National Microbial Genomics Framework 2024–2025

Endorsed by

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Foreword

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Glossary of key technical terms

For the purposes of the National Microbial Genomics Framework 2023-2026, key terms are defined as follows.

Term	Definition
Bioinformatics	The use of algorithms and software to analyse sequencing data.
DNA	Deoxyribonucleic acid—a self-replicating material which is present in nearly all living organisms as the main constituent of chromosomes. It is the carrier of genetic information.
Efficiency	A measure of whether health care resources are being used to get the best value for money. Includes technical, productive, and allocative efficiency.
Gene	The basic physical and functional unit of heredity. Genes, which are made up of DNA, act as instructions to make molecules called proteins.
Genome	The complete set of genetic information in an organism.
Genomics	The application of genome-based knowledge through the study of genes and other genetic information, their functions, and interrelationships for the benefit of human health.
Genomic data	Refers to data produced from DNA sequencing of a genome.
Genomic knowledge	Includes information about the interpretation of genomic data and the implications of these findings, as well as relevant non-genomic clinical information.
Genomic services	Genome sequencing and analysis available for research, screening, and diagnostic purposes.
Genomic surveillance	Involves the monitoring of pathogen evolution, transmission, and dissemination, including distribution and evolution of antimicrobial resistance determinants and lineages. This type of surveillance involves applying the principles of evolutionary biology to determine the relatedness of pathogens
Genomic testing	Involves the analysis of hundreds or even thousands of genes from a pathogen simultaneously using sophisticated computer-based algorithms.
Governance	The structures and processes by which the health system is regulated, directed, and controlled. It includes the obligations of stewardship—ensuring that the system is well sustained for the future as well as serving the needs of the present.

Lineage	A group of closely related organisms, such as viruses, with a common ancestor.
Metadata	A set of data that describes and gives information about other data.
Metagenomics	The study of all genetic material recovered from an environmental or clinical sample. Metagenomics is often used to study a specific community of microorganisms, or to identify an unknown microbial agent(s).
Microbe	A microorganism, such as bacteria, virus, or fungi, that can be seen only through a microscope.
Microbial genomics	The genomic study of microbes or microorganisms.
One Health	An approach to designing and implementing programs, policies, legislation, and research in which multiple sectors communicate and work together to achieve better public health outcomes.
Pathogen	An organism that can cause disease.
Pathogen genomics	The genomic study of a pathogen, a category of microbial genomics.
Proteomics	The study of proteomes and their functions. A proteome is a set of proteins produced in an organism, system, or biological context. Proteomes differ from cell to cell and can change over time.
RNA	Ribonucleic acid—a nucleic acid present in all living cells. Its principal role is to act as a messenger carrying instructions from DNA to initiate and control the synthesis of proteins, although in some viruses RNA rather than DNA carries the genetic information.
Strain	A strain is a genetic variant or subtype of microorganism.
Variant	An organism that is genetically distinct from a main strain, but not sufficiently different to be termed a distinct strain.
Whole genome sequencing	A laboratory process to determine the complete DNA sequence of an organism's genome.

Acronyms and abbreviations

Acronym	Meaning
ABLN	Australian (Counter) Bioterrorism Laboratory Network
AHPPC	Australian Health Protection Principal Committee
AMR	Antimicrobial resistance
ASTAG	Australian Strategic and Technical Advisory Group on AMR
CDC	United States Centers for Disease Control and Prevention
CDGN	Communicable Diseases Genomics Network
CDNA	Communicable Diseases Network Australia
COVID-19	Coronavirus disease 2019
DNA	Deoxyribonucleic acid
EMPaCT	Emerging Molecular Pathogen Characterisation Technologies
EQA	External Quality Assurance
FDA	United States Food and Drug Administration
GHFM	Genomics Health Futures Mission
GMI	Global Microbial Identifier
HCEF	Health Chief Executives Forum
Health	Australian Government Department of Health and Aged Care
LEADDR	Laboratories for Emergency Animal Disease Diagnosis and Response
MDU PHL	Microbiological Diagnostic Unit Public Health Laboratory
MRFF	Medical Research Future Fund
NATA	National Association of Testing Authorities
NHMRC	National Health and Medical Research Council
NPAAC	National Pathology Accreditation Advisory Council
OHP	Office of Health Protection
PHLN	Public Health Laboratory Network

PHU	Public Health Unit
PTP	Proficiency Testing Program
RCPA QAP	The Royal College of Pathologists of Australasia Quality Assurance Programs
UKHSA	United Kingdom Health Security Agency
WGS	Whole genome sequencing

Background

The genome of a microbe reveals its identity and ancestry, the ways in which it infects humans, and how it may evade antibiotic and other existing treatment and/or the immune system, at the highest possible resolution. Microbial genomics is the study and application of genome sequencing technologies to characterise and analyse microorganisms, including pathogens. It is a powerful and critical tool for the investigation and management of infectious disease and can be used to improve public health surveillance and inform public health decision making.

Public health applications of microbial genomics technology include:

- informing therapeutics and vaccine development and continuing susceptibility to existing treatment and vaccines
- informing public health infection control in food safety, across hospitals, and within community settings
- assisting to inform agricultural and water resource and management practices and to determine the persistence of microbes in the environment
- informing the development of sensitive and specific diagnostic tools
- supporting decision-making in health care service planning, and
- collaboration with law enforcement agencies in microbial forensics in the context of criminal or terrorist investigations.

Noting its utility, integration of whole genome sequencing into public health has been gradually building over many years. However, like any integration, there are challenges that impact the implementation of microbial genomics technology in Australia, including the following:

- public health laboratory and health unit systems do not currently have the capacity or capability to fully integrate microbial genomics data and metadata into existing surveillance systems from the sequencing laboratory right through to capture at the national level
- there is an essential need to undertake more extensive workforce planning and training in bioinformatics for pathologists, medical laboratory scientists and epidemiologists
- there is a need to expand upon developed policies and procedures to enable rapid national genomics data sharing and analysis to enhance public health surveillance and response beyond COVID-19 and across the human, animal, and environmental health sectors
- there is a role for national standardisation and definition of quality practices to assist in National Association of Testing Authorities (NATA) accreditation of microbial genomics analysis in public health laboratories in Australia
- there is a need for exploration of opportunities to further integrate or link microbial genomic data into surveillance infrastructures (for example, OzFoodNet, the National Notifiable Diseases Surveillance System, jurisdictional health databases, the National Tuberculosis Advisory Committee and the National Neisseria Network)
- there are differences in jurisdictional capacity, expectations, methodology, instrumentation, governance structures and requirements for microbial genomic technologies and information within both the laboratories and public health units (PHUs), and
- consideration needs to be given as to how the lessons from COVID-19 can be integrated into the design of the new Australian Centre for Disease Control.

Early work undertaken by the Communicable Diseases Genomics Network (CDGN), an Expert Reference Panel of Australia's Public Health Laboratory Network (PHLN) identified the need to formally establish a nationally agreed and consistent microbial genomics system, to better support coordination and implementation into Australian public health laboratories, acknowledging the variable capability and challenges that existed. It was determined that a national strategic framework would be the most appropriate mechanism to help drive this work forward.

In 2019, *the National Microbial Genomics Framework 2019-2022* (the Framework) was published as the first national strategic document for microbial genomics in Australia. The 2019-22 Framework provided a nationally consistent and strategic view for integrating microbial genomics in the Australian public health system, and for identifying microbial genomics policy issues and challenges that needed to be addressed. The Framework was consistent with, and complementary to, the *National Health Genomics Policy Framework (2018-21)* and placed a strong focus on issues that would benefit from collaboration across all jurisdictions and between PHLs and PHUs specifically.

An associated implementation plan (the Plan) which operationalised the Framework, was endorsed by the Australian Health Protection Principal Committee (AHPPC)[1] in early 2021. The purpose of the Plan was to identify actions, responsibilities, timeframes, priorities, and resourcing requirements for the integration of microbial genomics into the Australian public health system.

Since initial publication, the application of genomic surveillance to support outbreak response has accelerated the development of a nationally coordinated approach to sequencing and analysis. In 2023, this Framework has been renewed in line with these developments and lessons from the COVID-19 pandemic.

Purpose

This framework is to provide a consistent, national, and strategic view for integrating microbial genomics into the Australian health system and for identifying microbial genomics policy issues and challenges that need to be addressed.

Specifically, the Framework:

- continues to support better coordination and consistency of action between PHLs and PHUs to ensure the potential benefits of microbial genomics are harnessed in an efficient, effective, ethical, and equitable way
- provides high-level guidance for the continued enhancement of a nationally agreed microbial genomics system that allows organisms of public health importance to be identified within the auspice of a robust quality management system
- highlights that development of both domestic and international linkages for information sharing and communication are essential to drive this important public health initiative
- prioritises issues for consideration and indicates where further work is needed while also recognising that stakeholders have a role in addressing issues independently, and
- identifies other emerging issues with subsequent iterations as rapid development of sequencing technology and reduction in subsequently lower barriers to access.

[1] The Australian Health Protection Principal Committee is the key decision-making committee for health emergencies, comprising of all state and territory Chief Health Officers and is chaired by the Australian Chief Medical Officer.

Vision

To protect the health of all Australians from communicable disease and biological agent threats (including foodborne, zoonotic, and environmental) through:

- access to near real-time microbial genomics sequencing, nationally coordinated analysis and reporting technology
- timely, responsible, and transparent data sharing, and
- the gradual evolution of use in routine surveillance for all pathogens of public health significance.

Audience

This framework is designed primarily as a tool to provide guidance for the development and implementation of microbial genomic related policies, strategies, actions, and services and is directed at decision-makers and policymakers at state and territory and national health service levels.

Time frame

The time frame of the framework is three years, with a review anticipated in 2026 to inform the next iteration.

Sector consultation

A broad range of stakeholders were identified and consulted during the development of the Framework. This included expert advisory groups under the Australian Government Health Chief Executives Forum (HCEF) committee structure as well additional experts in public health and clinical service delivery, research, and private pathology.

Guiding principles

The development of the Framework was supported by the following guiding principles:

1. **National approach.**

   Developed jointly by Australian and state/territory governments, with the Framework facilitating national coordination and government priority setting and decision-making.

2. **High-level, strategic framework.**

   Identification of themes, principles, and considerations for embedding consistency and national coordination as enablers for more efficient, equitable, and effective utilisation of microbial genomics. It will be overarching and will align with existing, or to be developed, regulation, guidelines, and discussion papers addressing specific microbial genomics issues.

3. **System-focused.**

   An understanding of what the system can deliver and consideration of how a change within one system domain, including how

   - leadership and governance
   - system financing
   - human resources (workforce)
   - information systems, and

- service delivery

will impact, interact with, and change the other domains and affect the whole system. This system will be considered within the context of existing capacity and controls to remain consistent with and eventually embed into current communicable diseases surveillance infrastructure.

4. **Evidence-informed public policy.**

   Ensuring that the best available research and information is used to guide decisions at all stages of policy processes.

5. **Flexible to keep up with scientific advances.**

   Will contain flexibility to enable it to be adapted to reflect the evolving nature of microbial genomics technology and consider the latest scientific findings and advances and potential shifts in microbial genomics policy issues and challenges.

6. **Identifies priority areas.**

   Considers prioritising the microbial genomics policy issues and challenges that need to be addressed and identifies directions for change / opportunities for action and areas that require further work.

Enablers

To help guide decision-makers and policymakers in successfully implementing the framework, three key enablers have been identified:

1. **Collaborative governance and leadership.**
   Joint national and jurisdictional leadership with engagement from the Australian Government, states, and territories, CDGN, PHLN, Communicable Diseases Network Australia (CDNA), AHPPC and other relevant networks and stakeholders.

2. **Stakeholder engagement and action**
   Actively engage and cooperate with private and PHLs, research laboratories, clinical diagnostic laboratories, animal laboratories, environmental laboratories, PHUs, communicable disease control units, regulatory bodies, OzFoodNet and the Royal College of Pathologists Australasia Quality Assurance Programs (RCPA QAP).

3. **National and international partnerships**

   Establish and maintain genomics collaborations for information sharing, capacity and capability building and overarching, collective goal progression and attainment, between entities such as:

   - Australian Government Committees such as the:
     - PHLN
     - Australian (counter) Bioterrorism Laboratory Network (ABLN)
     - CDGN, and
     - CDNA

- related government initiatives such as the Department of Foreign Affairs and Trade's Indo-Pacific Centre for Health Security, and
- relevant international partners including, but not limited to:
    - WHO
    - United Kingdom Health Security Agency (UKHSA)
    - United States Centers for Disease Control and Prevention (CDC)
    - National Center for Biotechnology Information (NCBI)
    - Ministry of Health Singapore
    - Public Health Agency of Canada, and
    - Chinese Center for Disease Control and Prevention.

Strategic context

Microbial genomics continues to revolutionise the diagnosis, surveillance, and control of communicable diseases and antimicrobial resistance. Strengthening Australia's existing national genome sequencing capability and capacity, including workforce, and exploring potential ways for cross-sectoral and microbial-agnostic approaches to data sharing and analysis will be essential for disease preparedness as this technology becomes more accessible.

Several potential public health benefits of microbial genomics were identified in the Framework's first iteration which will be expanded on in this Framework, including the ability to:

- provide high-resolution and nationally and internationally compatible typing and characterisation data for communicable disease surveillance and bio-threat detection
- use near real-time genomic sequencing surveillance to inform the prevention, early detection, and management of disease outbreaks and bio-threats
- rapidly identify clusters of disease transmission
- more accurately and rapidly identify foodborne and waterborne outbreaks and investigate source attribution
- rapidly detect, characterise, and monitor emerging pathogens or new mechanisms of antibiotic resistance, and
- monitor and predict the effectiveness of treatments and vaccines for communicable disease pathogens.

Underpinning this renewed Framework is the One Health principle which recognises that the health of humans, animals, and the environment are all inter-connected and that there are opportunities to harness expertise across sectors to strengthen response activities.

As a pathogen which transcends human, animal, and environmental health, the detection of Japanese encephalitis virus (JEV) in South-eastern Australia in early 2022 highlighted the urgent need for cross-sectoral genomic sequencing efforts and data sharing for the purposes of surveillance, research, and development. However, the cross-cutting nature of zoonotic pathogens gives rise to additional challenges and requirements including the consolidation of national genomic information, especially where there are sensitivities surrounding the data and data sharing within and between sectors. There is significant variation in data collection needs and objectives across sectors, as well as differing maturity in genomic sequencing and pathogen surveillance systems. Data sharing is also at differing levels of integration between jurisdictions and across the One Health sectors.

In this Framework, consideration is given to these current challenges and opportunities that could arise from One Health collaboration to understand how best to improve testing and genomic surveillance procedures to ensure Australia is prepared to address priority public health and animal health challenges into the future.

Funding mechanisms are also reflected on within this framework. In Australia, states and territories are responsible for providing microbial whole genome sequencing (WGS) capability for the purposes of diagnosis and clinical patient management. Support for surveillance and research is cost-shared between states and territories and the federal government, and the levels of available resources and investments vary between sectors and depending on the objective of the activity. This framework aims to acknowledge the respective responsibilities of state, territory and the federal governments while outlining the need for a collaborative effort to address gaps and further drive national value.

In addition, consideration has been given as to how this framework may evolve and be integrated into planning for the design of the Australian Centre for Disease Control (ACDC) to ensure the challenges, vulnerabilities and areas for improvement identified throughout this process (including lessons from the COVID-19 pandemic), are explored, and supported by sustainable funding mechanisms.

Finally, this framework seeks to drive national effort on agreed priorities of coordinated sequencing activities across Australia for priority pathogens regardless of organism type—bacterial, viral, or fungal. The Framework provides an opportunity to act on divergent approaches to implementing microbial sequencing before they form impediments to successful integration of microbial genomics into the Australian health system. To provide further context, key national and international developments can be found in Annex A.

Strategic Priorities and Implementation

This framework sets out how the Australian Government and the states and territories will work collaboratively to integrate microbial genomic approaches into health care over time. The Framework includes actions, responsibilities, time frames, priorities, and resourcing to measure the progress and success of the Framework and allow for the monitoring of national and jurisdictional progress against activities and milestones outlined. While the Framework outlines an agreed national policy approach to microbial genomics integration, it does not identify all the specific actions needed to take the framework forward.

Evaluation

It is intended that every three years the Australian Government and the states and territories will evaluate the activity outcomes described in the Framework, including the cost-effectiveness, key achievements, sustainability, and challenges of integrating microbial genomics into the Australian public health system.

The Framework acknowledges that involving all governments, laboratory and public health sectors is key to harnessing the power and subsequent health benefits of microbial genomics. This new Framework encompasses a plan to operationalise priority outcomes. It proposes strategic projects and actions that will drive results over the longer term and high-priority actions for the short term. As the Framework has a long-term vision, some actions are expected to go beyond its three-year duration.

Indicative action timeframes

Indicative timeframes proposed for each activity are:

- short-term (1 – 1.5 years)
- medium-term (1.5 – 3 years), and
- long-term (more than 3 years).

Timeframes show the expected length of time needed to complete the proposed activity. Some activities flagged as long-term are ongoing and likely to go beyond the duration of this iteration of the Framework.

Priority key

Indicative priorities proposed for each activity are:

- low
- medium
- high

The level of priority is determined through consideration of:

- the need for implementation
- the sequential need for an activity, and
- the beneficial influence or impact the action will have on national capacity, capability, and utilisation of microbial genomics in the public health system.

Roles and responsibilities

Each level of government has specific roles and responsibilities across the range of health policies and programs that involve, or are becoming increasingly influenced by, microbial genomics. The Framework does not change the nature of these roles and responsibilities but looks to create a more cohesive approach across all governments. The Framework recognises coordinated and thorough planning is needed between all levels of government and across the laboratory and public health sectors. The Framework embodies this approach, with all levels of government involved in both its development and implementation.

The Framework is the responsibility of the federal, state and territory governments under HCEF governance arrangements[2]. The work and cooperation of public pathology laboratories, public health authorities, research organisations and educational leaders is essential to achieving the Framework's overall vision.

In the proposed implementation activities, 'National Action' infers the collective responsibility of states, territories, and the Australian Government.

[2] Formerly known as the Australian Health Ministers' Advisory Council (AHMAC).

Governance

Governance is key for driving and co-ordinating implementation of the Framework. To ensure the Australian Government and state and territory governments are involved, and work is progressed in a cohesive way, it is appropriate for the governance arrangements to be situated under the HCEF structure.

Australian Government Action	Roles	Timeframe	Lead Responsibility
Action i: The Australian Government and state and territory governments will continue to support governance arrangements through the HCEF structure. AHPPC will provide advice on the implementation of the Framework, ensuring ongoing national consistency.	Health will monitor this progress.	Short-term	Health and relevant committees
Action ii: The Australian Government and state and territory governments will evaluate the National Microbial Genomics Framework. This evaluation will begin in 2026 to inform the future directions in microbial genomics policy.	Health will lead an evaluation, including development of an evaluation plan.	Medium-term	Health

Accountability - measuring and reporting

Accountability requires appropriate frameworks to manage risk and maintain appropriate control frameworks to manage risks to promote the efficient, effective, economical and ethical use of public resources. The development of a national system performance framework will ensure implementation activities remain is fit for purpose, and achieve the defined objectives within the proposed timeframes.

Australian Government Action	Roles	Timeframe	Lead Responsibility
Action iii: Develop a mid-cycle report on implementation progress of the Framework.	Health in collaboration with relevant committees and networks.	Short-term	Health and relevant committees
Action iv: Develop a national system performance framework (with high level indicators to show what success looks like). This will monitor whether public health microbial genomics is being embedded in the laboratory and public health sectors in an equitable and efficient way. Development and future inclusion of ethical and cost-effectiveness indicators will be encouraged.	Health to support development of a performance framework in consultation with relevant committees and networks.	Medium-term	Health and relevant committees and networks

Strategic priorities

The National Microbial Genomics Framework outlines five strategic priorities that aim to:

- prioritise key microbial genomics policy issues and challenges
- provide directions for change
- highlight opportunities for action, and
- identify areas that require further work.

The priority areas are not necessarily discrete and there will be interrelationships and interdependencies. The five strategic priorities are as follows:

***Strategic Priority 1*—Standardised National Approach**

- Enhance governance arrangements to drive standardisation on microbial genomics matters of national significance, including rapid national data sharing.
- Grow and apply microbial genomic knowledge that is evidence based, standardised, and of high quality.

***Strategic Priority 2*—Technology and Data Governance**

- Establishing and enhancing nationally agreed and standardised data governance arrangements.
- Promoting the importance of ethical and equitable data sharing and understanding the risks (or perceived risks) that it may entail.
- Strengthening high-performance computing infrastructure to support data storage and sharing that can adapt to enhancing microbial genomics technologies.

Strategic Priority 3—Integration into Public Health

- Enhancing collaboration and strong linkages when and as appropriate between Australian laboratories (including diagnostic and non-human testing laboratories) and public health units to ensure the value of microbial genomics technology is recognised.
- Strengthening nationally consistent reporting structures that are compatible with existing public health surveillance systems.

Strategic Priority 4—Access and Workforce

- Enhancing and maintaining a competent multidisciplinary microbial genomics workforce.
- Ensuring microbial genomics capacity and capability is equitable across jurisdictions.

Strategic Priority 5—Financing

- Ensuring the funding model applied to microbial genomics considers the substantial establishment costs and is cost-effective and sustainable into the future.

The following values underpin the strategic priorities of the framework:

- The application of microbial genomic knowledge is ethically, legally, and socially responsible.
- Access to microbial genomics information is equitable within and between the jurisdictions and the Australian Government.
- The application of microbial genomics knowledge to improve public health outcomes is supported and informed by evidence and research.

Strategic Priority 1—Standardised National Approach

Despite rapid advancements and strong jurisdictional collaboration to strengthen microbial genomic capability, some jurisdictional differences remain in laboratory workflow and specimen processing, public health microbiology service reimbursement and epidemiological typing and characterisation for the purposes of surveillance. These result in national variability in capability, testing practices, turnaround times and reporting.

Without continued progress towards national coordination and standardisation of microbial genomic practices, some of the key risks include:

- inconsistency in analysis due to different bioinformatics pipelines
- incompatible data from different sequencing platforms
- inconsistency in the application of microbial genomics to public health and bio-threat issues
- fragmentation in data collection and storage
- protracted turnaround times for test results if need to seek other jurisdiction assistance for gap in capability
- lack of consistency in data analysis and output for surveillance and investigative efforts
- lack of collation and curation of national-level genomic data.

Some of the key challenges in achieving nationally consistent laboratory-based surveillance have been highlighted in the *National Framework for Communicable Disease Control*. These include:

- aligning governance and reporting models for public health laboratories and national centres
- harmonising laboratory-based surveillance methods between jurisdictional public health reference laboratories
- agreeing on an ethical and confidentiality dimension
- improving information sharing between laboratories, public health authorities and clinicians
- agreeing on sustainable financing mechanisms for public health laboratory activities.

What does the future look like?

- The application of microbial genomics to public health—infectious disease and biological agents of security concern control—is well understood by stakeholders.
- A coordinated and consistent approach has been developed around the application of microbial genomics in public health practice that increases efficiency and reduces duplication of effort.
- The approach has been adopted at a national level and is supported by all states and territories for communicable diseases and antimicrobial resistances of public health significance.
- The approach is sustainable and well supported by secure information technology (IT) infrastructure, quality assurance pathways and appropriate financing.

Prior and current activities

Many initiatives to support development of a standardised national approach have been completed

or are underway. The Australian Government and state and territory governments are supporting microbial genomics research and projects aimed at improving consistency and harmonisation among public health laboratory systems, with the majority being led by CDGN, including the following completed activities:

- development of a national framework (including SARS-CoV-2 analysis protocols) based on international best practice to facilitate consistency in the use of microbial genomics for public health in Australia
- in 2020 establishing an agreement with the RCPA QAP to support development, analysis, and reporting of proficiency testing programs for WGS, including supporting the analysis of the 2021 SARS-CoV-2 modules, and
- in 2021 developing the *CDGN Sampling Strategy for SARS-CoV-2 Genomic Surveillance,* so that Australia remained vigilant in responding to emerging variants.

The following activities are ongoing:

- promoting best practice sequencing methodologies, determined in consultation with internationally established best practices that are both cost and time effective, to garner the most value from microbial genomics sequencing to inform public health action
- providing ongoing support to laboratories with sequencing and analysis advice on a range of priority pathogens, including of SARS-CoV-2 to ensure capability continues to be enhanced
- in 2021 establishing a Salmonella and Listeria Working Group which continues to facilitate a national transition to WGS of *Salmonella* and *Listeria* for routine public health testing, and
- in 2021 establishing a Tuberculosis (TB) Working Group which continues to coordinate and standardise approaches to sequencing, analysis, and reporting of *Mycobacterium tuberculosis* for public health.

Outcome 1.1— Enhanced standardised policies and procedures

- Continue to develop common standards, nomenclature and reporting outputs and formats that are fit for purpose for public health surveillance and response.
- Progress the expansion of AusTrakka, the agreed national genomic surveillance platform which hosts bioinformatics pipelines and a data repository that is available to all public health laboratories.

National Action	Timeframe	Lead	Priority
Outcome 1.1 – Enhanced standardised policies and procedures			
1.1.1 Continue to ensure microbial genomics is considered in the context of any broader review of health technology and systems assessment to support national consistency and especially in the design of the new Australian Centre for Disease Control.	Short	Health	High
1.1.2 Review and update relevant existing guidelines and standards or develop new ones where appropriate to ensure microbial genomics applications are: • evidence-based • nationally consistent (where appropriate), and • in line with agreed national approaches.	Medium	CDGN, PHLN	Medium
1.1.3 Build on existing mechanisms, systems, and processes (where possible) to ensure nationally adopted supply of service and cohesive approaches to microbial genomics applications.	Medium	Health	Medium
1.1.4 Develop a consistent and, where appropriate, pathogen-agnostic and One Health approach to microbial genomics data analyses across jurisdictions, noting the challenges and approaches in analysis can depend on the organism.	Ongoing	CDGN	High
1.1.5 Continue to progress the development of AusTrakka for use as a national genomic surveillance platform for priority organisms of national public health concern.	Ongoing	CDGN, PHLN, Health	High

Outcome 1.2—Harmonisation of laboratory-based sequencing and surveillance methods

- Continue to develop nationally harmonised laboratory-based sequencing methodologies.
- Continue to develop nationally standardised microbial genomics surveillance methods.

National Action	Timeframe	Lead	Priority
Outcome 1.2 – Harmonisation of laboratory-based sequencing and surveillance methods			
1.2.1 Continue to develop and promote laboratory guidelines and decision support tools to clearly describe appropriate referral practices, in line with a One Health approach. That is, when should WGS be requested by general practitioners, diagnostic laboratories, or other public health clients to ensure use of resources is efficient.	Ongoing	CDGN, PHLN	Medium
1.2.2 Encourage engagement between governments, laboratories, PHUs and the research sector to discuss, discover and address any ethical and/or legal issues associated with microbial genomics (especially metagenomics), as they are identified.	Medium	CDGN, PHLN, Health	Medium
1.2.3 Involve health sector partners outside of core public health systems to promote awareness and understanding of microbial genomics and priority sample referral pathways, such as private pathology, remote area clinics, and hospitals.	Medium	CDGN, PHLN, Health	Medium
1.2.4 Design and provide a biennial survey for public health laboratories and public health professionals working with microbial genomics to measure the impact and progress of the modernization of national microbial genomics capability and capacity. This will also provide a practical evidence base for policymakers, discover areas for improvement, and disseminate best practices and lessons learned.	Medium	Health, CDGN	Medium
1.2.5 Identify and determine ways to enhance collaboration with non-human testing laboratory stakeholders to ensure harmonisation of practices beyond human health where necessary, and in a One Health context.	Medium	Health, PHLN, CDGN, DAFF, DCCEEW	Medium

Outcome 1.3—Establishment of quality services

- Continue to develop quality assurance and proficiency testing programs specific to microbial genomics.
- Strengthen technical competence and integrity within organisations offering microbial genomics services through collaboration with National Pathology Accreditation Advisory Council (NPAAC), NATA and the RCPA QAP.
- Promote sharing of sequence data nationally and to international repositories and / or directly with international laboratories upon request to inform detection and investigation of multi-jurisdictional and multi-country outbreaks.

National Action	Timeframe	Lead	Priority
Outcome 1.3 – Establishment of quality services			
1.3.1 Continue to develop nationally consistent and best-practice protocols. This includes providing input into development of accreditation protocols for public health sequencing laboratories with NATA and RCPA QAP.	Medium	CDGN, PHLN	High
1.3.2 Continue to support the development and implementation of microbial genomics-related PTP to be offered to laboratories through the RCPA QAP.	Ongoing	CDGN, PHLN, Health	High
1.3.3 Participate in QAP programs (Global Microbial Identifier (GMI), External Quality Assessment (EQA), RCPA) to maintain key microbial genomics-related technical skills and share best practices and lessons learned with other laboratories.	Ongoing	CDGN, PHLN	High
1.3.4 Generate high quality, locally relevant reference genomes for pathogens of public health significance in Australia. This is to be shared among jurisdictional laboratories, and across One Health sectors; and release these genomes to the wider international community.	Ongoing	Relevant PHLs	High
1.3.5 Harmonise governance and legal requirements between jurisdictions and amend guiding frameworks specifically for sequence and genomic data and associated metadata.	Medium	Health	High

Strategic Priority 2—Technology and Data Governance

There is recognition in the public health community of the importance of nationally agreed data sharing to improve public health surveillance and response. Identifying suitable approaches to data sharing ensures sensitive data remains protected while allowing for the benefits of genomic data to accrue for public health surveillance and technological advancements is an ongoing challenge. Microbial genomics data exchanged in this manner has been used as a tool for outbreak investigation and outbreak detection. It allows for finer resolution of outbreaks, and greater confidence in including or excluding isolates in a particular outbreak. The aim is to achieve real-time sequencing and data exchange to enable enhanced outbreak detection and response. International progress to address key issues relating to data governance, including equitability of access and benefits arising from the sharing of data, is already being made. Implementation of activities to strengthen Australia's data governance must ensure alignment with these standards and best practice models, which include the *WHO data sharing principles (2022)*, and IHR (2005). While progress has been made, effort is still required to ensure data sharing is routine and transparent across Australia. In addition, Australia will continue to support and strive for the timely sharing of data on trusted international repositories, such as the recently proposed WHO Pathogen Access and Benefit-Sharing System (PABS) in line with our international commitment to support pandemic preparedness and response initiatives. The value of genomic data, collected as part of genomic surveillance, for basic research and activities aligned with the One Health approach should be also acknowledged.

What does the future look like?

- A national data governance mechanism is in place to ensure real-time data sharing and data use in the nationally consistent application of microbial genomics in public health practice.
- Secure systems and IT infrastructure is established to support current and future national data sharing and storage requirements.

Prior and current activities

Jurisdictions continue to invest in developing standards, policies, and procedures to support infrastructure for capturing, analysing, and sharing microbial genomics data. However, inconsistencies remain in the technologies used and data governance, such as data storage infrastructure and bioinformatics analyses, raise challenges for rapid sharing of data, particularly across One Health sectors. Various initiatives are underway to address these challenges and improve data sharing between jurisdictions. These include the following completed activities:

- establishment of operational governance and data governance structures for the ongoing management of AusTrakka for *priority pathogens* public health significance
- establishment of the CDGN AusTrakka User Group to:
    - support platform optimisation
    - enhance, coordinate, and support jurisdictional capability and capacity in the implementation of WGS and metagenomics approaches
    - develop procedures and policies allowing rapid national genomic data sharing and analysis, to enhance public health outbreak detection and response
    - maintain validated national microbial bioinformatics pipelines

    - agree and develop procedures and policies that allow for rapid national genomic data sharing and analysis through AusTrakka to enhance disease outbreak detection and response, and

- development of AusTrakka version 2 that aims to allow more flexible and safe data sharing and visualisation.

The following activities are ongoing:

- maintenance of data sharing agreements established by CDGN, signed by jurisdictions. These agreements establish trust for cooperative, safe, and equitable data sharing between CDGN laboratories

- since January 2022, AusTrakka has focused on developing scalability and sustainability of the platform for the introduction of new pathogens of public health interest and the governance, data types and requirements that accompany it, including:
    - *Salmonella* Hvittingfoss
    - *Salmonella* Stanley
    - *Salmonella* Typhimurium
    - *Salmonella* Enteritidis
    - *Salmonella* Saintpaul
    - Japanese encephalitis virus
    - monkeypox virus
    - *Vibrio* parahaemolyticus, and
- given its success with COVID-19, AusTrakka is currently being explored as an appropriate mechanism for the national genomic investigation of JEV in Australia as a pilot One Health project.

Outcome 2.1—Technology

- Maintain comparable sequencing instruments across jurisdictions which have the flexibility to be configured for use securely in the Australian setting.
- Continue to develop and maintain high-performance computing infrastructure to support data storage and sharing that can adapt to emerging microbial genomics technologies.
- Continue to develop a pathogen-agnostic framework for data sharing and analysis, and in consideration of a One Health context.

National Action	Timeframe	Lead	Priority
Outcome 2.1 – Technology			
2.1.1 Progress the development of AusTrakka as a shared, access--controlled, scalable repository that allows laboratories to upload and share sequence data and associated contextual and epidemiological metadata across jurisdictions, One Health sectors, and internationally.	Medium	CDGN	High
2.1.2 Strengthen AusTrakka'a microbial genomics analysis and visualisation tool for integrated genomics data that can be accessed by public health laboratories undertaking sequencing.	Medium	CDGN, MDU PHL	Medium
2.1.3 Enable and maintain access to nationally agreed minimum sequence data, quality metrics, and protocols for sequence quality control and analysis for priority pathogens in AusTrakka.	Long	CDGN	High
2.1.4 Improve microbial genomics and bioinformatics capability and capacity in each jurisdiction.	Medium	CDGN, Health	High
2.1.5 Investigate feasibility of a centralised technological solution to enable enhanced data sharing and analysis across jurisdictions.	Medium	CDGN, Health	High

Outcome 2.2—Data sharing

- Maintain and enhance multi-directional microbial genomic data and critical metadata sharing across and within jurisdictions, to the Australian Government and internationally, including the provision of data and/or isolates to public health laboratories from non-reference laboratories, and across One Health sectors.
- Ensure data sharing is compliant with the appropriate national and jurisdictional legislation and guidelines such as the:
    - *Privacy Act 1988*
    - *National Health Security Act 2007*
    - *National Statement on Ethical Conduct in Human Research (2007)*
    - *National Digital Health Strategy and Framework for Action,* and
    - any organisational ethical frameworks for public health practice.

National Action	Timeframe	Lead	Priority
Outcome 2.2 – Data Sharing			
2.2.1 Maintain a national pathogen-agnostic data sharing agreement and protocol for the sharing of sequencing data, epidemiological metadata, and microbial isolates across the human public health sector.	Short	CDGN	High
2.2.2 Support sector engagement with international microbial genomics alliances to promote shared access to data for research and global harmonisation of data where appropriate.	Medium	CDGN, PHLN, CDNA, Health	Medium
2.2.3 Involve the private pathology sector in key data sharing discussions across laboratories through existing networks including (but not limited to) PHLN, CDGN, and Australian Pathology.	Medium	CDGN, PHLN, Health	Medium
2.2.4 Develop and maintain a common process for timely data and information sharing across One Health sectors in the event of a One Health emergency outbreak relevant to Australia.	Medium	CDGN, PHLN, Health	High
2.2.5 Evaluate the outcome of the pilot project to use AusTrakka for the national capture, analysis, and reporting of flavivirus sequences across the human, animal, and environmental sectors and action agreed next steps.	Medium	CDGN, PHLN, Health	High
2.2.6 Support the integration of microbial genomics data for non-human samples i.e., food, animal, and environmental.	Medium	CDGN	Medium
2.2.7 Invest in data integration or linkage as appropriate between PHLs and health departments' data management systems.	Long	Health	High
2.2.8 Adopt Open Science principles at organisational and jurisdictional levels.	Long	CDGN, PHLN, Health	Medium

Outcome 2.3—Data storage

- Continue to develop nationally agreed pathogen-agnostic standards for data collection, safe storage, data sharing, custodianship, analysis, reporting and privacy requirements, with consideration to other One Health sector requirements.
- Strengthen infrastructure to support secure storage of microbial genomic data.

National Action	Timeframe	Lead	Priority
Outcome 2.3 – Data storage			
2.3.1 Define minimum pathogen-agnostic security handling requirements that are aligned with national and international standards and best practice for microbial genomics data pipelines, systems, data sharing, and storage, with consideration to the different requirements across One Health sectors.	Short	CDGN, Health	High
2.3.2 Strengthen nationally accessible and sustainable data storage and computational infrastructure options, that is also accessible to appropriate One Health sector users, ensuring they are financially sustainable.	Medium	CDGN	High

Outcome 2.4—Use of data

- Maintain, develop, and promote common standards for the public health use of microbial genomics data across jurisdictions.
- Maintain, develop, and promote common reporting standards for microbial genomics.

National Action	Timeframe	Lead	Priority
Outcome 2.4 – Use of data			
2.4.1 Maintain, develop, and promote processes to identify, promote, monitor, and report best practice in microbial genomics for public health action. This includes the timely sharing of sequencing data and other related information across the One Health sector, where appropriate.	Medium	CDGN, PHLN	Medium
2.4.2 Promote and maintain nationally standardised reporting formats to communicate microbial genomic data to end-users for public health action.	Long	CDGN, PHLN	High

Outcome 2.5—Data governance

- Review legislation and regulation at both state and federal levels to identify whether there are any impediments to implementation of microbial genomics, particularly in relation to data sharing.
- Ensure data is being handled in an ethical and culturally appropriate way.
- Ensure meaningful and appropriate recognition of data sources by both users.
- Establish and maintain trust between data-sharing entities and encourage further data sharing among active and potential providers, including in a One Health context.
- Ensure data privacy and security is maintained throughout the data collection, handling, and storage process.

National Action	Timeframe	Lead	Priority
Outcome 2.5 – Data governance			
2.5.1 Review legislation and regulation at both state/territory and federal levels to identify any impediments to implementation of microbial genomics for public health action, particularly in relation to data sharing.	Short	CDGN, CDNA, Health	High
2.5.2 Develop a national microbial genomics One Health data governance framework that aligns with international frameworks, following evaluation of pilot flavivirus AusTrakka project.	Medium	CDGN, PHLN, CDNA, Health	Medium
2.5.3 Following the evaluation of the One Health AusTrakka pilot project develop nationally agreed standards for One Health data collection, safe storage, data sharing, custodianship, analyses, reporting and privacy requirements.	Medium	CDGN, PHLN, CDNA, Health	Medium

Strategic Priority 3—Integration into Public Health

The main utility of microbial genomics is in enhancing national and international surveillance and response to infectious diseases. Throughout the COVID-19 pandemic, the use of sequencing data has shown to form the basis of robust public health surveillance through rapid pathogen detection and identification; and monitoring that ultimately links to information on clinical, demographic, and exposure details.

To achieve maximal public health impact, it is critical that genomic data are appropriately linked to epidemiological and clinical data and that results from genomic data are rapidly disseminated back to 'end users' or even directly accessible.

Conceptually, this is directly aligned with several of the key outcomes in the *National Framework for Communicable Disease Control*. To fully achieve this aim requires ongoing strategic coordination and collaboration between existing groups and networks.

Given the vast amount of useful data that microbial genomics generates (related to pathogen transmission, resistance, virulence, and evolution) and the increasing popularity of culture-independent diagnostic tests in clinical laboratories and its potential impact on laboratory-based typing, microbial genomics sits directly at the interface between clinical epidemiological surveillance and laboratory-based surveillance. As such, it is critical that microbial genomics continues to integrate into existing epidemiological networks, as this would better enable:

- proactive and coordinated gathering and sharing of information
- detection and rapid response to disease outbreaks
- identification of disease clusters
- accurate and rapid source identification of foodborne, waterborne, and animal outbreaks
- accurate and rapid source attribution of foodborne, waterborne, and animal outbreaks, and
- rapid detection and characterisation of emerging pathogens or new mechanisms of antibiotic resistance.

However, COVID-19 response activities have highlighted potential risks to the successful integration of complete data for public health response. The increasing interest in use of point-of-care tests (POCT), including self-tests raises several issues to consider when developing public health data integration strategies, including:

- misinterpretation of results can have significant public health consequences, including inappropriate management of the individual and their contacts
- decrease the number of notified cases which can contribute to jurisdictional and national surveillance
- decrease in laboratory-confirmed cases which could lead to the failure to detect viral mutations that may impact the diagnostic accuracy of the test
- lower sensitivity and specificity of other laboratory-based tests, leading to false negative and false positive results, and
- most importantly, the inability to use the sample for onward testing, including genomic sequencing where appropriate.

However, with these risks comes certain opportunities as POCT can decrease time-to-treatment, increase accessibility to testing in regional and remote areas, and increase accessibility for those diseases that have high levels of stigma and discrimination associated with them, with individuals being able to test in the

privacy of their own home. When integrating both detection methodologies into public health, it will be important to work towards the connection POCT results to public health data surveillance repositories and ensuring genomic data collated is:

- representative,
- enables new pathogen variants to be identified, and
- provides reliable findings that facilitate public health action.

What does the future look like?

- Microbial genomics is fully integrated into national public health practice and in a One Health context.
- There is evidence from Australia that microbial genomics has contributed to improvements in the detection of outbreaks and enabled timely response.
- There is greater systematic collaboration with researchers and a process to maximise opportunities for improvement and expansion in the application of microbial genomics.

Prior and current activities

There is a collective effort by the Australian Government and state and territory governments to prioritise microbial genomics integration activities to improve public health outcomes. Completed activities include the following:

- In early 2021 CDNA endorsed the ongoing sharing of enhanced metadata in AusTrakka for the SARS-CoV-2, and
- CDGN hosted two symposia sessions at the Communicable Diseases and Immunisation Conference in Sydney in June 2022, with a focus on the utility for genomics for COVID-19 and other public health pathogens.

The following include ongoing activities:

- CDGN continues to advise and interact with laboratory and public health networks, government, policy makers, and other relevant stakeholders on pathogens of public health interest, including SARS-CoV-2
- research opportunities continue to be explored through leading research bodies and consortiums focusing on a range of microbial genomics issues. States and territories continue to engage in collaborative research partnerships to ensure evidence-based integration of public health microbial genomics in Australia, and
- CDGN regularly contributes to national SARS-CoV-2 surveillance, providing national genomics surveillance reports from data analysed through the AusTrakka platform as part of the Australian National Disease Surveillance Plan for COVID-19. To facilitate this, CDGN established the SARS-CoV-2 VoC WG
- in March 2021 to support Australia's national response to SARS-CoV-2 variants. Activities undertaken include:
    - Development and regular update of a VoC literature summary document, a 'live' list of variants and mutations of concern or interest relevant to Australia for

surveillance and reporting based on available literature and international classifications.
- Maintenance of the CDGN laboratory case definitions for SARS-CoV-2 VoC.
- Collaboration with the Department of Health and Aged Care, develop a standardised approach for reporting of SARS-CoV-2 variants and mutations across jurisdictions and nationally, to support recording SARS-CoV-2 variants in the National Notifiable Diseases Surveillance System (NNDSS).
- Ongoing review of the CDGN website to ensure content on the website is accurate and aligned with leading international organisations (for example, WHO, UKHSA).

Now is the time to consider how microbial genomics data for public health could be more broadly integrated into both existing and developing animal and environmental (One Health), food safety and AMR surveillance systems and networks. This will include identification of priority organisms to take full advantage of microbial genomics for real--time diagnostics, supporting timely outbreak investigation. Greater systemic collaboration with researchers is also required to boost opportunities for improvement and application of microbial genomics for public health action.

Outcome 3.1—Integration of microbial genomics data into epidemiological systems

- Facilitate integration into epidemiological and antimicrobial resistance surveillance systems.
- Facilitate integration into laboratory information systems.
- Facilitate integration into food safety and regulatory sector arrangements.
- Facilitate integration into animal, and environmental health sector arrangements.

National Action	Timeframe	Lead	Priority
Outcome 3.1 – Integration of microbial genomics into epidemiological systems			
3.1.1 Investigate how microbial genomics data and new laboratory information management systems and epidemiological surveillance systems can be integrated or linked to support decision-making. Determine how systems can facilitate seamless notification pathways for effective and real-time public health action.	Medium	CDGN, PHLN, CDNA	High
3.1.2 Maintain standardised reports and nomenclature for key pathogens of public health interest that effectively communicates data to end-users.	Long	CDGN, PHLN, CDNA	High
3.1.3 Using pilot implementation projects, such as that for JEV, look at the possibility of interoperable One Health routine microbial genomics sequencing for surveillance of priority organisms to measure and identify local transmissions for outbreak management and control.	Medium	CDGN, PHLN	Medium
3.1.4 Develop exercises to test the use of microbial genomics in the event of a human disease outbreak. These will assess and look at strengths and opportunities to improve Australia's integration of microbial genomics into public health responses.	Medium	Health, CDGN	Medium
3.1.5 Encourage the use of microbial genomics technology and the integration of genomics data from animal and environmental sources. Work towards a cross-sectorial integrated One Health approach to surveillance of communicable diseases and AMR. Achieve this through closer engagement with networks such as the Laboratories for Emergency Animal Disease Diagnosis and Response (LEADDR).	Long	CDGN, PHLN, CDNA	Medium

Outcome 3.2—Identification of priority organisms

- Continue to ensure preparedness to rapidly detect and characterise emerging and/or newly imported pathogens and other bio-threats.
- Improve knowledge on what type of microbial genomics information improves public health disease control and response and how this is applied in relation to priority organisms, particularly its role in maintaining national health security and biosecurity.
- Facilitate and encourage private microbiology laboratories to refer priority samples for sequencing and / or share microbial genomics related data for public health and surveillance purposes for priority organisms.

National Action	Timeframe	Lead	Priority
Outcome 3.2 – Identification of priority organisms			
3.2.1 Ensure laboratories have the necessary resources for the rapid detection and characterisation of emerging and/or newly imported pathogens and other bio-threats.	Medium	Health, PHLN, CDGN	High
3.2.2 Drawing from national and international experience, regularly review list of priority organisms where sequencing would enhance pathogen detection and public health response. This should be decided through consultation and collaboration with relevant stakeholders and include defining appropriate sampling frames, stages of implementation and indicators of effective implementation.	Ongoing	CDGN, PHLN, CDNA, Health	Medium
3.2.3 Through existing networks, reach out to and encourage One Health and human diagnostic pathology laboratories to share isolates of priority organisms for public health surveillance purposes.	Ongoing	CDGN, PHLN, Health	Medium

Outcome 3.3—Prioritisation of public health microbial genomics research

- Strengthen communication with microbial genomics researchers to identify gaps for improvement in infectious disease control for public health purposes.
- Maximise microbial genomics research opportunities to enhance public health outcomes.
- Ensure early identification of translational research priorities in microbial genomics.

National Action	Timeframe	Lead	Priority
Outcome 3.3 – Prioritisation of public health microbial genomics research			
3.3.1 Develop and promote a national research agenda for microbial genomics for public health action. Look at opportunities to link to Australian Government and state and territory government research priorities.	Medium	CDGN, PHLN, CDNA	Medium
3.3.2 Map current public health microbial genomics research activities and explore options to strengthen national coordination. This will inform development of a national research agenda to guide sustainable and strategic research investment.	Medium	CDGN, PHLN, CDNA, Health	Medium
3.3.3 Support translational research opportunities that can improve public health investigation, surveillance, and response through commissioning and consulting with relevant academic institutions (i.e., cutting-edge sequencing technologies, clinical metagenomics, and application of machine learning/artificial intelligence methodologies).	Medium	CDGN, PHLN, CDNA, Health	High

Strategic Priority 4—Access and Workforce

Currently, public health microbiology services are provided by public health laboratories through a network of jurisdictional specialist microbiology laboratories. These public health laboratories are either dedicated specialist (reference) facilities or are co-located within hospital-based facilities. Depending on jurisdictional size and capacity, public health laboratories provide a range of specialist functions, including:

- detailed typing and characterisation of communicable disease pathogens, underpinning national surveillance for communicable diseases
- laboratory contribution to outbreak investigation
- specialised reference diagnostics and confirmatory testing
- provision of scientific advice to public health networks and authorities
- state-based and national leadership in standardising the diagnosis and laboratory-based surveillance of communicable disease, and
- identification and application of new technological and scientific developments to public health microbiology practice.

Despite rapid advance, there remains varying capacity and capability across jurisdictions regarding the implementation of microbial genomics in public health laboratories, in part due to resource prioritisation and expense of equipment needed to fully integrate microbial genomic practices into the laboratory. To complicate implementation, the increased use of portable sequencing platforms and decentralised molecular diagnostic testing (including personal use in-vitro diagnostic devices) will challenge the traditional model of clinical sample referral to public health laboratories for specialist typing and characterisation as part of surveillance activities. Common protocols and collaboration between the clinical and public health laboratories will be key to ensuring quality and portability of genomic data across integrated laboratory information systems for surveillance purposes.

A growing number of pathology providers in public and private sectors are considering different models of genomics testing for hospital infection control and antimicrobial stewardship.

What does the future look like?

- A robust, sustainable national microbial genomics capacity and capability has been established to meet public health need and referral of priority specimens for genomics characterisation is maintained.
- Capacity and capability are well supported and will be maintained through national standardisation of equipment and levels of required expertise and workforce development.
- Microbial genomics literacy is maintained across all relevant stakeholders and there is national support for innovation.
- The genomics workforce is supported throughout all stages of their careers, building a well-trained and microbial genomics literate workforce to meet the increasing demand for genomics services in Australia.

Prior and current activities

The introduction of microbial genomics in the Australian public health laboratory and public health sector more broadly presents a major workforce development challenge. There is a clear need to upskill the

existing workforce through increasing capacity and capability in microbial genomics technologies, as well as bioinformatics. This will help build an appropriately skilled workforce that is literate in microbial genomics sequencing and analysis.

Invigorated by the COVID-19 pandemic, many states and territories have acted to better understand how the workforce should evolve to support microbial genomics as an integral part of mainstream laboratory testing. However, most of these activities are still being supported by existing resources and require sustainable funding to maintain the provision of training, workshops, and upskilling. This is true in particular for smaller jurisdictions with limited dedicated microbial genomics resources.

Health continues to support the CDGN to provide coordination and bioinformatics support to jurisdictions that are developing capability and capacity. The network has used this funding to upskill laboratory staff and improve bioinformatics literacy across jurisdictions that have limited dedicated bioinformaticians or bioinformatics expertise, which is also supported by the CDGN Teaching, Training and Curriculum Working Group.

The Australian Government is also progressing the development of a National Public Health Laboratory Strategy. While this is not microbial genomics-specific, it will assist to determine workforce needs more broadly in the public health laboratory system as a first step to understanding gaps and opportunities.

A workforce mapping exercise is needed to understand the specific gaps that need to be addressed to improve access to and build microbial genomics capability and capacity. The workforce mapping exercise should look at mechanisms for safe, equitable, efficient, effective, and informed service delivery. There is a pressing need for more bioinformaticians, computer scientists, genomic epidemiologists, translational genomics researchers, genomics-literate microbiologists, and data analysts. This will help to meet the growing demand for microbial genomics in the public health system.

The need for improved and standardised education opportunities that cover microbial genomics for laboratory, clinical, public health and government sector staff is widely recognised as being critical to maximising the potential benefits of microbial genomics for public health action.

Outcome 4.1—Enhanced capacity and capability

- Assess, foster, establish, and maintain national microbial genomics capacity and capability.
- Building and maintaining a skilled, multi-disciplinary and cross-trained workforce.
- Ensure equitable access to capability, including high-performance computing infrastructure, for all jurisdictions.
- Develop bioinformatics expertise, noting that this cannot be generalised across organism types.
- Maintain and build upon engagement with diagnostic laboratories and One Health laboratories.

National Action	Timeframe	Lead	Priority
Outcome 4.1 – Enhanced capacity and capability			
4.1.1 Maintain and develop a skilled and literate national public health microbial genomics workforce through development of workforce strategies and planning.	Long	CDGN, PHLN, CDNA, Health	Medium
4.1.2 Improve the microbial genomics literacy and capability of the health workforce. Do this through the development, delivery and ongoing maintenance of appropriate microbial genomics education, training, and skills.	Medium	CDGN, PHLN, CDNA, Relevant Training Providers & Institutions	Medium
4.1.3 Provide adequate resourcing dedicated to establishing surge capacity and pandemic preparedness, including One Health.	Long	Health	High
4.1.4 Maintain bioinformatics and analytical support in public and private laboratories (including public hospital laboratories) across jurisdictions. Find improvement opportunities that may benefit from national coordination.	Medium	CDGN	High
4.1.5 Provide outreach and education about the availability and utility of genomic analysis for high-priority health care facilities.	Short	CDGN, PHLN, CDNA, Relevant Training Providers & Institutions	Medium
4.1.6 Establish explicit pathways for requesting genomic analysis for high-priority facilities.	Short	CDGN, PHLN, CDNA	Medium

Outcome 4.2—Standardised microbial genomics equipment and expertise

- Maintain comparable instrumentation across jurisdictions.
- Maintain comparable levels of expertise across jurisdictions.

National Action	Timeframe	Lead	Priority
Outcome 4.2 – Standardised microbial genomics equipment and expertise			
4.2.1 Continue to identify barriers to equity of access for laboratories and develop a national approach to address these. Access is multi-dimensional and includes location, cost, availability, and appropriateness.	Medium	CDGN, PHLN, Health	high
4.2.2 Expand AusTrakka as a public health bioinformatics platform allowing standardised analyses across public health and One Health sequencing laboratories.	Long	CDGN, MDU PHL, DAFF, Health	High
4.2.3 Develop and maintain guidelines on public health microbial genomics testing and research as appropriate and encourage national adoption.	Medium	CDGN, PHLN, Health	Medium
4.2.4 Map the public health microbial genomics workforce initiatives underway and find opportunities to further develop the necessary capabilities. Also consider strategies to support the equitable supply and distribution of that workforce.	Medium	CDGN	Medium

Outcome 4.3—Encourage innovation

- Promote national and international collaboration and innovation across One Health laboratories, public health units and academia to keep pace with advances in microbial genomics technology, including non-culture-based approaches.

National Action	Timeframe	Lead	Priority
Outcome 4.3 – Encourage innovation			
4.3.1 Foster One Health and public health partnerships and stakeholder engagement to encourage innovation in microbial genomics to improve public health outcomes.	Medium	CDGN, PHLN, CDNA, Health, DAFF	Medium
4.3.2 Consult with private industry to explore opportunities for partnerships to support development and sustainable application of public health microbial genomic knowledge.	Medium	CDGN, PHLN, Health	Medium
4.3.3 Strengthen metagenomic capability for public health. Harness its ability to investigate unidentified pathogens in clinical isolates or the environment, where standard laboratory practices may fail to detect viruses.	Long	CDGN, PHLN	Low

Outcome 4.4—Workforce development

- Promote establishment, improvement, and maintenance of genomics literacy and related skills in both laboratory and non-laboratory settings (for example, public health clinicians and epidemiologists) through microbial genomics education, training, and quality assurance.
- Promote workforce training strategies and planning to ensure consistent and equal access to upskilling opportunities across jurisdictions and microbiology service providers.
- Facilitate collaboration, partnerships, and networks between professional colleges and societies to promote and support the sharing of knowledge.

National Action	Timeframe	Lead	Priority
Outcome 4.4 – Workforce development			
4.4.1 Involve relevant professional bodies and colleges who oversee and inform workforce training to streamline public health microbial genomics curricula. Ensure a consistent approach to teaching and training of microbial genomic sequencing for use in public health.	Medium	PHLN, CDNA, Health	Medium
4.4.2 Involve relevant stakeholders, sectors, and subject matter experts to improve genomics health literacy. Share experiences and lessons learned and raise awareness of the integration of microbial genomics into the Australian public health system.	Medium	CDGN, PHLN, CDNA, Health	Medium
4.4.3 Provide coordination and bioinformatics training and support across jurisdictions to ensure equitable sharing of practices, knowledge, and information to all jurisdictions.	Medium	CDGN	High

Strategic Priority 5—Financing

Public health laboratories have identified common challenges to the routine implementation of microbial genomics in their laboratories. These include:

- lack of sustainable funding for maintaining a microbial genomics service in public health laboratories post COVID-19, particularly in those that receive relatively low specimen numbers, noting also that public expectation regarding service delivery and fast turn-around time remains high
- limited bioinformatics expertise in some jurisdictions
- limited infrastructure in some jurisdictions in relation to sequencing, data storage and computational capacity, and
- lack of standardisation of bioinformatics analysis between jurisdictions.

Sustainable funding is essential for the success of a nationally consistent and comprehensive microbial genomics program. In May 2018, the Australian Government announced an investment of $500 million over 10 years for an Australian Genomics Mission under the MRFF. The Australian Genomics Mission will help to save or transform the lives of more than 200,000 Australians through research on better testing, diagnosis, and treatment.

In April 2019, it was announced that a grant opportunity under the MRFF would be dedicated a Genomics Health Futures Mission (GHFM) Flagship for pathogen genomics. This flagship recognises the application of genome sequencing technologies to the characterisation and analysis of pathogens. This informs clinical and public health investigations of, and responses to, infectious disease. Key programs awarded under this grant opportunity include AusPathoGen, H2Seq, and the Meta-GP program.

While the added value of microbial genomic services for public health has been recognised, agreement needs to be reached between clinical and public health services with regard to funding for service development and delivery where the microbial genomics services have a dual clinical and public health benefit—for example, drug resistance and antimicrobial stewardship.

What does the future look like?

- A sustainable funding model has been established, linked to broader public health laboratory testing, outbreak investigation and public health response.
- The funding model is agile so it can respond to emerging technologies and expanding application of microbial genomics to public health.

Prior and current activities

An evidence base to support the value of microbial genomics has now been established due to the COVID-19 pandemic, however further work needs to be progressed to understand the cost-effectiveness of microbial genomics in the Australian context for other pathogens of public interest. This can be done by exploring, evaluating, and reporting on economic evidence that supports the integration of microbial genomics into Australian laboratories. This is necessary to inform how a sustainable funding model could be established that considers the cost-effectiveness of services and acknowledges the clinical and/or public health applications of pathogen genomics.

The application of microbial genomics in public health has the potential to reduce the financial burden of infectious disease management and outbreak investigation and response. This is through earlier characterisation of outbreaks and implementation of public health intervention measures. Without sustainable funding, laboratories are limited in their capacity to provide microbial sequencing services for the purposes of clinical and/or public health value. Support for, and investment in, advancing technology is needed to drive innovation and capability in this rapidly evolving environment.

Starting in 2021, AusPathoGen is undertaking an economic evaluation of genomic-based public health responses. The program aims to compare the incremental cost and effectiveness of WGS compared to current methods of testing and typing, and so assess the incremental cost effectiveness of WGS as the core tool for surveillance of these pathogens.

Outcome 5.1—Establishment of a sustainable funding model

- Develop a sustainable funding model involving a partnership between the Australian Government and the states and territories.
- Improve flexibility to keep pace with advances in technology and the expanding role of microbial genomics.

National Action	Timeframe	Lead	Priority
Outcome 5.1 – Establishment of a sustainable funding model			
5.1.1 Continue to explore and advocate for equitable financing and purchasing models to inform the appropriate integration of safe, effective, and cost-efficient public health microbial genomics delivery. This will be particularly important in the context of establishment of the new Australian Centre for Disease Control.	Medium	CDGN, PHLN, CDNA, AHPPC, Health	Medium
5.1.2 Investigate funding opportunities at both the national and state and territory level, for example, through grant opportunities, to enhance microbial sequencing capability and capacity. Funding opportunities that focus on public health and One Health surveillance and / or to inform individualised patient care should be targeted.	Ongoing	CDGN, PHLN, CDNA	High
2.1.1 Develop robust business cases to seek funding opportunities required for the establishment, maintenance, and advancement of public health laboratory capacity and capability in microbial genomics.	Long	CDGN, PHLN	High

Outcome 5.2—Establishment of cost-effectiveness

- Ensure the cost of introducing and maintaining microbial genomic technology results in savings accrued from improvement in patient care and replacement of existing technologies. Initial implementation will result in a short-term increase in costs while development of new workflow processes and replacement of outdated testing methods occur.
- Establish a mechanism to regularly review risks and challenges associated with the integration of microbial genomics into public health.

National Action	Timeframe	Lead	Priority
Outcome 5.2 – Establishment of cost-effectiveness			
5.2.1 Evaluate and report on the value and cost-effectiveness of implemented microbial genomics services through evaluation activities of AusPathoGen.	Medium	CDGN, PHLN, CDNA, Health	Medium
5.2.2 Develop partnerships, funding, and data sharing approaches for microbial genomics that promote access to safe, efficient, and cost-effective services, including for a One Health context both nationally and regionally recognising that regional investment mutually benefits Australia.	Medium	CDGN, PHLN, CDNA, Health	Medium
5.2.3 Collaborate across governments and stakeholders to maximise investment, reduce duplication of effort, and use resources efficiently.	Long	CDGN, PHLN, CDNA, AHPPC, Health	Medium
5.2.4 Establishing a mechanism to regularly review risks and challenges associated the integration of microbial genomics into public health.	Medium	Health	High

Annex A

National developments

Since the publication of the first *National Microbial Genomics Framework 2019-2022,* the integration of microbial genomics in public health has been fast-tracked due to the COVID-19 pandemic. However, while activities over 2020-2023 were largely focused on the COVID-19 response, developments have been made in other critical areas including training and workforce and establishing sequencing pipelines and methods for other diseases and antimicrobial resistances of public health significance. This progress was largely due to, and facilitated by, the CDGN.

Communicable Diseases Genomics Network

The CDGN was established in 2015 with an overarching aim of implementing genomics into clinical and public health microbiology in Australia. The CDGN includes representatives from PHLs across all jurisdictions in Australia, and New Zealand.

CDGN's vision is to advance public health in Australia and New Zealand through the implementation of microbial genomics to support communicable disease control activities. Since its establishment, CDGN continues to provide PHLN with technical advice on genomics and to progress activities under this Framework.

To address the aims of the Network, CDGN has established several working groups covering the following topics:

- pathogen and topic-specific expert advisory groups, such as the SARS-CoV-2 variants of concern working group
- workforce training and curriculum development in microbial genomics
- development of a secure platform for rapid, equitable and ethical data sharing (i.e., AusTrakka), and
- standardisation and implementation of genomic technologies in laboratories (including clinical metagenomics). This includes development and support for the RCPA QAP in microbial genomics.

CDGN has also played a critical role in Australia's response to COVID-19 and continues to actively monitor and report on domestic and international SARS-CoV-2 variants.

In Focus: CDGN Teaching and Training

Since the formation of CDGN, teaching and training within the field of pathogen genomics for public health has been a central focus for the Network. CDGN's teaching and training activities are undertaken by the Teaching, Training and Curriculum Working Group (TTC WG), established to enhance Australia's genomics capacity through the promotion and implementation of high-quality teaching and training resources across all jurisdictions. The multidisciplinary working group is comprised of members from CDGN laboratories with expertise across microbial genomics, bioinformatics, medical microbiology, and genomic epidemiology, who meet monthly to progress key TTC WG activities.

In 2021, the TTC WG developed a genomics-based end-to-end Training Framework to align training approaches nationally, informed by the group's experience and expertise working within public health and clinical laboratories across Australia.

In 2022, the TTC WG translated the Training Framework into a three-part webinar series titled '*Introduction to Pathogen Genomics for Public Health*', which was implemented across the year and covered wet-lab processes for WGS, bioinformatic analysis for clinical and public health, and reporting considerations for WGS. Evaluation surveys from the webinar series found participants strongly valued "the up-to-date information on technology changes" and the explanation of "difficult information in a concise manner". The TTC WG activities directly align with strategic priority 4 of the *Implementation Plan for the National Microbial Genomics Framework 2021-2022*, which seeks to foster national microbial genomics capacity and capability and promote improvement and maintenance of genomics literacy in both laboratory and non-laboratory settings.

Microbial genomics and the COVID-19 response

Enhanced expertise was, and remains, essential to guide Australia's national approach to SARS-CoV-2 genome sequencing and analysis to support the Australian Government response to the COVID-19 pandemic and its transition to management under standard communicable disease control measures. Microbial genomics has been recognised as an important public health tool that can enhance epidemiological investigation of COVID-19 cases by:

- supporting the identification of the source of infection in cases arising without known epidemiological links
- supporting field investigations to identify and more precisely characterise outbreaks
- identifying clusters of infection, and
- defining possible transmission networks to enhance targeted implementation of public health measures and prevent or slow onward transmission.

Integration and implementation of a nationally coordinated approach to sequencing was accelerated and became a critical pillar in Australia's public health response to the COVID-19 pandemic. The need to rapidly characterise SARS-CoV-2 lineages using genome sequencing was apparent early in the pandemic, due to the virus' ability to quickly evolve and impact, transmissibility, severity, immune evasion, and treatment efficacy.

With support of Australia's collaborative network of public health laboratories and CDGN, all states and territories were quickly able to increase their sequencing capability and capacity in the early stages of the pandemic. Over the course of the pandemic the outputs of sequencing analysis have influenced decision making in different ways; for example, informed decisions to introduce public health and social measures, such as mask wearing, social distancing, or lockdowns.

With increased sequencing capability arose the need for more effective management and harmonisation of sequencing information, and the establishment of a nationally coordinated approach to genomic surveillance. In early 2020, a nationally agreed approach to sequence and minimal metadata sharing for SARS-CoV-2 was established, led by CDGN. This included development of a governance framework for data sharing, which was critically public health focussed and enabled custodianship of the data to remain with contributing sequencing laboratories.

SARS-CoV-2 Variants of Concern

As COVID-19 variants began to emerge in late 2020, the international public health community rallied to determine the impact of circulating variants on current diagnostics and therapeutics, disease severity, and overall transmissibility. In response, CDGN identified the need for a dedicated taskforce to provide Australia with a nationally coordinated mechanism for understanding and responding to emerging variants. The CDGN multi-disciplinary Variant of Concern Working Group (VOC WG) was formed to address this need, comprising of medical microbiologists, virologists, bioinformaticians, genomic epidemiologists, phylodynamic modelers, and government representatives.

The CDGN VOC WG has supported a nationally coordinated response to SARS-CoV-2 variants, and implemented near real-time genomic surveillance and consistent reporting of circulating lineages, particularly through regular publication of a VOC Literature Summary containing up to date information on lineages circulating globally and nationally, maintenance of a national VOC Laboratory Case Definition, and regular briefings on emerging lineages in response to requests from governments and key stakeholder groups. The CDGN continues to provide expert advice to the Australian Government on SARS-CoV-2 variants and mutations of interest relevant to Australia for surveillance and reporting based on available literature and international classifications.

Due to the broader circulation of COVID-19 in the community in late 2021, Australia's sequencing laboratories moved from a comprehensive sequencing strategy (attempt to sequence every case) to a targeted surveillance approach focussed more on surveillance and detection of variants or mutations of concern. This led to the publication of the *CDGN Sampling Strategy for SARS-CoV-2 Genomic Surveillance*. The Strategy aimed to ensure the data collected is:

- Representative
- Still enables new introductions to the identified, and
- Provides reliable findings that impact public health action.

The Strategy outlined suggested priority groups for targeted sampling, this included patients admitted to hospital and/or intensive care, to identify whether any virus lineages are associated with increased disease severity.

WGS Proficiency Testing for SARS-CoV-2

To ensure capability was developed and maintained across jurisdictions, over 2019-2022, Health supported the RCPA QAP Biosecurity program to develop a proficiency testing program (PTP) for SARS-CoV-2 WGS. This was offered to interested laboratories for free. The PTP provided important insights into established WGS practices and how performance and standardisation may be improved. Following the successful first pilot WGS PTP, further modules were offered over 2020-21. These modules monitored the quality of sequencing practices in Australian public health laboratories.

AusTrakka

AusTrakka was developed in response to key reports to the Office of Health Protection on the need to better facilitate public health genomics data sharing and analysis in Australia in a nationally coordinated way. In 2020, national endorsement was provided for the use of AusTrakka, as Australia's national genomic surveillance system for SARS-CoV-2 located at the University of Melbourne. AusTrakka provides for near

real-time analysis of integrated pathogen genomic data for public health across Australia, providing a central, secure, and private online location to share, store, analyse and view aggregated national and jurisdictional data.

In September 2020, AHPPC endorsed the *Framework for data sharing and analysis for SARS-CoV-2 in the AusTrakka system*. This framework provides a mechanism for rapid data sharing and genomic analysis within and between jurisdictions, and nationally. While not legally binding, it formalised the endorsement for public health laboratories to rapidly share all SARS-CoV-2 genomics data to the AusTrakka platform through their nominated public health laboratory for national near real-time surveillance. This enabled the public health system to track transmission and identify new and emerging SARS-CoV-2 clusters to improve surveillance of COVID-19. This rapid sharing of genomic data now consistently contributes meaningfully to response activities and informs decision making on public health interventions, where required.

AusTrakka is continuing to grow as new public health pathogens are embedded. In its expansion, AusTrakka aims to facilitate the rapid and coordinated responses in four areas of national need:

- foodborne diseases (see Case Study 2, *page XX*),
- respiratory and vaccine-preventable diseases,
- sexually transmitted infections (see Case Study 3, *page XX)*, and
- antimicrobial resistance (AMR) (Case Study 4, *page XX*) and emerging pathogens (biothreat agents).

Case Study 1: Multijurisdictional outbreak of *Salmonella* Typhimurium

In 2021 a national genomic surveillance investigation of *Salmonella* Typhimurium cases across Australia was conducted in AusTrakka, triggered by an increasing number of Typhimurium outbreaks across jurisdictions. For this outbreak, traditional epidemiological approaches were unable to identify clear links between clusters or potential sources as differing typing methods in each state prevented comparison based on laboratory results alone. OzFoodNet Australia requested a national comparison of all genomic sequences collected within a six-month period be conducted in AusTrakka. This included samples that were part of separate outbreaks in Queensland and Victoria.

An initial comparison identified 32 multijurisdictional genomic clusters of varying sizes within the 629 sequences submitted. In-depth genomic analysis revealed highly related groups within clusters that would not have otherwise been discovered. This enabled the identification and exclusion of suspected transmission chains between jurisdictions and potential sources. This was one of the first large-scale genomics-led exploratory investigations into *Salmonella* Typhimurium transmissions across Australia. The outcomes of this investigation informed OzFoodNet of potential links between cases and sources for further investigation, enabling a more targeted approach to the response. This is an example of an innovative response to national surveillance and outbreak investigation in line with the Australian Foodborne Illness Reduction Strategy.

Case Study 2: Monitoring multi- and extensively-drug-resistant *Shigella* species

The emergence and increased circulation of multi- and extensively-drug-resistant (MDR/XDR) *Shigella* strains across the globe means there is significant risk of the introduction and establishment of these highly resistant pathogens in Australia. Genomic studies undertaken in Victoria and Queensland has provided key insights to the different aspects of this threat: the introduction and transmission of XDR *Shigella sonnei* among gay, bisexual, and other men who have sex with men (GBMSM) in Australia[3,4], co-circulation of multiple MDR *Shigella* species in Australia[5], and the transfer of a MDR plasmid to an endemic strain of *Shigella flexneri* that disproportionally affects Aboriginal and Torres Strait Islander children[6]. This expertise now underpins the efforts towards real-time nationally harmonised surveillance of *Shigella* species, undertaken as one of the key pathogens in the Medical Research Future Fund (MRFF) funded national AusPathoGen program; directly meeting the priority area of using evidence-based surveillance and monitoring data to inform action and responses outlined in Australia's National Antimicrobial Resistance Strategy.

Case Study 3: Clinical and public health utility of *Mycobacterium* tuberculosis whole genome sequencing[7]

For patients with *Mycobacterium* tuberculosis, WGS has been shown to be of real value as it enables patients to received tailored treatment and is able to differentiate between relapse and re-infection. Contamination, mixed infections, clusters, and transmission pathways can also be determined more accurately using whole genome sequencing compared to traditional methods. Surveillance of antimicrobial resistance is an additional advantage, particularly for high-burden countries.

In Australia, WGS of *Mycobacterium* tuberculosis for the purpose of drug susceptibility testing at the time of diagnosis and in the event of a recurrence has been added to the Medical Benefits Scheme on advice from MSAC[8].

[3] Williamson DA, Ingle DJ, Howden BP. (2019) Extensively drug-resistant Shigellosis in Australia among men who have sex with men. New England Journal of Medicine.

[4] Ingle DJ, Andersson P, Valcanis M et al. (2020) Prolonged outbreak of multidrug-resistant Shigella sonnei harbouring blaCTX-M-27 in Victoria, Australia. Antimicrobial Agents and Chemotherapy.

[5] Ingle DJ, Easton M, Valcanis et al (2019) Co-circulation of multidrug-resistant Shigella among men who have sex with men in Australia. Clinical Infectious Diseases.

[6] Guglielmino CJD, Kakkanat A, Forde BM et al (2021) Outbreak of multi-drug-resistant (MDR) Shigella flexneri in northern Australia due to an endemic regional clone acquiring an IncFII plasmid. European Journal of Clinical Microbiology and Infectious Diseases.

[7] Gordon, A. K., Marais, B., Walker, T. M., & Sintchenko, V. (2021). Clinical and public health utility of Mycobacterium tuberculosis whole genome sequencing. International Journal of Infectious Diseases, 113, S40-S42.

[8] Australian Government (2022, May 31). Medical Services Advisory Committee, Public Summary Document, Application No. 1646 – Whole genome sequencing of antimicrobial-resistant pathogens. Retrieved 17 February 2023 from MSAC - 1646 – Whole genome sequencing of antimicrobial-resistant pathogens

Translational research initiatives

In 2020, the Australian Government announced $27 million in funding under the MRFF through the Genomics Health Futures Mission to support large scale pathogen genomics research studies that are late in the research and development pipeline. These projects aim to demonstrate clinical and/or public health utility, cost-effectiveness, and translational capacity, in recognition that such evidence is critical to the adoption of genomics in the mainstream health system.

AusPathoGen

The Australian Pathogen Genomics (AusPathoGen) Program aims to deliver precision in public health for Australia through integrated pathogen genomics. Commencing in 2021, AusPathoGen, a consortia of program partners led by CDGN, aims to build on the success of the COVID-19 genomics response to further implement and evaluate large-scale integration of pathogen genomics, epidemiological and surveillance data at the public health interface.

The AusPathoGen program aims to address the rise in infectious diseases and antimicrobial resistance, adhering to international models for optimal use of pathogen genomic data. This includes:

- Accelerating translational research to inform the establishment of genomics-enabled surveillance and public health interventions,
- Evaluation of its cost-effectiveness and public health impact, and
- Strengthening the pathogen genomics community in Australia and internationally.

The Program also aims to reduce the impact of infectious diseases and AMR on public health by improving pathogen characterisation and optimising responses, to enhance public health action and patient care in Australia. This work will support activities under this Framework.

H2Seq

Human immunodeficiency virus (HIV) and hepatitis C (HCV) are among the most rapidly mutating, genetically diverse, pathogenic RNA viruses. Mutations observed in circulating viruses are influenced by challenges posed by the human immune system, antiviral treatments, and human behaviours allowing transmission – as well as constraints associated with efficient viral replication. Understanding the interaction of viral mutations and each of these influencing factors are key to inform preventive and therapeutic strategies for these conditions.

H2Seq is a national collaborative network that aims to develop, implement, and evaluate platforms for HIV and HCV pathogen genomics for 'near real time' molecular epidemiology. Integrated with this is the development of a full-length genome next-generation sequencing (NGS) protocol for diagnostic use for both HIV and HCV.

Already, H2Seq has significantly impacted current understanding of:

- how HCV evolves at both epidemiological level and during a single infection within the host
- how human behaviours and population movements have impacted the global HCV epidemic
- what measures would be useful in constraining epidemic spread
- what impacts surveillance of the potential emergence of resistance to directly acting antiviral (DAA) treatments as these new agents are rolled out worldwide
- how some patients spontaneously clear the virus with major implications for development of a preventive vaccine, and
- the strengths and vulnerabilities of human immune system against HCV and other RNA viruses.

Metagenomics Platform (Meta-GP)

Clinical metagenomic next-generation sequencing (mNGS) is a transformative approach in microbial diagnostics and patient care, due to its use in detecting and characterising all known pathogens – bacterial, viral, fungal, parasitic – in one single test. Meta-GP aims to develop and implement clinical metagenomic diagnostics for infectious diseases in Australia.

At the conclusion of Meta-GP, Australia will have a nationally accessible network of laboratories that can apply metagenomic approaches in patient care to rapidly detect, prevent, and respond to infectious threats, including antimicrobial resistance.

Meta-GP aligns with the *National Microbial Genomics Framework* strategic priorities and principles by delivering the following objectives:

- the ability to rapidly identify the cause of any infectious disease within a clinically actionable timeframe and hence transform individual patient care
- a clear understanding of the range of microbial pathogens that impose a major disease burden in Australia, and
- ensure public health surveillance can occur in the face of culture independent diagnostic tests.

International developments

Due to the emergence of SARS-CoV-2 and its rapidly emerging and evolving variants, the ability to perform genome sequencing has now been established in more than two-thirds of Member State countries[9]. However, there remains marked variation between different countries regarding the degree to which:

- infrastructure and systems enable nationwide genomic surveillance of communicable diseases, and
- genomic data is able to be shared for public health purposes.

Below is a brief snapshot of activities undertaken by key organisations, collaborations, and countries to enhance pathogen genomic capability and capacity.

World Health Organization

The World Health Organization (WHO) acknowledges that the application of microbial genome analysis has emerged as an essential feature in infectious disease control, with the intention of:

- identification and diagnosis of infectious diseases, and
- demonstrating infection movement between human and/or animal hosts, including:
    - Evolution mapping of infectious agents
    - Gene phenotypic properties assignment, such as infectivity and pathogenicity, and
    - Drug sensitivity or resistance evaluation of an infectious agent.

To drive the progression of its integration, the WHO has released the *Global genomic surveillance strategy for pathogens with pandemic and epidemic potential 2022-2032*[10] which urges Member States to strengthen

[9] World Health Organization (2022) Global genomic surveillance strategy for pathogens with pandemic and epidemic potential, 2022–2032. Retrieved 17 February 2023 from WHO global genomic surveillance strategy for pathogens with pandemic and epidemic potential 2022-2032

[10] World Health Organization (2022) Global genomic surveillance strategy for pathogens with pandemic and epidemic potential, 2022–2032. Retrieved 17 February 2023 from WHO global genomic surveillance strategy for pathogens with pandemic and epidemic potential 2022-2032

their genomic surveillance capacity and capabilities. It aims to address public health needs while recognising that most countries will require assistance to develop their own capabilities. The five objectives of the strategy are to:

- improve access to tools for better geographic representation
- strengthen the workforce to deliver at speed, scale, and quality
- enhance data sharing and utility for streamlined local to global public health decision-making and action
- maximise connectivity for timely value-add in the broader surveillance architecture, and
- maintain a readiness posture for emergencies.

This global strategy aims to guide countries in their expansion of genomic surveillance efforts and promote a harmonised local-to-global approach. Supporting the Strategy's mandate is the recently formed WHO Western Pacific Region (WPR) Emerging Molecular Pathogen Characterisation Technologies (EMPaCT) Surveillance Network. The Network identifies that there is a need for a systems approach to re-visit and re-organise available resources to meet new demand for surveillance to include genomic information in the WPR. A seven-step approach was proposed to facilitate this vision which strives to support the development of sustainable, resilient, and nationally coordinated in-country genomic surveillance systems which have the potential to detect and characterise new threats [11].

Understanding the complexities of genomic integration, in July 2022 WHO published the *Accelerating access to genomics for global health: promotion, implementation, collaboration, and ethical, legal, and social issues: a report of the WHO Science Council*[12]. The report acknowledges the impediments to integration of genomics in low- and middle-income countries include high cost of equipment and reagents, and lack of trained personnel. In this report, fifteen actions are recommended to achieve the goal of accelerating access to genomics for global health under four themes:

- promotion of genomics through advocacy
- implementation of genomic methodologies
- collaboration among entities engaged in genomics, and
- attention to the ethical legal, and social issues raised by genomics.

Recognising the global response to the COVID-19 pandemic was disjointed and hindered by inadequate sharing, WHO published the *WHO guiding principles for pathogen genome data sharing*[13] in November 2022. The guidance acknowledges pathogen genomics capacity is advancing rapidly and recognises risks created by gaps in global surveillance. New technology is not equally accessible and potentially negative effects from

[11] World Health Organization: Regional Office for the Western Pacific (2022). Meeting Report: Inaugural Meeting of the Western Pacific Region Emerging Molecular Pathogen Characterization Technologies (EMPaCT) Surveillance Network. Retrieved on 17 February 2023 from Inaugural Meeting of the Western Pacific Region Emerging Molecular Pathogen Characterization Technologies (EMPaCT) Surveillance Network, Virtual meeting, 21-22 September 2021: meeting report (who.int)

[12] World Health Organization (2022). Accelerating access to genomics for global health: promotion, implementation, collaboration, and ethical, legal, and social issues. A report of the WHO Science Council. Retrieved 17 February 2023 from Accelerating access to genomics for global health: promotion, implementation, collaboration, and ethical, legal, and social issues: a report of the WHO Science Council

[13] World Health Organization (2022). WHO Guiding principles for pathogen genome data sharing. Retrieved 17 February 2023 from WHO guiding principles for pathogen genome data sharing

reporting the emergence of new and dangerous pathogens can act as a deterrent to data sharing. WHO encourages timely pathogen genome data sharing and the guidance suggests 13 foundational principles on which pathogen genome data sharing should be based:

- capacity development
- collaboration and cooperation
- high-quality, reproducible data
- global and regional representativeness
- timeliness
- acknowledgement and intellectual credit
- global and regional representativeness
- equitable access to health technologies as a benefit
- as open as possible and as closed as necessary
- interoperability and relevance for national, regional, and global decision-makers
- trustworthiness and ease of use
- transparency
- consistency with applicable law and ethical regulations, and
- compliance and enforcement.

To facilitate pathogen genomic surveillance, in May 2023 the WHO launched the International Pathogen Surveillance Network (IPSN), a global network of pathogen genomic stakeholders, hosted by the WHO Hub for Pandemic and Epidemic Intelligence. The IPSN's aims is to accelerate progress on the deployment of pathogen genomics and improve public health decision-making. To achieve its mission, the IPSN has identified five areas of work:

1. Communities of practice to solve common challenges
2. Country scale-up accelerator to align efforts and enable South-South exchange
3. Funding to improve equity and to power IPSN projects
4. High-level advocacy and communications to keep genomic surveillance on the agenda
5. Global partners forum for pathogen genomics to bring partners together

The Quadrilateral Security Dialogue and the G20

The Quadrilateral Security Dialogue (the Quad) is a strategic security dialogue between Australia, India, Japan, and the United States (US). On 24 September 2021, the Quad committed to better preparing member countries and the world for the next pandemic, as part of the Build Back Better Health Security initiative[14]. In its commitment, the Quad agreed to continue building multi-lateral COVID-19 response and health-security efforts in the Indo-Pacific, and further strengthen science and technology cooperation. This included support for the development of a "global pandemic radar" to improve viral genomic surveillance, and working to strengthen and expand the WHO Global Influenza Surveillance and Response System (GISRS). Through the Science and Technology cooperation, genomic surveillance was, and continues to be, a key priority of the Quad to accelerate efforts to end this pandemic and build better health security.

The Group of Twenty (G20) is an intergovernmental forum comprising 19 countries and the European Union. It works to address major issues related to the global economy, such as international financial stability, climate change mitigation, and sustainable development. The G20 Bali Leaders' Declaration of 15-16

[14] Fact Sheet: Quad Leaders' Summit - The White House

November 2022 assured that the G20 remained committed to embedding a multisectoral One Health approach to enhancing global surveillance, including genomic surveillance, to detect pathogens and AMR that may threaten human health. In addition, the G20 encouraged sharing of pathogen data in a timely manner on shared and trusted platforms in collaboration with WHO to enable global pathogen surveillance as part of our commitment to implement the International Health Regulations (IHR) (2005) and encourage sharing of benefits arising from the utilisation of pathogens consistent with applicable national laws.

In addition to the global networks described above, countries around the world have established frameworks and ambitious programs to progress pathogen surveillance. While this Framework focuses programs based in the UK, US, Canada and Singapore, this list is not exhaustive and provides only a small snapshot of activities underway.

United Kingdom

In September 2020, the UK published their *Genome UK: the future of healthcare*[15] which aims to extend their leadership in genomic health and research over the next ten years. The three pillars of the Strategy are defined as: diagnosis and personalised medicine, prevention, and research. Recognising the critical role of surveillance in responding to the pandemic[16], in 2021 to 2022 the UK committed to progress on the following ambitions relating to pathogen genomics[17]:

- deliver and analyse SARS-CoV-2 viral genomes together with genomes from affected individuals to inform diagnostics, vaccines, prevention, and containment strategies in response to the global pandemic
- expand viral genome sequencing and analysis capacity and capability to establish a world leading pathogen genomics system to detect and provide local, regional, and national surveillance of infectious threats with strategies to provide this capability within the regional and national health and public health framework.

Case Study 4: Multi-country outbreak of *Salmonella* Typhimurium[18]

In 2021, the UK used WGS to link a geographically dispersed cluster of cases of *Salmonella* Typhimurium with unknown origin. Based on the data generated, a further connection was then established between the human outbreak cases and *Salmonella* Typhimurium contamination identified in a buttermilk tank at a chocolate factory in Belgium. Investigations found that the implicated food products had been distributed to at least 113 countries and led to more than 300 cases of infection in 16 different countries being reported. Information provided by investigations informed public health control measures.

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[15] Department of Health and Social Care. (2020, September 26). Genome UK: the future of healthcare. GOV.UK. Retrieved 17 October 2022 from https://www.gov.uk/government/publications/genome-uk-the-future-of-healthcare

[16] The COG-UK consortium a national pathogen sequencing service was rapidly formed in March 2020 to provide SARS-CoV-2 genome sequencing and analysis to inform public health policy and action.

[17] GOV.UK (2021, May 19). Genome UK: 2021 to 2022 implementation plan. Retrieved 26 October 2022 from Genome UK: 2021 to 2022 implementation plan - GOV.UK (www.gov.uk)

[18] World Health Organization (2022, April 26). Disease Outbreak News; Multi-country outbreak of *Salmonella* Typhimurium linked to chocolate products – Europe and the United States of America. Retrieved 30 September, 2022, from https://www.who.int/emergencies/disease-outbreak-news/item/2022-DON369

Canada

Canada acknowledges that global interest in genomics has increased, and precision health, environmental protection, food, and energy security are just some examples of where genomics research can be utilised and combined with other fields[19]. To prevent falling behind other countries, more than $400 million dollars over 6 years was proposed during Canada's Budget 2021 to fund the development of a Pan-Canadian Genomics Strategy (PCGS) which aims to increase the implementation of genomics and related technologies in Canada and progress genomics commercialisation.

United States

In March 2022, the US CDC announced $90 million in funding for a new competitive agreement that will support the establishment of the US Pathogen Genomics Centers of Excellence (PGCoE)[20]. The PCGoE network provides an opportunity for genomic surveillance advancement through partnerships between academic institutions and health agencies and aims to improve public health response to infectious disease threats. Recipients of the 5-year awards were announced in September 2022 with all five centers consisting of a health department and one or more academic institutions. Working as a network, the PGCoE's intend to[21]:

- perform a landscape analysis of gaps, needs, and opportunities for pathogen genomics in the United States public health system
- pilot and implement genomics technologies and applications for public health
- provide training in pathogen genomics for the public health workforce, and
- prepare for and respond to infectious disease threats.

In addition to the creation of the PGCoE, CDC's Advanced Molecular Detection program effort has been expanded by a $1.7 billion, multi-year US government investment from the American Rescue Plan Act of 2021 to help prepare states, communities, and the nation for future disease outbreaks by investing in computer power, data-sharing, and education[22].

Singapore

In June 2022, the Centre for Outbreak Preparedness (COP) was launched by the Duke-NUS Medical School to strengthen regional research capacity and capabilities and a partnership with Bill and Melinda Gates Foundation announced to develop the Asia Pathogen Genomics Initiative (APGI)[23]. The Duke-Nus COP aims

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[19] Government of Canada (2022, June 29). Consultation Paper: Developing a Pan-Canadian Genomics Strategy. Retrieved 20 February 2023 from Consultation-Paper-Developing-a-Pan-Canadian-Genomics-Strategy.pdf (canada.ca)

[20] Centers for Disease Control and Prevention (2022, September 22). CDC announces $90M funding to support new Pathogen Genomics Centers of Excellence network. Retrieved 20 February 2023 from Announcement Pathogen Genomics Centers of Excellence (cdc.gov)

[21] Centers for Disease Control and Prevention (2022, September 22). CDC announces $90M funding to support new Pathogen Genomics Centers of Excellence network. Retrieved 20 February 2023 from Announcement Pathogen Genomics Centers of Excellence (cdc.gov)

[22] Centers for Disease Control and Prevention (2022, January 26). Investments in AMD. Retrieved 20 February 2023 from Investments in AMD | Advanced Molecular Detection (AMD) | CDC

[23] Duke-NUS Medical School (2022, June 10). Duke-NUS Centre for Outbreak Preparedness launched in Singapore to enhance regional capacity for future health threats. Retrieved 20 February 2023 from Duke-NUS Centre for Outbreak Preparedness launched in Singapore to enhance regional capacity for future health threats

to enhance regional health security across South and Southeast Asia by working to improve regional surveillance and laboratory capacity for early detection of disease threats and supporting other countries in the region in early detection and variant analysis through enhanced genomic surveillance and data sharing via the APGI.