8th Southern Cross Travel and Tropical Medicine Conference

12-14 September 2025

ABSTRACT BOOK

Table of Contents

Free Communications (Oral presentations) 2

Poster presentations 12

Free Communications (Oral presentations)

The first Dengue outbreak in a *Wolbachia* established setting

Scott Lyons, Kyra Thompson, Mikaela Seymour, Kate Murton, Katherine Malone, Jesse Fryk

Background: Dengue is an acute febrile flavivirus which has caused historical outbreak in North Queensland. The Wolbachia program was launched in the Townsville region in 2011, which led to a rapid reduction in dengue notifications. Between 2020-2024 there was no identified local transmission of dengue in Townsville. This outbreak report presents the first locally transmitted dengue outbreak since widespread establishment of Wolbachia in Townsville.

Method and results: In January 2025 the Townsville Public Health Unit (TPHU) was notified of two cases of dengue with no associated domestic or international travel in their exposure period. The cases' homes were within 500m of each other. An outbreak was declared and a public health response initiated. Outbreak case definitions were in line with the Communicable Disease Network of Australia guidelines. A total of 16 cases were associated with this outbreak, 12 confirmed and 4 probable. This report will present an epidemiological curve of cases, demonstrating effectiveness of indoor residual spraying interventions, and Geo mapping of cases and intervention locations. It will also provide descriptive data on case demographics, including hospitalisation status. Dengue genetic typing will also be presented, demonstrating this was an outbreak of the same strain.

Conclusions: Since the widespread dissemination of Wolbachia, dengue control efforts and community public health messaging have been significantly defunded and deprioritised. This outbreak report raises potential questions regarding the long-term effectiveness of Wolbachia. These authors believe it represents the new normal since the resumption of international travel post COVID19 and believe it supports ongoing advocacy for dengue control, even in Wolbachia penetrant areas.

Can serosurveillance provide early warning of vaccine preventable disease outbreaks: measles seroprevalence before and after a national outbreak in Samoa

Harriet Lawford, Helen Mayfield, Filipina Amosa-Lei Sam, Satupaitea Viali, Tito Kamu, Robert Thomsen, Stefanie Vaccher, Fiona Angrisano, Leanne Robinson, Colleen Lau

Background: Serosurveillance of vaccine preventable diseases (VPDs) is the gold standard for assessing population immunity. In October 2019, a measles outbreak in Samoa caused >5700 cases and 83 deaths, prompting nationwide mandatory vaccination targeting those aged 6 months-19 years and non-pregnant women 20-35 years. In 2018 in Samoa, measles vaccination coverage was 41% in ≤1-year-olds, well below the target of 95% to minimise the risk of outbreaks. This study aimed to assess the utility of serosurveillance to provide early warning of VPD outbreaks.

Methods: Longitudinal serosurveys of community members aged ≥5 years took place in the same 8 villages in Samoa in 2018, 2019 and 2023. Multiplex bead assays were used to detect antibodies to measles (Mev Ab+) and other diseases. Logistic regression was used to estimate associations between Mev Ab+ and year, age and sex. Seroprevalence by age and year was estimated using post-estimation margins.

Results: 3384 participants were included (881 in 2018; 1022 in 2019; 1034 in 2023). Year (χ^2=157.0; p<0.001) and age (χ^2=96.3; p<0.001) were strong predictors of Mev Ab+. 375 (43.3%; 95% Confidence Interval: 40.0-

46.6%) participants were Mev Ab+ in 2018, 447 (46.0%; 42.9-49.1%) in 2019 and 971 (97.4%; 96.2-98.2%) in 2023. From 2018-2023, predicted prevalence increased significantly ($p<0.001$) among 5-35-year-olds from 34.0% (30.5-37.6%) in 2018 to 96.6% (95.1-98.0%) in 2023; and among ≥36-year-olds from 77.8% (71.7-83.8%) in 2018 to 99.7% (99.1-100.0%) in 2023. By 2023, the only age group with Mev Ab+ below 95% was 20-29-year-olds (94.5%; 89.4-97.2%).

Conclusions: The increase in Mev Ab+ from pre- to post-outbreak, especially among 5-35-year-olds, reflects the substantial increase in population immunity from both infection and vaccination. These findings demonstrate the utility of serosurveys to provide early warning of potential outbreaks of VPDs by identifying immunity gaps that can inform national vaccination strategies and catch-up campaigns targeting subgroups with low immunity.

Combining Forces: Integrating Infectious Disease and NCD Surveillance in Niue's National STEPS Survey

Adam Craig, Harriet Lawford, Grizelda Mokoia, Tonia Marquardt, Colleen Lau

Background: This study explored the feasibility and cost-efficiency of integrating infectious disease (ID) and non-communicable disease (NCD) surveillance in Niue—a small Pacific Island developing state. The integrated approach aimed to overcome resource constraints, validate the elimination of lymphatic filariasis, and assess population immunity for 15 priority vaccine-preventable, vector-borne, and neglected tropical diseases.

Methods: Data were collected through qualitative interviews, direct observation, and cost analysis. The Consolidated Framework for Implementation Science guided thematic analysis.

Results: Successful integration hinged on early and consistent collaboration between Niue's health authorities, who led the NCD survey, and the ID serosurveillance team. This fostered trust and mutual understanding. In the context of high transactional costs and limited capacity, flexibility and respect for local workflows were key. The ID team's practical support—particularly in staffing blood collection points—strengthened the partnership and demonstrated added value. Integration was recognised as a more efficient alternative to conducting separate, parallel surveys in the future.

Despite initial concerns about workflow disruption, issues were resolved collaboratively, and the integrated approach was ultimately seen as both holistic and beneficial. Collecting ID and NCD data at the individual level enabled richer analysis and reduced the burden on communities. Cost savings were achieved through improved process efficiencies and the elimination of duplicated fieldwork.

Conclusion: This is the first documented example of integrated ID-NCD surveillance in the Pacific—and potentially globally. It provides timely, practical insights into what makes integration work in small island settings. As countries seek more efficient, people-centred approaches to public health surveillance, this study offers a compelling model. Its findings will inform national practices and contribute to evolving WHO guidance on integrated surveillance.

Integrated serosurveillance and spatial epidemiology of vaccine preventable diseases and lymphatic filariasis in Samoa, 2018-2019

Selina Ward, Harriet Lawford, Benn Sartorius, Helen Mayfield, Filipina Amosa-Lei Sam, Tito Kamu, Sarah Sheridan, Patricia Graves, Robert Thomsen, Satupaitea Viali, Colleen Lau

Background: Serosurveillance measures population-level prevalence of antibodies to identify burden of current and/or past infections (or immunisation) and immunity gaps to vaccine preventable diseases (VPDs). Integrating surveillance of multiple infectious diseases (ID), as opposed to a siloed approach, can highlight health disparities and immunity gaps to enable targeted public health intervention. Inclusion of lymphatic filariasis (LF) is particularly relevant given ongoing global elimination efforts. This study examined seroprevalence and spatial clustering of select VPDs and LF in Samoa from 2018-2019.

Methods: Dried blood spots (DBS) were collected from two nationally representative community surveys in 2018-2019. Multiplex bead assays (MBA) were used to detect antibodies (Ab) for diphtheria, measles, rubella, tetanus and LF (Bm14 and Wb123). Seroprevalence estimates were adjusted for study design, age, and sex. Spatial cluster analysis was conducted using SatScan.

Results: Of 8849 participants (2018 in 4419; 2019 in 4909), 8394 (94.8%; mean age±SD: 19.9±19.2years) had valid MBA results. Seropositivity to measles, rubella, diphtheria and tetanus were 46.9% (95%CI:45.8-48.0), 79.8% (95%CI:78.8-80.9), 83.1% (95%CI:82.1-84.1) and 90.7% (95%CI:89.9-91.4), respectively. 106 people (1.2%; mean age 11.4±7.6years) were seronegative to all VPDs. For LF in 2019, seroprevalence was 22.7% for Bm14 Ab and 50.3% for Wb123 Ab. Spatial clustering ($p<0.05$) was found for seronegativity to measles, and seropositivity to Bm14.

Conclusions: Substantial immunity gaps to VPDs were identified, including clustering of those seronegative to measles. The surveys were conducted prior to the large measles outbreak in 2019, highlighting the potential of serosurveys to provide early warning of outbreaks, and guide targeted vaccination campaigns. Prevalence of LF Ab can provide valuable insights for monitoring and evaluation of elimination programs. Integrated serosurveillance is both cost-efficient and highly efficient, ideal for low resource settings. Furthermore, recognizing spatial patterns of IDs can enable design of integrated interventions for at-risk communities.

Insights from Integrated Serosurveillance for Measles, Rubella, Tetanus, and Diphtheria in Vanuatu

Mohamad Assoum, Dorothy Machalek, Elizabeth Nguyen, Arunasingam Abayasingam, Prudence Rymil, Mackline Katenga, Stephanie Tabe, Eithandee Aung, Fernando Santiago, Gladymar P Chacon, Claire Dyer, David Kennedy, Md Islam, Julie Jacobson, John Kaldor, Susana Vaz Nery

Background: Monitoring population-level immunity to vaccine-preventable diseases (VPDs) is essential for evaluating immunisation programme impact. This study assessed seroprevalence of measles, rubella, tetanus, and diphtheria in Tafea, Sanma, and Shefa provinces in Vanuatu and compared findings with WHO-reported vaccination coverage.

Methods: The Vanuatu Ministry of Health, with support from the PINE Project conducted Integrated serological surveys between 2021 and 2023 alongside mass drug administration campaigns. Dried blood spots were collected from participants across the three provinces and analysed using a multiplex bead assay. Cluster adjusted seroprevalence estimates for anti-MeV (measles), anti-RuV (rubella), anti-TetTox (tetanus), and anti-DipTox (diphtheria) antibodies were calculated per province and stratified by age and sex. Results were compared with WHO/UNICEF Estimates of National Immunisation Coverage (WUENIC) for the corresponding years.

Results: Measles seroprevalence among children aged 1–14 years ranged from 39.5% in Tafea to 50.9% in Shefa, generally below the WHO-estimated vaccination coverage of 50%–70%. Rubella seropositivity was higher, ranging from 70.4% to 90.3% across the provinces, consistently exceeding reported coverage levels. Tetanus antibody prevalence ranged from 69.6% in Tafea to 94.4% in Shefa, with levels increasing by age and aligning well with WHO DTP3 coverage data. Diphtheria seroprevalence in children aged 1–14 ranged from 52.7% in Tafea to 79.3% in Sanma, with general agreement between seroprevalence and coverage data in Sanma and Shefa.

Conclusion: Serological data revealed disparities in population immunity across provinces and antigens. While rubella and tetanus showed high immunity levels, gaps in measles and diphtheria seroprevalence, especially among young children require further investigation and interpretation in the context of case and immunisation data.

The importance of measles vaccination prior to travel

Janet Strachan, Miriam O'Hara, Annelise Plummer, Ellie Robinson, Fiona Moran, Mihaela Ivan, Min-Ho Jung, Catherine Radkowski*

Background: Australia was declared to have eliminated endemic measles by the World Health Organization in 2014 with nearly all cases since then being imported or import related. Interruptions to global childhood immunisation programs due to COVID-19 restrictions and post-pandemic vaccine hesitancy have led to an increase in vaccine-preventable diseases including measles in many countries. In 2025, although most Victorian cases occur among overseas travelers, there has been an increase in locally-acquired cases where the source is unknown.

Methods: We descriptively analysed public health surveillance data from all confirmed measles cases notified in Victoria from 1 January to 30 April 2025.

Results: From 1 January – 30 April 2025, 25 confirmed measles cases were notified in Victoria. Cases were aged from 6 months to 60 years old. Ten cases were admitted to hospital. Thirteen cases were acquired in countries with high measles incidence; eight in Vietnam, three in Indonesia and two in Pakistan. Four overseas-acquired cases were unvaccinated infants aged 6-11 months. The other nine cases were aged 20-60 years, with two-thirds (6/9) either being unvaccinated or unsure of their vaccination status. There were 10 locally-acquired measles cases in Victoria with an unknown source and two with known sources. Preliminary genomic analysis indicated these cases formed three clusters. Comparison with international sequencing databases found the strains matched viruses recently seen overseas. Follow-up of the 25 measles cases required extensive contact tracing across a large number of exposure sites and placed significant demands on public health and healthcare services.

Conclusions: Travel-related measles cases pose a threat to Australia’s measles elimination status. The majority of Victorian overseas-acquired cases in 2025, were eligible for free measles vaccination.

**Presenter: Sophie Wilson*

Once bitten, twice shy: an unusual case of dual malaria infection with Plasmodium falciparum and Plasmodium ovale

Tara Grayson, Maxwell Braddick, Thomas Brasher, Eugene Athan

Background: Malaria is a vector-transmitted parasite that infects 249 million people annually. Co-infection of Plasmodium falciparum and P. vivax is well-documented; however, co-infection with other malaria species is rarely described. Notably dual infection with *P. falciparum* and *P. ovale* presents a diagnostic challenge due to its hypnozoite stage and additional therapies required to achieve parasite clearance.

Methods: We report a 67-year-old gentleman with a past medical history of type two diabetes mellitus, chronic plaque psoriasis and previously treated latent tuberculosis. He was first diagnosed with malaria following travel to South Sudan in 2023. Thick and thin (T&T) blood films were positive for *P. falciparum* (parasite count 0.10%) and malaria PCR detected *P. falciparum* alone with a CT (cycle threshold) of 22. He was treated with a six-dose course of artemether/lumefantrine 20/120mg (per local guidelines). He did not travel overseas again.

Results: Six months later he presented febrile (38.70C) with acute confusion post-cataract repair. He had lymphopaenia (0.9x109/L) and a CRP of 53.5mg/L. Cerebrospinal fluid was normal, except for a glucose of 9.0mmol/L, and culture was negative. T&T blood films revealed trophozoites, schizonts and gametocytes resembling P. ovale (parasite count 0.05%) and malaria PCR detected *P. ovale* (CT 24). He was managed with six doses of artemether/lumefantrine 20/120mg and 14 days of primaquine 30mg daily, following exclusion of G6PD deficiency - with clearance confirmation six weeks later by T&T blood films. Cognition improved to baseline with treatment.

Conclusions: We report an unusual case of dual infection with *P. falciparum* and *P. ovale*. For potential *P. ovale* infection, the absence of recent travel or negative PCR testing should not deter clinicians from considering co-infection, given the parasite's hypnozoite stage. Presumptive anti-relapse therapy should be considered for patients with *P. falciparum* malaria who have visited *P. ovale* endemic regions.

Comparison between initial clinical and laboratory profiles between dengue fever and dengue hemorrhagic fever in patients presenting at a university hospital in Suburban Bangkok: A ten-year analysis

Thanabadee Kulveeraaree, Soravit Thummawatwimon, Anchalee Khanijou, Sakarn Charoensakulchai, Manasvin Onwan

Background: Dengue fever (DF) is a mosquito-borne viral infection endemic to countries like Thailand and increasingly prevalent worldwide. Its severe form, dengue hemorrhagic fever (DHF), characterized by plasma leakage and abnormal bleeding, has cost detrimental burden on global healthcare due to its serious complications related to multi-organ failure. Most patients present during the febrile stage, making early prediction of disease severity a clinical challenge. This study aimed to compare clinical and laboratory profiles at presentation between DF and DHF cases to support early severity prediction.

Methods: A retrospective cross-sectional study was conducted at H.R.H. Princess Maha Chakri Sirindhorn Medical Center, Nakhon-Nayok, Thailand, from 2014 to 2023. A total of 706 patients diagnosed with dengue infection were reviewed. Data were collected using a standardized case report form (CRF), including initial clinical and laboratory features. Cases were classified using the WHO 1997 criteria. Chi-square and independent t-tests were used for analysis.

Results: A total of 658 DF and 48 DHF cases were identified. Chills ($p<0.01$), myalgia ($p<0.01$), impaired consciousness ($p<0.01$), fatigue ($p=0.02$), and headache ($p=0.03$) were more common in DHF than DF significantly. Signs such as hepatomegaly ($p<0.01$), petechiae ($p<0.01$), and severe bleeding (epistaxis, gum bleeding, hematemesis, and melena; $p<0.01$) were more common in DHF than DF significantly. Laboratory results showed higher mean hematocrit levels in DHF than DF (44.24%±5.36% and 40.47%±4.06%; $p<0.01$). DHF had lower mean platelet counts than DF (78,512±53,362 cells/mm^3 vs. 167,312±71,986 cells/mm^3; $p<0.01$).

Conclusions: Specific clinical signs and laboratory markers—particularly hematocrit and platelet counts—can help distinguish DHF from DF at presentation. These findings may support earlier identification and improved management of severe dengue. Further multicenter studies and diagnostic performance analyses are recommended to validate these indicators.

Impact of Temperature on Dengue Virus Transmission by Aedes aegypti in New Caledonia

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Background: Dengue virus (DENV) is a major public health concern in tropical and subtropical regions, with transmission dynamics strongly influenced by environmental factors. Temperature is recognized as a major driver of transmission by mosquito vectors. In the Pacific region, where the impact of climate change is increasingly noticeable, understanding how rising temperatures may alter transmission is essential to better anticipate future dengue risk and disease burdens.

Methods: This study aimed to evaluate how temperature variations influence the transmission potential of DENV by Aedes aegypti mosquitoes from New Caledonia. Mosquitoes were orally exposed to infectious blood meals containing two different DENV titres (1.10^5 and 1.10^7 FFU/mL) and incubated under constant (26.6°C, 28.1°C, 29.6°C, and 31.1°C). Mosquitoes were collected at several time points post-infection (3, 5, 7, 10, and 14 days) and analysed by immunofluorescence to determine DENV presence in their bodies, heads, and saliva. Viral titres in bodies and heads of mosquitoes exposed to an infectious blood meal at 1.107FFU/mL was determined.

Results: Preliminary analyses demonstrated that infection rates were higher at 28.1°C, regardless of the viral blood meal titre used. In contrast, significantly higher viral titres were observed in the bodies and heads of mosquitoes held at 31.1°C compared to 26.6°C (bodies: $p=0.0063$; heads: $p=0.0091$). We were unable to test if this increase could also be observed for saliva.

Conclusions: Although high temperatures do not promote infection rates, they do appear to increase the viral replication in infected Ae. aegypti mosquitoes. These results highlight the importance of studying the effects of temperature on DENV transmission in the vector in a context of climate change.

Mapping Arboviral Risk in Brazil: Targeting High-Risk Tourist Areas for Dengue, Chikungunya, and Yellow Fever

Sebastian Vernal Carranza, Eloise Skinner, Beatris Martin, Benn Sartorius, Luis Furuya-Kanamori

Background: Brazil is a popular travel destination, attracting >6.6M visitors in 2024 alone. At the same time, the country faces recurrent outbreaks of arboviral diseases —including dengue, chikungunya, and yellow fever (YF)— posing risks to both local populations and international travellers. Our study aimed to identify areas of high arboviral infection risk and develop a user-friendly mapping interface to inform travel health recommendations.

Methods: We conducted a retrospective analysis of laboratory-confirmed arboviral cases and deaths reported to Brazil's national notification system from 2019-2024 (2015-2023 for YF), aggregated by 133 intermediate regions (IR). Incidence rates were calculated per 100,000. To identify high-risk areas, we first considered whether transmission of each arbovirus was endemic within an IR (>10 cases/month), then scored annual case counts within each IR into quartiles based on national data. These scores were summed over the study period to estimate cumulative risk. For YF, we overlaid vaccination coverage data; for dengue, we mapped the recent distribution of the TAK-003 vaccine. Spatiotemporal maps were generated and incorporated into a user-friendly interface.

Results: We analysed 4.3M dengue, 707K chikungunya, and 2.3K YF cases, with 7.7K, 589, and 787 deaths, respectively. Dengue risk was widespread (100% IRs), but the highest risk was concentrated in the Midwest, coinciding with prominent tourist destinations such as the Pantanal. Chikungunya risk was also widespread (93.9% IRs), but the highest risk was in areas in the Northeast, where popular beaches such as Recife are found. YF risk was not widespread (16.5% IRs), was particularly high around the Southeast (16.5% of IR), especially São Paulo, a hub for business travel.

Conclusions: This spatially integrated approach provides a novel decision-support tool for travel medicine. By using an intuitive map to map arboviral risk in tourist-frequented areas, healthcare providers can tailor preventive advice and immunisation recommendations.

Challenges and opportunities for post-validation surveillance of lymphatic filariasis in Tonga, 2024: a qualitative study

Holly Jian, Harriet Lawford, Adam Craig, Angus McLure, Ofa Tukia, Joseph Takai, Colleen Lau

Background: Tonga was validated by the World Health Organization (WHO) as having eliminated lymphatic filariasis (LF) as a public health problem in 2017. Following validation, WHO recommends conducting post-validation surveillance (PVS) to monitor for LF recrudescence. However, no PVS was implemented in Tonga until 2024. A targeted survey identified persisting LF transmission in 2024, indicating the need for ongoing PVS. To be sustainable, PVS must be tailored for Tonga's capacity and context. This study aimed to identify challenges and opportunities for the implementation of PVS in Tonga.

Methods: We conducted semi-structured key informant interviews with 13 Tonga Ministry of Health staff who worked on the 2024 PVS survey. Interview questions and thematic data analysis were guided by the Consolidated Framework for Implementation Research, and examined systemic, organisational, and operational factors affecting PVS implementation.

Results: Systemic challenges to implementing PVS in Tonga included low awareness of LF's public health risks. Additionally, ongoing impacts of misinformation during the COVID-19 pandemic led to some 2024 PVS survey participants being reluctant to be tested for LF, due to misunderstanding that they were being vaccinated. Organisational challenges included limited awareness of the requirement for PVS among decision-makers, workforce limitations and reliance on external funding and technical support. Opportunities included potential integration of LF surveillance with existing programs, such as the WHO STEPwise approach to NCD risk factor surveillance (STEPS) survey. Operational factors included logistical challenges in reaching remote populations, while opportunities exist in leveraging local knowledge and well-established stakeholder networks.

Conclusions: To be feasible, LF PVS must be designed for Tonga's unique systemic, organisational and operational context. Sustainable PVS will require effective streamlining of domestic resources, including through integration of LF surveillance with existing health programs. PVS initiatives should be driven by national health authorities to effectively leverage local knowledge and long-standing stakeholder partnerships.

Comparing Human and Vector-Based Indicators of Lymphatic Filariasis Transmission in Samoa: Results from 2023–2024

Helen Mayfield, Angus McLure, Brady McPherson, Benn Sartorius, Donna McKenzie, Lisa Rigby, Patricia Graves, Robert Thomsen, Satupaitea Viali, Colleen Lau

Background: Effective surveillance is essential for supporting disease elimination efforts. For vector-borne diseases such as lymphatic filariasis (LF), surveillance can target infection markers in humans — such as antigen (Ag) or microfilariae (Mf) — or in mosquitoes by testing for pathogen DNA. This study aimed to compare the impact of the 2023 triple-drug (ivermectin diethylcarbamazine, albendazole) mass drug administration (MDA) in Samoa on Ag, Mf, and molecular xenomonitoring (MX) indicators.

Methods: We surveyed up to 25 randomly selected households in each of eight primary sampling units in Samoa in March 2023 (6 months pre-MDA) and August 2024 (11 months post-MDA). Finger-prick blood samples were collected from community members aged ≥5 years and tested for Ag and Mf. Prevalence was calculated (adjusted for age and sex). For MX, traps were placed at 15 households per village for 48 hours. Female mosquitos were sorted by species, pooled and tested for filarial DNA using PCR, and prevalence of PCR-positive mosquitoes was estimated using the PoolTestR software.

Results: We obtained Ag and Mf results for 623 and 1075 participants, and tested 4,798 and 3,196 female Aedes mosquitos (438 and 305 pools) in 2023 and 2024, respectively. There was no significant decline in human prevalence from 2023 to 2024 for Ag (9.9% to 9.0%, OR 0.79, 95% CI:0.52-1.22) or Mf (5.1% to 2.7%, OR 0.63, 95% CI:0.30-1.32). In contrast, prevalence of filarial DNA in Aedes mosquitos was significantly lower in 2024 compared to 2023 (OR: 0.42; 95% CrI: 0.24-0.69).

Conclusion: These findings support growing evidence that mosquito-based indicators may respond sooner to changes in LF transmission following MDA compared to Ag and Mf. This highlights the potential of MX to provide critical early indications of changes in LF transmission levels and complement human-based monitoring and surveillance for supporting elimination efforts, including evaluating the impact of MDA.

Eye spy with my little eye: has Australia eliminated trachoma as a public health problem?

Alison Jaworski, Carleigh Cowling, Sergio Sandler, Absar Noorul, Susana Vaz Nery, John Kaldor

Background: Trachoma is the world's leading infectious cause of preventable blindness. Australia remains the only high-income country with endemic trachoma, found in remote First Nations communities in western and central jurisdictions. In 2022 Australia reached World Health Organization (WHO) benchmarks for elimination as a public health problem (EPHP): trachomatous inflammation-follicular (active trachoma) prevalence <5% in children and trichiasis (severe advanced disease) prevalence 'unknown to the health system' <0.2% in adults, within formerly endemic jurisdictions. 2024 was the final year of monitoring against these benchmarks, before being eligible to apply for EPHP validation.

Methods: WHO grading criteria was used to classify trachoma in children aged 5–9 years by trained graders. Trichiasis rates are derived from public health surveillance, visiting optometry services, and Adult Health assessments (715 checks). Jurisdictions also submit data on implementation of the SAFE strategy for trachoma control: Surgery to correct trichiasis, Antibiotics to treat infection, Facial cleanliness and Environmental improvements to reduce transmission and prevent reinfection.

Results: In 2024, 86 at-risk communities were screened for trachoma. Overall trachoma prevalence was 2.1% in the Northern Territory, 1.3% in Western Australia and 0% in South Australia. Several communities still report hyper-endemic trachoma (>20% prevalence). In total, 1,674 doses of antibiotics were administered in 25 communities to treat active infection. Trichiasis in screened persons aged 15+ years was 0.04%, with six surgical interventions.

Conclusions: Australia has met criteria for EPHP validation; however, systemic efforts are needed to prevent recrudescence. Ownership by and accountability to First Nations people must underpin post-EPHP strategies developed. Surveillance and control will need to be maintained in at-risk communities and may include the use of biomarker assessments in partnership with ACCHOs and primary care. Focusing on improving social and environmental determinants of health, changing focus from "SAFE" to "EFAS", will be critical to maintaining elimination status.

Opening a can of worms: A qualitative study on the feasibility and acceptability of One Health approaches to Soil-Transmitted Helminthiases (STHs) in rural Northern Australia

Anna Duan, Yvonne Cadet James, Frank Mills, Maxine Whittaker

Background: NTDs such as soil-transmitted helminthiases (STHs), disproportionately affect remote Aboriginal and Torres Strait Islander communities in Northern Australia. Despite their impact, STHs remain underprioritized in public health policy. One Health (OH) is a transdisciplinary approach that recognizes the interconnected health of people, animals, and environments. Although applied internationally, the feasibility and acceptability of OH strategies for STH control in Australia remain unexplored.

Methods: This qualitative study used semi-structured interviews with eleven key informants, spanning human, animal, and environmental health sectors in regional/rural/remote Far North Queensland across Townsville, Cairns and surrounding regions including Torres Strait Islands and Weipa. A modified Health Beliefs Model approach was used, with guidance and consultation with an Aboriginal and Torres Strait Islander advisory committee. Qualitative thematic analysis was undertaken through a mixture of inductive and deductive approaches.

Results: Participants acknowledged STHs as underrecognized due to their asymptomatic nature and limited public awareness. While OH was seen as valuable for addressing underlying social determinants of health, significant barriers emerged, including professional silos, unclear roles, limited intersectoral communication, and funding constraints. Community trust and buy-in, cultural considerations (pet ownership as part of Indigenous identity), and workforce transience impacted feasibility and continuity of OH approaches. Despite these challenges, practitioners in remote areas highlighted existing informal cross-disciplinary collaboration and emphasized the need for community ownership and sustained engagement. Education, policy support, and integration into undergraduate health curricula were seen as vital enablers of OH uptake.

Conclusion: STHs in remote Australian communities are a case study in neglect that could benefit from a OH approach. While conceptually supported by stakeholders, operationalizing OH requires structural change, targeted education, funding, and culturally grounded strategies. Successful OH implementation depends not only on interprofessional collaboration but also on empowering communities to co-lead health initiatives, addressing both biomedical and socio-cultural determinants of health.

Geostatistical analysis of national soil-transmitted helminth surveys in Timor-Leste 2012-2021

Adam Bartlett, Luzia Freitas, Rita Alves, Angela Cadavid Restrepo, Peter McMinn, Jose Liu Fernandes, Susana Vaz Nery

Background: Soil-transmitted helminth (STH) control in Timor-Leste has been integrated with lymphatic filariasis control, involving albendazole and diethylcarbamazine preventive chemotherapy in 2005-2008, then 2015-2018, adding ivermectin in 2019. To track STH endemicity, the Ministry of Health conducted school surveys in 2012, 2015, 2017, 2019 and 2021, revealing variable prevalence across municipalities. Here we report geostatistical analyses of the surveys to better define the spatial distribution of STHs.

Methods: Parasitological data from surveys conducted 2012-2021 were linked with environmental and climatic data to develop risk prediction models from each survey. Final models were selected through non-spatial multivariable regression with the lowest akaike information criteria and all variables with a variance influence factor <10. Residual spatial autocorrelation was investigated using semivariograms, and if present, models were fitted with the Matérn covariance. Risk prediction maps were then developed using the final non-spatial or spatial models.

Results: Overall STH prevalence was 28.9% (from 2,198 schoolchildren, 30 schools, 13 municipalities; school range 1.8–81.3%) in 2012, 11.9% (658 schoolchildren, 11 schools, 6 municipalities; range 0–34.4%) in 2015, 10.8% (1,408 schoolchildren, 28 schools, 13 municipalities; range 0–14.0%) in 2017, 24.3% (1,121 schoolchildren, 6 schools, 3 municipalities; range 1.5–49.2%) in 2019, and 28.4% (1,121 schoolchildren, 6 school, 3 municipalities; range 7.6–47.3%) in 2021. Geographic representation varied across surveys and was limited in 2019 and 2021. Risk prediction maps for each survey year suggest different higher risk areas when considering only the year data; with higher risk in southern areas in 2012; in the north and centre of the country in 2015; and in northwestern, southwestern and northeastern corners in 2019 and 2021.

Conclusion: This series of geostatistical analyses suggest different locations of higher STH infection risk across years. Future work to optimise predictive models to guide control strategies and monitoring activities is required.

Poster presentations

Risky Encounters Abroad: Attitude and Behaviour Towards Sexually Transmissible Infections Among Australian Travellers

Wondimeneh Shiferaw, Deborah Mills, Kenneth Koh, Judith A Dean, Stanley Khoo, Michael Tooth, Jenny Visser, David Rutherford, Colleen Lau, Luis Furuya-Kanamori

Background: Changes in travellers' sexual behaviours, driven by opportunities during travel, contribute significantly to the acquisition of sexually transmissible infections (STIs). However, research on travellers' risk perception, intentions regarding new sexual partners, and adherence to STI prevention measures remains limited. This study aims to evaluate the risk-perceptions, attitudes, and sexual behaviours among Australian travellers attending pre-travel consultations.

Methods: A cross-sectional online survey, conducted from July 2023 to September 2024, recruited people (aged ≥18 years and planning to travel overseas within six months) from five Travel Medicine Alliance (TMA) clinics and a sexual health clinic in Australia. Analysis focused on participants travelling without partners to assess intentions regarding new sexual partnerships. Subgroup analyses explored variations in socio-demographics and behaviour by clinic type.

Results: Of the 205 respondents, 172 (83.9%) were from TMA clinics, and 33 (16.1%) from a sexual health clinic. Among these, 51% (n=105) were female, with a mean age of 42.5 ± 16 years. Twenty-nine (22.7%) intended to engage in sexual activity with new partners while travelling (21 [18.6%] from TMA clinics; 8 [53.3%] from the sexual health clinic). Among these, 21 of 29 (72.4%) perceived their risk of contracting STIs as low despite reporting intention to engage in risk-related behaviours, e.g. 7 of 25 (28.0%) reported no intention to use condoms and 7 of 29 (24.1%) intention to engage with sex workers. Post travel, 9 of 26 (34.6%) reported no plans for STI testing. Nearly half (12 of 29, 41.4%), identified a need for better STI-related pre-travel information, highlighting gaps in awareness.

Conclusions: A significant proportion of travellers planning new sexual encounters during travel underestimated their STI risk and demonstrated little intention of using preventive practices. These findings underscore the importance of integrating comprehensive sexual health counselling into pre-travel consultations to address knowledge gaps and mitigate STI risks.

Forced Migration and Mortality: Health Disparities Among Venezuelan Migrants in Peru and Colombia from 2017 to 2021

Liuyi Chen-Cao, Angela Cadavid Restrepo, Miguel Cabada, Kasim Allel, Wondimeneh Shiferaw, Deborah Mills, Colleen Lau, Luis Furuya-Kanamori

Background: Venezuela's political and socio-economic crisis has precipitated one of South America's largest population displacements, with over 7.7 million Venezuelans fleeing their country. This study aimed to compare mortality patterns among international travellers in Colombia and Peru, which host the largest number of Venezuelan migrants.

Methods: We conducted a cross-sectional study using death certificates of international travellers in Peru and Colombia from 2017 to 2021. Causes of death were categorised into non-communicable diseases (NCDs), communicable diseases and injuries. We quantified causes of death by demographic characteristics to assess differences between Venezuelan migrants and non-migrant travellers.

Results: A total of 1,514 deaths were reported in Peru and 3,653 in Colombia. Migrants accounted for 28.3% of deaths in Peru and 75.6% in Colombia. More deaths were observed in males in both Venezuelan migrants (65.0% [Peru], 62.9% [Colombia]) and non-migrant travellers (64.0% [Peru], 63.1% [Colombia]). Venezuelan migrants died at a younger age (median age 39.3 years interquartile range [IQR]: 25.7-56.0 [Peru]; 32.6 years, IQR: 16.0-57.2 [Colombia]) compared to non-migrant travellers (55.0 years, IQR 38.0-68.8 [Peru]; 54.4 years, IQR 35.5-65.8 [Colombia]). NCDs were the leading cause of death among non-migrant travellers in Peru (43.7%, n=424), and both non-migrant travellers (69.7%, n=620) and Venezuelan migrants (53.2%, n=1,470) in Colombia. A high proportion of NCD-related deaths in Colombia occurred among children under 10 years, primarily attributed to malnutrition. Communicable diseases were the most common cause of deaths among Venezuelan migrants in Peru (39.5%, n=156). Injuries were twice as common among Venezuelan migrants (27.3%) than non-migrant travellers (14.9%) in Colombia, while in Peru, injuries accounted for a similar proportion (~24%) in both groups.

Conclusions: This study identified health disparities between Venezuelan migrants and non-migrant travellers in Peru and Colombia. These findings may facilitate multisectoral targeted efforts to address health services gaps for vulnerable migrant populations.

Spectrum of Illness Among Returning International Travellers: Insights from a Travel Clinic in China

Xinyu Wang, Xian Zhou

Background: As outbound travel from China continues to expand, clinicians are increasingly confronted with a broad range of imported infectious diseases, many of which are uncommon or unfamiliar in domestic practice. This study explores the diagnostic diversity observed at a travel medicine clinic in a tertiary centre in Shanghai.

Methods: We conducted a retrospective review of returning travellers who presented with febrile or systemic illness after visiting tropical, subtropical, or rural regions worldwide. Diagnoses were confirmed through microbiological, serological, molecular, or histopathological methods.

Results: A diverse array of infectious diseases was identified. Cases of malaria included *Plasmodium falciparum*, *P. vivax*, *P. ovale*, and *P. malariae*, acquired in sub-Saharan Africa and Papua New Guinea. Arboviral diseases were represented by dengue fever in travellers from India, Indonesia, Malaysia, and southern China. Bacterial infections included typhoid fever (Malaysia), Q fever (Sichuan, Yunnan), scrub typhus (Jiangsu), and psittacosis (Brazil). Parasitic infections ranged from schistosomiasis (Zimbabwe), fascioliasis, and clonorchiasis (Guangdong), to African trypanosomiasis (Gabon), onchocerciasis (DRC), and cutaneous larva migrans (Indonesia). Myiasis (Peru) and eosinophilic syndromes were also observed. Fungal diseases included coccidioidomycosis (US, Mexico) and systemic histoplasmosis linked to cave exploration in Anhui, China.

Conclusions: The clinical spectrum of imported diseases among returning travellers is highly diverse, reflecting the complex interplay between global mobility and infectious risk. Accurate diagnosis requires awareness of endemic exposures, recognition of key clinical patterns (e.g., fever with rash, eosinophilia, thrombocytopenia), and access to specialised laboratory testing. These findings highlight the critical need to build diagnostic capacity, enhance clinician training, and strengthen travel health surveillance systems in China to address both timeless threats and newly emerging infections.

Risks, regulations and reality: the three Rs of travel health – sorting fact from fiction to make informed decisions

Irene Lai

Background: The internet and the World Wide Web have enabled unprecedented access to data and information. The vast amount of information available continues to grow exponentially and news can cross the planet instantly. Travellers can research in great detail almost every aspect of their intended itinerary before booking their trip. However, whilst there is good quality information available, it is increasingly difficult to maintain a high "signal to noise ratio". The advent of artificial intelligence adds to the complexity. How should travellers and travel health professionals manage the infodemic? What guidelines are available?

Method: Recent examples of health information relevant for travellers reported in the media are "fact-checked" against reliable resources and analysed for accuracy and potential adverse outcomes. The landscape of information regulation will be briefly introduced. Recommendations on how to analyse reliability of sources will be presented.

Results: Both poor- and high-quality travel health information is available. Guidelines and regulations to address the abundance of information and to counter misinformation are limited.

Conclusions: Travellers and travel health professionals need to stay abreast of risks, regulations and reality. Understanding the heath information landscape and potential pitfalls and developing and utilising a robust system to remain informed are essential.

Human infections with zoonotic soil transmitted helminths, Gabon, Central Africa

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Background: Deforestation and environmental degradation in Central Africa have increased human exposure to zoonotic soil-transmitted helminths (STH) from non-human primates (NHPs). Recent reports of *Necator gorillae* and *Strongyloides fuelleborni fuelleborni* infections in researchers working with NHPs in the Central African Republic suggest these zoonotic STH might occur extensively in forest-edge human communities. We explored the occurrence of these zoonotic STH in villagers from Gabon, Central Africa, using microscopy and faecal metabarcoding analysis.

Methods: We conducted a parasitological survey of 226 human stool samples from six forest-edge communities in Ngounie Province, Gabon. Samples were analysed by formalin ethyl acetate sedimentation microscopy. DNA extracts from samples containing Strongylid eggs underwent metabarcoding analysis of partial mitochondrial cytochrome c oxidase subunit I (cox1) and/or 18S rRNA hypervariable region IV (HVR-IV).

Results: Microscopy identified hookworm eggs in 16 samples, *S. f. fuelleborni* eggs in seven (3% prevalence), and *Strongyloides* spp. larvae in one (20 samples total, some with co-infections). Of the 14 samples yielding cox1 sequence data, 11 contained Necator spp. and three contained S. f. fuelleborni. Four of the *Necator* infections were identified as *N. gorillae* (1.8% prevalence), three of which were coinfected with *N.*

americanus. The remaining *Necator* infections were *N. americanus*. 18S rRNA HVR-IV sequences were obtainable from six *Strongyloides* samples; five identified as *S. f. fuelleborni* and one as *S. stercoralis*.

Conclusion: We report human infections with the NHP helminths *N. gorillae* and *S. f. fuelleborni* in Gabon, Central Africa. These infections occurred in a forest-edge region where localised environmental disturbance may have increased contact between humans and NHPs, leading to greater exposure to NHP STH parasites. Further surveillance is needed to determine the extent of human infections with zoonotic NHP STH in areas where populations overlap, and to define the clinical impact and most appropriate treatment for these infections.

Seasonal and Demographic Trends of Dengue in Suburban Central Thailand during 2014 to 2023: A Ten-Year Retrospective Review at a University Hospital

Praosirin Tungkiatsilp, Aticha Leelachiawchankul, Sakarn Charoensakulchai, Manasvin Onwan

Background: Dengue remains a significant public health challenge in Thailand. With population growth and an increasingly aging society, recent evidence suggests a demographic shift in the disease burden, particularly in the age groups most affected. Climate change and rapid urbanization may also be altering dengue's seasonal patterns. This study aims to explore epidemiological trends over the past decade to reflect both the national and potentially global dengue situation.

Method: A retrospective cross-sectional study was conducted at H.R.H. Princess Maha Chakri Sirindhorn Medical Center in Nakhon-Nayok, Thailand, covering the period from 2014 to 2023. Data were collected on patient demographics (age, gender), diagnosis, and month of presentation.

Results: A total of 706 dengue cases were identified over the study period. Of these, 655 cases (92.8%) were diagnosed as dengue fever, while 51 cases (7.2%) were classified as dengue hemorrhagic fever, including one fatality. There was a slight predominance among females (52.1%). The highest incidence occurred among individuals aged 20–24 years (18.1%), followed by those aged 15–19 years (15.6%). Seasonal trends showed that 67.9% of cases occurred during the rainy season. Case numbers began rising in late April, peaked between August and November, and declined thereafter.

Conclusions: This study highlights a shift in the age group most affected by dengue, from children to older adolescents and young adults, consistent with findings from other Thai studies. The warm, humid rainy season facilitates Aedes mosquito proliferation, extending its lifespan and increasing transmission. Effective dengue control in tropical climates is challenging. It requires comprehensive strategies, including public education, environmental management to eliminate breeding sites, and cautious use of insecticides. Although vaccination remains the most promising preventive tool, limited availability and affordability continue to hinder widespread implementation in Thailand.

Rare, But Real: Schistosomiasis in Myanmar

Catherine Gordon, Darren Gray

Background: Schistosomiasis was historically considered non-endemic in Myanmar, however reports from the early 2010's identified both *Schistosoma japonicum* and *S. mekongi* occurring in Myanmar, however clarification of species distribution and endemicity—particularly through molecular diagnostics—

is urgently needed. There has been a lot of political unrest in Myanmar, with the movement of refugees and decreased access to clean water and hygiene infrastructure, and decreasing socio-economic status likely leading to lead to increased spread of parasitic diseases in Myanmar.

Methods: In 2016 we collected stool samples from 264 school-aged children for KK and qPCR from Bago Region, Myanmar. These samples were initially tested for soil-transmitted helminths, with 78% identified as positive for at least one STH infection. In 2024 we re-tested the DNA samples for strongyloidiasis, and schistosomiasis using two different primer sets that amplify both *S. japonicum* and *S. mekongi*.

Results: A total of 264 samples were analysed by qPCR, of those only two samples were positive for schistosomiasis using one of the qPCR assays. We attempted to sequence the positive *Schistosoma* spp. amplicon, but were unable to. We plan to use generic *Schistosoma* spp. primers to amplify and sequence the single positive and clarify the infecting species.

Conclusions: While only two samples were positive for schistosomiasis, this represents further evidence that schistosomiasis is more wide-spread in Myanmar than previously thought. Bago state neighbours Rakhine state, the site of a schistosomiasis outbreak in 2018; both are far removed from the previous endemic area around Lake Inlay. Continued political unrest leading to disruption of treatment programs has likely only increased the prevalence and spread of schistosomiasis. Further information on snail hosts and genetic identification of species will be crucial for any control programs.

Yaws truly: the role of active and passive surveillance systems for yaws elimination in Vanuatu

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Background: Yaws, a skin neglected tropical disease (NTD), is targeted for elimination in Vanuatu by 2030. Azithromycin mass drug administration (MDA) is integral to elimination but requires surveillance data to inform delivery. From 2021 to 2024, MDA for yaws, scabies and soil-transmitted helminths was conducted in Tafea, Sanma and Shefa provinces supported by the Pacific Integrated NTD Elimination (PINE) project. This analysis reports passive and active surveillance yaws data throughout the project and their roles in identifying endemic communities.

Methods: Passive yaws data (January 2021 – June 2024) was collated from health facility reporting across all six provinces. MDA campaigns in Tafea (2021, 2023), Sanma (2022) and Shefa (2023) provinces included self-reporting and screening of yaws cases. All suspected cases were confirmed using the Dual Path Platform (DPP) test, while those identified during the MDA were also analysed using a multi-bead assay (MBA) for anti-Rp17 and anti-TmpA antibodies.

Results: 1,143 cases were reported by health facilities and 58 cases detected through MDA campaigns. Of the total 1,201 cases, 77.0% (925/1,201) were in Tafea, 15.7% (188/1,201) in Shefa and 7.2% (86/1,201) in Sanma. There was one case each in Malampa and Penama, and no cases in Torba. Monthly case reporting detected low numbers in Tafea in 2021 followed by a large increase in late 2022 and 2023. Monthly case reporting in Sanma and Shefa remained stable. Of 12 DPP-positive children, 9 (75.0%) were positive for both anti-Rp17 and anti-TmpA antibodies. There were 19 DPP-negative children with suspected yaws, all also negative on the MBA.

Conclusions: Passive surveillance is integral for monitoring yaws by providing longitudinal data on cases and their location. MDA with active surveillance is also an effective strategy to identify active cases. Both can inform the location of endemic communities and the need for targeted interventions to achieve yaws elimination.

High prevalence of hookworms and *Strongyloides stercoralis* in school-age children and in cohabiting dogs in Cambodia despite long-term bi-annual mass drug administration: a One Health approach study

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Background: Despite ongoing efforts, soil-transmitted helminths (STHs) remain a public health burden across tropical and sub-tropical regions. The World Health Organization (WHO) aims to eliminate STHs as a public health problem by 2030. However, mass drug administration (MDA) targeting only school-aged children (SAC), coupled with inadequate diagnostics, may hinder progress. Moreover, the presence of large populations of dogs, as potential zoonotic reservoirs, has the potential to further complicate control efforts. This study evaluated the effectiveness of STH-control strategies in a Cambodian commune that underwent five years bi-annual MDA and explored zoonotic STH transmission between SAC and co-habiting dogs using molecular tools.

Methods: Faecal samples from 706 SAC and 457 dogs across 14 villages in Ta Ches commune, Kampong Chhnang Province, were screened using multiplex-PCRs for hookworms, Ascaris, Trichuris, and *Strongyloides spp*. Dog samples were screened for canine hookworms and *Strongyloides spp*. Genetic characterization and regression models were used to investigate zoonotic transmission.

Results: Using qPCR, STHs were detected in 46% of SAC, with hookworms being most prevalent (43.4%). Moderate-heavy hookworm infections exceeded the 2% WHO-2030 threshold control targets. Zoonotic STHs were found in all villages, infecting 84% of dogs. *Ancylostoma ceylanicum* and/or *S. stercoralis* occurred in 77% of villages, infecting 6.1% of SAC overall and up to 15.7% in some villages. A strong correlation ($\rho=0.62$, $p<0.0001$) between infections in dogs and SAC suggests zoonotic transmission. Genetic characterization revealed the presence of zoonotic haplotypes in both SAC and dogs infected with *A. ceylanicum* and *S. stercoralis*, bolstering the hypothesis of inter-host transmission.

Conclusions: These findings show that hookworms and *Strongyloides* persist despite bi-annual long-term MDA. Our One-Health approach highlights the need for improved measures to assess the effectiveness of intervention strategies and the need to elucidate the role of animal reservoirs to achieve WHO-2030 STH control targets.

Integrated Serosurveillance as a Tool for Monitoring of Neglected Tropical Disease in Vanuatu

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Background: Neglected tropical diseases (NTDs) remain a public health concern in Vanuatu despite recent elimination efforts. Integrated serological surveillance can help monitor ongoing or residual transmission and support post-MDA decision-making by providing population-level data on pathogen exposure.

Methods: Between 2021 and 2023, the Vanuatu Ministry of Health (MoH), with support from the Pacific Integrated Neglected Tropical Diseases Elimination (PINE) project, conducted two rounds of mass drug administration (MDA) with ivermectin, albendazole, and azithromycin, alongside integrated serological surveys across Sanma, Shefa, and Tafea provinces. Dried blood spots (DBS) were collected in a subset of villages for multiplex analysis of 31 antigens, including key neglected tropical diseases (NTDs).

Results: Yaws seroprevalence (dual anti-rp17 and anti-TmpA positivity) in children aged 1-14 was 3.7% in Tafea (11/297), 1.5% in Shefa (2/133), and 0% in Sanma (0/161), with 13 children testing double-positive. Trachoma (anti-Pgp3) seroprevalence in 1-14-year-olds was 21.4% in Tafea, 29.0% in Sanma, and 28.9% in Shefa. Seroconversion rates ranged from 2.3 to 4.0 per 100 children annually. Despite its elimination in 2022, trachoma antibodies remain detectable, likely reflecting historical exposure. Lymphatic filariasis antibodies (anti-bm14, bm33, wb123) were present in children in all provinces, but no triple positives were detected among those aged 1-14. Two triple-positive cases—both females aged 40-49—were identified in Sanma and Shefa, suggesting residual exposure. Strongyloidiasis (anti-NIE) seroprevalence in 1-14-year-olds was 1.8%, with highest prevalence in Sanma (3.6%). Taeniasis (anti-rES33) was 0.91% overall, and cysticercosis (anti-T24H) was 1.2%, with all provinces represented. Highest T24H positivity was observed in Tafea (2.1%).

Conclusions: These findings highlight new and residual exposure. These results will inform MoH planning for future NTD interventions and demonstrate the value of integrated serology for multi-disease surveillance in resource-limited settings. Continued data validation and age-stratified analysis are planned to refine interpretation of exposure trends.

Using genomics to identify transmission patterns of *Wuchereria bancrofti*, the parasite that causes lymphatic filariasis in Samoa

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Background: Over the last 20 years, lymphatic filariasis (LF) was validated as eliminated from 8 Pacific Island countries. However, despite multiple mass drug administration (MDA) campaigns using diethylcarbamazine, albendazole, and recently, ivermectin, LF persists in 8 countries and territories, with recent reports of post-elimination resurgence of transmission. The spatial scale of transmission (e.g., within the household, community, or between islands) strongly impacts the optimal drug distribution strategy needed to reach elimination. This study aimed to help improve intervention strategies in Samoa using parasite genomics to identify transmission among villages.

Methods: We sequenced the whole genomes of 73 *Wuchereria bancrofti* microfilariae collected in 2023 from 17 people from 15 villages in Samoa and identified 515,485 autosomal variants. Whether geographic location and genetic variation were correlated was assessed using discriminant analysis of principal components.

Results: We found that *W. bancrofti* across the north-western coast on the island of Upolu were genetically similar, with a posterior probability (PP) of correctly identifying a parasite's geographic location based on genetic variants of only 0.65; i.e., the parasites in different communities were not strongly genetically distinct. In contrast, Fusi, to the south of Upolu, had genetically distinct parasites (PP = 1.0). Parasites from rural villages on the island of Savai'i were genetically distinct from each other and from Upolu (PP = 1.0), with the exception of Salelologa, where travel to and from Upolu is more common (PP = 0.67).

Conclusions: Our results indicate that parasite transmission is impacted by increased travel within northwest Upolu, with localized transmission due to the short flight range of the mosquito vectors elsewhere. This suggests a role for more targeted intervention in hotspots of high prevalence. We will be applying the results from genomic analyses to improve geostatistical, agent-based models for assessing alternative interventions.

Utility of lymphatic filariasis antibody serosurveillance for post-validation surveillance in Tonga

Harriet Lawford, 'Ofa Tukia, Joseph Takai, Sarah Sheridan, Selina Ward, Holly Jian, Beatris Martin, Stefanie Vaccher, Fiona Angrisano, Reynold 'Ofanoa, Leanne Robinson, Colleen Lau

Background: Tonga eliminated lymphatic filariasis (LF) as a public health problem in 2017 and conducted post-validation surveillance (PVS) in 2024. LF antibody (Ab) may be more sensitive than antigen (Ag) to detect early transmission signals. We investigated the utility of Abs for PVS by measuring Ab prevalence, risk factors for Ab-positivity (Ab+) and the sensitivity and specificity of Ab to identify Ag-positives (Ag+).

Methods: Targeted PVS was conducted in Tonga in May–July 2024. Ag was detected by Filariasis Test Strips (FTS) and blood slides examined for microfilariae (Mf). Multiplex bead assays (MBA) were used to detect Ab+ (Bm14Ab, Wb123Ab) using Ab-specific magnetic fluorescence intensity (MFI-bg) cut-offs. Logistic regression was used to identify risk factors for Ab+ and pairwise comparisons for mean difference in Bm14Ab and Wb123Ab MFI-bg in Ag+ vs Ag-.

Results: 1727/1787 participants (97%) had FTS and MBA results (mean age 29 years; range 5-89). 5/1727 (0.3%) were Mf+, 39 (2%) Ag+, 53 (3%) Bm14Ab+, 88 (5%) Wb123Ab+, and 100 (6%) positive to at least one Ab (Ab+). More participants were Ab+ than Ag+ (χ^2=45.9;p<0.001). Risk factors for Ag+ and Ab+ were male sex (Ab+ adjusted odds ratio [aOR]=2.0; 95% Confidence Interval=1.3-3.1; Ag+ aOR=5.0;2.3-10.7), age >19 years (Ab+ aOR=4.0;2.4-6.5; Ag+ aOR=5.0;2.2-11.6) and residing in outer islands (Ab+ aOR=7.1;4.3-11.6; Ag+ aOR=11.5;4.5-29.8). Ab had high specificity (95.8%;94.7-96.7) and moderate sensitivity (74.0%;57.9-87.0) for identifying Ag- and Ag+, respectively. Ag+ had higher mean MFI-bg than Ag- for Bm14Ab (3.1 v 1.3;p<0.001) and Wb123Ab (3.4 v 1.9;p<0.001).

Conclusions: Ab+ was moderately sensitive to identify Ag+ and highly specific to identify Ag-. MFI-bg values show potential to discriminate between Ag+ and Ag-. Most Ag+ would be detected by MBA if Ag testing was not possible. Integration of LF into serological surveys using MBA could be a cost-efficient PVS strategy.

Assessing the prevalence of hookworm species and Strongyloides spp. in Vanuatu: the role of molecular diagnostics

Adam Bartlett, Paolo Bareng, Sze Fui Hii, Stephanie Tabe, Garae Mackline, Fasihah Taleo, Vito Colella, Prudence Rymill, Susana Nery

Background: The Vanuatu Ministry of Health, supported by the Pacific Integrated Neglected Tropical Diseases Elimination (PINE) project, aimed to deliver two rounds of mass drug administration (MDA) to accelerate control of multiple NTDs, including soil-transmitted helminths (STHs). Surveys were integrated with each round of MDA to assess the prevalence of STHs pre- and post- the first MDA round. We used molecular techniques to investigate the prevalence of the different hookworm species and the presence of *Strongyloides* spp.

Methods: Cluster surveys were conducted in a random selection of approximately 30 villages per province in Tafea (November 2021, December 2023), Sanma (August 2022) and Shefa (April 2023, May 2024). A stool sample was collected from 137-932 participants in each survey and analysed by quantitative polymerase chain reaction (qPCR). Cluster adjusted prevalence estimates were calculated.

Results: Tafea had the highest hookworm prevalence of 33.6% (range 19.8-50.8%) pre-MDA and 35.5% (range 25.4-47.1%) post-MDA. In Shefa, the pre-MDA hookworm prevalence was 22.8% (range 14.2-34.6%), and 11.5% post-MDA (range 7.2-17.8%). In Sanma, the pre-MDA hookworm prevalence was 19.1% (range 12.8-27.4%). Necator americanus was the most prevalent hookworm species in Tafea (pre-MDA: prevalence 31.4%, range 17.8-49.2%; post-MDA: prevalence 34.9%, range 24.6-46.8%). Of note is the high prevalence of the zoonotic hookworm *Ancylostoma ceylanicum* in Sanma (12.1%, range 2.8–24.4% pre-MDA) being the most prevalent hookworm; and Shefa (11.9%, range 0–21.1% pre-MDA; 6.3%, range 0–14.3% post-MDA), similar to the prevalence of *N. americanus*. Most area councils had a *Strongyloides* spp prevalence <5%, though a prevalence of >10% was found in several area councils in Shefa.

Conclusions: Many area councils in Tafea, Sanma and Shefa provinces remain at high risk of hookworm infection, including the zoonotic hookworm, requiring control efforts. The use of qPCR identified areas that would benefit from interventions for zoonotic reservoirs and the use of ivermectin for strongyloidiasis.

Point-of-care diagnostics (POCs) development for schistosomiasis in the Philippines

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Background: Schistosomiasis in the Philippines remains prevalent across endemic communities with sustained morbidities despite decades of preventative chemotherapy. The country has recently shifted to the multi-disciplinary One Health approach to address and eliminate the parasite in humans, animals and the environment. However, such efforts are hindered by the limited sensitivity of the current diagnostics in the field, resulting in underestimated disease burden and undermining the effectivity and efficiency of control strategies.

Methods: We have recently developed semi-point-of-care diagnostics (POCs) for schistosomiasis: 1) an equipment-free cotton-syringe DNA extraction device combined with a portable quantitative PCR for detection of parasite DNA in stool samples and 2) a latex microsphere-based lateral flow immunoassay (LM-based LFIA) for detection of anti-SjSAP4 antibodies in serum samples.

Results: Using infected human samples, the POCs were validated to have comparable diagnostic performance with their lab-based counterparts (91.7% concordance of results of cotton-syringe with magnetic bead-based kit DNA extraction, and 80.60% concordance of results of LM-based LFIA with SjSAP4 enzyme-linked immunoassay), gaining their sensitivity but with fewer steps and simpler equipment. To assess their suitability in the field and inform further diagnostic development, the POCs were field-tested in six endemic villages in the Philippines. Community health workers were recruited and trained to use the POCs to test residents (n=250 per village) in the field, and their acceptability of the POCs were evaluated through questionnaires and focus group discussions.

Conclusions: Preliminary results identify pain points in the POC testing such as the undesirability of stool sample among health workers and bottleneck in the sample homogenization step of the cotton-syringe DNA extraction. Addressing these issues will ensure better adoption of these POCs in situ for their use in schistosomiasis surveillance and monitoring.

Modelling Environmental and Climatic-sensitive Infectious Syndromes in the Pacific Region (2011-2020)

Liuyi Chen-Cao, Behzad Kiani, Angela Cadavid Restrepo, Benn Sartorius

Background: Climate and environmental change will increasingly have a significant impact on infectious disease (ID) burden. However, the role of these factors (and interactions thereof) is poorly understood in the Pacific, particularly vulnerable to warming climate and with sensitive local environments. The Pacific Syndrome Surveillance System (PSSS) provides weekly syndromic notifications by country, offering opportunities for examining these relationships in the region. We aim to better understand IDs syndromic spatial-temporal patterns and climatic associations in the Pacific region to inform targeted surveillance and early warning systems for climate-sensitive diseases.

Methods: We utilised weekly PSSS data across 21 countries for three syndromes pre-COVID19: diarrhoea and prolonged fever (PF) from 2011, dengue-like illness (DLI) from 2017. We employed hierarchical mixed-effects negative binomial regression models for each syndrome to analyze associations with various climatic/environmental factors (both current and lagged). Additionally, we developed a separate model for DLI additionally incorporating normalized difference vegetation index (NDVI) tertiles to better capture this non-linear relationship.

Results: We found significant associations between various climatic/environmental factors and syndromic-specific incidence. Higher NDVI was associated with reduced incidence risk of diarrhoea (IRR=0.66, p<0.001) and PF (IRR=0.77, p<0.001). One-week lagged minimum precipitation showed similar protective effects for both diarrhoea/PF syndromes. Conversely, a 1°C rise in lagged average minimum temperature significantly increased diarrhoea (IRR=1.55,p<0.001) and PF (IRR=1.80,p<0.001) incidence. Higher DLI incidence was significantly associated with increased minimum precipitation (IRR=1.09,p=0.048) and greater temperature range (IRR=1.43,p=0.007) in the preceding week and highest NDVI tercile (IRR=2.58,p<0.001).

Conclusions: Climatic/environmental factors show non-linear, context-specific associations with ID syndromes in the Pacific, highlighting the critical need for local strategies to better prepare for and mitigate the impacts of climate change. Our findings underscore the urgency of integrating disease and climatic/environmental forecast data into local public health strategies to protect vulnerable communities across the Pacific region.

A method to estimate population immunity levels

Nicolas Smoll, Gabriel Parker

Background: Optimal population immunity levels reduce the spread of communicable diseases. Immunity levels are associated with vaccination coverage and natural infections. When rates of population level immunity are at 'herd immunity' levels, there's reduced infection transmission. A measure of immunity over time can provide estimates of when and how to intervene to maintain acceptable immunity levels.

Methods: We present a method of measuring immunity using the estimated effectiveness of naturally or vaccine-acquired immunity over time. This mathematical model incorporates immunity levels for a pathogen with time decay functions. This method can be used on populations of many sizes (from small to large).

Results: I represents population immunity level at time T(IT). Examples are used to demonstrate the model. For large populations it can be used to identify regions with low vaccination coverage but high infection rates and high overall immunity levels. For small populations it can be used to guide future booster dose allocations e.g., prior to military unit deployments, or in an aged care facility that has experienced a recent outbreak.

Conclusion: Population immunity levels can be measured for a disease and immunity inducing events. Measuring immunity over time can provide a guide for public health interventions to maintain herd immunity.

Geostatistical Modelling of Lymphatic Filariasis in Samoa Using Molecular Xenomonitoring and Human Antigen Data

Angus McLure, Helen Mayfield, Angela Cadavid Restrepo, Brady McPherson, Lisa Rigby, Patricia Graves, Robert Thomsen, Satupaitea Viali, Colleen Lau, Benn Sartorius

Background: Lymphatic filariasis (LF) remains endemic in Samoa despite repeated rounds of mass drug administration. Molecular xenomonitoring (MX) — testing disease vectors for infection markers — complements human surveillance. Previous research shows substantial clustering of infection markers within households and villages. This study investigates the relationship between infection markers in humans and mosquitos, and environmental factors to improve predictions of human infection risk.

Methods: We used geolocated data from a 2019 community survey that tested 1,815 people for filarial antigen and 34,299 pooled mosquitos for LF DNA. Environmental and demographic variables, including temperature, elevation, land cover, and population density, were compiled for each sampled location and at unsampled locations for prediction. Bayesian geostatistical models estimated risk surfaces for positive mosquitos and antigen-positive humans separately and in a joint "shared components" model.

Results: Individual geostatistical models revealed marked spatial variation in LF risk across Samoa, identifying persistent transmission hotspots. Higher prevalence of human and mosquito infection markers were associated with lower temperature and population density, and higher Normalized Difference Vegetation Index (NDVI) and slope. Strong spatial correlation was observed between infection in humans and Aedes mosquitos, supporting infection in mosquitoes as a proxy for human infection risk. A Joint model of MX and human antigen status produced more precise and accurate estimates risk compared to modelling outcomes separately.

Conclusions: Our novel approach to integrating MX and human data in a shared geostatistical framework provides a powerful tool for LF surveillance. The integrated spatial approach enables identification of high-risk areas and key environmental drivers, supporting more targeted and cost-effective interventions. Integrating mosquito and human data improves the precision of estimates of infection markers. As Samoa moves toward elimination, joint geostatistical modelling can enhance decision-making in the programmatic endgame and serve as a model for surveillance of LF and other vector-borne diseases in other settings.

A Transmission Model for Understanding *Strongyloides stercoralis* Transmission Dynamics among Humans, Dogs, and the Environment

Mackrina Winslow, Vito Colella, Juan Pablo Villanueva-Cabezas, Patricia Therese Campbell

Background: *Strongyloides stercoralis* is a soil-transmitted helminth that affects over 600 million people and 6% of dogs globally. Its complex life cycle, characterised by parthenogenesis and auto-infection, allows for lifelong infection within hosts. Molecular phylogenetic studies based on a short fragment of the *S. stercoralis* genome have identified two genetic lineages: one infecting both humans and dogs (zoonotic) and another restricted to dogs (non-zoonotic). However, the role of dogs as a source of human *S. stercoralis* infection remains uncertain.

Methods: We developed a novel compartmental transmission model to explore the potential role of dogs in human infection. The model incorporates two environmental reservoirs, dogs and humans stratified by age. Parameter combinations were generated using Latin Hypercube Sampling, and demographic and epidemiological data from Cambodia for both humans and dogs were used for model calibration and parameter estimation. We evaluated the impact of annual Mass Drug Administration (MDA) targeting humans and/or dogs to assess effectiveness under zoonotic and non-zoonotic transmission assumptions.

Results: Model simulations showed that community-wide annual MDA reduced human prevalence approximately 10 times more effectively than child-only treatment. With 100% efficacy and coverage, human-only MDA sustained control in non-zoonotic scenarios, but in zoonotic settings, the mean prevalence rebounded above 5% within 17 years post-MDA, indicating that the involvement of dogs alone is sufficient to maintain transmission.

Conclusions: These results emphasise the necessity of community-wide treatments compared to targeted treatments for effective infection control in humans. Even with ideal coverage and efficacy, treating humans alone is insufficient if zoonotic transmission occurs. These findings highlight the importance of dog treatment and underscore the need for empirical studies to identify the role of dogs in transmitting *S. stercoralis* to humans. Future work will explore varying levels of coverage, efficacy, and dog infection prevalence to inform sustainable intervention strategies.

From Evidence to Action: Quantifying the impact of changing climate on mosquito borne diseases in vulnerable small island nations with focus on Mauritius

Mohabeer Teeluck, Oyelola Adegboye, Stephan Karl, Diana Iyaloo, Eloise Skinner, Benn Sartorius, Emma McBryde

Background: Tropical Island nations, highly vulnerable to climate change, are increasingly recognized as high-risk hotspots for mosquito-borne diseases (MBDs), posing a significant public health concern for countries like Mauritius. Although MBDs are not endemic to Mauritius, dengue outbreaks have escalated in frequency and intensity in recent years, largely attributable to imported cases and climate variability. Capturing the lagged effects of meteorological factors is essential to improving prediction and strengthening outbreak preparedness. The aim of the systematic review was to synthesis existing evidence assessing the relationship between meteorological variables and MBDs outbreaks in small islands with vulnerable public health systems, with a view to improving prediction and preparedness strategies for emerging outbreaks in Mauritius.

Methods: A PRISMA-based systematic review was chosen to methodically ascertain the existing knowledge gaps associating the changing climate with MBDs in vulnerable small islands. The study population consisted of only independent small island nations with the most climate-vulnerable public health systems.

Results: Sixteen studies met the inclusion criteria. Overall, the quality of studies was rated high. Most (9/16; 56%) originated from Sri Lanka while the remainder were distributed across Pacific and Atlantic Ocean islands. Ten of 14 (72%) studies assessing temperature demonstrated a positive relationship with MBDs transmission. Eleven of 13 studies (84%) assessing rainfall reported a positive association with the propagation of MBDs. All six articles assessing humidity showed a positive association with MBDs transmission. Among 6 studies assessing windspeed, 4 (67%) demonstrated a negative association with MBDs. Findings varied by island context and study design, further precluding the use of a meta-analysis.

Conclusions: This review highlights the scarcity of studies and significant gaps in MBD transmission modelling in South-western Indian Ocean islands. This underscores the urgency to build regional predictive modelling capacity to inform early warning systems/outbreak preparedness and climate-resilient health strategies in resource-limited island nations such as Mauritius.

“Montezuma’s Revenge” with Neurological Disorder: A Nightmare in Remote Location of Nepal

Aakash Sherpali, Subash Dawadi

Background: Traveler's Diarrhea (TD), sometimes referred as Montezuma’s Revenge, is usually bacterial, and *Campylobacter* is one of the major causes of acute bacterial diarrhea. TD is a major problem encountered by trekkers in remote areas of Nepal. Guillain-Barré Syndrome (GBS) is a common acute inflammatory demyelinating polyneuropathy often triggered by *Campylobacter jejuni*, viral infection, or post-immunization.

Methods: Case report of GBS following diarrhea while traveling to the remote Himalayas of Nepal.

Results: Case Presentation: A 65-year-old male from Australia without comorbidities was evacuated by Helicopter from remote part of the western Himalayas with complaints of decreased sensation over his legs, impaired balance, burning sensation, and pain over thighs, and shoulders for the past 3 days. He had been trekking for the past two weeks. In the initial days, he had diarrhea, fever, and vomiting. He first could not feel cold or warm over feet, progressing to impaired balance. On Neurological examination, GCS was full with impaired sensation over C8-T1 areas bilaterally over upper limbs and impaired sensation to touch, vibrations, and pain with no clear sensory level, absent reflexes (knee and ankle), and mute planters. CSF showed albumin cytological dissociation and was negative for viral infections. MRI showed marked enhancement on the conus medullaris, nerve root of cauda equina, and other degenerative changes in the spine. Nerve conduction velocity tests later suggested acute motor and sensory axonal neuropathy. He was managed symptomatically and 5 days Immunoglobulin was administered. After recovery, he had repatriation back to his home country.

Conclusions: TD, while common in remote Nepal, can sometimes have a serious complication such as GBS which needs prompt recognition, medical evacuation from remote locations, and treatment as soon as possible.

Travellers Must Be Alert to the Risks of Severe Fever with Thrombocytopenia Syndrome Virus (SFTSV)

Xian Zhou, Xinyu Wang

Background: Severe fever with thrombocytopenia syndrome (SFTS), caused by the novel tick-borne SFTS virus (SFTSV), is an emerging infectious disease predominantly reported in East Asia, particularly China, South Korea, and Japan. Travellers visiting endemic areas, especially those participating in rural or outdoor activities, may be at increased risk. However, awareness of SFTSV among travellers and clinicians globally remains limited, highlighting a critical knowledge gap in travel medicine practice.

Methods: We conducted a systematic literature review using databases (PubMed, CNKI, J-STAGE) in English, Chinese, and Japanese from 2005 to 2025, focusing on recent epidemiological patterns, clinical manifestations, diagnostic methods, therapeutic advances, and preventive strategies related to SFTSV. Key findings relevant to travel medicine and traveller-associated risks were summarised.

Results: SFTS cases have steadily increased over the past decade, primarily during spring to autumn months, aligning with peak tick activity periods. Infection commonly presents with high fever, thrombocytopenia, gastrointestinal symptoms, and multi-organ dysfunction. Severe cases have a fatality rate ranging from 5% to over 20%. Recent studies reported occasional person-to-person transmission via direct contact with blood or bodily fluids. Diagnostic advancements include rapid and portable tests such as CRISPR-based assays, enabling early detection in field conditions. Although no specific antiviral therapies are officially approved, favipiravir has shown promising results in preliminary clinical trials. Vaccine candidates, including mRNA and inactivated vaccines, are currently under investigation but not yet commercially available.

Conclusions: Travellers visiting endemic regions, particularly rural East Asia, must be adequately informed about SFTSV transmission risks, preventive measures (such as tick avoidance and protective clothing), and early symptoms. Clinicians should include SFTS in differential diagnoses for travellers returning with febrile illness and thrombocytopenia from these areas. Enhanced awareness and rapid diagnosis are essential to prevent severe outcomes and limit disease transmission.

Insecticide resistance status of sand fly vectors of leishmaniasis in Na Thawi District, Songkhla, Southern Thailand

Atchara Phumee, Sudarat Katatho, Leena Kepan, Nisareen Upamma, Tasnim Doloh, Padet Siriyasatien

Background: Sand flies serve as crucial vectors in various medical and veterinary diseases. Sand fly-borne diseases pose a significant public health burden globally, as the causative agents can infect a diverse range of hosts, leading to severe consequences such as leishmaniasis and sand fly fevers. Additionally, the widespread use of insecticides for agricultural purposes and mosquito control is not specifically targeted at sand flies, potentially leading to resistance development. This study aims to survey sand fly species composition and evaluate insecticide resistance at the Vgsc domain IIS6 region using molecular diagnostic tools in Na Thawi District, Songkhla Province, Thailand.

Methods: Sand flies were collected using CDC light traps. The collected sand flies were then identified to species level using molecular techniques. Subsequent analyses the identification of pyrethroid resistance mutations within the voltage-sensitive sodium channel (Vgsc) domain IIS6 gene, followed by sequence analysis.

Results: Molecular identification of sand fly species revealed these sand flies belonged to nine species including *Sergentomyia khawi* (63.5%), *Se. barraudi* (12.9%), *Phlebotomus stantoni* (7.1%), *Sergentomyia* spp. (4.7%), *Se. hivernus* (3.5%), *Ph. betisi* (3.5%), *Se. anodontis* (2.4%), *Se. slyertica* (1.2%), and *Se. bailyi* (1.2%). The results revealed that all 85 samples (100%) showed no kdr mutation at codon 1014, with the presence of the wild-type allele (leucine, TTA). There was no replacement of leucine with serine (L1014S, TCA) or with phenylalanine (L1014F), which can occur through two alleles (TTC and TTT) compared to references sequences.

Conclusions: The results of this study provide valuable information on insecticide resistance in sand flies. The insecticide resistance status in sand flies has the potential to significantly improve risk assessments and guide targeted vector control efforts in Thailand.

Patent Infections by zoonotic *Trichostrongylus* nematodes in children and adults from Vietnam

Patsy A. Zendejas-Heredia, Justin Alway, Lucas G. Huggings, Sze Fui Hii, Dinh Ng-Nguyen, Rebecca J. Traub, Susana Vaz Nery, Vito Colella

Background: Zoonotic trichostrongyloses, primarily caused by *Trichostrongylus axei*, *T. colubriformis*, and *T. orientalis*, are neglected parasitic diseases transmitted from livestock to humans through the faecal-oral route. Clinical manifestations often resemble those of hookworm disease. The eggs of *Trichostrongylus* spp. are morphologically similar to those of hookworms, leading to frequent misidentification in microscopy-based surveys. While cases have been reported globally, no human infections had been documented in Vietnam.

Methods: During a cluster-randomised trial for hookworms in Vietnam, a portion of samples screened were qPCR negative, but showed hookworm-like eggs under microscopy, suggesting potential misidentification with hookworm-like nematodes. A subset of 1,126 faecal samples from school-age children (6–14 years) and adults (15–80 years) were screened using qPCR for *Trichostrongylus* spp. Positive samples were genetically characterized via long-read amplicon sequencing targeting the complete ribosomal ITS region and phylogenetic analyses were conducted to confirm species identification.

Results: *Trichostrongylus* spp. infections were identified in 2.25% of adults and 0.23% of children. Sequencing confirmed the presence of *T. colubriformis* in children and both *T. axei* and *T. colubriformis* in adults. These species typically infect goats, sheep, and cattle, suggesting zoonotic transmission linked to close human-livestock contact.

Conclusions: The detection of patent zoonotic *Trichostrongylus* infections in Vietnam highlights a previously undocumented public health concern. This study provides molecular evidence of *T. axei* and *T. colubriformis* in humans in Vietnam, emphasizing the need for integrated, molecular-based surveillance. Moreover, widespread benzimidazole resistance in livestock could compromise treatment efficacy in humans if resistant strains establish in humans. Therefore, molecular monitoring of zoonotic helminths in humans will be critical to improving control strategies and mitigating future treatment failures due to drug resistance.

Emergence of Novel Zoonotic Filarial Species in Humans and Dogs: Implications for Post-Validation Surveillance in the Asia–Pacific

Vito Colella, Ushani Atapattu, Lucas Huggins, Ralph Manzanell, Neil D. Young, Virak Khieu, Robin B. Gasser, Indeewarie Gunaratna

Background: Zoonotic filariases are important but often neglected tropical diseases caused by filarial parasites of the family *Onchocercidae*, transmitted from animals to humans via arthropod vectors. *Brugia* spp. and *Dirofilaria repens* are the most commonly implicated agents. However, limitations in microscopy-based diagnostics have hindered accurate identification of novel or cryptic species, restricting our understanding of the role of zoonotic filariases in the Asia–Pacific region.

Methods: We employed a combined morphological and molecular method to characterise a novel zoonotic *Dirofilaria* species from dogs in Sri Lanka. Additionally, we applied a newly developed next-generation sequencing-based metabarcoding platform to detect zoonotic filarial parasites in dogs from Cambodia and Bhutan, and in both dogs and humans from Sri Lanka.

Results: We provide a comprehensive morphological description of adult females, males, and microfilariae, along with mitochondrial genome characterisation of a previously unrecognised *Dirofilaria* genotype, now designated *Dirofilaria asiatica*. Metabarcoding revealed that dogs serve as reservoirs of *D. asiatica* in Sri Lanka, Bhutan, and Cambodia. Phylogenetic and sequence type analyses further showed that *Brugia* sequences from dogs were identical to those from human infections in Sri Lanka, and distinct from *B. malayi* strains circulating in Southeast Asia.

Conclusions: Our findings highlight the critical role of advanced molecular tools in detecting cryptic zoonotic filarial species in both dogs and humans. We demonstrate that *D. asiatica* likely accounts for the majority of zoonotic *Dirofilaria* infections across southern and southeastern Asia, including imported cases in travellers from these regions to Australia and Europe. We also provide evidence that dogs are reservoirs of a novel zoonotic *Brugia* species infecting humans in Sri Lanka. These findings have important implications for filariasis control strategies in the post-validation surveillance phase across the Asia–Pacific.

Increasing number of Sapovirus outbreaks in Beijing (2014-2021): Dominance of Genotypes GII.3 and GI.2.

Fan Yu, Lingyu Shen, Hanqiu Yan, Baiwei Liu, Weihong Li, Yu Wang, Yi Tian, Lei Jia, Peng Yang, Quanyi Wang, Daitao Zhang, Zhiyong Gao

Background: Sapovirus, a re-emerging calicivirus, is increasingly recognized as an under-characterized cause of acute gastroenteritis globally. Frequently underrecognized, sapovirus has driven several outbreaks across South Asia, Europe, and North America. This growing burden highlights critical gaps in our understanding of the epidemiological dynamics and genetic diversity of sapovirus, hindering timely public health response and the development of effective control strategies.

Methods: We aim to examine temporal, regional, and demographic patterns, clinical features, genotypes, and recombination events of sapovirus outbreaks in Beijing (2014-2021). Detection used real time RT-PCR, with genotype and phylogenetic analyses based on Viral Protein 1 and RNA-dependent RNA polymerase regions via BEAST, and jModelTest software for using model the Hasegawa-Kishino-Yano model, alongside whole genome sequencing.

Results: From 2014 to 2021, 216 sapovirus-related outbreaks were identified (95 sapovirus only and 21 mixed). Peaks occurred in 2017, 2019, and 2021; 78% were in transitional months between seasons. Most occurred in kindergartens (76.4%) and primary schools (19.0%), with person-to-person the dominant mode of transmission (97.7%). Outbreaks in suburbs had longer median durations (8 days, IQR:6-10). Higher attack rates were seen in comprehensive schools (21.6%, IQR:10-35) and kindergartens (18.12%, IQR:13.5-22.7). More cases were associated with foodborne outbreaks (8 cases, IQR:14-20). Vomiting was more common in ≤5-year-olds, and diarrhea in >5-year-olds. 8 genotypes were identified (GI.1–3, 5–6; GII.1, 3, 5) with no recombination. A shift from GII.3 (2016–2019) to GI.2 (2020–2021) occurred, with novel clades showing significant nucleotide and amino acid changes.

Conclusions: Sapovirus is an emerging cause of gastroenteritis outbreaks, particularly foodborne outbreaks in kindergartens. Targeted interventions such as hand hygiene, food safety, and outbreak monitoring in childcare settings are essential. Given the rise of new genotypes, ongoing surveillance, genotyping, and whole-genome sequencing are critical for timely response and global public health preparedness.

Serological and Molecular Screening of Leptospira Infection in Patients with Acute Febrile Illness After Flash Flood Exposure in Southern Thailand

Issara Prachongsai, Arthit Malert, Krittaya Sodthip, Nattida Kongprasert, Pornthep, MD. Dechphol, Wiwit Tantibhedayangkul, Tiwaporn Nualkaew

Background: Leptospirosis is a globally neglected tropical disease, commonly associated with heavy rainfall and flooding. It is part of Thailand’s national disease surveillance program, particularly during the rainy and post-flood seasons. Nakhon Si Thammarat, located in southern Thailand, is a tropical and flood-prone province known to be endemic for leptospirosis. In recent years, immunochromatographic assays have been widely used for laboratory screening of acute leptospirosis due to their rapid turnaround time and convenience. This study aimed to evaluate the diagnostic performance of serological and molecular methods for screening among patients exposed to flash flooding in this high-risk area.

Methods: From November to December 2024, serum samples were collected from 64 patients presenting with acute febrile illness following flash flood exposure in Thasala and Promkiri districts, Nakhon Si Thammarat. Two commercial Leptospira IgM test kits were used: Lepkit, which detects anti-lipopolysaccharide (LPS) IgM, and Citest Leptospira IgM, which primarily detects anti-Leptospira IgM. An in-house multiplex quantitative polymerase chain reaction (qPCR) was used for molecular confirmation.

Results: Among the 64 serum samples, Lepkit identified 16 positive cases (25.0%), whereas Citest detected 2 positive cases (3.1%). Multiplex qPCR confirmed Leptospira DNA in 2 samples (3.1%), both of which were also positive by Lepkit, indicating 100% concordance with PCR-confirmed cases. The 2 Citest-positive cases were not confirmed by PCR.

Conclusions: In endemic areas or following flash flood events, timely screening for leptospirosis is critical for early diagnosis and outbreak control. Our findings suggest that detection of anti-leptospiral LPS IgM can capture all PCR-confirmed cases, supporting its role as a primary screening tool. However, high positivity rates from rapid tests alone may reflect lower specificity, potentially leading to overestimation. Molecular techniques such as multiplex qPCR offer higher specificity. The combination of serological and molecular techniques may improve diagnostic accuracy and strengthen public health responses.

Increasing Genome assembly of Simulium damnosum, a vector of Onchocerciasis in Ghana

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Background: Human onchocerciasis, or river blindness, is caused by the parasitic nematode Onchocerca volvulus, which is transmitted by the bites of blood-sucking blackflies of the genus *Simulium*. These blackflies are not only vectors for onchocerciasis but are also significant pests of livestock. Despite their medical importance, there is a lack of molecular data characterizing *Simulium* species, with current classification based largely on cytotaxonomy, which is dependent on expert microscopy examination of chromosomal banding patterns in the larval silk gland. The complexities of cryptic species further complicate taxonomy, and poor morphological identification of adult blackflies further limits speciation efforts. The WHO recommends alternative strategies to augment drug treatment programs for the elimination of onchocerciasis transmission, including transmission zone delineation, which is influenced by vector competence and dispersal patterns. However, knowledge of species critical for understanding vector dispersal, remains limited.

Methods: In this study, we present the first nearly complete genome assembly of an adult *Simulium damnosum* collected from Ghana. We used Oxford Nanopore long-read sequencing (2,915,146 million reads) and Illumina short-read whole genome sequencing (16,385,843 paired-end 2x150 bp) obtained from *Simulium* genomic DNA to assemble the genome.

Results: The assembled genome was ~260 million base pairs long with 90.5% completeness, and 15,894 predicted genes. Population genetics analysis of 273 adult blackflies collected from 21 sites across Ghana, using the assembled genome as a reference, identified three distinct lineages, molecular operational taxonomic units (MOTUs), with further differentiation within one MOTU into a sub-MOTU.

Conclusions: This genome assembly serves as a valuable resource for studying blackfly ecology, vector dispersal, crucial for understanding onchocerciasis transmission dynamics. Future improvements, including the integration of Hi-C data for haplotype phasing, will further enhance our understanding of the *Simulium* chromosomal evolution and speciation.

Impact of extreme weather events on leptospirosis burden in the Caribbean region

Beatris Mario Martin, Zhonghan Zhang, Sebastian Vernal, Holly Jian, Luis Furuya-Kanamori, Benn Sartorius, Collen L. Lau

Background: The last global-level estimates of leptospirosis annual morbidity and mortality, based on data up to 2008, identified the Caribbean region (CR) as the third most affected region globally. Poor, vulnerable communities and small islands were found to bear the highest burden. Recently, extreme climate events have shifted the epidemiological patterns of leptospirosis. This study aimed to better understand the recent burden of leptospirosis in the CR.

Methods: We conducted a systematic review of publications on morbidity (incidence or prevalence) and/or mortality of leptospirosis from 2008-2023 across five databases (PubMed, Web of Science, Embase, Scopus, LILICAS) and grey literature. We included studies in English, Spanish, or French, conducted in Caribbean islands (excluding mainland countries and territories). The number of reported cases was extracted from eligible studies/reports. A mixed-effects hierarchical country-level Poisson model incorporating precipitation, temperature, percentage of urbanisation in country and gross domestic product was used to estimate annual case numbers by country, including predictions for country-years with no data.

Results: Of 110 full texts reviewed, 15 met the inclusion criteria. Another 11 grey literature reports were included. The estimated average leptospirosis incidence in the CR was 4.4 cases/100,000 population/year. However, incidence rates were above this average in 2008 (5.8), 2011 (5.2), 2018 (7.8), 2019 (7.9) and 2023 (5.3), years associated with intense Atlantic hurricane seasons. The average incidence during these high-burden years (6.4) was nearly twice the average of the other years (3.4). St. Vincent and the Grenadines, Martinique, and Guadeloupe were consistently estimated to have the highest incidence across all years, with Guadeloupe reaching 40.2 cases/100,000 in 2019.

Conclusions: Spikes during hurricane years highlight the potential escalation of leptospirosis burden with climate change, and the urgent need for more resilient surveillance, early warning, prevention, and response strategies.

Spatial distribution and socio-ecological factors of strongyloidiasis in Australia

Fasil Shiferaw, Kefyalew Alene, Darren Gray

Background: Strongyloidiasis, caused by the soil-transmitted helminth *Strongyloides stercoralis*, remains a neglected public health issue in Australia, particularly affecting socioeconomically disadvantaged and remote Indigenous populations. This study aimed to map the spatial distribution of strongyloidiasis and investigate associated socioecological factors to identify high-risk areas and guide targeted interventions in Australia.

Methods: We used data from a previous nationwide survey conducted between 2012 and 2016, which included 80,556 individuals across 324 statistical area levels 3 (SA3) regions in Australia. Socio-ecological and environmental variables were extracted from publicly available online sources to explore their relationship with strongyloidiasis. Spatial patterns were analysed using Global Moran's I and Getis-Ord statistic to identify clusters of high and low disease prevalence. A Bayesian geostatistical modelling was applied to investigate whether socio-climatic factors explain the spatial distribution of strongyloidiasis in Australia.

Results: The predicted prevalence map showed substantial spatial heterogeneity of strongyloidiasis, with the highest prevalence identified in regions of the Northern Territory and northern Queensland. Bayesian geostatistical analysis indicated significant positive associations between strongyloidiasis prevalence and higher temperature (β: 0.081; 95% CrI: 0.044, 0.118) and elevated soil pH (β: 0.243; 95% CrI: 0.052, 0.435). Conversely, a higher Socio-Economic Indexes for Areas (SEIFA) score was negatively associated with the strongyloidiasis prevalence (β: -0.097; 95% CrI: -0.169, -0.026).

Conclusions: Our findings reveal significant geographical variation in strongyloidiasis prevalence across Australia, highlighting hotspots particularly in northern Queensland and the Northern Territory, where climatic factors, soil characteristics, and socioeconomic conditions shape the spatial distribution of the disease. Geographically tailored strategies targeting vulnerable areas are essential for effective prevention and control.

A critical review and update of the epidemiology, transmission and prevention of Buruli Ulcer in Australia.

Andjela Arandjelovic

Background: The rising incidence and geographic spread of Buruli Ulcer in southeastern Australia, particularly in temperate coastal Victoria, highlights the importance of understanding its epidemiological patterns, modes of transmission and feasible prevention strategies. This review aimed to evaluate current epidemiological trends, transmission pathways, and prevention strategies for Buruli Ulcer in Australia.

Methods: A narrative review was conducted using EMBASE and PubMed databases. Search terms included "Buruli Ulcer" OR "Mycobacterium ulcerans" AND "epidemiology" OR "transmission" OR "prevention" AND "Australia". The search was limited to English-language publications from January 2015 to April 2025, including peer-reviewed articles, books and government public health reports. Studies unrelated to Australia or published in non-English languages were excluded.

Results: This review synthesised findings from epidemiological studies, environmental microbiology and public health research to outline the current understanding of Buruli Ulcer in Australia. A total of fifteen publications were included in this review. In Australia, Buruli Ulcer exhibits distinct epidemiological patterns, with marked concentration in coastal areas including the Bellarine and Mornington Peninsulas. Evidence suggests transmission may occur through environmental exposure (e.g. contaminated soil or water), vector-borne pathways (notably via mosquitoes), and zoonotic reservoirs (possums). An incubation period of 4-5 months and average diagnostic delay of 1-2 months warrants development of early detection methods. Surveillance of possum faeces may assist in identifying emerging endemic regions, to allow for early intervention. Prevention strategies should also focus on education, mosquito bite prevention, reduction in mosquito and possum burden and environmental management.

Conclusion: The ongoing rise in Buruli Ulcer in Australia warrants improved understanding in the transmission pathways of the disease. Targeted prevention strategies informed by current evidence are essential to mitigate the spread of this debilitating and emerging public health threat.

Diagnostic Validation of Seegene GI Helminth Allplex Assay in a High Endemicity Population

Anna Duan, Francesca Azzato, Eileen Hor, Jee Hinaut, Huan Zhao, Matthew Watts, Polydor Mutombo, Rodrigue Mintsa, Richard Bradbury

Background: Although traditional microscopy techniques remain the gold standard for diagnostic parasitology testing. Molecular diagnostics, including multiplex PCR panels, offer a high sensitivity and specificity alternative for targeted parasites. The AllplexTM GI-Helminth (I) assay (Seegene Inc, Seoul, South Korea) simultaneously detects eight intestinal helminths. This study aimed to evaluate the diagnostic performance of the Allplex GI-Helminth (I) Assay in samples collected from a population highly endemic for soil transmitted helminth (STH) infections.

Methods: 222 human fecal samples from Gabon, West Africa underwent formalin ethyl-acetate concentration microscopy. 70% EtOH preserved samples were DNA extracted using Qiagen Powersoil and then subjected to Allplex GI-Helminth (I) Assay analysis. Diagnostic accuracy was assessed using a microscopy and composite reference standard (CRS).

Results: The sensitivity of the Allplex GI-Helminth (I) assay compared to microscopy alone and a composite reference standard of microscopy and Allplex GI Helminth (I) PCR results was; 97.6% and 98.3%

(respectively) for *Ascaris lumbricoides*, 81.8% and 88.2% for *Trichuris trichiura*, 75.0% and 91.3% for the hookworms and 57.1% and 88.9% for *Strongyloides spp*. Specificity vs microscopy alone was 78.4% for *A. lumbricoides*, 68.3% for *T. trichiura*, 87.9% for the hookworms and 92.1% for *Strongyloides* spp. These samples contained many *S. fuelleborni* infections, which were detected by the Allplex GI-Helminth (I) *Strongyloides* primers.

Conclusions: Integrating helminth PCR assays into diagnostic workflows has the potential to improve the reliability of STH detection. When compared to FES microscopy, the *Strongyloides* PCR target demonstrated relatively low sensitivity. However, this is likely attributable to the inherently low sensitivity of FES for detecting *S. stercoralis*, rather than a limitation of the PCR assay itself. Further evaluation of the *Strongyloides* target with a coprological larval culture reference standard is required.

Multi-locus sequence typing of *Trichomonas vaginalis* isolates from North India

Abhishek Mewara, Taruna Kaura, Urvashi Rahi, Aashima Arora, Sunil Sethi, Rashmi Bagga, Sumeeta Khurana

Background: *Trichomonas vaginalis* is most common nonviral sexually transmitted disease (STD) pathogen worldwide. There is extensive genetic diversity in *T. vaginalis*, suggested to be associated with metronidazole susceptibility and other factors, however, there is not much information about the population structure of *T. vaginalis* from India. We studied the genetic diversity of *T. vaginalis* isolates by multi-locus sequence typing (MLST) in this work.

Methods: Endocervical/vaginal swabs of patients suspected of STDs were subjected to microscopy and T. vaginalis-specific repeat sequence PCR. The seven housekeeping genes tryptophanase (P1), glutaminase (P3), family T2 asparaginase-like-threonine peptidase (P6), alanyl tRNA synthetase (P8), DNA mismatch repair protein (P13), serine hydroxy methyltransferase (P14), and mannose 6- phosphate isomerase (P16) were amplified and sequenced for MLST analysis; goeBURST algorithm was used to study the phylogenetic relationship by generation of minimum spanning trees (MST).

Results: Of 876 patients, 21 (2.4%) were positive for *T. vaginalis* by microscopy and 23 (2.6%) by PCR. High quality sequences were obtained from 9 isolates for the different seven housekeeping genes. PubMLST analysis of the housekeeping genes revealed 13 polymorphic nucleotide sites and 8 different alleles among the isolates. Novel sequence types (STs) which were different from the 72 STs in PubMLST database were observed—2 isolates had the same ST, while 7 had unique STs. The Simpson’s diversity index was 0.083; index of association (IAS) was 0.0249 for all the isolates, and 0.0185 for STs only. The isolates divided into distinct clades—7 were in clade A, one in clade B, and one remained as a mixed unassigned ST.

Conclusions: The PCR-MLST of seven single-copy housekeeping genes of *T. vaginalis* clinical isolates revealed multiple circulating alleles with few synonymous and non-synonymous mutations, showing a diverse T. vaginalis population. Further, the differences between the genotypes with respect to drug resistance will be studied.

Modelling African Swine Fever Epidemiology: A Systematic Review of Statistical, Mechanistic, and Machine Learning Approaches

Kim Dianne Ligue-Sabio, Kien Quoc Do, Benn Sartorius, Luis Furuya Kanamori, Yoni Nazarathy, Yusuf Sucol, Colleen Lau

Background: African swine fever (ASF) is an emerging infectious disease with complex, climate-sensitive transmission dynamics involving ecological and anthropogenic factors. Understanding ASF spread across tropical and temperate regions offers valuable insights for preparedness not only for ASF but also for zoonoses. Modelling plays a critical role in surveillance and control. However, a comprehensive synthesis of applied methodologies remains lacking. This study aims to review models used to understand ASF epidemiology and how these methods could potentially be applied to zoonoses.

Methods: We conducted a PRISMA systematic literature review of modeling studies on ASF published in English across PubMed, Web of Science, Embase, and Scopus up to November 2024. Studies that modeled ASF outbreak data using statistical, mechanistic, or ML techniques were eligible. Extracted data included modelling objectives, methods, temporal and geographic coverage, explanatory variables, assumptions, error metrics, and policy implications.

Results: A total of 153 studies were included: 90 used mechanistic models, 56 employed statistical methods, and 16 applied ML. The most common approaches were compartmental models (63.2%), generalized linear models (63.3%)—primarily logistic regression—and maximum entropy modeling (71.4%). Few studies applied hybrid frameworks. Most studies assessed transmission drivers, control strategies, or spatiotemporal trends. Nearly all (99.3%) were published from 2011–2024, focusing largely on Europe and Asia. Predictors included animal, farm, anthropogenic, and environmental data, though integration of these across modelling approaches was often limited.

Conclusion: This review highlights the critical role of modeling in ASF research, particularly through mechanistic approaches. ML remains underutilised despite its capacity to harness complex data. Future efforts should integrate diverse data through a One Health lens and explore hybrid models to support advanced outbreak prediction and targeted control. Lessons from ASF modelling could inform zoonotic disease preparedness, where interdisciplinary data integration is essential.

Molecular Docking-Guided Identification of Quercetin and Kaempferol Glycosides as Adjuncts to Vaccine Strategies Against *Acinetobacter baumannii*

Jutathip Jeeramanaphong, Techit Thavorasak, Witawat Tunyong, Thida Kongngoen, Dararat Horpet, Nitaya Indrawattana, Sirijan Santajit

Background: Vaccine-preventable diseases remain a significant global health challenge, further exacerbated by antimicrobial resistance (AMR) and the emergence of multidrug-resistant (MDR) pathogens. While vaccines play a critical role in infection prevention, complementary antimicrobial strategies are essential for controlling resistant bacterial infections, particularly in travel and tropical medicine. This study explores the potential of Paederia foetida Linn., a medicinal plant with known bioactive compounds, to combat bacterial infections through molecular docking-aided discovery and experimental validation.

Methods and results: Using computational approaches, quercetin and kaempferol glycosides were identified as potent inhibitors targeting quorum-sensing (QS) regulators—AbaR (*Acinetobacter baumannii*). The ethanolic extract exhibited antimicrobial activity, biofilm disruption, and virulence gene suppression in in vitro assays. Additionally, computational ADMET predictions confirmed favorable pharmacokinetics, supporting the potential of these natural compounds as adjunct therapies alongside vaccines.

Conclusions: This study highlights the synergy between bioinformatics-driven drug discovery and traditional medicine in addressing vaccine-preventable bacterial infections. By integrating plant-derived antimicrobials into global health strategies, these findings contribute to the development of novel interventions to mitigate AMR threats and support vaccine efficacy in travel and tropical medicine.

Lymphatic Filariasis resurgence and intervention options in a Pacific Island country: a predictive model for policy makers

Claire Brereton

Background: Lymphatic Filariasis (LF) is a mosquito-transmitted Neglected Tropical Disease which causes disability, chronic pain and social stigmatisation in endemic Pacific Island countries. The disease, often leading to elephantiasis and hydrocele, is caused by parasite *Wuchereria bancrofti*. The worm's life cycle involves both a human host where adult worms live and reproduce and a mosquito host where larvae develop. The asymptomatic infectious period may last for many years and clinical symptoms may never appear. These characteristics make LF a difficult disease to eliminate. A predictive modelling approach aims to give health policy makers in Pacific Island Countries a tool to compare options for reduction, control and elimination of LF.

Methods: Two models were created. First, a qualitative Causal Loop Diagram describing the LF infection cycle was built and agreed with an expert panel including NTD clinicians and a parasitologist. This formed the basis of a quantitative, dynamic Susceptible, Exposed, Infected, Recovered (SEIR) model, which was calibrated to community surveys of antigen levels and infections for the country. Potential interventions including Mass Drug Administration (MDA) and Targeted Test and Treat (TTT) in infection hotspots were applied to the model.

Results: Modelled results show that multiple rounds of MDA have not reduced disease prevalence enough to stop ongoing transmission, despite meeting the World Health Organization elimination guidance target of less than 1% antigen positivity. An interactive interface for policy makers enables experimentation in real time to predict results of potential future interventions including MDA and TTT.

Conclusions: The World Health Organization elimination guidance target is unsuitable for Pacific Island countries, possibly because the local vector, *Aedes polynesiensis*, is a 24-hour biter and possibly because of other local factors. Options for combinations of interventions can now be compared to determine the most appropriate approach for the country.

Adjunct Antimicrobial Potential of Paederia foetida Linn. Leaf Extract: In Vitro–In Silico Insights Against *Staphylococcus aureus* Infections

Sirijan Santajit, Techit Thavorasak, Witawat Tunyong, Thida Kongngoen, Dararat Horpet, Wampen Chaicumpa, Nitaya Indrawattana

Background: Antimicrobial resistance (AMR) threatens the effectiveness of vaccines against bacterial infections, particularly with *Staphylococcus aureus*, a major vaccine-preventable pathogen capable of biofilm formation and quorum sensing (QS)-regulated virulence. In response to this challenge, this study investigates the potential of Paederia foetida Linn., a medicinal plant rich in bioactive compounds, as an adjunct antimicrobial strategy to enhance infection control alongside vaccination efforts.

Methods and Results: Using an integrated in vitro–in silico approach, the ethanolic P. foetida leaf extract demonstrated significant antimicrobial activity against *S. aureus*, including methicillin-resistant strains (MRSA), and effectively disrupted biofilm formation. Quantitative reverse transcription polymerase chain reaction (qRT-PCR) analysis confirmed downregulation of key biofilm and virulence genes, indicating interference with QS mechanisms. Biofilm assays further validated the extract's ability to prevent and eradicate established biofilms. LC-MS/MS analysis identified quercetin and kaempferol glycosides as major bioactive constituents, and molecular docking confirmed their strong binding affinity to the QS transcriptional regulator SarA. Computational ADMET predictions revealed favorable intestinal absorption, though concerns regarding permeability and drug-likeness due to flavonoid glycoside structures remain.

Conclusions: By integrating natural antimicrobials with vaccine-based strategies, this study highlights the potential of plant-derived bioactive compounds to enhance infection prevention, reduce bacterial virulence, and support vaccine efficacy in controlling S. aureus infections. These findings provide new insights into developing adjunct therapies to complement vaccination programs, addressing the growing threat of AMR in global health.

Sunshine Coast Improving Immunisation Project (SCIIP) – Barriers to vaccination

Gabriel Parker, Nicolas Smoll

Background: The rate of fully vaccinated children (<5y/o) on the Sunshine Coast, Queensland is <88%, well below the state target of 95%. In an effort to improve this the Sunshine Coast Public Health Unit developed a targeted vaccination program (Sunshine Coast Improving Immunisation Program - SCIIP) which was designed to improve vaccination coverage in a cohort of previously fully vaccinated children (n = 276) by providing them with the one vaccination (4y/o Infanrix IPV or Quadracel immunisation) required to get them up to date with their immunisation schedule. As part of the program non-vaccinating parents were contacted by staff at the unit to organise vaccinations and responses from parents were collected.

Methods: A quali-quantitative single level analysis of responses was conducted using the World Health Organisation's (WHO) Behavioural and Social Drivers (BeSD) of Vaccination framework. This framework categorises modifiable drivers of vaccination into four domains: Thinking & Feeling, Motivation, Social Processes, and Practical Issues. Responses collected from non-vaccinating parents during the program were analysed and matched to these domains.

Results: The program resulted in 44 vaccination events (16% of cohort). There were 21 comments from parents who declined or were undecided about vaccinating their child that were classifiable under the WHO BeSD framework. The primary driver of non-vaccination was concern over vaccine safety (50% of responses). Other drivers included concerns within the Thinking & Feeling domain (25%), Social Processes (10%) and Motivation (25%).

Conclusions: The SCIIP intervention achieved limited success in improving vaccination coverage among previously fully vaccinated children. Analysis using the WHO BeSD framework revealed that the primary barrier to vaccine uptake for non-vaccinating parents on the Sunshine Coast were concerns over vaccine safety. These findings highlight the need for tailored public health strategies that address vaccine safety perceptions and enhance parental confidence in immunisation to achieve vaccination targets.

Urban Gentrification and Infectious Diseases: An interdisciplinary narrative

Behzad Kiani, Gabriel Parker, Senobar Naderian, Colleen Lau, Benn Sartorius

Background: Urban gentrification—the socioeconomic transformation of neighbourhoods due to the influx of higher-income residents—leads to displacement of lower-income communities and has significant but understudied public health implications. This study examines how gentrification influences infectious disease dynamics by exploring sociodemographic disparities, economic conditions, housing instability, and urban environmental changes.

Methods: A systematic narrative literature review was conducted using PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar, with search terms "gentrification" and "infectious disease." Snowballing methods were applied to identify additional relevant studies. After screening 542 articles, 14 studies met inclusion criteria. Studies were categorised by infectious disease type and data was extracted using a consensus-driven approach.

Results: Findings indicate that gentrification alters infectious disease risks through multiple pathways. Blood-borne and sexually transmitted infections (STIs) are exacerbated by reduced access to essential healthcare services, disproportionately affecting marginalized populations, including female sex workers and LGBTQ+ communities. Airborne diseases are linked to increased overcrowding and displacement, leading to worsening health inequalities. Changes in urban landscapes contribute to vector-borne disease risks especially among displaced populations. Spatial epidemiology approaches are recommended to better understand and visualize these complex dynamics.

Conclusions: Gentrification influences infectious disease patterns by reshaping healthcare access, housing conditions, and population distributions. Spatial epidemiology offers a valuable tool for mapping these risks and informing targeted public health interventions. Future research should focus on quantifying these impacts using advanced geospatial epidemiological techniques thus aiding development of mitigation strategies to address health disparities in gentrifying urban areas.

From Barnyards to B-Cells: A review of the evidence linking *Coxiella burnetii* to haematological malignancy risk

Anna Duan, Robert Norton

Background: Q fever, caused by *Coxiella burnetii*, is a zoonotic infection recognised for its chronic immune-modulating effects. While *C. burnetii* is known to trigger autoimmune and inflammatory syndromes, emerging evidence suggests a potential link with non-Hodgkin lymphoma (NHL). However, this association remains poorly defined. This review provides the first structured synthesis and critical appraisal of published mechanistic and epidemiological data examining the link between Q fever and haematological malignancy.

Methods: A structured narrative synthesis was conducted using literature from PubMed, Scopus, CINAHL, and Google Scholar. Studies were appraised across two themes: (1) the immunopathogenesis of *C. burnetii* and its theoretical contribution to lymphomagenesis; and (2) epidemiological associations with haematological malignancy. Key findings were assessed using Bradford Hill's causality framework.

Results: Mechanistically, *C. burnetii* induces chronic inflammation, immune evasion, and IL-10–mediated immunosuppression, fostering an environment conducive to lymphoid transformation. Transcriptomic profiling in persistent Q fever identified upregulation of genes implicated in NHL, supporting biological plausibility. *C. burnetii* DNA has also been detected in lymphoid tissue in some NHL cases, although no specific tropism has been confirmed. A French retrospective study found a significant association between chronic Q fever and NHL (OR 5.10; 95% CI: 1.43-18.14), particularly for DLBCL and follicular lymphoma. In contrast, a large Dutch cohort reported no increased risk (aHR 1.02; 95% CI: 0.78-1.33). Case reports provide additional anecdotal support but are limited by their scope. Overall, the evidence base is constrained by heterogeneity, small sample sizes, and absence of prospective data.

Conclusions: Bradford Hill analysis supports biological plausibility and analogy; however, criteria such as temporality, strength, and consistency are weak. The proposed link between *C. burnetii* and NHL is best described as weak to moderate. Routine screening is not indicated, but clinicians should remain vigilant. Prospective studies are needed to clarify risk and guide practice.