



CENTRE FOR
PATHOGEN
GENOMICS

BIENNIAL CENTRE REPORT

2024-2025

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EXECUTIVE SUMMARY

Established in 2022, the Centre for Pathogen Genomics is a University of Melbourne Research and Research Training Centre, bringing together world-leading expertise across pathogen genomics, bioinformatics, microbiology, epidemiology, public health, innovation, training and evaluation science to address infectious diseases of national and global importance.

Over the past two years, the Centre has made substantial progress against its strategic objectives of enabling innovative pathogen genomics research to address infectious diseases and emerging threats, foster the next generation of research leaders, and delivering impact and leadership in global health across the Asia-Pacific. The Centre has advanced its research agenda through the development of a Centre Research Strategy and delivered innovative high-impact research (>80 peer reviewed publications) across antimicrobial resistance (AMR), tuberculosis, influenza, emerging pathogens, and the microbiome. The Centre launched an inaugural Seed Grant Scheme, with initial strategic investment in 11 collaborative projects to foster research partnerships across the Centre and with Asia-Pacific partners, and generate early evidence for scalable, high-impact research.

The Centre is supporting the next generation of genomics leaders, with 16 PhD students, and >150 scientists, bioinformaticians, epidemiologists, and policy makers trained across 19 countries.

The Centre has strong global leadership in the development and deployment of advanced bioinformatic tools and platforms through the Bioinformatics Hub. Through the Training Hub, the Centre is also enhancing pathogen genomics capabilities across Australia and the Asia-Pacific through its PhD program, delivering practical workshops and in-country training and fostering regional communities of practice.

Collectively, the achievements outlined in this report demonstrate that the Centre for Pathogen Genomics is delivering strongly on its mission and strategic objectives, with a growing portfolio of high-impact research, significant external funding, an expanding skilled workforce, and clear evidence of national and international influence in shaping the future of pathogen genomics research.



RESEARCH

OVERVIEW

The Centre for Pathogen Genomics was established in 2022 with the mission, *accessible pathogen genomics for better health*. The Centre is co-led by Prof Tim Stinear, Prof Ben Howden and Dr Chuan Lim, and brings together a team of world-leading experts in pathogen genomics, epidemiology, bioinformatics, microbiology, clinical and public health, evaluation science, and capacity building and training. Collectively, the Centre Team has decades of experience in applying cutting edge genomic technologies to address infectious diseases of national and global importance. The Centre's research program focusses on optimising the use of pathogen genomics to inform public health action and spans eight key research themes: antimicrobial resistance (AMR), the microbiome, One Health, surveillance, data sharing, evolutionary genomics, metagenomics and evaluation science. The Centre team is also at the forefront of global efforts to develop and implement novel computational approaches to enhance genomic data utilisation..

RESEARCH STRATEGY

The Centre for Pathogen Genomics Research Strategy 2024-2027 sets out an ambitious agenda to position the Centre as a global leader in infectious diseases research across Australia and the Asia-Pacific through:

- Undertaking innovative and transformational research, from discovery to implementation, that leads to significant advancement of knowledge and health impacts
- Building research capacity and excellence in Australia and the Asia Pacific region
- Developing relationships and building networks across the Asia Pacific to strengthen and build critical mass of genomics research in our region
- Linking world-leading research in Australia with novel, interdisciplinary, collaborative approaches to address the most challenging and significant infectious diseases problems.
- Providing high-quality postgraduate and postdoctoral training environments for the next generation of pathogen genomics researchers

The implementation of the research strategy is supported by the research strategy group, which brings together emerging leaders across each of the Centres Scientific Themes.

Key Activities

The Centre's research program is underpinned by four key activities that together foster leadership, innovation. Additionally, the Bioinformatics, Innovation and Training Hubs, which provide the foundational expertise, infrastructure, and workforce development required to enable high-quality research (Figure 1).

Flagship Programs

The Centre is enabling the development and delivery large-scale, complex research programs, through its diverse network of expertise across academia, clinical and public health, industry and government.

Research Projects

In addition to our Flagship Programs, the Centre supports a diverse range of research projects that bring together diverse expertise from across the University as well as partners nationally and internationally.

Seed Grant Scheme

This Scheme aims to stimulate collaboration and enhance genomics capacity across the Asia-Pacific by funding research that addresses regional health priorities, including AMR, multi-drug-resistant tuberculosis and dengue.

Research Forum

This series brings together researchers from across the Centre to foster collaboration and communication among groups and showcase the breadth of the Centre research network.

RESEARCH STRATEGY

SCIENTIFIC THEMES



AMR



Microbiome



One Health



Surveillance



Data Sharing



Evolutionary Genomics



Metagenomics



Evaluation

OUR APPROACH



Flagship Programs



Research Projects



Seed Grants



Research Forum

ENABLING CAPABILITIES



Bioinformatics Hub



Innovation Hub



Training Hub

OUR IMPACT



>100
Publications



55
Presentations



18
Awards



19
Asia-Pacific
collaborations



11
Seed grants
awarded



\$35M
Grant funding

FLAGSHIP PROGRAMS



The Metagenomics Platform (Meta-GP) was an MRFF funded national, multi-centre cohort study that advanced the development and implementation of accredited clinical metagenomics diagnostics for infectious diseases in Australia.

Building on this success, the Metagenomics and Integrated Transcriptomics for Infectious Disease Genomics and Translational Evaluation (MITIGATE) program is now developing a next-generation diagnostic platform that integrates genomic and host immune profiling to enable rapid identification of complex infections.



AUSTRALIAN PATHOGEN GENOMICS PROGRAM

Integrating pathogen genomics into public health

The Australian Pathogen Genomics Program (AusPathoGen) will implement and evaluate a nationally synchronised approach to public health pathogen genomics.

This MRFF-funded program will utilise the AusTrakka platform for consistent analysis and reporting and collaborate with health departments and public health laboratories to facilitate rapid and coordinated genomics-based responses to major infectious disease threats.

RESEARCH

EXEMPLAR RESEARCH PROJECTS



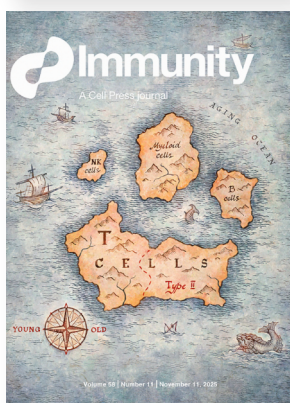
Rifaximin prophylaxis causes resistance to the last-resort antibiotic daptomycin

Multidrug-resistant bacterial pathogens like vancomycin-resistant *Enterococcus faecium* (VREfm) pose critical threat to human health. Daptomycin is a last resort antibiotic for VREfm infections but has widely reported unexplained resistance. This study, published in Nature, established that rifaximin, an unrelated antibiotic prescribed to patients with liver disease, causes cross-resistance to daptomycin in VREfm, overturning assumptions that rifaximin carries minimal resistance risk.



Mosquitoes provide a transmission route between possums and humans for Buruli ulcer in southeastern Australia

Published in Nature Microbiology, this study identified mosquitoes as the primary vector transmitting *Mycobacterium ulcerans* from the environment to humans, solving an 80-year mystery surrounding Buruli ulcer transmission. These findings represent a significant advancement in our understanding of the epidemiology of Buruli ulcer and provide an evidence base to support strengthened vector surveillance, targeted mosquito control and community-level prevention initiatives to control Buruli ulcer.



Microbiota-derived butyrate promotes FOXO1-induced stemness program and preserves CD8+ T cell immunity against melanoma

This study, published in Immunity, demonstrated that microbiota-derived butyrate regulates the differentiation of tumour-specific CD8+ T cells and reduces melanoma progression in pre-clinical cancer models. Metabolic flux modelling also predicted enhanced microbial production of butyrate in melanoma patients with complete therapeutic responses to immune checkpoint blockade, highlighting the influence of microbial metabolite production on cancer immunotherapy outcomes.



Successful management of a multi-species outbreak of carbapenem-resistant organisms in Fiji: a prospective genomics-enhanced investigation and response

Fiji is a Pacific Island nation grappling with the increasing threat of AMR. While genomic technologies are increasingly used to understand the emergence and spread of AMR globally, its application to inform outbreak responses in low-and middle-income settings remains limited. Through an established capacity building program, genomics was applied to identify multiple concurrent outbreaks of carbapenem-resistant organisms in a major Fiji hospital, highlighting the urgent risk posed by AMR pathogens in the Pacific and the importance of access to genomic technologies in resource limited settings.

SEED GRANT SCHEME

The inaugural Centre for Pathogen Genomics Seed Grant Scheme funded 11 innovative research projects (Table 3) that exemplify scientific excellence, foster regional collaboration, and align with the vision and objectives of the Centre. This approach seeks to catalyse new partnerships with researchers in low to middle income countries (LMICs) and generate foundational data to support future, larger-scale competitive funding applications. Each of the awarded projects demonstrates a commitment to using genomics for real-world impact, advancing local expertise, and building stronger regional research networks.

TABLE 3: SEED GRANTS AWARDED IN 2025

LEAD APPLICANT	PROJECT
Dr Courtney Lane Ms Keeley Allen	Genomic epidemiology of carbapenem-resistant organisms in Sri Lanka
Dr Prashanth Ramachandran	Custom hybrid-capture metagenomic sequencing for paediatric CNS infections in low-resource settings: a Vietnam pilot
Dr Kathryn Edenborough	Genomic surveillance of dengue virus imported in Victorian returned travellers (DIVRT)
Dr Khrisdiana Putri	Genomic insights into <i>Enterococcus</i> and <i>Salmonella</i> from cattle and poultry in Yogyakarta, Indonesia
Dr Mun Hua Tan	Exploring hidden reservoirs of malaria parasite diversity in humans
Ms Tilda Thomson Dr Courtney Lane	Genomic epidemiology of enteric pathogens from human clinical infections and water sources in Papua New Guinea
Dr Aneley Getahun Strobel	Investigation of emerging antimicrobial resistance in Fiji: a One Health approach
Dr Sarah Baines	Coordinated multi-country genomic snapshot of antimicrobial resistant pathogens: a pilot study of carbapenemase-producing <i>Acinetobacter baumannii</i> in Bhutan, Nepal and Papua New Guinea
Dr Patiyan Andersson	Capacity building for whole genome sequencing of multidrug-resistant tuberculosis and assessment of 10-colour Xpert MTB/XDR assay for second-line drug resistance in Bhutan
Dr Natasha Jansz	Genetic and structural diversity underlying distinct disease outcomes of HTLV-1 infection
Dr Jake A. Lacey	Genomic bioprospecting of antimicrobial, probiotic, and extremophilic bacteria from Nepal

TRAINING

TRAINING STRATEGY

The Training Hub was established to develop the next generation of pathogen genomics researchers across Australia and the Asia-Pacific. The Centre's training program spans microbial genomics, bioinformatics, genomic epidemiology, evaluation and policy, and aims to build a genomics research and public health workforce equipped to effectively generate and use genomic data, and support the translation of genomics science into accessible, actionable public health insights. Training is delivered through multiple complementary pathways including a PhD program, practical workshops and in-country training activities, flagship programs and the development of regional communities of practice networks (Figure 2).

Key Activities

Global Health Forum

The Global Health Forum is a regional, collaborative meeting that brings the Centre's trainee network to further develop their skills in pathogen genomics. Each session includes a mix of case studies and updates from the Centre team and trainees across laboratory, bioinformatics, genomic epidemiology, policy and practice. The meeting also provides a supportive environment to share ideas, troubleshoot challenges, and seek advice on projects, workflows and protocols.

Micro-credentials

The Training Hub delivers a series of University of Melbourne micro-credentials focussed on microbial genomics each year. These micro-credentials, designed for health professionals, provide an overview of the science behind DNA sequencing, best-practice approaches for generating and analysing sequence data and, how microbial genomics can help address the public health challenges of our times. Each year, these micro-credentials attract 30-40 enrolments across both units.

PhD Program

The Centre Team demonstrates strong capability and sustained commitment to mentoring higher-degree research students across diverse scientific and institutional settings, collectively supervising a cohort 16 PhD candidates, three master's students, and two Honours students across multiple institutions and research groups. This cohort includes students from seven countries across the Asia-Pacific and Africa, providing an internationally focused, diverse community to foster a collaborative culture.



TRAINING STRATEGY

OUR CAPABILITIES



Laboratory



Bioinformatics



Genomic
Epidemiology



Policy and
Governance

WHO WE WORK WITH



Governments and
Ministries of Health



Clinical and Public
Health Laboratories



Universities and Medical
Research Institutes



Global Health Agencies
and Funders

OUR APPROACH



PhD Program



Microcredentials



Global Health
Forum



Practical
workshops



Flagship
Programs

OUR IMPACT



16

PhD Students



150+

Microcertificate
completions



12

Workshops
delivered



150+

Trained



20+

Countries

TRAINING

FLAGSHIP PROGRAMS



Funded by the Department of Foreign Affairs and Trade (DFAT), this program aims to support implementation of public health pathogen genomics across the Asia-Pacific region.

Working with in-country partners in Malaysia, Fiji and the Philippines, the program supports the development and implementation of national pathogen genomics surveillance strategies, strengthens the integration and use of genomics data within infectious disease surveillance systems, delivers targeted workforce training, and enhances regional connectivity and collaboration in pathogen genomics across the Asia-Pacific region.



PulseNet Asia Pacific (PNAP) was established in 2002 as a regional arm of PulseNet International (PNI). The primary objective of this program is to establish a regionally connected network of national laboratories to strengthen genomics-informed enteric pathogen surveillance and outbreak response across the Asia-Pacific.

Since being appointed as regional coordinators in 2022, the Centre has facilitated hands-on training, developed and optimised standard operating procedures, and provided ongoing mentorship through monthly Office Hours sessions. This initiative is funded by the Association of Public Health Laboratories and the US Centres for Disease Control.

EXEMPLAR RESEARCH PROJECTS



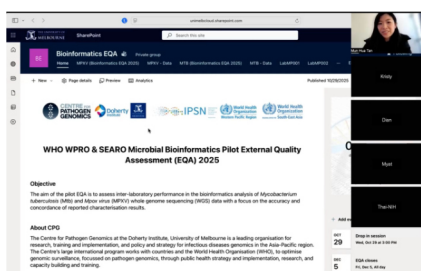
DFAT Australia Awards Fellowships

Through this program, the Centre hosted 11 public health professionals from Bangladesh, Bhutan, Cambodia, Fiji, Malaysia and the Philippines for an intensive five-week training program in genomics-informed surveillance and diagnosis of infectious diseases. The program provided practical training in the generation, analysis and interpretation of genomic data. Fellows were also paired with a senior academic mentor to further support skill development. The Fellows are now being supported to apply these skills to enhance local infectious disease surveillance programs in their respective countries.



Genomic sequencing of emerging high threat pathogens

Following the WHO's declaration of mpox as a public health emergency of international concern in August 2024, the Centre was engaged by the WHO to deliver a one-week training program on genomics sequencing of monkeypox virus (MPXV) for 25 public health professionals from 20 laboratories across the Asia-Pacific region. The Centre is continuing to support the trainees to implement genomic sequencing of MPXV in their laboratories, enhancing regional capacity to detect and respond to mpox.



Regional bioinformatics external quality assessment (EQA) program

One of the major challenges to the implementation of public health pathogen genomics is a lack of robust, standardised bioinformatics and data analysis systems. To address this, the Centre, working in partnership with the WHO, developed and delivered a pilot bioinformatics EQA program focussed on benchmarking and strengthening bioinformatics workflows for MPXV and *M. tuberculosis*. More than 20 scientists from 12 laboratories across nine countries participated in the pilot. Based on strong engagement and clear regional demand, the Centre is planning to expand the EQA program in 2026.



SeqAsia

SeqAsia is a training and capacity building project. Delivered in conjunction with the Danish Technical University and supported by the Fleming Fund, this 12-month initiative provided online and intensive in-country training to strengthen Thailand's position as a regional leader in genomics-based AMR surveillance. SeqAsia also hosted regional webinars to enhance collective knowledge and develop a network of genomics-informed AMR professionals across the Asia-Pacific region.

BIOINFORMATICS HUB

OVERVIEW

The Bioinformatics Hub brings together a multidisciplinary team of bioinformaticians, computational biologists and software engineers, dedicated to both supporting Centre's program of work and undertaking independent research. A major focus of the Hub is to develop and implement best-practice approaches for microbial genomic data analysis and foster collaboration with other University initiatives including the Doherty Institute Computational Science Initiative (CSI) and Melbourne Integrated Genomics (MIG). The Hub also provides Centre researchers with access to high-performance computing resources to support data analysis and storage. Working with the Training Hub, the Bioinformatics Hub also aims to enhance the genomics capabilities of Centre researchers, contributes to regional capacity building initiatives and fosters a community of practice for pathogen genomics across the Asia-Pacific region.

KEY ACTIVITIES AND PROJECTS

Bioinformatics Analysis Portal

The Bioinformatics Analysis Portal is a browser-based platform that streamlines genomic data analysis and visualisation. By transforming complex genomics pipelines into a point-and-click web interface, it enables users to move from raw sequencing to actionable insights, without the need for command-line bioinformatics expertise. The Portal reduces technical barriers, ensures reproducibility, and enables scalable pathogen genomics analysis for outbreak investigations and national surveillance programs. Its browser-based design and minimal infrastructure requirements make it suitable for use in resource-limited settings, expanding participation in genomic surveillance across diverse contexts.

PathoGenTrakka

This project will adapt AusTrakka, Australia's secure genomic surveillance platform, to PathoGenTrakka, a genomic data integration, analysis, visualisation and reporting platform that can be managed and deployed in-country on either government infrastructure or in the cloud. By providing locally deployable bioinformatics and surveillance solutions, PathoGenTrakka will enhance genomic surveillance capacity in resource-limited settings, and remove barriers to data analysis, integration and public health action.

Tool Development

The Centre Team has led or contributed to the development of numerous tools that support microbial genomics data analysis, visualisation and use. Key examples are outlined below, and a full list is provided in Appendix C.

Autocycler: Generates accurate bacterial genome assemblies by combining multiple alternative long-read assemblies of the same genome.

TbtAMR: A comprehensive pipeline to predict Mycobacterium tuberculosis drug susceptibility from genomic data, validated and accredited to ISO standards.

Core-SNP-Filter: Filters sites in a FASTA-format whole-genome alignments based on variability and conservation.

Pango-collapse: Simplifies and automates SARS-CoV-2 reporting by collapsing Pango sub-lineages into user-defined parent lineages.

SonneiTyper: Genotype-calling and lineage-assignment tool for Shigella Sonnei.

The screenshot shows the homepage of the Centre for Pathogen Genomics Bioinformatics Analysis Portal. At the top, there is a search bar with the text "Search the Portal" and a navigation menu with "About". The main header features the Centre for Pathogen Genomics logo and the tagline "Explore and run tools from the most talented and accomplished scientists ready to take on your next project". Below this, there are two buttons: "Sign Up" and "Learn More". The main content area displays a grid of tool cards. Each card includes a title, a brief description, and a list of tags. The tools shown are: abriTAMR (Antimicrobial gene detection in assembled genomes from WGS data...), terrier (Transposable Element Repeat Result classifier), mlst (MLST scans contig files against traditional PubMLST typing schemes to determine the sequence type (ST) of...), Seqkit Stats (Simple statistics of FASTA/Q files using Seqkit: A cross-platform and ultrafast toolkit for FASTA/Q file manipulation.), tbtAMR (tbtAMR implements custom logic developed at MDU-PHL to identify mutations linked to antimicrobial...), and TraDIS-ONT (A set of Python scripts for processing Oxford Nanopore sequencing reads from Transposon-Directed Insertion Sit...).

INNOVATION HUB

OVERVIEW

The Innovation Hub operates within a framework of collaborative partnerships to empower researchers to harness the power of pathogen genomics to address significant human and animal health challenges. It supports research partners across the University and externally by providing access to genome sequencing capacity, technical expertise and critical training (Figure 3). The Innovation Hub integrates discovery research with practical applications, focussing on infectious diseases, AMR and the microbiome. Since its establishment in 2014, the Innovation Hub has been involved in more than 200 projects (testing >34,000 samples), contributed to more than 150 publications and numerous grant applications attracting over \$25 million in funding.

KEY ACTIVITIES AND PROJECTS

Lifeblood Partnership

Faecal Microbiota Transplantation (FMT) emerging as an effective therapy for recurrent *Clostridioides difficile* infection, with its potential for clinical use expanding following recent Therapeutic Goods Administration approval for the manufacture and distribution of FMT products by Lifeblood. Through this partnership the Innovation Hub will generate the first comprehensive evidence base connecting FMT safety, quality and efficacy, positioning Lifeblood as a national leader in evidence-based microbiome therapeutics, ready to evaluate new clinical applications of FMT across diverse disease settings.

Microbiome Platform

In recent years, the Innovation Hub has expanded its capacity to support research into the role of the microbiome in human health and disease by providing expertise in sequencing, interpretation and reporting of the microbiome. To further strengthen capability in this area, the Hub has recently established a microbiome biobank to catalogue and characterise microorganisms within the human microbiome, creating a valuable resource that will enable research into microbiome-health interactions.

Macrophage MR1 antigen presentation promotes MAIT cell immunity and lung microbiota modulation

This study, published in Science, examined how mucosal-associated invariant T (MAIT) cells are activated by microbial antigens to support tissue homeostasis and antimicrobial immunity. Tissue-resident macrophages were identified as the main cell type expressing MHC class I-related protein (MR1) and presenting microbial vitamin B-derived antigens. Loss of MR1 in myeloid cells altered microbiota composition and impaired MAIT cell responses against bacterial infections, demonstrating a critical role for macrophages in MR1 antigen presentation and MAIT cell immunity.

Benchmarking reveals superiority of deep learning variant callers on bacterial nanopore sequence data

This study demonstrates that combining the latest generation of Oxford Nanopore Technology (ONT) long read sequence data with state-of-the-art variant callers enables bacterial variant discovery at an accuracy comparable to or exceeding the current gold standard of Illumina short read sequencing. These results highlight the potential of ONT sequencing to replace traditional short-read sequencing methods in bacterial genomics, particularly in resource limited-settings.

INNOVATION HUB STRATEGY

OUR CAPABILITIES



Advice on
Study Design



Whole Genome
Sequencing



Metagenomics



Microbiome
Profiling



Plasmid / Clone
validation



Bioinformatics



Training



Access to
Instruments

WHO WE WORK WITH



Medical Research Institutes

Burnet Institute
The Florey Institute
The Kids Research Institute



Universities

Monash University
University of Sydney
University of Queensland



Industry

CSL
360biolabs
Lifeblood



Hospitals

Royal Children's Hospital
Austin Hospital
Royal Melbourne Hospital

OUR IMPACT



200+
collaborative
research projects



> 20
research groups
supported



150
publications



> \$25M
in grant funding

LEADERSHIP

POLICY AND ADVISORY ROLES

The Centre Team hold key leadership and advisory roles across Australia and globally. A summary of these roles is provided below (Table 4).

TABLE 4: POLICY AND ADVISORY ROLES

ROLE	CENTRE TEAM MEMBER
Public Health Laboratory Network (PHLN) member	Prof Ben Howden Dr Chuan Lim
PHLN AMR expert reference panel member	Prof Ben Howden A/Prof Norelle Sherry
Communicable Diseases Genomics Network (CDGN) chair	A/Prof Norelle Sherry
CDGN member	Prof Ben Howden Prof Tosten Seemann
Australian Biosecurity Laboratory Network state representative	Dr Chuan Lim
Member of the National Working Group on drug-resistant Neisseria gonorrhoea	A/Prof Norelle Sherry
Member of Australian Strategic and Technical Advisory Group on AMR	Prof Ben Howden
Founding chair for Melbourne TB Community	A/Prof Sarah Dunstan
Director WHO Collaborating Centre for Mycobacterium ulcerans	Prof Tim Stinear
WHO Buruli ulcer Technical Advisory Group member	Prof Tim Stinear
Director WHO Collaborating Centre for Antimicrobial Resistance	Prof Ben Howden
Temporary advisor to the WHO Western Pacific Region Emerging Molecular Pathogen Characterization Technologies (EMPACT) Surveillance Network	Dr Courtney Lane Dr Norelle Sherry
Expert advisor to the Member State negotiations at the Intergovernmental Working Group in relation to the Pathogen Access and Benefit-Sharing	Prof Ben Howden
Public Health Alliance for Genomic Epidemiology Bioinformatics Pipelines and Visualisation Working Group member	Prof Torsten Seemann
Co-Director, WHO Rotavirus Regional Reference Laboratory for the Western-Pacific Region	Dr Celeste Donato
OIE/FAO Network of Expertise on Animal Influenza member	Dr Michelle Wille
National Avian Influenza Wild Bird Surveillance Steering Group member	Dr Michelle Wille
Scientific Committee for Antarctic Research member	Dr Michelle Wille
Commonwealth Environmental Water Hold (CEWH) High Pathogenicity Avian Influenza Advisory Group member	Dr Michelle Wille
Bioplatforms Australia Animal Disease 'Omics Initiative' Advisory Group member	Dr Michelle Wille
East Asian Australian Flyway Partnership Avian Disease Working Group member	Dr Michelle Wille
Population and Conservation Status Working Group of the Agreement for the Conservation of Albatrosses and Petrels (ACAP), High pathogenicity H5N1 Avian Influenza Intersessional Group member	Dr Michelle Wille

LEADERSHIP

PARTNERSHIP WITH THE WHO INTERNATIONAL PATHOGEN SURVEILLANCE NETWORK (IPSN)

The IPSN was established in 2023 to help protect people from infectious disease threats through the power of pathogen genomics. The Centre has been one of the earliest members of the network and contributed expertise in governance, evaluation, epidemiology, bioinformatics and public health. The partnership with IPSN has driven new collaborations, linkages with the global genomics community, capacity building and training initiatives, and development of key resources in the IPSN toolkit. One of the Centre's key activities with the IPSN has been the development of a Monitoring and Evaluation Tool (M&E) for the IPSN toolkit, Capacity Strengthening Framework for Pathogen Genomics Informed Surveillance Systems. This tool is aligned with other IPSN tools and resources and structured to support implementation of WHO's Global Genomic Surveillance Strategy. It aims to provide countries, funders, and implementers with a standardised approach to systematically assess progress towards implementing the established goals for a public health pathogen genomics surveillance system.

CONFERENCE ORGANISATION

3rd International *Mycobacterium ulcerans* Conference (IMUC-III)

The Centre led the delivery of IMUC-III, hosted by the WHO Collaborating Centre for *Mycobacterium ulcerans* in partnership with the Doherty Institute. Held in Melbourne in November 2024, the conference brought together 153 experts from 21 countries to share progress in addressing the challenges of Buruli ulcer, including treatment, transmission, pathogenesis, and diagnosis.

Global Microbial Identifier 15 (GMI15)

The Centre hosted the Global Microbial Identifier 15 (GMI15) meeting in Melbourne in September 2025. This meeting brought together more than 100 international scientists and policy makers from over 30 countries, to advance equitable implementation of pathogen genomics, promote global data sharing and address policy and legislative challenges for data access and benefits sharing.

PulseNet International Meeting

In September 2025, the Centre co-hosted a joint PulseNet Asia Pacific and PulseNet Africa meeting. This meeting was attended by 28 scientists from 18 countries and facilitated knowledge sharing among laboratories and regions, and planning for the 2026 work year.

IPSN Global Partners Forum

The Centre co-hosted the IPSN Global Partners Forum with the WHO South-East Asian and Western Pacific Regional Offices in November 2024. The Forum provided a platform for public health practitioners, academics, policy makers and financial institutions to build partnerships, introduce innovations and accelerate the deployment of pathogen genomics.

Surveillance of Pathogens in Oceania and the Pacific (SPOP)

The Centre represented the Doherty Institute at the SPOP Workshop, organised by Institut Pasteur New Caledonia. The workshop focused on advancing genomic surveillance of pathogens in the Pacific region through a One Health approach and marked a significant milestone in fostering collaboration among Pacific Island Countries and Territories.

11th International Symposium on Avian Influenza

In June 2025, Centre Dr Michelle Wille co-convened the 11th International Symposium on Avian Influenza in Canada. The symposium convened scientists, biologists, veterinarians, medical researchers, and government regulators to share the latest evidence on avian influenza and address national and international issues through a One Health lens.

AWARDS

The Australian Museum Eureka Prize for Infectious Diseases Research Finalist (2024 and 2025)

Beating Buruli Team (led by Prof Tim Stinear)

Victorian Public Healthcare Award (2024)

Beating Buruli Team (led by Prof Tim Stinear)

Australian Society for Microbiology Distinguished Orator Award (2025)

Prof Tim Stinear

NHMRC 10 of the best (2025)

Prof Ben Howden

Australian Biosecurity Award - Environmental Biosecurity (2024)

Dr Michelle Wille

Victorian Tall Poppy Award (2024)

Dr Michelle Wille

Catton Prize for Impact in Public Health

AusPathoGen Leadership Team

The Australian Society for Microbiology Frank Fenner Award (2025)

Dr Danielle Ingle

A/Prof Sacha Pidot

Dean's Award for Excellence in PhD Thesis (2025)

Adrianna Turner

Highly Cited Researchers (2024 and 2025)

Dr Claire Gorrie

Dr Ryan Wick

The Australian Society for Microbiology Dena Lyras ECR Award (2025)

Dr Chris Connor

eMERGE Bridging Fellowship (2025)

Dr Sarah Baines

Microbial Genomics Best Talk at Mircoseq (2025)

Munazzah Maqbool

Best Sessional Talk, Indo-Pacific Futures Leaders in AMR Student Symposium (2025)

Jia Qi Beh

PUBLICATIONS AND PRESENTATIONS

PUBLICATIONS

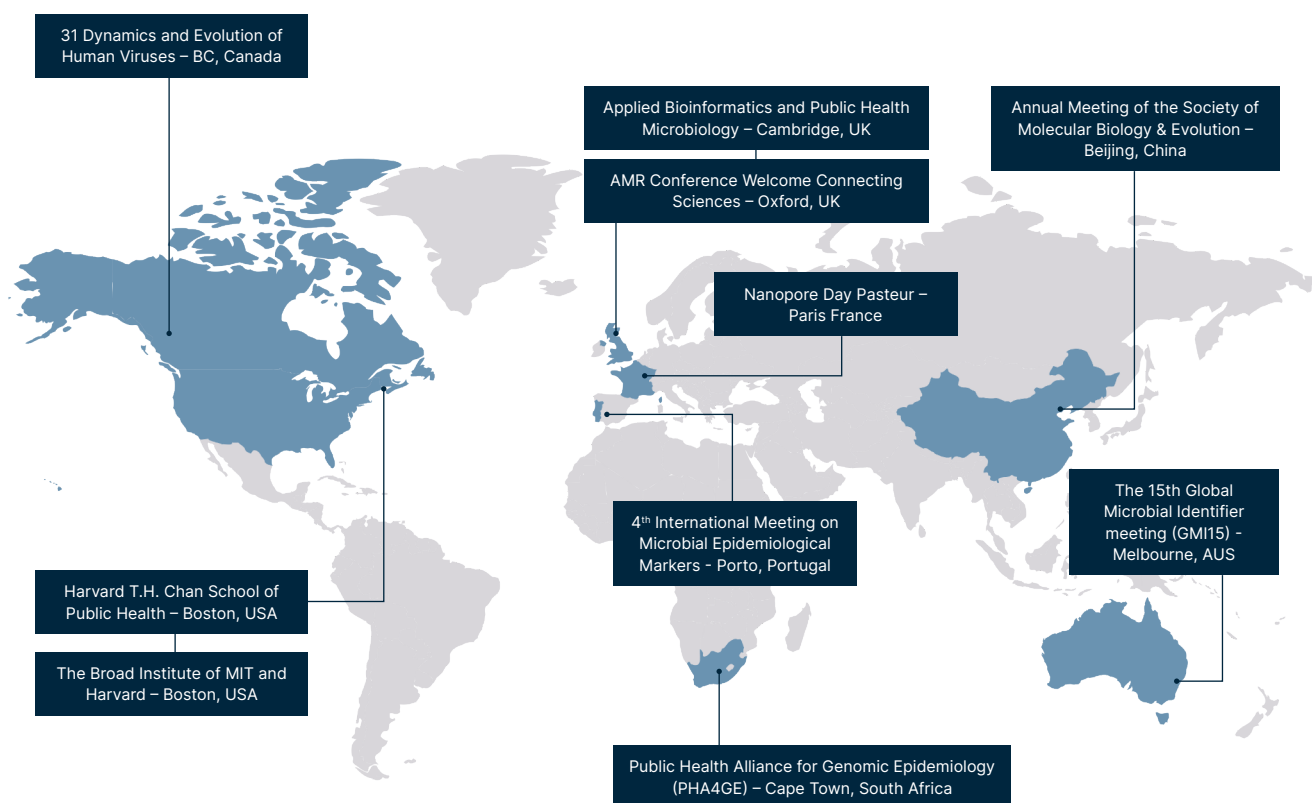
During 2024-2025, the Centre produced over 100 publications, applying pathogen genomics to infectious diseases surveillance, AMR, the microbiome and One Health and encompassed discovery and translational research, as well as methodological and bioinformatic advances. The Centre's research was published in leading high-impact international Journals, including Nature, Science, Nature Communications, Lancet Microbe, Lancet Regional Health – Western Pacific, eLife, Immunity, Genome Medicine, Microbial Genomics, and Antimicrobial Agents and Chemotherapy, reflecting both scientific excellence and global impact. Collectively, these studies advanced understanding of pathogen evolution, transmission and resistance, demonstrated the importance of genomics informed surveillance systems for public health decision making in Australia and the Asia-Pacific.

PRESENTATIONS

The Centre Team delivered over 55 presentations across nine countries at national and international conferences, meetings and symposia in 2024 and 2025. This included presentations at major international conferences the 15th Global Microbial Identifier (Melbourne), Congress of the European Society of

Clinical Microbiology and Infectious Diseases (Austria), ASM Microbe (USA), Applied Bioinformatics and Public Health Microbiology (UK), and Dynamics and Evolution of Human Viruses (Canada) (Figure 4).

Key presentations highlighted the development and application of innovative computational tools including WebAssembly, a powered client-side bioinformatics software, Snippy-NG for next generation microbial variant calling and Barbet, a deep learning approach for bacterial taxonomic classification. Centre researchers also addressed critical aspects of public health genomics, including the implementation of AMR surveillance programs, ISO accreditation of bioinformatic pipelines, and the coordination of national pathogen genomics initiatives (AusPathoGen), demonstrating the translation of genomic research into applied public health practice. Central themes across these engagements included the enhancement of accessibility and automation in genomic analyses, reinforcing the Centre's commitment to advancing both methodological innovation and public health impact.



GRANTS AND FUNDING

TABLE 6: ACTIVE GRANTS AND FUNDING AWARDED TO THE CENTRE TEAM

SCHEME / PROJECT	CENTRE CIS	AMOUNT	YEARS
ARC FUTURE FELLOWSHIPS: Preparing Australia for the next panzootic	Dr Michelle Wille	\$1,131,187	2025 - 29
ARC DISCOVERY EARLY CAREER RESEARCH AWARD: High-throughput bacterial genome assemblies with perfect accuracy	Dr Ryan Wick	\$387,071	2024 - 28
NHMRC INVESTIGATOR GRANTS: Elimination of <i>Mycobacterium ulcerans</i> infection (Buruli ulcer)	Prof Tim Stinear	\$3,014,025	2026 - 30
Genomics-driven innovations to tackle drug-resistant bacterial infections	Prof Ben Howden	\$2,668,202	2026 - 30
Understanding complex genomic and biochemical landscapes in human health microbiology	Prof Tim Stinear	\$2,210,520	2021 - 25
Genomics for combating antimicrobial resistant bacterial pathogens	Prof Ben Howden	\$2,027,364	2021 - 25
MRFF GENOMICS HEALTH FUTURES MISSION: The Australian Pathogen Genomics Program (AusPathoGen)	Prof Ben Howden	\$2,995,437	2026 - 29
Metagenomics and Integrated Transcriptomics for Infectious Disease Genomics and Translational Evaluation (MITIGATE)	Dr Prashanth Ramachandran	\$2,955,490	2025 - 30
AusPathoGen	Prof Ben Howden	\$9,999,499	2021 - 24
MetaGP	Prof Tim Stinear	\$6,984,360	2021 - 24
ARC DISCOVERY PROJECT: Unravelling Toxic Cyanobacterial Ecosystem Challenges in Wastewater Reuse	Prof Ben Howden	\$758,537	2025 - 27
CUMMING GLOBAL CENTRE FOR PANDEMIC THERAPEUTICS FOUNDATION GRANT: Customisable biotherapeutics against pandemic pathogens	Prof Ben Howden	\$600,000	2024 - 27
CHAN ZUCKERBERG INITIATIVE: Bacterial variant calling with Snippy	Prof Torsten Seemann	\$400,000	2024 - 26
DFAT STRATEGIC PARTNERSHIP Building resilience to infectious diseases globally through genomics	Prof Ben Howden	\$1,562,312	2024 - 27
DFAT AUSTRALIA AWARDS FELLOWSHIPS: Strengthening genomics-informed surveillance, diagnosis and control of infectious diseases across the Asia-Pacific	Prof Ben Howden	\$218,418	2024 - 25
CONTRACTS AND OTHER FUNDING		\$7,887,965	2024 - 25
TOTAL		\$45,803,387	

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Dr Chuan Lim

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APPENDICES

APPENDIX A: CENTRE PUBLICATIONS

- Acharya J, Jha R, Bhatta RR, Shrestha L, Sharma BK, Chapagain S, *et al.* Extended spectrum beta-lactamase producing *Escherichia coli* and antimicrobial resistance gene sharing at the interface of human, poultry and environment: results of ESBL tricycle surveillance in Kathmandu, Nepal. *One Health Outlook.* 2025;7(1):25.
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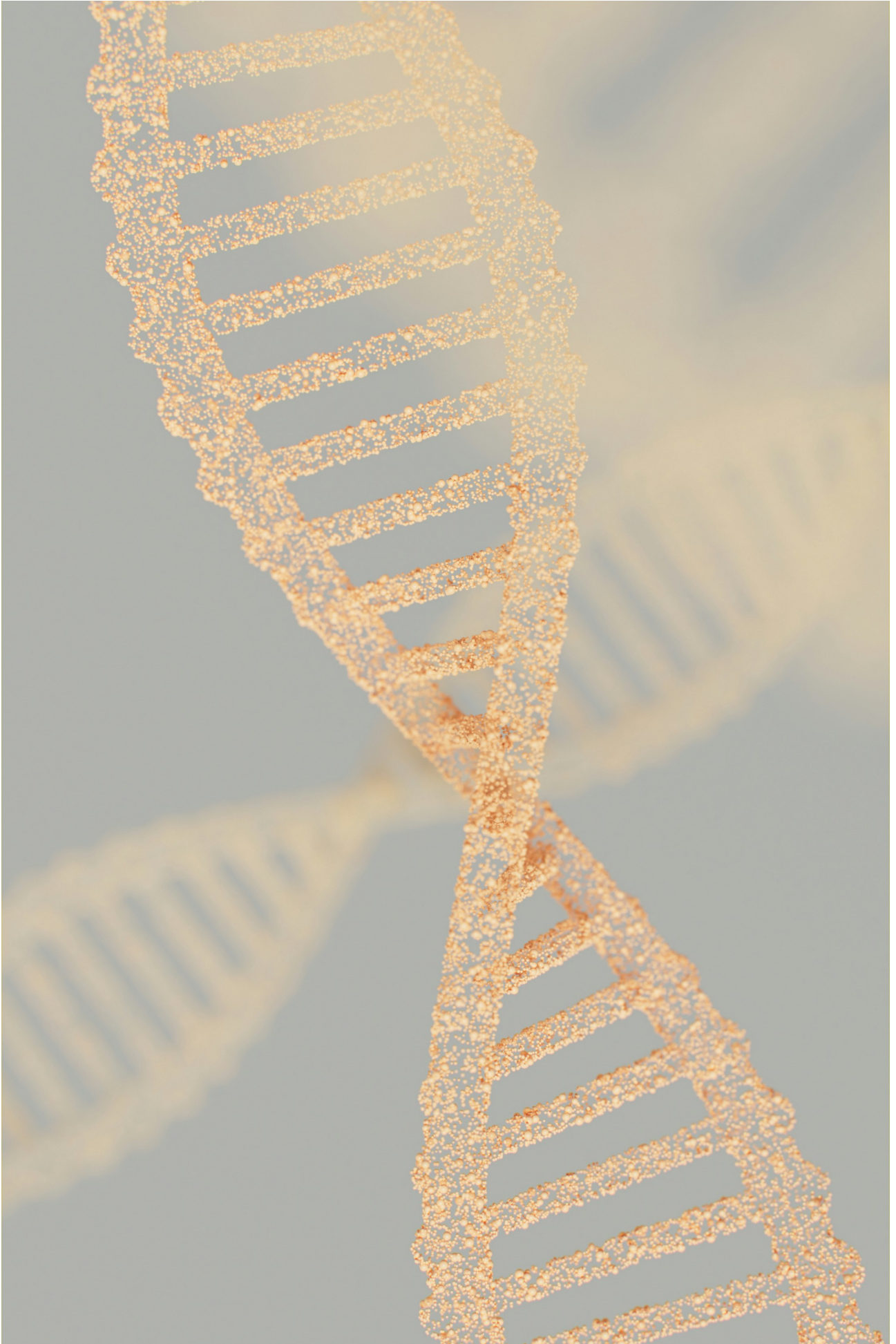
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APPENDICES

APPENDIX B: BIOINFORMATICS TOOLS

NAME	DESCRIPTION	LINK
Prokka	Prokka is a software tool to annotate bacterial, archaeal and viral genomes quickly and produce standards-compliant output files.	https://github.com/tseemann/prokka
Snippy	Rapid haploid variant calling and core genome alignment.	https://github.com/tseemann/snippy
Mlst	Scans contig files against traditional PubMLST typing schemes.	https://github.com/tseemann/mlst
Abricate	Mass screening of contigs for antimicrobial and virulence genes.	https://github.com/tseemann/abricate
Unicycler	An assembly pipeline for bacterial genomes.	https://github.com/rrwick/Unicycler
Autocycler	Generates accurate bacterial genome assemblies by combining multiple alternative long-read assemblies of the same genome.	https://github.com/rrwick/Autocycler
Porechop	Porechop is a tool for finding and removing adapters from ONT reads.	https://github.com/rrwick/Porechop
Filtlong	Filtlong is a tool for filtering long reads by quality.	https://github.com/rrwick/Filtlong
Bohra	A pipeline for bioinformatics analysis of bacterial genomes	https://github.com/MDU-PHL/bohra
AbritAMR	abriTAMR is an AMR gene detection pipeline that runs AMRFinderPlus on a single (or list) of given isolates and collates the results into a table, separating genes identified into functionally relevant groups. This pipeline has been accredited by NATA for use in reporting the presence of reportable AMR genes in Victoria Australia	https://github.com/MDU-PHL/abritamr
tbTAMR	A comprehensive pipeline for to predict Mycobacterium tuberculosis drug susceptibility from genomic data, validated and accredited to ISO standards.	https://github.com/MDU-PHL/tbtamr
Panaroo	A pipeline for running AMRfinderPlus and collating results into functional classes.	https://github.com/gtonkinhill/panaroo
fastBAPS	A fast approximation to a Dirichlet Process Mixture model (DPM) for clustering genetic data.	https://github.com/gtonkinhill/fastbaps
PanStripe	Panstripe improves the post processing of bacterial pangenome analyses by replacing the dubious but popular pangenome accumulation curves.	https://github.com/gtonkinhill/panstripe
Shovill	Assemble bacterial isolate genomes from Illumina paired end reads.	https://github.com/tseemann/shovill
Core-SNP-Filter	Filters sites in a FASTA-format whole-genome alignment based on variability and conservation.	https://portal.cpg.unimelb.edu.au/tools/Core-SNP-filter
Pango-collapse	Simplifies and automates SARS-CoV-2 reporting by collapsing Pango sub-lineages into user-defined parent lineages.	https://github.com/MDU-PHL/pango-collapse
SonneiTyper	Genotype-calling and lineage-assignment tool for shigella sonnei.	https://github.com/katholt/sonneityping





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