Butel-Simoes G, Eden JS, Neave MJ, Mileto P, Hueston L, Freeman K, Ellem J, Caly L, Sikazwe C, Levy A, Thomas A, Taylor C, Kurucz N, Smyth K, Jennison A, Moore P, Wright R, Mee PT, Feldman R, Dwyer D, O'Sullivan MV, Mahony AA, Warner MS, Papanicolas L, Schlebusch S, Lim, C K, Baird, R, Speers, D, Williams, D T, Currie, B J, Kok, J

The Lancet Microbe, Published June 20, 2025

https://doi.org/10.1016/j.lanmic.2025.101089

Background

An outbreak of Murray Valley encephalitis virus (MVEV), the largest since 1974, was observed in Australia between Jan 1 and July 31, 2023. This study aims to characterise the utility of diagnostic platforms, testing algorithms, and genomic characteristics of MVEV to facilitate a comprehensive framework for MVEV testing and surveillance in the outbreak setting.

Methods

In this observational study, we assessed flavivirus diagnostics for all patients with suspected Murray Valley encephalitis in Australia from Jan 1 to July 31, 2023. We included all patients with confirmed Murray Valley encephalitis, probable Murray Valley encephalitis, or acute unspecified flavivirus infection using the Communicable Diseases Network Australia case definition. Cases were excluded if an alternative diagnosis was identified. We collected blood, serum, cerebrospinal fluid, brain tissue, urine, or a combination of these samples, as appropriate and at the discretion of the treating clinician. We conducted multimodal diagnostic testing, which included flavivirus-specific serological and nucleic acid amplification testing. Metagenomic next-generation sequencing, including next-generation deep sequencing, target-enrichment, and targeted amplification, was conducted on human and representative mosquito-derived samples obtained from established mosquito population surveillance programmes for phylogenetic analysis.

Findings

27 patients with encephalitis were assessed for MVEV between Jan 1, 2023, and July 31, 2023, 23 (85%) of whom fulfilled national case definitions for confirmed Murray Valley encephalitis. Patient ages ranged from 6 weeks to 83 years (median 62·0 years [IQR 31·0-67·5]) and patients were mostly male (21 [78%] male patients and six [22%] female patients). Incidence varied widely by geographical region and was highest in the Northern Territory (32·0 per 1 000 000 population). Diagnostic specimen collection generally occurred promptly (median 6·0 days [IQR 4·0–14·5] from symptom onset to diagnostic specimen collection). In seven patients, case assignation relied on convalescent serum samples to assess for seroconversion or an appropriate rise in antibody titre (to four times the initial value or greater), or both. MVEV-specific IgM was detectable in serum samples of 17 (81%) of 21 patients tested by day 7 and MVEV IgG or total antibody (TAb) were detected in 18 (100%) of 18 patients tested by day 30. MVEV-specific IgM (or TAb) and MVEV RNA were detected in cerebrospinal fluid collected within 14 days of symptom onset in nine (39%) of 23 patients and seven (28%) of 25 patients, respectively. Phylogenetic analysis revealed two circulating MVEV genotypes, G1A and G2, in mosquitoes and humans in 2023. In southeast Australia, only G1A was detected and probably introduced from enzootic foci in northern Australia.

Interpretation

This study provides a comprehensive overview of the diagnostic workflows and phylogenetic evaluations used during the 2023 MVEV outbreak in Australia, emphasising the importance of a multimodal approach for accurate and timely confirmation of flavivirus infection. Further One Health surveillance for MVEV and other zoonotic flaviviruses is key, given potential expanded ecological niches in the context of episodic climatic events.

Keywords: Murray Valley encephalitis, Murray Valley encephalitis virus, flavivirus, encephalitis, One Health, climate change, zoonosis, pathogen genomics

Temporal and geographical lineage dynamics of invasive *Streptococcus pyogenes* in Australia from 2011 to 2023: a retrospective, multicentre, clinical and genomic epidemiology study

Xie O, Chisholm R H, Featherstone L, Nguyen A N T, Hayes A J, Jespersen M G, Zachreson C, Tellioglu N, Tonkin-Hill G, Dotel R, Spring S, Liu A, Rofe A, Duchene S, Sherry N L, Baird R W, Krause V L, Holt D C, Coin L J M, Rai N J, O'Sullivan M V N, Bond K, Corander J, Howden B P, Korman T M, Currie B J, Tong S Y C, Davies M R

The Lancet Microbe Volume 6, Issue 6, June 2025, 101053

https://doi.org/10.1016/j.lanmic.2024.101053

Background

Defining the temporal dynamics of invasive *Streptococcus pyogenes* (group A Streptococcus) and differences between hyperendemic and lower-incidence regions provides crucial insights into pathogen evolution and, in turn, informs preventive measures. We aimed to examine the clinical and temporal lineage dynamics of *S pyogenes* across different disease settings in Australia to improve understanding of drivers of pathogen diversity.

Methods

In this retrospective, multicentre, clinical and genomic epidemiology study, we identified cases of invasive *S pyogenes* infection from normally sterile sites between Jan 1, 2011, and Feb 28, 2023. Data were collected from five hospital networks across low-incidence regions in temperate southeast Australia and the hyperendemic, tropical, and largely remote Top End of the Northern Territory of Australia. The crude incidence rate ratio (IRR) of bloodstream *S pyogenes* infection comparing the Top End and southeast Australia and in First Nations people compared with non-First Nations people was estimated by quasi-Poisson regression. We estimated odds ratios (ORs) of intensive care unit (ICU) admission, in-hospital mortality, and 30-day mortality for the Top End versus southeast Australia using logistic regression. Retrieved and successfully sequenced isolates were assigned lineages at whole-genome resolution. Temporal trends in the composition of co-circulating lineages were compared between the two regions. We used an *S pyogenes*-specific multistrain simulated transmission model to examine the relationship between host population-specific parameters and observed pathogen lineage dynamics. The prevalence of accessory genes (those present in 5–95% of all genomes) was compared across geographies and temporal periods to investigate genomic drivers of diversity.

Findings

We identified 500 cases of invasive *S pyogenes* infection in patients in the Top End and 495 cases in patients in southeast Australia. The crude IRR of

bloodstream infection for the Top End compared with southeast Australia was 5·97 (95% CI 4·61–7·73) across the entire study period; in the Top End, infection disproportionately affected First Nations people compared with non-First Nations people (5·41, 4·28–6·89). The odds of in-hospital mortality (OR 0·43, 95% CI 0·26–0·70), 30-day mortality (0·38, 0·23–0·63), and ICU admission (0·42, 0·30–0·59) were lower in the Top End than in southeast Australia. Longitudinal lineage analysis of 642 *S pyogenes* genomes identified waves of replacement with distinct lineages in the Top End, whereas southeast Australia had a small number of dominant lineages that persisted and cycled in frequency. The transmission model qualitatively reproduced a similar pattern of replacement with distinct lineages when using a high transmission rate, small population size, and high levels of human movement—characteristics similar to those of communities in the hyperendemic Top End. Using a lower transmission rate, larger population size, and lower levels of migration similar to those of communities in urbanised southeast Australia, the transmission model qualitatively reproduced a pattern of dominant lineages that cycled in frequency. Despite distinct circulating lineages, the prevalence of accessory genes in the bacterial population was maintained across geographies and temporal periods.

Interpretation

In a hyperendemic setting, the replacement of distinct *S pyogenes* lineages occurred in waves, which could be linked to the disproportionate burden of disease and sparse human population in this setting. The maintenance of bacterial gene frequency could be consistent with multilocus selection. These findings suggest that lineage-specific interventions—such as vaccines under development—should consider disease setting and, without broad cross-protection, might lead to lineage replacement.

Population sequencing for phylogenetic diversity and transmission analyses

Pearson T, Furstenau T, Wood C, Rigas V, Drake K, Sahl J, Maltinsky S, Currie B J, Mayo M, Hall C, Keim P, Fofanov V

Proc Natl Acad Sci U S A. 2025 Jun 10;122(23):e2424797122.

DOI: [10.1073/pnas.2424797122](https://doi.org/10.1073/pnas.2424797122)

Genomic diversity in pathogen populations is foundational for evolution and adaptation. Understanding population-level diversity is also essential for tracking sources and revealing detailed pathways of transmission and spread. For bacteria, culturing, isolating, and sequencing the large number of individual colonies required to adequately sample diversity can be prohibitively time-consuming and expensive. While sequencing directly from a mixed population will show variants among reads, they cannot be linked to reveal allele combinations associated with phylogenetic inheritance patterns. Here, we describe the theory and method for using population sequencing directly from a mixed sample, along with a minimal number of individually sequenced colonies, to describe the phylogenetic diversity of a population without haplotype reconstruction. To demonstrate the utility of population sequencing in capturing phylogenetic diversity, we compared isogenic clones to population sequences of *Burkholderia pseudomallei* from sputum of a single patient. Our results point to the pathogen population being highly structured, suggesting that for some pathogens, sputum sampling may preserve structuring in the lungs and thus present a noninvasive alternative to understanding

colonization, movement, and pathogen/host interactions. We also analyzed population sequences of *Staphylococcus aureus* derived from different people and different body sites to reveal directionality of transmission between hosts and across body sites, demonstrating the power and utility for characterizing the spread of disease and identification of reservoirs at the finest levels. We anticipate that population sequencing and analysis can be broadly applied to accelerate research in a wide range of fields reliant on a foundational understanding of population phylogenetic diversity.

Keywords: deep sequencing; pathogen evolution; pathogen population diversity; pathogen population sequencing; pathogen transmission directionality.

Improving access to ivermectin for Aboriginal and Torres Strait Islander people in Australia: Big gains from a small change

Cox VRV, Stephens M, Singh GR, Currie BJ

Australian and New Zealand Journal of Public Health Volume 49, Issue 3, June 2025, 100237

https://doi.org/10.1016/j.anzjph.2025.100237

No abstract available

Key words: Australian Aboriginal and Torres Strait Islander Peoples; Pharmaceutical Benefits Scheme; access to medicine; best practice; ivermectin; scabies

"Hurts less, lasts longer"; a qualitative study on experiences of young people receiving high-dose subcutaneous injections of benzathine penicillin G to prevent rheumatic heart disease in New Zealand

Cooper J, Enkel SL, Moodley D, Dobinson H, Andersen E, Kado JH, Barr RK, Salman S, Baker MG, Carapetis JR, Manning L, Anderson A, Bennett J

PLOS ONE May 14, 2024
https://doi.org/10.1371/journal.pone.0302493

Background

Four-weekly intramuscular (IM) benzathine penicillin G (BPG) injections to prevent acute rheumatic fever (ARF) progression have remained unchanged since 1955. A Phase-I trial in healthy volunteers demonstrated the safety and tolerability of high-dose subcutaneous infusions of BPG which resulted in a much longer effective penicillin exposure, and fewer injections. Here we describe the experiences of young people living with ARF participating in a Phase-II trial of SubCutaneous Injections of BPG (SCIP).

Methodology

Participants (n = 20) attended a clinic in Wellington, New Zealand (NZ). After a physical examination, participants received 2% lignocaine followed by 13.8mL to 20.7mL of BPG (Bicillin-LA®; determined by weight), into the abdominal subcutaneous tissue. A Kaupapa Māori consistent methodology was used to explore experiences of SCIP, through semi-structured interviews and observations taken during/after the injection, and on days 28 and 70. All interviews were recorded, transcribed verbatim, and thematically analysed.

Principal findings

Low levels of pain were reported on needle insertion, during and following the injection. Some participants experienced discomfort and bruising on days one and two post dose; however, the pain was reported to be less severe than their usual IM BPG. Participants were 'relieved' to only need injections quarterly and the majority (95%) reported a preference for SCIP over IM BPG.

Conclusions

Participants preferred SCIP over their usual regimen, reporting less pain and a preference for the longer time gap between treatments. Recommending SCIP as standard of care for most patients needing long-term prophylaxis has the potential to transform secondary prophylaxis of ARF/RHD in NZ and globally.

Cutaneous Larva Migrans Refractory to Therapy with Ivermectin: Case Report and Review of Implicated Zoonotic Pathogens, Epidemiology, Anthelmintic Drug Resistance and Therapy

Currie BJ, Hoopes J and Cumming B

Trop. Med. Infect. Dis. 2025, 10(6), 163; https://doi.org/10.3390/tropicalmed10060163

Cutaneous larva migrans (CLM) is attributed to zoonotic infection with animal hookworm larvae penetrating the human skin, usually the feet and legs. There is, however, a broad range of differential diagnoses, with the implicated hookworm species usually remaining speculative. Single-dose ivermectin is the most recommended current therapy, with repeat ivermectin doses sometimes required. With the massive global expansion of macrocytic lactone use in both livestock and companion animals, ivermectin resistance is being increasingly described in both helminths and ectoparasites. A case of CLM involving the foot of a healthy 37-year-old is described, with the failure of two doses of ivermectin 15 mg (240 μg/kg) a week apart. This occurred in the context of a remote work environment in tropical Australia with both companion animals (dogs and cats) and wildlife exposed to antiparasitic agents including ivermectin. A combination regimen of multiple doses of albendazole and ivermectin was curative. Parasites with multidrug resistance being described from animals now include hookworms in dogs which are resistant to pyrantel, benzimidazoles such as mebendazole and ivermectin. For relapsed CLM we now recommend a combination of ivermectin and albendazole therapy. This report supports the critical role for a One Health/Planetary Health approach to surveillance and response for emerging zoonoses and antimicrobial resistance in human and animal pathogens. This requires support for systematic approaches to foster and normalize communications and collaborations between human and animal health professionals, environmental scientists and ecologists and First Nations scientists who are the holders of Indigenous knowledge.

Keywords: cutaneous larva migrans; zoonoses; One Health; ivermectin; albendazole; hookworms; antimicrobial resistance; Planetary Health.

Evaluating the effectiveness and sustainability of a primary healthcare strategy to reduce the prevalence of strongyloidiasis in endemically infected Indigenous communities in Northern Australia

Page WA, Blair D, Dempsey K, Biggs BA, Judd JA

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DOI: 10.1371/journal.pntd.0013136

Background: Strongyloidiasis is endemic in many remote Indigenous communities in Australia. Early diagnosis, treatment, and follow-up of chronic strongyloidiasis can prevent life-threatening clinical complications and decrease transmission in these endemic communities. The aim of this paper is to evaluate the effectiveness and sustainability of a primary healthcare strategy designed to measure and reduce the prevalence of strongyloidiasis in four remote communities in northeast Arnhem Land.

Methodology: The primary healthcare strategy was a prospective, longitudinal, health-systems intervention designed to integrate serological testing for chronic strongyloidiasis into the Indigenous preventive adult health assessment utilising the electronic health-record systems in four Aboriginal health services. Positive cases were recalled for treatment, and opportunistic follow-up serology after six months. Results were tracked using Strongyloides reports generated by the electronic health-record system. This paper describes the changes in prevalence, effectiveness of treatment, and reinfection during the implementation phase, 2012-2016. An improved Strongyloides electronic report was developed to evaluate the effectiveness and sustainability of the intervention to the end of 2020.

Principal findings: During the entire period 2012-2020, 84% (2390/2843) of the resident adults in the four communities were tested for strongyloidiasis at least once. Prevalence was reduced from 44% (1056/2390) ever-positive to 10% (232/2390) positive on their last test. Of positive, treated cases with a follow-up serology test, the last test was negative in 85% (824/967) of individuals. Point prevalence continued to decrease in each community four years after the end of the implementation phase.

Conclusions: The results provided practice-based evidence of a significant decrease in the prevalence of strongyloidiasis attributable to the strategy which could be replicated in other health services utilising electronic health-record systems. The final evaluation demonstrated the sustainability and ongoing benefits for endemically infected communities, and the key role that health services can play in strongyloidiasis prevention and control programs.

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