

Table S1. Clinical and genomic epidemiology of infectious diseases in the Northern Territory.

Pathogen	Clinical epidemiology	Genomic epidemiology	References
Skin pathogens			
<i>Sarcoptes scabiei</i> (scabies)	<ul style="list-style-type: none"> Scabies hyperendemic in remote NT communities In East Arnhem region between 2001-2005, by age 1 year 68% had had first episode scabies 	<ul style="list-style-type: none"> First genotyping globally, using multilocus microsatellite markers <i>S. scabiei</i> populations in humans are distinct from those in dogs in remote NT communities Recurrent scabies driven by reinfestation from inadequately treated contacts 	[1-4]
Community-associated methicillin-resistant <i>Staphylococcus aureus</i>	<ul style="list-style-type: none"> Emerged north Western Australia 1980s Cases reported NT Top End early 1990s By early 2000s incidence of bacteraemia in Aboriginal people in Top End 172 per 100,000 (5.8 per 100,000 in non-Indigenous population) 	<ul style="list-style-type: none"> ST93 dominant in NT, harbours Panton-Valentine leucocidin (PVL) toxin Among cases of <i>S. aureus</i> infection at Royal Darwin Hospital, PVL associated with double odds of sepsis Molecular dating suggests ST93 arose from MSSA in northern Australia in 1970s, with methicillin resistance acquired on three separate occasions, expansion and spread of clade harbouring staphylococcal cassette chromosome <i>mec</i> IVa to east coast by 2000 	[5-11]
Group A <i>Streptococcus</i> (<i>Streptococcus pyogenes</i>)	<ul style="list-style-type: none"> Impetigo associated with scabies in children Incidence of invasive infection and immunologic sequelae especially acute rheumatic fever amongst the highest globally In East Arnhem region between 2001-2005, by age 1 year 82% had had first episode impetigo 2018 prevalence rheumatic heart disease in 5-20 year-olds in Maningrida $\geq 10\%$ 	<ul style="list-style-type: none"> Diverse <i>emm</i> types not unique to NT and found internationally, no dominant <i>emm</i> type No rheumatogenic or hypervirulent strains identified to date in NT Sporadic outbreaks of acute post-streptococcal glomerulonephritis associated with nephritogenic strains, including 2005 outbreak associated with <i>emm55</i> Concerns that <i>emm</i> diversity in NT will not be adequately covered by M-based vaccines 	[4,12-22]
Vaccine-preventable infections			
<i>Streptococcus pneumoniae</i> (invasive pneumococcal disease)	<ul style="list-style-type: none"> Associated with influenza, seasonal increases 0-4 year-olds and >65 year-olds most affected First Nations people disproportionately affected nationally including in NT 	<ul style="list-style-type: none"> National Enhanced Invasive Pneumococcal Disease Surveillance Program identified serotype replacement following universal funding of PCV7 Multijurisdictional outbreak of 245 serotype 1 invasive pneumococcal disease cases in NT, Queensland, and Western Australia 2011-2012 	[23-26]
Influenza virus	<ul style="list-style-type: none"> Dry season peak in cases corresponding to southern winter, with inter-seasonal transmission and wet season outbreaks in some years NT First Nations incidence 5.6x higher among 55-64 year-olds and 4.3x higher in 0-4 year-olds than non-Indigenous population NT First Nations 6.5x more likely to be hospitalised and 5.5x more likely to 	<ul style="list-style-type: none"> Minimal mid-year influenza activity Australia-wide in 2018, followed by detection of influenza A(H1N1)pdm09 subclade in Darwin October 2018 - associated with large peak in Darwin cases and expansion across Australia leading to increased transmission in southern states early 2019 - Australia-wide May 2019 notifications 12-fold 	[27-31]

	<p>die from influenza than non-Indigenous people</p> <ul style="list-style-type: none"> In 2009, seroprevalence for and hospitalisation with influenza A(H1N1)pdm09 markedly higher in First Nations people 	<p>higher than average for preceding 3 years</p> <ul style="list-style-type: none"> Record low influenza case numbers Australia-wide in 2021, NT received returned travellers to the Howard Springs Quarantine Facility and highest number of cases nationally, NT strain used to develop Southern Hemisphere 2022 influenza vaccine 	
SARS-CoV-2 (COVID-19)	<ul style="list-style-type: none"> No sustained community transmission until November 2021 	<ul style="list-style-type: none"> In-flight transmission of B.1.617.2 (Delta) on flights from India to Australia, April 2021 Genomic sequencing commenced at Territory Pathology October 2021, used to link B.1.617.2 (Delta) clusters and detect B.1.1.529 (Omicron) 	[32-34]
<i>Neisseria meningitidis</i> (meningococcal disease)	<ul style="list-style-type: none"> Outbreaks in Central Australia 1987-1991 (60 confirmed cases), 1997-1998 (11 confirmed cases), 2017 (31 confirmed cases) 	<ul style="list-style-type: none"> 1987-1991 outbreak group A 1998 outbreak group B 2017 outbreak group W 	[35-40]
Rotavirus	<ul style="list-style-type: none"> Outbreaks in central and northern Australia, resulting in hospitalisations especially in 0-5 year-olds Rotavirus vaccination program in NT implemented October 2006 (Rotarix, includes live attenuated G1P[8] virus) Hospitalisations of First Nations children >20 times higher than for non-Indigenous children in remote central and northern Australia in 2007-2010, despite >70% vaccine coverage Clinical trial in progress to determine optimal vaccination schedule 	<ul style="list-style-type: none"> Outbreaks in post-vaccination era due variety of genotypes, including G1P[8] (the genotype in Rotarix vaccine), G9P[8], G2P[4] Novel G10P[14] virus identified in Central Australia in 2011, predicted to have originated in an even-toed ungulate 	[41-49]
Mycobacterial infection			
<i>Mycobacterium tuberculosis</i>	<ul style="list-style-type: none"> Incidence in NT First Nations falling by ~5% per year but remains high (15 per 100,000, compared to <1 per 100,000 in Australian-born non-Indigenous nationally) Multidrug-resistant TB incidence low (~1.5% notified cases), no First Nations multidrug-resistant TB cases Incidence childhood TB the highest nationally, most child cases First Nations Increased cases associated with overseas arrivals (fishers from Indonesia, asylum seekers and crew, 1999 humanitarian evacuation from Timor-Leste) 	<ul style="list-style-type: none"> Half of sequenced cases 1989-2020 belonged to genomic clusters, 86% First Nations, 76% remote region Genomic clusters with overseas-born case as first case small (2-5 cases) Interval between cases and epidemiologically- and genomically-linked contacts 4.5 months-24 years Genomics linked mystery cases to clusters No evidence of transmission of multidrug-resistant TB Phylogenetics consistent with multiple introductions from Europe and Asia 	[50-56]
Vector-borne diseases			
Murray Valley encephalitis virus	<ul style="list-style-type: none"> Enzootic in Kimberley region Western Australia and Top End NT, <i>Culex annulirostris</i> mosquitos and wading water birds 	<ul style="list-style-type: none"> Four genotypes identified (G1-4), G1 and G2 recently in Australia NT under-sampled 	[57-62]

	<ul style="list-style-type: none"> • Virus activity during wet season with human infections February-July • Surveillance includes mosquito-trapping and identification, and serosurveillance of vertebrate hosts 	<ul style="list-style-type: none"> • G1B in Western Australia, Queensland, New South Wales, and Victoria • G1A and G2 in Western Australia and NT 	
Japanese encephalitis virus	<ul style="list-style-type: none"> • First locally-acquired NT case reported on Tiwi Islands February 2021 	<ul style="list-style-type: none"> • Diagnosis made by metagenomic sequencing of brain tissue 	[63-65]
Environmental pathogens			
<i>Burkholderia pseudomallei</i> (melioidosis)	<ul style="list-style-type: none"> • Reservoir soil and surface water • Majority of cases during wet season November-April • Increased case numbers associated with urban construction, increased rainfall, and severe weather events • Diabetes, hazardous alcohol consumption, chronic kidney disease key risk factors 	<ul style="list-style-type: none"> • Populations in Australia, Asia, Africa, and Americas remain distinct, enabling prediction of geographic origin of emergent strains • Water supplies and contaminated products confirmed to be source of case clusters • Neurological melioidosis associated with the <i>bimA_{Bm}</i> variant, hypothesised nerve root translocation • Rare cases of antimicrobial resistance during treatment due to mutations in core genes • Genome reduction and loss of virulence associated with chronic carriage in cystic fibrosis • Genotyping reveals recent importation of Asian strains to NT 	[66-80]
<i>Acinetobacter baumannii</i>	<ul style="list-style-type: none"> • Community-onset bacteraemic pneumonia mostly wet season November-April • Hazardous alcohol consumption and diabetes key risk factors • Community isolates sensitive to gentamicin, ciprofloxacin, meropenem 	<ul style="list-style-type: none"> • NT community isolates do not belong to major international global clones, but are not unique to NT • Half of cases ST10, with closely related isolates in Vietnam and USA, MRCA for clade 1957 (spread possibly associated with Vietnam war) • Variable presence of virulence genes not associated with differences in severity • 3/30 (10%) survivors had reinfection during 21-year study 	[81-85]
Foodborne pathogens			
<i>Salmonella</i>	<ul style="list-style-type: none"> • Incidence ~5x national average • 0-4 year-olds most affected • Outbreaks uncommon, have been associated with sea turtle and barramundi • Non-Typhimurium <i>Salmonella</i> more common than in southeastern Australia 	<ul style="list-style-type: none"> • Common clinical serovars isolated from large proportion of homes, including from animal faeces (frog, lizard, gecko, dog), vacuum cleaner contents, soil, and sandpit samples 	[86-91]
<i>Shigella</i>	<ul style="list-style-type: none"> • Incidence 119 per 100,000 in 2019 compared to 12 per 100,000 for whole Australia • >80% NT cases in First Nations people • 0-4 year-olds most affected 	<ul style="list-style-type: none"> • Increase in <i>S. flexneri</i> serotype 2b in NT and Queensland since 2017 • Emergence of multidrug-resistance-conferring <i>bla_{ADH}</i> plasmid in Queensland in 2018 • None of 12 NT isolates carried this plasmid, two NT isolates carried <i>bla_{CTX-M}</i> extended-spectrum beta-lactamase plasmid, and one isolate carried <i>bla_{TEM-1B}</i> and <i>mphA</i> (associated with macrolide resistance) 	[92,93]

Sexually-transmitted infections			
<i>Neisseria gonorrhoeae</i>	<ul style="list-style-type: none"> Prevalence 9.5% and incidence 23.4-26.1 new infections per 100 person-years in 16-19 year-olds in remote northern and Central Australia Treatment guidelines vary by region; azithromycin, amoxycillin, and probenecid standard of care in remote NT regions 	<ul style="list-style-type: none"> AMR surveillance using 8 PCR assays used to detect genes and mutations associated with resistance to penicillin, third-generation cephalosporins, ciprofloxacin, and azithromycin <5% remote samples predicted to have penicillin resistance, 0.2% azithromycin resistant 	[94,95]
<i>Treponema pallidum</i> (syphilis)	<ul style="list-style-type: none"> Multijurisdictional syphilis outbreak in remote northern Australia since 2011, cases in Queensland, NT, South Australia and Western Australia Cases of congenital syphilis, including deaths 	<ul style="list-style-type: none"> <i>T. pallidum</i> has been successfully sequenced from clinical samples using bait capture approach 25 NT <i>T. pallidum</i> specimens sequenced, phylogenetically interspersed with Australian and global genomes, 87% of all Australian specimens in study genotypically macrolide resistant 	[96-99]
<i>Chlamydia trachomatis</i> (including non-sexually acquired serotypes that cause trachoma)	<ul style="list-style-type: none"> Sexually-transmitted <i>C. trachomatis</i> prevalence 11.1% and incidence 23.4-29.2 new infections per 100 person-years in 16-19 year-olds in remote northern and Central Australia Trachoma community-wide screening and treatment led to reduction in prevalence from 29% in 2008 to 4% in 2012 but remains endemic in central Australia; the only developed nation globally to not have eradicated trachoma 	<ul style="list-style-type: none"> <i>C. trachomatis</i> outer membrane protein A (<i>ompA</i>) genotypes A-C are associated with trachoma, genotypes D-K are associated with non-invasive urogenital infection, and genotypes L1-L3 are associated with invasive infections and lymphogranuloma venereum <i>C. trachomatis</i> from NT children with trachoma 1985-1993 was not within the classical trachoma lineage on whole genome phylogenetic analysis, instead belonging to two urogenital clades but with recombination at <i>ompA</i> (replacement with <i>ompA</i> B, Ba and C, characteristic of ocular strains) 	[100,101]
Bloodborne viruses			
Hepatitis B virus	<ul style="list-style-type: none"> First description hepatitis B surface antigen ('Australia antigen') in Australian First Nations man Prevalence in NT First Nations people 6% 	<ul style="list-style-type: none"> All NT First Nations cases to date C4 genotype, Australian MRCA >51,000 years ago (approximate time of arrival of modern humans) Phylogeographic clustering of HBV genomes from Daly River, Katherine, Tiwi Islands, West Arnhem, East Arnhem 20/35 genomes had ≥1 mutation associated with either rapid liver disease progression or hepatocellular carcinoma C4 has <i>ayw3</i> serotype, divergent from A2 vaccine serotype <i>adw2</i>, however vaccine effective at preventing chronic HBV in NT First Nations people 	[102-108]
Human T lymphotropic virus type 1 (HTLV-1)	<ul style="list-style-type: none"> Estimated prevalence in central Australia 33% 	<ul style="list-style-type: none"> HTLV-1c is endemic in Central Australia, two clades distinct from other countries in the Western Pacific, most recent common ancestor estimated to have occurred 9,120 years ago (38,000-4,500 years ago) 	[109-111]

References

- Walton SF, Choy JL, Bonson A, et al. Genetically distinct dog-derived and human-derived *Sarcoptes scabiei* in scabies-endemic communities in northern Australia. *Am J Trop Med Hyg* **1999**, 61, 542-7. doi: 10.4269/ajtmh.1999.61.542
- Walton SF, McBroom J, Mathews JD, et al. Crusted scabies: A molecular analysis of *Sarcoptes scabiei* variety hominis populations from patients with repeated infestations. *Clin Infect Dis* **1999**, 29, 1226-30. doi: 10.1086/313466
- Walton SF, Dougall A, Pizzutto S, et al. Genetic epidemiology of *Sarcoptes scabiei* (Acari: Sarcoptidae) in northern Australia. *Int J Parasitol* **2004**, 34, 839-49. doi: 10.1016/j.ijpara.2004.04.002
- McMeniman E, Holden L, Kearns T, et al. Skin disease in the first two years of life in Aboriginal children in East Arnhem Land. *Australas J Dermatol* **2011**, 52, 270-3. doi: 10.1111/j.1440-0960.2011.00806.x
- Udo EE, Pearman JW, Grubb WB. Genetic analysis of community isolates of methicillin-resistant *Staphylococcus aureus* in Western Australia. *J Hosp Infect* **1993**, 25, 97-108. doi: 10.1016/0195-6701(93)90100-e
- Maguire GP, Arthur AD, Boustead PJ, et al. Emerging epidemic of community-acquired methicillin-resistant *Staphylococcus aureus* infection in the Northern Territory. *Med J Aust* **1996**, 164, 721-3. doi: 10.5694/j.1326-5377.1996.tb122270.x
- Tong SY, Bishop EJ, Lilliebridge RA, et al. Community-associated strains of methicillin-resistant *Staphylococcus aureus* and methicillin-susceptible *S. aureus* in Indigenous northern Australia: epidemiology and outcomes. *J Infect Dis* **2009**, 199, 1461-70. doi: 10.1086/598218
- Tong SY, Lilliebridge RA, Bishop EJ, et al. Clinical correlates of Panton-Valentine leukocidin (PVL), PVL isoforms, and clonal complex in the *Staphylococcus aureus* population of Northern Australia. *J Infect Dis* **2010**, 202, 760-9. doi: 10.1086/655396
- Stinear TP, Holt KE, Chua K, et al. Adaptive change inferred from genomic population analysis of the ST93 epidemic clone of community-associated methicillin-resistant *Staphylococcus aureus*. *Genome Biol Evol* **2014**, 6, 366-78. doi: 10.1093/gbe/evu022
- Turnidge J, Coombs G, Daley D, et al. MRSA: A Tale of Three Types. 15 years of survey data from AGAR. Sydney: ACSQHC. 2016. https://www.safetyandquality.gov.au/sites/default/files/2020-09/mrsa_-_a_tale_of_three_types.pdf (accessed 25 July 2021).
- van Hal SJ, Steinig EJ, Andersson P, et al. Global scale dissemination of ST93: a divergent *Staphylococcus aureus* epidemic lineage that has recently emerged from remote northern Australia. *Front Microbiol* **2018**, 9, 1453. doi: 10.3389/fmicb.2018.01453
- McDonald MI, Towers RJ, Andrews R, et al. The dynamic nature of group A streptococcal epidemiology in tropical communities with high rates of rheumatic heart disease. *Epidemiol Infect* **2008**, 136, 529-39. doi: 10.1017/S0950268807008655
- Marshall CS, Cheng AC, Markey PG, et al. Acute post-streptococcal glomerulonephritis in the Northern Territory of Australia: a review of 16 years data and comparison with the literature. *Am J Trop Med Hyg* **2011**, 85, 703-10. doi: 10.4269/ajtmh.2011.11-0185
- Towers RJ, Carapetis JR, Currie BJ, et al. Extensive diversity of *Streptococcus pyogenes* in a remote human population reflects global-scale transmission rather than localised diversification. *PLoS One* **2013**, 8, e73851. doi: 10.1371/journal.pone.0073851
- Romani L, Steer AC, Whitfield MJ, et al. Prevalence of scabies and impetigo worldwide: a systematic review. *Lancet Infect Dis* **2015**, 15, 960-7. doi: 10.1016/S1473-3099(15)00132-2
- Boyd R, Patel M, Currie BJ, et al. High burden of invasive group A streptococcal disease in the Northern Territory of Australia. *Epidemiol Infect* **2016**, 144, 1018-27. doi: 10.1017/S0950268815002010
- Bowen AC, Harris T, Holt DC, et al. Whole genome sequencing reveals extensive community-level transmission of group A *Streptococcus* in remote communities. *Epidemiol Infect* **2016**, 144, 1991-8. doi: 10.1017/S095026881500326X
- Davies MR, McIntyre L, Mutreja A, et al. Atlas of group A streptococcal vaccine candidates compiled using large-scale comparative genomics. *Nat Genet* **2019**, 51, 1035-43. doi: 10.1038/s41588-019-0417-8
- Francis JR, Gargan C, Remenyi B, et al. A cluster of acute rheumatic fever cases among Aboriginal Australians in a remote community with high baseline incidence. *Aust N Z J Public Health* **2019**, 43, 288-93. doi: 10.1111/1753-6405.12893
- Giffard PM, Tong SYC, Holt DC, et al. Concerns for efficacy of a 30-valent M-protein-based *Streptococcus pyogenes* vaccine in regions with high rates of rheumatic heart disease. *PLoS Negl Trop Dis* **2019**, 13, e0007511. doi: 10.1371/journal.pntd.0007511
- Katzenellenbogen JM, Bond-Smith D, Seth RJ, et al. Contemporary incidence and prevalence of rheumatic fever and rheumatic heart disease in Australia using linked data: the case for policy change. *J Am Heart Assoc* **2020**, 9, e016851. doi: 10.1161/JAHA.120.016851
- Francis JR, Fairhurst H, Hardefeldt H, et al. Hyperendemic rheumatic heart disease in a remote Australian town identified by echocardiographic screening. *Med J Aust* **2020**, 213, 118-23. doi: 10.5694/mja2.50682
- Staples M, Graham RM, Jennison AV, et al. Molecular characterization of an Australian serotype 1 *Streptococcus pneumoniae* outbreak. *Epidemiol Infect* **2015**, 143, 325-33. doi: 10.1017/S0950268814000648
- Marmor AM, Harley D. Evaluation of Australia's Enhanced Invasive Pneumococcal Disease (IPD) Surveillance Program. *Commun Dis Intell (2018)* **2018**, 42. doi: 10.1017/S0950268814000648
- Meder KN, Jayasinghe S, Beard F, et al. Long-term impact of pneumococcal conjugate vaccines on invasive disease and pneumonia hospitalizations in Indigenous and non-Indigenous Australians. *Clin Infect Dis* **2020**, 70, 2607-15. doi: 10.1093/cid/ciz731
- Cook HM, Giele CM, Jayasinghe SH, et al. An outbreak of serotype-1 sequence type 306 invasive pneumococcal disease in an Australian Indigenous population. *Commun Dis Intell (2018)* **2020**, 44. doi: 10.33321/cdi.2020.44.66
- Flint SM, Davis JS, Su JY, et al. Disproportionate impact of pandemic (H1N1) 2009 influenza on Indigenous people in the Top End of Australia's Northern Territory. *Med J Aust* **2010**, 192, 617-22. doi: 10.5694/j.1326-5377.2010.tb03654.x
- Trauer JM, Laurie KL, McDonnell J, et al. Differential effects of pandemic (H1N1) 2009 on remote and Indigenous groups, Northern Territory, Australia, 2009. *Emerg Infect Dis* **2011**, 17, 1615-23. doi: 10.3201/eid1709.101196

29. Barr IG, Deng YM, Grau ML, et al. Intense interseasonal influenza outbreaks, Australia, 2018/19. *Euro Surveill* **2019**, 24. doi: 10.2807/1560-7917.ES.2019.24.33.1900421
30. Weinman AL, Sullivan SG, Vijaykrishna D, et al. Epidemiological trends in notified influenza cases in Australia's Northern Territory, 2007-2016. *Influenza Other Respir Viruses* **2020**, 14, 541-50. doi: 10.1111/irv.12757
31. WHO Collaborating Centre for Reference and Research on Influenza. Annual Report 2021. http://www.influenzacentre.org/documents/publications_reports/Annual%20Report%202021.pdf (accessed 5 June 2022).
32. Douglas NM, Meumann EM, Krause VL, et al. Successful containment to date of SARS-CoV-2 transmission in the Northern Territory. *Med J Aust* **2021**, 214, 218-9. doi: 10.5694/mja2.50840
33. Hogarth F, Coffey P, Goddard L, et al. Genomic evidence of in-flight SARS-CoV-2 transmission, India to Australia, April 2021. *Emerg Infect Dis* **2022**, 28. doi: 10.3201/eid2807.212466
34. Meumann EM, Menouhos D, Christofis S, et al. Local genomic sequencing enhances COVID-19 surveillance in the Northern Territory of Australia. *Pathology* **2022**, 54, 659-662. doi: 10.1016/j.pathol.2022.03.005
35. Creasey SA. Epidemic meningococcal meningitis in central Australia in the 1970s. *Med J Aust* **1991**, 155, 725-6. doi: 10.5694/j.1326-5377.1991.tb94004.x
36. Patel MS, Merianos A, Hanna JN, et al. Epidemic meningococcal meningitis in central Australia, 1987-1991. *Med J Aust* **1993**, 158, 336-40. doi: 10.5694/j.1326-5377.1993.tb121793.x
37. Hansman D, Ashton F. Serotype and serosubtype distribution of strains of *Neisseria meningitidis* isolated in South Australia and the Northern Territory of Australia: 1971-1989. *Pathology* **1994**, 26, 318-20. doi: 10.1080/00313029400169741
38. Farmer B. Meningococcal disease in Central Australia 1998. *The Northern Territory Disease Control Bulletin* **1999**, 6, 1-6. doi: 10.1016/j.1326-5377.1999.tb121793.x
39. McMullin T, Peacock D. Meningococcal disease in the Northern Territory between 1991 and 2000. *The Northern Territory Disease Control Bulletin* **2001**, 8. doi: 10.1016/j.1326-5377.1999.tb121793.x
40. Sudbury EL, O'Sullivan S, Lister D, et al. Case manifestations and public health response for outbreak of meningococcal W disease, Central Australia, 2017. *Emerg Infect Dis* **2020**, 26, 1355-63. doi: 10.3201/eid2607.181941
41. Gelbart B, Hansen-Knarhoi M, Binns P, et al. Rotavirus outbreak in a remote Aboriginal community: the burden of disease. *J Paediatr Child Health* **2006**, 42, 775-80. doi: 10.1111/j.1440-1754.2006.00976.x
42. Newall AT, MacIntyre R, Wang H, et al. Burden of severe rotavirus disease in Australia. *J Paediatr Child Health* **2006**, 42, 521-7. doi: 10.1111/j.1440-1754.2006.00915.x
43. Snelling TL, Andrews RM, Kirkwood CD, et al. Case-control evaluation of the effectiveness of the G1P[8] human rotavirus vaccine during an outbreak of rotavirus G2P[4] infection in central Australia. *Clin Infect Dis* **2011**, 52, 191-9. doi: 10.1093/cid/ciq101
44. Dey A, Wang H, Menzies R, et al. Changes in hospitalisations for acute gastroenteritis in Australia after the national rotavirus vaccination program. *Med J Aust* **2012**, 197, 453-7. doi: 10.5694/mja12.10062
45. Donato CM, Cannan D, Bogdanovic-Sakran N, et al. Characterisation of a G9P[8] rotavirus strain identified during a gastroenteritis outbreak in Alice Springs, Australia post Rotarix vaccine introduction. *Vaccine* **2012**, 30 Suppl 1, A152-8. doi: 10.1016/j.vaccine.2011.07.119
46. Cowley D, Donato CM, Roczo-Farkas S, et al. Novel G10P[14] rotavirus strain, Northern Territory, Australia. *Emerg Infect Dis* **2013**, 19, 1324-7. doi: 10.3201/eid1908.121653
47. Donato CM, Cowley D, Snelling TL, et al. Characterization of a G1P[8] rotavirus causing an outbreak of gastroenteritis in the Northern Territory, Australia, in the vaccine era. *Emerg Microbes Infect* **2014**, 3, e47. doi: 10.1038/emi.2014.47
48. Middleton BF, Danchin M, Quinn H, et al. Retrospective case-control study of 2017 G2P[4] rotavirus epidemic in rural and remote Australia. *Pathogens* **2020**, 9. doi: 10.3390/pathogens9100790
49. Middleton BF, Danchin M, Jones MA, et al. Immunogenicity of a third scheduled dose of Rotarix in Australian Indigenous infants: a phase IV, double-blind, randomised, placebo-controlled clinical trial. *J Infect Dis* **2022**. doi: 10.1093/infdis/jiac038
50. Krause VL, Britton WJ. Tuberculosis in the tropics. *Med J Aust* **1993**, 159, 412-5. doi: 10.5694/j.1326-5377.1993.tb137920.x
51. Kelly PM, Scott L, Krause VL. Tuberculosis in East Timorese refugees: implications for health care needs in East Timor. *Int J Tuberc Lung Dis* **2002**, 6, 980-7. doi: 10.1093/infdis/jiac038
52. Gray NJ, Hansen-Knarhoi M, Krause VL. Tuberculosis in illegal foreign fishermen: whose public health are we protecting? *Med J Aust* **2008**, 188, 144-7. doi: 10.5694/j.1326-5377.2008.tb01556.x
53. Teo SS, Tay EL, Douglas P, et al. The epidemiology of tuberculosis in children in Australia, 2003-2012. *Med J Aust* **2015**, 203, 440. doi: 10.5694/mja15.00717
54. Judge D, Krause VL. Multidrug-resistant tuberculosis in the Northern Territory: a 10-year retrospective case series. *Commun Dis Intell Q Rep* **2016**, 40, E334-9. doi: 10.33321/cdi.2019.43.10
55. The National Tuberculosis Advisory Committee for the Communicable Diseases Network Australia. The strategic plan for control of tuberculosis in Australia, 2016-2020: towards disease elimination. *Commun Dis Intell* (2018) **2019**, 43. doi: 10.33321/cdi.2019.43.10
56. Meumann EM, Horan K, Ralph AP, et al. Tuberculosis in Australia's tropical north: a population-based genomic epidemiological study. *Lancet Reg Health West Pac* **2021**, 15, 100229. doi: 10.1016/j.lanwpc.2021.100229
57. Burrow JN, Whelan PI, Kilburn CJ, et al. Australian encephalitis in the Northern Territory: clinical and epidemiological features, 1987-1996. *Aust N Z J Med* **1998**, 28, 590-6. doi: 10.1111/j.1445-5994.1998.tb00653.x
58. Spencer JD, Azoulas J, Broom AK, et al. Murray Valley encephalitis virus surveillance and control initiatives in Australia. National Arbovirus Advisory Committee of the Communicable Diseases Network Australia. *Commun Dis Intell Q Rep* **2001**, 25, 33-47. doi: 10.1016/j.lanwpc.2021.100229

59. Williams DT, Diviney SM, Niazi AU, et al. The molecular epidemiology and evolution of Murray Valley encephalitis virus: recent emergence of distinct sub-lineages of the dominant genotype 1. *PLoS Negl Trop Dis* **2015**, 9, e0004240. doi: 10.1371/journal.pntd.0004240
60. Floridis J, McGuinness SL, Kurucz N, et al. Murray Valley encephalitis virus: an ongoing cause of encephalitis in Australia's north. *Trop Med Infect Dis* **2018**, 3. doi: 10.3390/tropicalmed3020049
61. Russell JS, Caly L, Kostecki R, et al. The first isolation and whole genome sequencing of Murray Valley encephalitis virus from cerebrospinal fluid of a patient with encephalitis. *Viruses* **2018**, 10. doi: 10.3390/v10060319
62. Caly L, Davidson N, Ghimire R, et al. Extended detection and isolation of Murray Valley encephalitis virus in whole blood and urine. *Med J Aust* **2019**, 211, 499-500 e1. doi: 10.5694/mja2.50423
63. Gibson J. Health authorities issue mosquito warning after person dies on Tiwi Islands. 20 March 2021. <https://www.abc.net.au/news/2021-03-20/nt-mosquito-borne-virus-warning-following-tiwi-islands-death/100019152> (accessed 24 October 2021).
64. Australian Government Department of Health. Japanese encephalitis virus (JEV). <https://www.health.gov.au/health-alerts/japanese-encephalitis-virus-jev/about> (accessed 5 June 2022).
65. Furuya-Kanamori L, Gyawali N, Mills DJ, et al. The emergence of Japanese encephalitis in Australia and the implications for a vaccination strategy. *Trop Med Infect Dis* **2022**, 7. doi: 10.3390/tropicalmed7060085
66. Kaestli M, Mayo M, Harrington G, et al. Landscape changes influence the occurrence of the melioidosis bacterium *Burkholderia pseudomallei* in soil in northern Australia. *PLoS Negl Trop Dis* **2009**, 3, e364. doi: 10.1371/journal.pntd.0000364
67. Pearson T, Giffard P, Beckstrom-Sternberg S, et al. Phylogeographic reconstruction of a bacterial species with high levels of lateral gene transfer. *BMC Biol* **2009**, 7, 78. doi: 10.1186/1741-7007-7-78
68. Price EP, Sarovich DS, Mayo M, et al. Within-host evolution of *Burkholderia pseudomallei* over a twelve-year chronic carriage infection. *mBio* **2013**, 4. doi: 10.1128/mBio.00388-13
69. McRobb E, Sarovich DS, Price EP, et al. Tracing melioidosis back to the source: using whole-genome sequencing to investigate an outbreak originating from a contaminated domestic water supply. *J Clin Microbiol* **2015**, 53, 1144-8. doi: 10.1128/JCM.03453-14
70. Sarovich DS, Garin B, De Smet B, et al. Phylogenomic analysis reveals an Asian origin for African *Burkholderia pseudomallei* and further supports melioidosis endemicity in Africa. *mSphere* **2016**, 1. doi: 10.1128/mSphere.00089-15
71. Price EP, Sarovich DS, Smith EJ, et al. Unprecedented melioidosis cases in Northern Australia caused by an Asian *Burkholderia pseudomallei* strain identified by using large-scale comparative genomics. *Appl Environ Microbiol* **2016**, 82, 954-63. doi: 10.1128/AEM.03013-15
72. Kaestli M, Grist EPM, Ward L, et al. The association of melioidosis with climatic factors in Darwin, Australia: A 23-year time-series analysis. *J Infect* **2016**, 72, 687-97. doi: 10.1016/j.jinf.2016.02.015
73. Sarovich DS, Chapple SNJ, Price EP, et al. Whole-genome sequencing to investigate a non-clonal melioidosis cluster on a remote Australian island. *Microb Genom* **2017**, 3, e000117. doi: 10.1099/mgen.0.000117
74. Chewapreecha C, Holden MT, Vehkala M, et al. Global and regional dissemination and evolution of *Burkholderia pseudomallei*. *Nat Microbiol* **2017**, 2, 16263. doi: 10.1038/nmicrobiol.2016.263
75. Viberg LT, Sarovich DS, Kidd TJ, et al. Within-host evolution of *Burkholderia pseudomallei* during chronic infection of seven Australasian cystic fibrosis patients. *mBio* **2017**, 8. doi: 10.1128/mBio.00356-17
76. Pearson T, Sahl JW, Hepp CM, et al. Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year *Burkholderia pseudomallei* infection. *PLoS Pathog* **2020**, 16, e1008298. doi: 10.1371/journal.ppat.1008298
77. Madden DE, Webb JR, Steinig EJ, et al. Taking the next-gen step: comprehensive antimicrobial resistance detection from *Burkholderia pseudomallei*. *EBioMedicine* **2021**, 63, 103152. doi: 10.1016/j.ebiom.2020.103152
78. Currie BJ, Mayo M, Ward LM, et al. The Darwin Prospective Melioidosis Study: a 30-year prospective, observational investigation. *Lancet Infect Dis* **2021**, 21, 1737-46. doi: 10.1016/S1473-3099(21)00022-0
79. Meumann EM, Kaestli M, Mayo M, et al. Emergence of *Burkholderia pseudomallei* sequence type 562, northern Australia. *Emerg Infect Dis* **2021**, 27, 1057-67. doi: 10.3201/eid2704.202716
80. Webb JR, Mayo M, Rachlin A, et al. Genomic epidemiology links *Burkholderia pseudomallei* from individual human cases to *B. pseudomallei* from targeted environmental aampling in northern Australia. *J Clin Microbiol* **2022**, 60, e0164821. doi: 10.1128/JCM.01648-21
81. Anstey NM, Currie BJ, Withnall KM. Community-acquired *Acinetobacter* pneumonia in the Northern Territory of Australia. *Clin Infect Dis* **1992**, 14, 83-91. doi: 10.1093/cid/14.1.83
82. Anstey NM, Currie BJ, Hassell M, et al. Community-acquired bacteremic *Acinetobacter* pneumonia in tropical Australia is caused by diverse strains of *Acinetobacter baumannii*, with carriage in the throat in at-risk groups. *J Clin Microbiol* **2002**, 40, 685-6. doi: 10.1128/JCM.40.4.685-6.2002
83. Davis JS, McMillan M, Swaminathan A, et al. A 16-year prospective study of community-onset bacteremic *Acinetobacter* pneumonia: low mortality with appropriate initial empirical antibiotic protocols. *Chest* **2014**, 146, 1038-45. doi: 10.1378/chest.13-3065
84. Meumann EM, Anstey NM, Currie BJ, et al. Whole-genome sequencing to differentiate relapse from reinfection in community-onset bacteremic *Acinetobacter baumannii* pneumonia. *Open Forum Infect Dis* **2019**, 6, ofz263. doi: 10.1093/ofid/ofz263
85. Meumann EM, Anstey NM, Currie BJ, et al. Genomic epidemiology of severe community-onset *Acinetobacter baumannii* infection. *Microb Genom* **2019**. doi: 10.1099/mgen.0.000258
86. O'Grady K, Krause V. An outbreak of salmonellosis linked to a marine turtle. *The Northern Territory Disease Control Bulletin* **1998**, 5, 1-5. doi: 10.1080/14467659808838888

87. Wallace P, Kirk MD, Munnoch SA, et al. An outbreak of *Salmonella* Litchfield on a car rally, Northern Territory, 2009. *Commun Dis Intell Q Rep* **2010**, 34, 124-6. doi:
88. Williams S, Patel M, Markey P, et al. *Salmonella* in the tropical household environment--Everyday, everywhere. *J Infect* **2015**, 71, 642-8. doi: 10.1016/j.jinf.2015.09.011
89. Ford L, Glass K, Veitch M, et al. Increasing Incidence of *Salmonella* in Australia, 2000-2013. *PLoS One* **2016**, 11, e0163989. doi: 10.1371/journal.pone.0163989
90. Draper AD, Morton CN, Heath JN, et al. An outbreak of salmonellosis associated with duck prosciutto at a Northern Territory restaurant. *Commun Dis Intell Q Rep* **2017**, 41, E16-E20. doi:
91. Hamilton NJ, Draper ADK, Baird R, et al. Invasive salmonellosis in paediatric patients in the Northern Territory, Australia, 2005-2015. *J Paediatr Child Health* **2021**. doi: 10.1111/jpc.15473
92. Draper A, Markey P. *Shigella flexneri* 2b in the Northern Territory in 2017. *The Northern Territory Disease Control Bulletin* **2017**, 24, 1-9. doi:
93. Guglielmino CJD, Kakkanat A, Forde BM, et al. Outbreak of multi-drug-resistant (MDR) *Shigella flexneri* in northern Australia due to an endemic regional clone acquiring an IncFII plasmid. *Eur J Clin Microbiol Infect Dis* **2021**, 40, 279-86. doi: 10.1007/s10096-020-04029-w
94. Silver BJ, Guy RJ, Wand H, et al. Incidence of curable sexually transmissible infections among adolescents and young adults in remote Australian Aboriginal communities: analysis of longitudinal clinical service data. *Sex Transm Infect* **2015**, 91, 135-41. doi: 10.1136/sextrans-2014-051617
95. Whiley DM, Trembizki E, Buckley C, et al. Molecular Antimicrobial Resistance Surveillance for *Neisseria gonorrhoeae*, Northern Territory, Australia. *Emerg Infect Dis* **2017**, 23, 1478-85. doi: 10.3201/eid2309.170427
96. Nogrady B. Sixth child dies from congenital syphilis in northern Australia. *BMJ* **2018**, 360, k1272. doi: 10.1136/bmj.k1272
97. Beale MA, Marks M, Sahi SK, et al. Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. *Nat Commun* **2019**, 10, 3255. doi: 10.1038/s41467-019-11216-7
98. Chen W, Smajs D, Hu Y, et al. Analysis of *Treponema pallidum* strains from China using improved methods for whole-genome sequencing from primary syphilis chancres. *J Infect Dis* **2021**, 223, 848-53. doi: 10.1093/infdis/jiaa449
99. Taouk ML, Taiaroa G, Pasricha S, et al. Characterisation of *Treponema pallidum* lineages within the contemporary syphilis outbreak in Australia: a genomic epidemiological analysis. *Lancet Microbe* **2022**, 3, e417-e26. doi: 10.1016/S2666-5247(22)00035-0
100. Cowling CS, Liu BC, Snelling TL, et al. Australian trachoma surveillance annual report, 2013. *Commun Dis Intell Q Rep* **2016**, 40, E255-66. doi:
101. Andersson P, Harris SR, Smith H, et al. *Chlamydia trachomatis* from Australian Aboriginal people with trachoma are polyphyletic composed of multiple distinctive lineages. *Nat Commun* **2016**, 7, 10688. doi: 10.1038/ncomms10688
102. Blumberg BS, Alter HJ, Visnich S. A "New" antigen in leukemia sera. *JAMA* **1965**, 191, 541-6. doi: 10.1001/jama.1965.03080070025007
103. Alter HJ, Blumberg BS. Further studies on a "new" human isoprecipitin system (Australia antigen). *Blood* **1966**, 27, 297-309. doi:
104. Davies J, Littlejohn M, Locarnini SA, et al. Molecular epidemiology of hepatitis B in the Indigenous people of northern Australia. *J Gastroenterol Hepatol* **2013**, 28, 1234-41. doi: 10.1111/jgh.12177
105. Littlejohn M, Davies J, Yuen L, et al. Molecular virology of hepatitis B virus, sub-genotype C4 in northern Australian Indigenous populations. *J Med Virol* **2014**, 86, 695-706. doi: 10.1002/jmv.23888
106. Davies J, Li SQ, Tong SY, et al. Establishing contemporary trends in hepatitis B sero-epidemiology in an Indigenous population. *PLoS One* **2017**, 12, e0184082. doi: 10.1371/journal.pone.0184082
107. Cheah BC, Davies J, Singh GR, et al. Sub-optimal protection against past hepatitis B virus infection where subtype mismatch exists between vaccine and circulating viral genotype in northern Australia. *Vaccine* **2018**, 36, 3533-40. doi: 10.1016/j.vaccine.2018.01.062
108. Yuen LKW, Littlejohn M, Duchene S, et al. Tracing ancient human migrations into Sahul using hepatitis B virus genomes. *Mol Biol Evol* **2019**, 36, 942-54. doi: 10.1093/molbev/msz021
109. Cassar O, Einsiedel L, Afonso PV, et al. Human T-cell lymphotropic virus type 1 subtype C molecular variants among indigenous australians: new insights into the molecular epidemiology of HTLV-1 in Australo-Melanesia. *PLoS Negl Trop Dis* **2013**, 7, e2418. doi: 10.1371/journal.pntd.0002418
110. Grivas R, Freeman K, Baird R. Human T-lymphotropic virus-1 serology in the Northern Territory: 2008-2011. *Pathology* **2014**, 46, 644-8. doi: 10.1097/PAT.0000000000000164
111. Einsiedel L, Pham H, Talukder MRR, et al. Pulmonary disease is associated with human T-cell leukemia virus type 1c infection: a cross-sectional survey in remote Aboriginal communities. *Clin Infect Dis* **2021**, 73, e1498-e506. doi: 10.1093/cid/ciaa1401