Implementing a national programme of pathogen genomics for public health: the Australian Pathogen Genomics Program (AusPathoGen)

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Delivering large-scale routine pathogen genomics surveillance for public health is of considerable interest, although translational research models that promote national-level implementation are not well defined. We describe the development and deployment of the Australian Pathogen Genomics Program (AusPathoGen), a comprehensive national partnership between academia, public health laboratories, and public health agencies that commenced in January, 2021. Successfully establishing and delivering a national programme requires inclusive and transparent collaboration between stakeholders, defined and clear focus on public health priorities, and support for strengthening national genomics capacity. Major enablers for delivering such a programme include technical solutions for data integration and analysis, such as the genomics surveillance platform AusTrakka, standard bioinformatic analysis methods, and national ethics and data sharing agreements that promote nationally integrated surveillance systems. Training of public health officials to interpret and act on genomic data is crucial, and evaluation and cost-effectiveness programmes will provide a benchmark and evidence for sustainable investment in genomics nationally and globally.

Introduction

A goal listed by WHO in their Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032 is to strengthen genomic surveillance for pathogens of public health significance.[1] Increasing evidence supports the broader utilisation of pathogen genomics for the control of infectious diseases and antimicrobial resistance (AMR) globally, including that from the early leaders in pathogen-specific genomic surveillance in the UK and the USA.[2–10] In Australia, during the COVID-19 pandemic, genomics was essential to disease control strategies, enabling the country to remain largely disease free for 2 years when the population was vaccinated.[11–15] Thus, the pandemic showed that implementation of routine genomics into public health was crucial to enhance surveillance, despite challenges associated with a federated health system in Australia.[16]

As a federation, Australia's six states and two territories are independently responsible for public health activities. Although national coordination occurs through health-related committee structures, systematic sharing of laboratory and public health data is not routine. The transition of pathogen genomics from a research tool into an established method for enhanced infectious disease surveillance and response for public health presents substantial challenges, especially across jurisdictional and national borders.[3,17–20] These include (1) equitable access to genomics technologies,[21–23] (2) appropriate data ownership, governance, and rapid sharing approaches,[24–27] (3) standardised bioinformatics analyses and reporting that meet ISO standards,[28,29] (4) data sharing platforms that are fit for purpose at the public health interface,[30,31] (5) training of end users to ensure genomics data are turned into public health action, and (6) capturing the impact of genomics to inform sustainable funding models.[32–34] In Australia and New Zealand, the Communicable Diseases Genomics Network (CDGN) was established in 2015 as an expert reference panel of Australia's Public Health Laboratory Network to develop and support the integration of genomics in public health and contribute to Australia's first National Microbial Genomics Framework (2019–22).[35]

To accelerate the establishment of a pathogen-agnostic approach to genomic surveillance in Australia, the Australian Government Department of Health and Aged Care's Medical Research Future Fund provided AU$10 million under the Genomic Health Futures Mission[36] for the establishment of the Australian Pathogen Genomics Program (AusPathoGen; 2021–25). AusPathoGen brings together 180 stakeholders from 48 organisations across Australia and New Zealand ranging from public health laboratories (PHLs), public health agencies (PHAs), and academic organisations. They collectively aim to generate evidence to support the integration of genomics for surveillance of pathogens of public health significance in an equitable and nationally consistent manner. AusPathoGen aims to nationally harmonise and optimise genomics-based surveillance, train the future genomics workforce, implement and integrate analysis in existing surveillance systems for genomics-informed responses, and evaluate the utility and cost-effectiveness of genomics-based public health responses. Here, we provide our perspective on the foundations of AusPathoGen, focusing on research collaboration, data governance and data sharing infrastructure, ethics protocols, development of national projects for

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For **CDGN** see https://www.cdgn.org.au/

For **The AusPathoGen Executive Group** see https://www.auspathogen.org.au/our-team-categories/executive-group

priority pathogens from an Australian perspective, and approaches implemented to realise the aims. Our approach to national coordination and implementation of pathogen genomics surveillance into public health can be adopted by countries with federal systems to improve genomics integration and use at the public health interface.

Overview of the establishment of AusPathoGen

Programme inception

The AusPathoGen Executive Group, composed of PHL directors, Australian government representatives, leaders in bioinformatics and One Health, and evaluation scientists, was formed to design the programme through (1) existing academic partnerships that have led to advancement in the use of genomics for public health, and (2) a coordinated national network of PHLs working to harmonise and implement pathogen genomics for public health in Australia, the CDGN.

Stakeholder engagement

AusPathoGen conducted a review of stakeholders across PHLs, government agencies at the national and jurisdictional levels, academic institutions, existing relevant programmes, industry, and international agencies and organisations to obtain views on pathogen genomics needs, which led to the development of a comprehensive stakeholder list and engagement plan. Invitations to the programme were based on (1) their role in public health service delivery, (2) expertise and existing activities in pathogen genomics research, and (3) their ability to influence and drive public health policy. Stakeholders received a verbal and written briefing on the programme objectives, engagement strategy, and partners and intended outcomes. They also received an opportunity to provide feedback.

Priority pathogen list and genomic capacity

To establish a list of priority pathogens of public health significance for the programme, we undertook an assessment of the infectious disease burden and emerging trends in Australia by compiling publicly available data from the National Notifiable Disease Surveillance System for years 2016–19. Data on the number of isolates collected across key Australian PHLs were obtained for infectious diseases with substantial disease burden (eg, *Salmonella*, owing to high case numbers) to provide information on anticipated sample numbers that would be available for the programme. We also provided a scoping survey to PHLs to investigate jurisdictional capacity and readiness to sequence and share data on potential priority pathogens. The potential pathogen priority list was presented to key national bodies and committees (eg, Australian Health Protection Principal Committee, Communicable Diseases Network Australia, Public Health Laboratory Network) for consultation to ensure alignment with broader national surveillance strategies and priorities.

Formation of national working groups

The AusPathoGen executive group established the pathogen-specific working groups and invited stakeholders with the goal of achieving representation across all relevant disciplines responsible for creating national initiatives for priority pathogens. The initiatives included harmonising genomic surveillance systems for rapid responses to outbreaks and AMR and for the implementation of findings into routine national surveillance. An evaluation reference group, consisting of representatives from PHLs, PHAs, and end users of pathogen genomic data of priority pathogens, ensuring balance across jurisdictions, was established to guide and provide input to the evaluation and implementation programme.

Data management platform

AusPathoGen uses the AusTrakka platform, which was developed and deployed as Australia's government-endorsed public health genomic surveillance platform during the COVID-19 pandemic. AusTrakka provides a secure mechanism for the management, analysis, and visualisation of genomic data, with strict access control enabling the inclusion and sharing of sensitive metadata. The platform functionality has been further developed and adapted to meet the needs of AusPathoGen as a translational research programme. AusPathoGen has since been used to support national outbreak investigations of several other pathogens, including *Salmonella*, *Shigella*, and *Vibrio parahaemolyticus*.[16]

Ethics, research, and data governance

Operational frameworks supporting national public health data sharing across PHLs and agencies developed and facilitated by the CDGN PHLs were used to create the data sharing framework for the research activities in AusPathoGen. Collaborations within the programme were formalised through multi-institutional agreements between academic institutions, service agreements with PHLs, and collaboration agreements with PHAs and industry partners. Data transfer and data access agreements govern the sharing of and access to data. Cumulatively, the agreements and national ethics that form the governance of the programme clearly define data custodianship, uses of contributed data, data access, recognition of intellectual contributions, and funding of activities. Ensuring that the agreements are operationally compatible with existing jurisdictional public health processes and notifiable disease surveillance systems beyond the end of the programme is important for sustained implementation.

Development of an evaluation programme

A crucial and broad aspect of translational research, and a core element of AusPathoGen, is the evaluation of the public health usefulness of genomics. Here, we followed the Pathogen Genomics in Public HeAlth Surveillance Evaluation (PG-PHASE) Framework previously defined by members of the AusPathoGen evaluation team.[37] Informed by systems thinking, the evaluation and implementation

programme was designed to address issues of public health utility of pathogen genomics across all stages, from prioritisation of pathogens for sequencing to interpretation and visualisation of data.

Lessons learnt since the establishment of AusPathoGen

Programme governance and ethics

Extensive stakeholder consultation during the design phase of AusPathoGen created opportunities and enhanced engagement with the programme and supported contributions to research activities, and established formal partnerships to provide support and guidance for the programme through advisory roles and participation in working groups. The programme has stakeholders across the public health spectrum (PHLs and PHAs) and academia, ensuring a high probability of its successful translation, integration, and sustainability (appendix pp 1–2).

The executive group established a clear governance structure (figure 1). Data governance and advisory committees provide programme guidance, with implementation of outcomes enabled by the CDGN PHLs and PHAs, and academic partners providing subject matter expertise. Projects were developed and conducted in multidisciplinary pathogen-specific working groups, led by PHL directors and AusPathoGen Research Fellows, consisting of up to 80 members. Pathogen-specific bioinformatics sub-working groups included bioinformaticians and PHL genomic epidemiologists who worked together on standardising data analysis and interpreting results. Working groups followed terms of reference and authorship guidelines developed and endorsed by the executive group.

A range of agreements and frameworks underpin AusPathoGen activities. Financial aspects are managed through a head funding agreement and multi-institutional agreement for the distribution of grant funds, and jurisdictional sub-agreements detailing support for equipment, consumables, and workforce. National genomic data sharing in the programme is underpinned by a pathogen-agnostic genomic data sharing framework in place between the PHLs, and data transfer and access agreements. In Australia, the custodians are the PHLs (sequence and sample data) and PHAs (case metadata), with the custodianship of sequence and associated sample metadata remaining with the contributing organisations. The data sharing framework outlines the procedure for data usage, including ensuring consultation and approval of data custodians before any future use of the data. Data transfer and access agreements outline permissions to access and use data for analysis purposes in the projects and list the authorised personnel conducting this work at respective organisations, allowing regular audits to ensure secure membership.

The AusPathoGen ethics team developed the approved ethics protocol under Australia's National Mutual Acceptance system, providing a single ethical and scientific review for a PHL and PHA from each jurisdiction to contribute data and engage in the programme, with subsequent site-specific governance approval at each of the participating organisations. The ethics protocol covers the contribution of metadata and sequences and genomic epidemiological analysis across 18 pathogens from every Australian jurisdiction, providing a powerful blueprint beyond AusPathoGen for the implementation of collaborative research across Australia.

Pathogen prioritisation identified pathogens of immediate national focus

Pathogen prioritisation relied on National Notifiable Diseases Surveillance System data on disease burden and isolate numbers at each jurisdictional PHL and consultation with key stakeholders. At the time of prioritisation, few PHLs routinely sequenced many pathogens; thus, prioritisation was not influenced by available sequences. Consultations with the CDGN and Communicable Diseases Network Australia achieved consensus on high-priority pathogens in Australia and identified 18 priority pathogens (appendix p 4), with three pathogens selected for immediate focus for AusPathoGen: *Salmonella enterica* as it has a high disease burden, and is frequently associated with community outbreaks;[38] *Shigella* spp because of the introduction of many extensively drug-resistant strains into Australia, which have spread to individuals at high risk and clinically vulnerable populations;[39,40] and *Mycobacterium tuberculosis* as it is associated with high disease burden, disproportionally affecting Indigenous Australians.[41]

National sequencing capability

At the commencement of AusPathoGen, five of eight jurisdictions had public health genomics capacity at PHLs, with distinct variations in the annual throughput in 2018: from 100 to 1000 sequences (n=1) and 1000–10 000 sequences (n=2) to more than 10 000 sequences (n=2). AusPathoGen supported the establishment of, or access to, genomic sequencing platforms in three jurisdictions with limited capability and enhanced the capacity in those with existing capability, including the development of infrastructure (next generation sequencing platforms and bioinformatics hardware) and genomic workforce capacity (genomic epidemiologists, bioinformaticians, and laboratory scientists and clinicians). Facilitating equitable access allowed all jurisdictions to contribute data to the programme, further enabling increased local contribution to public health outbreak investigations and supporting the development of business and use cases to attain sustainable government funding.

Development of flagship national projects

Flagship projects for *M tuberculosis*, *Shigella* spp, and *S enterica* were developed by pathogen-specific working groups defining relevant sampling timeframes with minimum and enhanced metadata variables. To enhance

For **the National Notifiable Diseases Surveillance System** see https://www.health.gov.au/our-work/nndss

See **Online** for appendix

For **Communicable Diseases Network Australia** see https://www.directory.gov.au/portfolios/health-and-aged-care/department-health-and-aged-care/communicable-diseases-network-australia

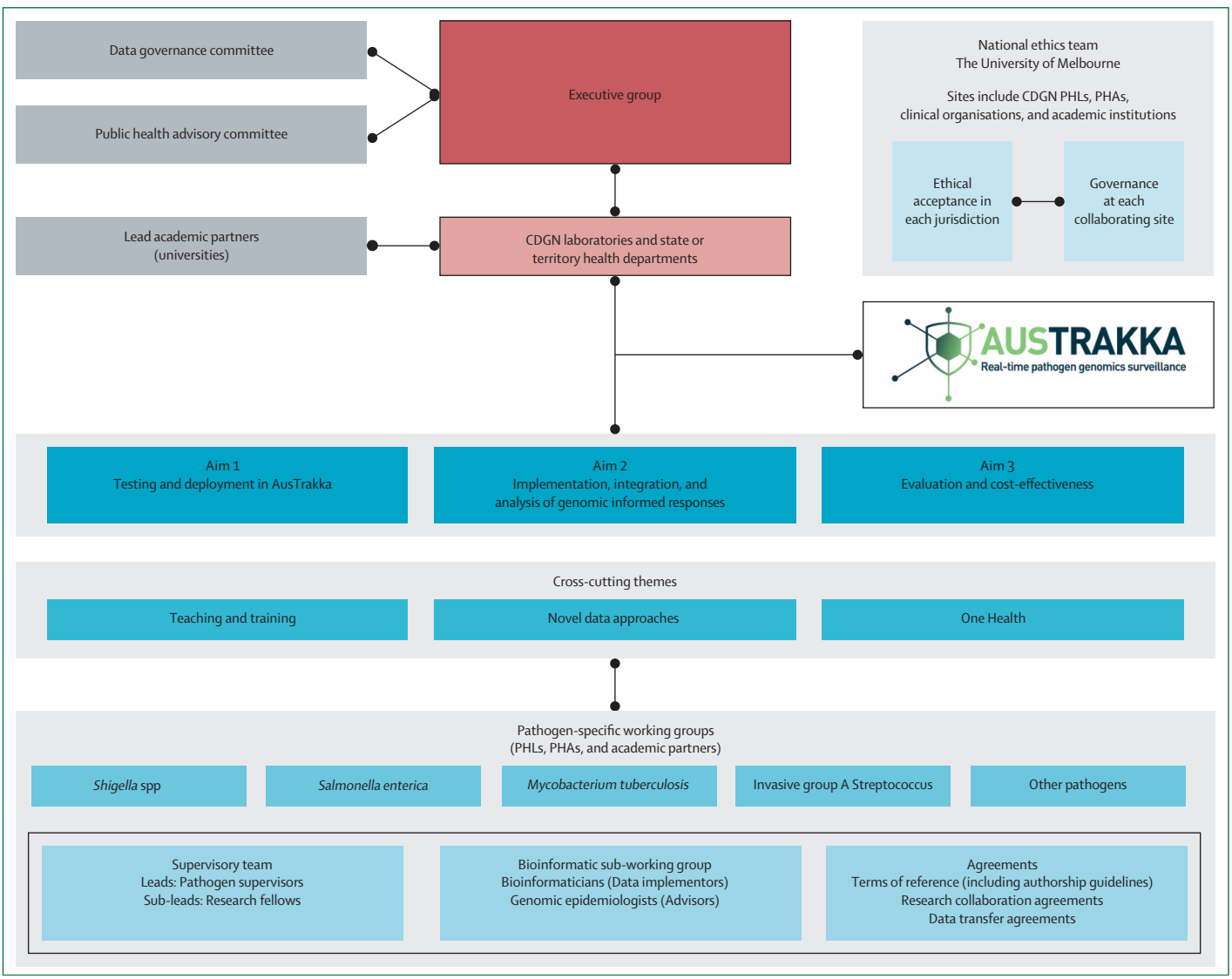

Figure 1: **Schematic illustration of the AusPathoGen governance structure**
Data governance and advisory committees provide programme guidance, and projects and outcome implementation are facilitated by the CDGN PHLs and PHAs. Academic partners provide subject matter expertise. Projects were developed and conducted within multidisciplinary, pathogen-specific working groups, led by PHL directors and AusPathoGen Research Fellows. The working groups comprise up to 80 members from all Australian jurisdictions and include academics, laboratory scientists, genomic epidemiologists, bioinformaticians, medical microbiologists, PHA members, and policy makers. Pathogen-specific bioinformatics sub-working groups include bioinformaticians and PHL genomic epidemiologists who collaborate on standardising data analysis and interpreting results. Working groups adhere to the terms of reference and authorship guidelines developed and endorsed by the executive group. AusPathoGen=Australian Pathogen Genomics Program. CDGN=Communicable Diseases Genomics Network. PHL=public health laboratory. PHA=public health agency.

longitudinal representation, retrospective projects spanned four years for *S enterica* and seven years for *Shigella* spp and *M tuberculosis*, for capturing temporal genetic diversity due to lower national case numbers and inherent slow growth or mutation rates. Bioinformatics sub-working groups developed nationally agreed bioinformatics and genomics epidemiological analysis plans. The projects addressed programme aims, standardising genomic approaches to identify case clusters and AMR using large retrospective and prospective national datasets and informing the establishment of pathogen-specific genomic surveillance systems in Australia. The steps taken for project development are described (figure 2).

Representative datasets collected through large national snapshots: To generate truly representative datasets for each of the three flagship pathogens *M tuberculosis*, *Shigella* spp, and *S enterica*, each jurisdiction attempted to sequence all notified pathogen samples available to the PHLs during a snapshot period, the length of which was informed by the incidence of the pathogen. For *S enterica*, a 3-month summer period from January to March, 2023, was selected to encompass the peak of annual incidence, whereas for

Shigella spp and *M tuberculosis*, a 12-month period (2022–23) was selected to capture sufficient data to assess changes in AMR and case clusters. All cases of these pathogens received by the PHLs during the snapshots were attempted to be sequenced. However, approximately 50% of shigellosis notifications tested positive for nucleic acid amplification but were culture negative, and 10–15% of tuberculosis notifications were diagnosed by clinical or radiological evidence only, which means that samples for these cases were not available for sequencing.

During national snapshots, a high proportion of notified pathogen cases were sequenced and contributed to AusTrakka by jurisdictional PHLs. In total, 27 456 sequences contributed to the retrospective (23 406 sequences) and three snapshots (4050 sequences), with 6884 (retrospective 6037, snapshot 847) for *M tuberculosis*, 4467 (retrospective 3753, snapshot 714) for *Shigella* spp, and 16 105 (retrospective 13 616, snapshot 2489) for *S enterica*, generating valuable Australian datasets (figure 3).

Metadata variable requirements are pathogen-specific: Working groups developed an agreed set of metadata standards (minimum [sample data] and enhanced [epidemiological data]) for contextualising genomic data to be incorporated into national surveillance systems (appendix pp 2–3). For international and national consistency, variables were aligned with those outlined by the Public Health Alliance for Genomic Epidemiology (PHA4GE) and with Australia's National Notifiable Diseases Surveillance System.[42] Minimum metadata standardised across all pathogens included: date collected, date received at PHL, date sequenced, jurisdiction, sex, age, species, minimum inhibitory concentration, minimum inhibitory concentration interpretation, and antimicrobial susceptibility testing standard. Enhanced metadata requirements were pathogen-specific, reflecting the epidemiology and sensitivities of each pathogen. For example, Australian rates and transmission of extensively drug-resistant *Shigella* spp in men who have sex with men and First Nations people are high. Thus, we captured the data to flag the increase and transmission of extensively drug-resistant *Shigella* spp in Australia.[39,43] The epidemiology of *S enterica* in Australia consists of a mix of endemic transmission and continuous importation from international sources. Therefore, data on recent travel as a proxy for potential overseas exposure was captured.

Building pathogen genomic surveillance system foundations in AusTrakka: The AusPathoGen flagship projects accelerated the development of AusTrakka,[16] including a sophisticated interface capable of handling pathogen-specific and project-specific user groups, pathogen-specific data integration models, and novel dashboard and data result visualisation formats, to enhance communication of genomic surveillance data to end users and policy makers. The AusTrakka platform is hosted in the Microsoft Azure cloud, providing automatic back-up services of both sequences and metadata. The platform uses distinct user roles, each defining specific levels of data access. Roles such as uploader and viewer are defined within governance documents, allowing regular access audits. Sequence data were mirrored over to compartmentalised folders on the AusPathoGen server and accessed by the multi-jurisdictionally represented implementer group for analysis, with resulting analysis data made visible through the AusTrakka platform. The data management ecosystem in the platform provides the foundations for a seamless transition to routine national genomic surveillance for these pathogens.

Standardisation of genomic analysis through a collaborative network: Genomics analysis plans have been developed to assess genomic epidemiological trends among large datasets and identify the best genomic approaches for cluster and AMR identification to inform Australian surveillance guidelines. As AusPathoGen is a multi-jurisdictional programme, we established governance for the development and stakeholder endorsement of genomic analysis plans. Lead research fellows drafted pathogen-specific data

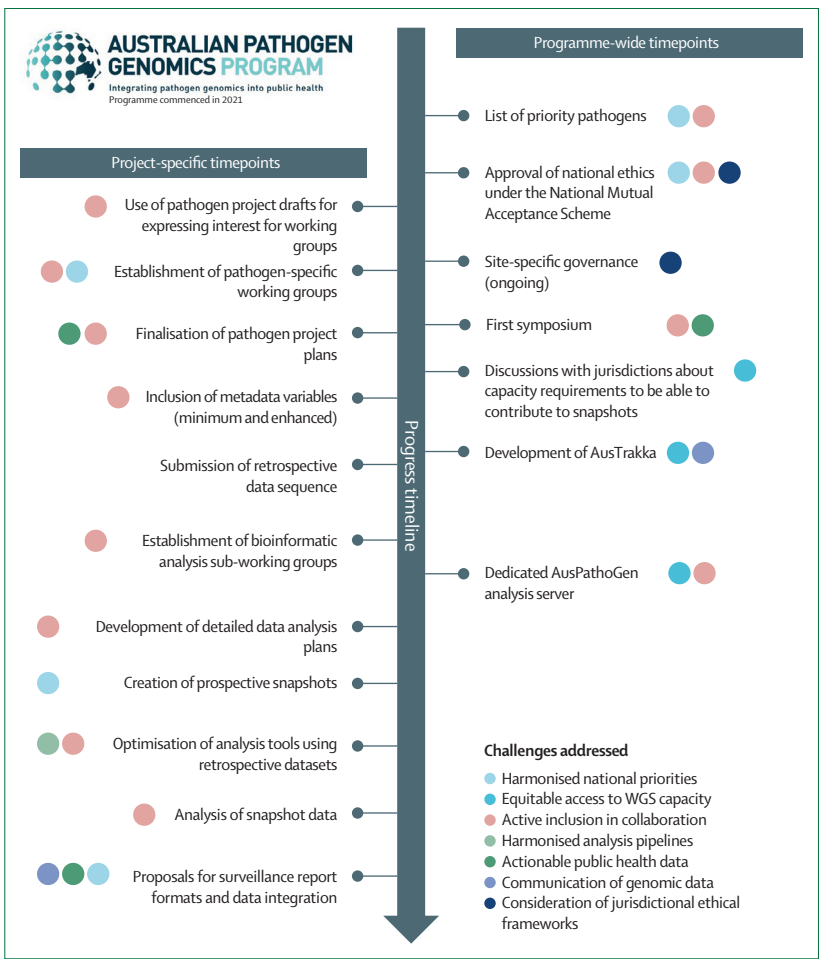

***Figure 2*: Timeline of key events and challenges addressed during the first year of AusPathoGen**
Working groups established relevant sampling timeframes and minimum and enhanced metadata variables, and bioinformatics sub-working groups developed nationally agreed-upon bioinformatics and genomics epidemiological analysis plans. The projects addressed the programme aims of standardising genomic approaches to identify case clusters and AMR using large retrospective and prospective national datasets and informing the establishment of pathogen-specific genomic surveillance systems in Australia. AMR=antimicrobial resistance. AusPathoGen=Australian Pathogen Genomics Program. WGS=whole-genome sequencing.

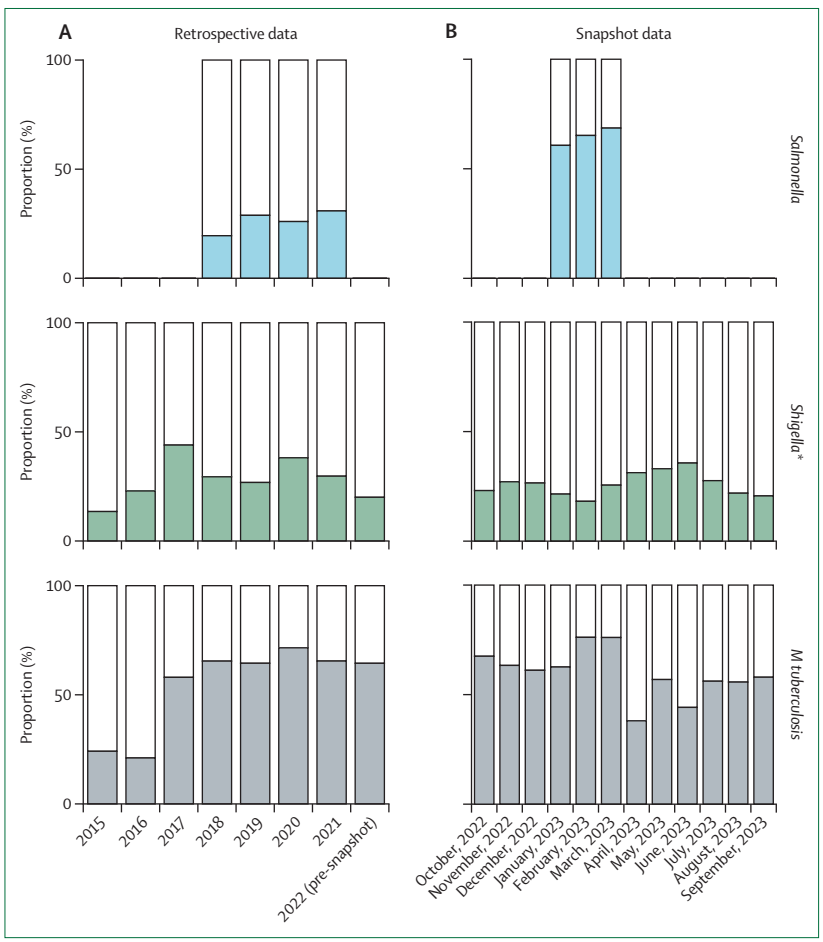

***Figure 3*: Proportion of notified pathogen cases sequenced for *Mycobacterium tuberculosis*, *Shigella* spp, and *Salmonella enterica* in Australia, as sequenced by jurisdictional PHLs and contributed to AusPathoGen via the AusTrakka platform**

Retrospective data (A) and proportion (B) of notifiable pathogens sequenced during national snapshots. A total of 27 456 sequences were contributed: 23 406 sequences from retrospective data and 4050 sequences from three snapshots. These sequences generated valuable Australian datasets and included 6884 sequences (retrospective 6037, snapshot 847) for *M tuberculosis*, 4467 sequences (retrospective 3753, snapshot 714) for *Shigella* spp*, and 16 105 sequences (retrospective 13 616, snapshot 2489) for *S enterica*. AusPathoGen=Australian Pathogen Genomics Program. PHL=public health laboratory. *Only approximately 50% of *Shigella* notifications in Australia are culture positive and thus available for sequencing.

analysis plans outlining genomic analysis steps and tools for assessing sequence and assembly quality, strain typing, identification of AMR genes or mutations, virulence factors, plasmids, phylogenetics, and cluster analysis. Data analysis plans were refined by the nationally representative bioinformatics analysis sub-working group, harnessing collective expertise to assess and optimise analysis approaches for nationally standardised genomics pipelines. Refined plans were presented to the wider working groups for endorsement, and final plans were then executed by the bioinformatics analysis sub-working group on an AusPathoGen-dedicated secure high-performance computer cluster. The dedicated server functions as a collaborative workspace and a resource for all partners. Genomics results are presented to pathogen working groups, and input from end users represented in the working group is used to develop and optimise reporting formats for disseminating genomics data and integrating it into new and existing public health surveillance systems.

Established model for project development enabled rapid deployment of secondary projects: The steps described for developing flagship projects (figure 2) facilitated the rapid design and implementation of national projects for infections caused by group A *Streptococcus* (ie, invasive group A streptococcal disease), *Streptococcus pneumoniae* (ie, invasive pneumococcal disease), and *Candida auris*. These initiatives were achieved by promptly establishing national working groups for these pathogens in response to public health concerns surrounding the increasing incidence of disease and AMR nationwide in 2022.[44,45] Given the importance of a One Health approach to infectious disease surveillance, including AMR,[46] an AusPathoGen One Health working group was established that incorporated academic leaders and stakeholders from the human health, animal health, and environmental health sectors. This working group has designed and implemented both retrospective and prospective projects using *Escherichia coli* as a representative One Health pathogen.

Identifying and responding to training needs

Discussions with PHAs and policy makers revealed considerable gaps in training resources catered towards individuals with minimal expertise in pathogen genomics, and we realised that broad training in pathogen genomics was required. A teaching and training cross-cutting activity was designed, where AusPathoGen-funded personnel were integrated into the existing CDGN Teaching, Training and Curriculum working group to bolster capacity for developing resources aimed at end users of genomics data. The working group designed and launched a four-part webinar series held throughout 2022–23, which focused on introducing key concepts and considerations related to sequencing, analysing, and reporting of microbial genomics for public health purposes. Registration and evaluation surveys highlight the pronounced reach and strong demand for genomics resources within the scientific community. A total of 354 individuals attended the webinars from Australia, New Zealand, Africa, Asia, Europe, Latin America, and the USA. Starting in June, 2024, the programme has been hosting a series of Public Health Implementation and Policy Workshops with representatives from each jurisdictional PHA, with the aim of creating an open forum to discuss and identify optimal approaches for integrating findings from AusPathoGen into public health surveillance approaches.

Design of the evaluation and implementation programme

The evaluation and implementation programme consists of a series of integrated projects. A comprehensive situation assessment has been designed to provide a detailed snapshot of the current landscape of pathogen genomics by jurisdiction, including all Australian PHLs. The

Panel: **Enablers underpinning the early success and sustainability of AusPathoGen**

Examples of early success enablers

Existing collaboration and laboratory-based network

- The Communicable Diseases Genomics Network (CDGN), led by public health laboratories (PHLs), facilitated strong long-term collaboration and information sharing, serving as a foundation for developing trusted relationships
- Formalising the CDGN within national health protection committee structures provided a forum for advocating and communicating public health genomics opportunities
- A national data sharing agreement across PHLs

Programme governance to promote collaboration

- A strong programme governance structure enabling oversight, contribution, and engagement from all stakeholders
- A dedicated collaborative and shared data analysis server to facilitate a collaborative approach to implementation

Multidisciplinary partnerships across academia and public health

- Academic institutions provide the expertise to develop tools, test models, and apply data approaches to define best practices for implementation
- Active multidisciplinary engagement across the public health spectrum is crucial for understanding public health needs, optimising metadata variables, and ensuring that analyses are relevant for informing public health actions
- Shared funding among partners, leveraging resources and opportunities for mutual benefit
- Promoting public health impacts and research outcomes

Secure platform for data sharing and integrated analysis

- The Australian Pathogen Genomics Program (AusPathoGen) uses the AusTrakka platform, which serves as a secure platform for consistent, pathogen-agnostic data sharing, integration, management, and visualisation
- AusTrakka facilitates outbreak investigations and provides agility to include other pathogens for future surveillance

Capacity building and training for data generators and users

- Capacity building in jurisdictions has ensured equitable access to whole-genome sequencing capabilities and data generation, allowing the collation of nationally representative sequences and metadata
- Training of end users and stakeholders to use genomics data for public health action has garnered government support for genomics surveillance

Examples of sustainability enablers*

Evidence for utility of public health genomics

- Equitable access to sequencing capacity
- Availability of data generated during AusPathoGen for further research
- Translation of analysis and interpretation approaches into national public health surveillance

Evidence for cost-effectiveness of genomics

- Systematic review of cost-effectiveness[8]
- Cost-effectiveness studies of genomics implementation into PHLs
- Proposals for joint funding models (involving both federal and state or territory governments)

Promote alignment and integration with public health priorities

- Expert elicitation with public health authorities to identify the mechanisms and priority pathogens for pathogen genomics
- Inclusion of public health stakeholders and leaders on to AusPathoGens executive group
- Alignment of AusPathoGens activities with national and international pathogen genomics surveillance and implementation strategies

*These factors are still in development

situation assessment includes four surveys focusing on (1) administrative processes, (2) sample and isolate processing and referral, (3) data collection and bioinformatics, and (4) costs and staffing. In addition to providing clarity regarding current sequencing capacity and practice, this data is used to inform the economic evaluation. The economic evaluation uses both real-world data and available literature to examine the cost-effectiveness of pathogen genomics in addressing foodborne diseases.[8] In conjunction with the situation assessment providing evidence of current jurisdictional capacity, an expert elicitation study uses the Delphi survey methodology to establish consensus among generators and users of pathogen genomic data regarding criteria and mechanisms for prioritisation of pathogens for sequencing. A series of case studies are being used to (1) examine the ethical, legal, and social implications of public health pathogen genomics, (2) assess the public health impact of genomics across the identified priority pathogens, and (3) identify crucial enablers and facilitators that support the

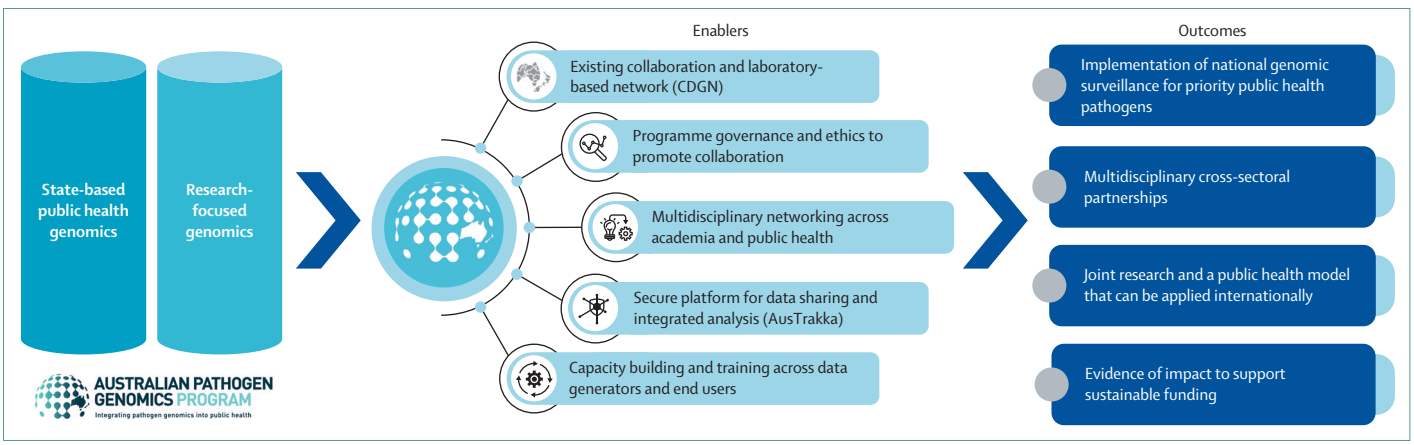

Figure 4: **Key enablers for establishing a national public health genomics initiative at the academic–public health interface**
Summary of activities that facilitated the advancement of the national public health genomics programmes and their anticipated outcomes. Further details are provided in the panel. CDGN=Communicable Diseases Genomics Network.

utility of pathogen genomics in public health interventions and decision making.

Considerations and future directions

To the best of our knowledge, this work provides the first description of a national, multi-pathogen, multidisciplinary research programme designed to directly inform the implementation of genomics-enhanced public health surveillance on a national scale. Sustaining the advances in pathogen genomics capacity and capability achieved during the pandemic and expanding these improvements to other pathogens are global health priorities. Emphasis should be placed on sustainability, cost-effective implementation and application, and equitable access to the data and benefits.[32,47] AusPathoGen aligns with these efforts, contributing to the global pathogen genomics community by sharing data, outcomes, and learnings, while also adopting best practices for genomic surveillance at a national level. The collation of highly representative national datasets provided a unique opportunity to develop nationally standardised bioinformatics approaches and generate data on genomic epidemiology, case clusters, and AMR of the priority organisms *M tuberculosis*, *Shigella* spp, and *S enterica*. These insights are instrumental in establishing genomics-informed surveillance systems in Australian public health settings. The key enablers for establishing a national public health genomics initiative at the academic–public health interface, based on the early success of AusPathoGen, are summarised in the panel and figure 4. In the absence of central coordination of public health application of pathogen genomics, it is essential that research efforts in the area promote a national, and ultimately international approach to avoid the risk of siloed implementation, therefore, avoiding issues in the disconnected analysis and interpretation of the data.[4,48]

AusPathoGen adopted a highly inclusive approach, incorporating expertise from academia, PHLs, and jurisdictional and federal PHAs, as well as national health protection committees and health departments, all as formal partners in the programme. Enablers for these partnerships are highlighted in the panel. This approach not only optimised the quality and relevance of the research conducted but also ensured that workflows and governance were complementary to existing systems, while remaining flexible and adaptable to innovative approaches and public health needs. The pre-existing relationships within the CDGN were a significant enabler for the programme, driving public health-focused research and ensuring implementation and use of CDGN-developed initiatives such as AusTrakka and national collaborative bioinformatics processes. Initiatives in different regions of the world have similarly identified the formation of cross-disciplinary networks as a key component of successful implementation.[49–51]

The teaching and training and the evaluation components of AusPathoGen are enhancing the baseline understanding of genomics across the public health spectrum and ensuring sustainability beyond the programme. The evaluation of the impact of applying pathogen genomics in public health, both within and beyond the AusPathoGen activities, including cost-effectiveness studies, allows participating organisations to see the true value measured and provide crucial inputs for building business cases.[8,37]

The formation of a bioinformatics network working collaboratively on a dedicated analysis server ensured effective data sharing and equitable access to resources, technology, and expertise, significantly enhancing bioinformatics capacity for interpreting genomics surveillance data at each PHL. Furthermore, it helped to establish a model for a seamless transition to service delivery, supported by familiar working relationships, optimising information sharing and dissemination pathways, and providing tangible personnel structures for funding proposals.

A key enabler of early success in the programme was the unified genomics data integration and analysis platform, AusTrakka, which served as a recognisable and trusted resource for public health responses. This platform provides secure access to data, allowing the inclusion of potentially

sensitive metadata variables for integrated analysis with genomics data, thereby optimising the utility of the resulting surveillance data.[16] Conducting research using the same platform architecture that will subsequently be used for public health implementation and incorporating platform improvements facilitate the streamlined translation of findings into public health action.

The programme's investment in sequencing a high proportion of notified cases during snapshot periods yielded truly representative national datasets. These datasets are crucial for determining relevant and feasible strategies for genomic surveillance for each pathogen. The data allows end users and policy makers to assess the true impact of the data, inform resource allocations, and avoid misdirected or unnecessary sequencing efforts that do not result in public health action.[52] Alignment with international data standards further enhances interoperability with international repositories, facilitates future sharing of the data collection, supports participation in international networks, and contributes to the refinement of genomics data resources, such as the WHO catalogue of *M tuberculosis* AMR.[53] The establishment of these foundational projects has served as a blueprint for similar initiatives targeting other priority pathogens in the programme, and the results from these projects will be reported in future research publications. Finally, the unified data management through AusTrakka and the collation of harmonised metadata variables ensure that the data support a common language for cross-jurisdictional result comparisons. This consistency allows the data to serve as a nationally reliable resource, providing context for future public health investigations. During the first years of the programme, the data already contributed to the establishment of national outbreak investigations and subsequent public health action by recognising multi-jurisdictional clusters of *M tuberculosis* and multidrug-resistant *Shigella*. Further, AusPathoGen data outputs are shaping Australian government policy, with its *M tuberculosis* leads collaborating with the National Tuberculosis Advisory Committee to develop government guidelines on using genomics to detect *M tuberculosis* clusters across Australia.

Pathogen genomics is increasingly being integrated into infectious disease surveillance and control, with many countries strengthening their national capabilities in this area.[10,49,54] As a translational research programme, ongoing implementation and impact is reliant on longer term commitments to funding from PHAs. In this context, the sustainability of AusPathoGen is a major consideration for the executive group, and factors supporting the programme's sustainability are summarised in the panel. To date, AusPathoGen has built on the public health surveillance improvements and collaborative relationships developed during the COVID-19 pandemic. The programme has supported equitable access to genomics technology across Australia and showed the measurable impact of genomics surveillance on public health responses, with engagement across the public health spectrum ensuring its success. AusPathoGen is informing how pathogen genomics can strengthen national surveillance systems within the evolving framework of the proposed Australian Centre for Disease Control. The programme serves as a global exemplar, offering a model for other nations to emulate in harmonising and implementing pathogen genomics for public health action.

Contributors

BPH, CL, AVJ, VS, TS, and MDK designed AusPathoGen and secured funding. JRW, PA, TH, BPH, AVJ, and VS designed this study; BPH is the programme lead, and AVJ and VS provided strategic oversight to AusPathoGen. Other public health laboratory directors or genomics leads (LEXL, DS, LC, KK, RB, CL) provided strategic input for the programme development and deployment. TS and CS developed and deployed AusTrakka and the national bioinformatics server for AusPathoGen. KG, TS, KH, AZ, ES, AEW, MLC, SPD, AF, CS, JEA, and DM provided crucial input and discussions towards this project and the broader development of AusPathoGen projects, including aspects of evaluation; JRW, PA, and BPH wrote the first draft; and all authors contributed to the final manuscript. All authors had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Declaration of interests

We declare no competing interests.

Data sharing

Training materials are publicly available on the AusPathoGen website (https://www.auspathogen.org.au/log-in), with the other resources to be made public through future publications.

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