

Towards Equitable Access to Public Health Pathogen Genomics in the Western Pacific

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Summary

The COVID-19 pandemic has increased interest and understanding of the utility of pathogen genomics across the Western Pacific region. Access to genomic data enhances surveillance and response to COVID-19, and will also support surveillance of other infectious diseases and antimicrobial resistant pathogens. Models of access can be determined based on intended purpose, use and sustainability. Achieving equitable access to genomics across the Western Pacific will contribute to the development of a regional public health genomics network to respond to major disease threats in the future.

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Background and context

Universal access to healthcare and healthcare associated technology is required to improve public health globally. Pathogen whole genome sequencing (genomics) is a transformative technology that enables rapid, precise, and accurate characterisation of pathogens to support clinical interventions and public health responses.

While genomics has, until recently, been considered a “cutting-edge research technology”, the COVID-19 pandemic has highlighted its utility to enhance infectious disease management for public health. International agencies, such as the World Health Organization (WHO), are interested in supporting equitable access to the technology for countries across the Western Pacific region.

To date, there has been limited investment toward equitable access to genomics across the Western Pacific region. With 37 countries and over a quarter of the world’s population, the Western Pacific region contains a wide range of health systems and services. Access to genomics for public health is highly variable across the region, with limited or no access across many countries, or access through referral pathways with genomics-enabled public health laboratories.^{1,2} Many high income countries across the region, including Australia,

Singapore, Japan, South Korea, Hong Kong and New Zealand, have robust sequencing capabilities to support public health. Some countries with genomics capabilities have established referral networks with countries without sequencing capacity, providing access to genomics across several Pacific Island Countries and countries across Southeast Asia, including Fiji, Timor-Leste and Papua New Guinea, and technical guidance through these networks to support plans to improve sequencing capacity.

Access to genomics will enhance COVID-19 surveillance and response, with longer term benefits in preparedness for future pandemics, and addressing other major infectious disease and public health threats across the region, including tuberculosis, influenza, dengue, and the spread of antimicrobial resistance across hospital and community settings.³ The barriers to equitable access are, however, significant, limited by workforce, infrastructure, logistical challenges, and sustainable investment. Equitable access to genomics is contingent on capacity building that currently relies on support from collaborative partnerships and networking across the region.

Use of pathogen genomics in the COVID-19 era

Pathogen genomics has contributed remarkably to the COVID-19 response, enhancing surveillance and

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informing public health decision making.⁴ Genomic analysis has been critical to support detection of outbreaks and importation events, enhanced understanding of transmission dynamics, surveillance of emerging mutations and variants of concern, and estimation of disease spread across the Western Pacific region.^{4–7} Access to genomic sequencing has allowed for contribution of data from the region to global SARS-CoV-2 genomic surveillance efforts, resulting in better understanding of disease spread worldwide. In Australia, where there is high sequence coverage and a relatively low burden of COVID-19, genomics has played a critical role in identifying the source of disease outbreaks, and measuring the impact of public health interventions.⁵

Key steps in the public health pathogen genomics process

Use of genomic data for public health requires a specialised end-to-end process, encompassing; (i) designing a COVID-19 sequencing strategy, including rapid and representative access to clinical samples; (ii) RNA extraction and generation of sequences in the laboratory; (iii) sequencing quality control; (iv) bioinformatic analysis and integration with epidemiological data; and (v) interpretation and reporting to public health agencies.⁸ Genomic sequence data can also be shared to enable critical research activities, such as modelling viral evolution and spread, vaccine design, and further refinement of diagnostics.

Laboratory whole genome sequencing (WGS) use benchtop workflows to generate the genome of an organism. Bioinformatic analyses is then applied to reconstruct the genome of the pathogen using specialised software and pipelines, assess data quality, undertake characterisation to detect mutations, and comparison between genomes from different clinical cases to determine potential clusters and transmission.

Following computational analysis, a combined genomic and epidemiological approach is critical to the interpretation of data for public health. The high-resolution and specificity of pathogen genomics has the capacity to identify transmission events and detect outbreaks that may not be identifiable from epidemiological data alone, however, requires epidemiology to provide context and confirm transmission dynamics. Integration through the emerging specialty of “genomic epidemiology” enhances interpretation and improves the value of genomic results for public health, repeatedly highlighted during the COVID-19 pandemic.^{5–7}

Critical to the value of genomics is supporting public health officials and policy makers to understand and interpret results to support decision making. Collaboration between laboratories and Ministries of Health to establish jointly agreed methodologies for reporting ensures genomic data is appropriately utilised and

integrated into broader surveillance programs, embedding genomics into public health responses for COVID-19 and other pathogens in future.

Capacity building approaches to enhance genomic literacy is crucial to implementation, both at the laboratory to facilitate meaningful reporting and communication of results to public health officials, and with policy makers, to accurately utilise genomic data and understand implication of findings for public health action.⁵

Models of access and the value of networking for public health pathogen genomics

International best-practice models highlight the importance of building genomics capacity within existing public health structures.^{2,3} A networked approach that places public health laboratories as the central driver for implementation allows for integrated coordination and engagement with government and policy makers (Figure 1). Public health laboratories have established remit to communicate and establish governance frameworks with Ministries of Health and public health surveillance units, to facilitate sharing of epidemiological data and embed reporting of results into public health surveillance programs. In some settings, partnership with academic institutions may be an important facilitator of progress, however, public health agencies should take the lead where possible.

Genomics implementation requires significant resource and workforce investment. Models for equitable access need to consider value for money, feasibility and sustainability of approach, ability to meet public health objectives and to align with international best practice approaches to promote interoperability of data.^{8,9} Considerations for current and required laboratory, data analysis and data storage infrastructure, workforce capacity and training requirements, and ongoing maintenance and long-term integration into the public health system is required, and can be assessed through the development and implementation of a readiness assessment framework.¹⁰

Assessment of intended purpose for accessing genomic technology will provide rationale for development and deployment of a genomics implementation model in some countries. Implementation strategies need to consider required throughput to justify ongoing maintenance of WGS workflows, balanced with the long-term public health need for rapid access to genomic data where international referral of samples may cause delays, and sustainability of investment and integration into public health programs.

In settings where in-country deployment is not the short-to-medium term solution, an alternative model that establishes partnerships with genomics reference laboratories, or local research institutions with genomic capabilities, may be more suitable as a mechanism for

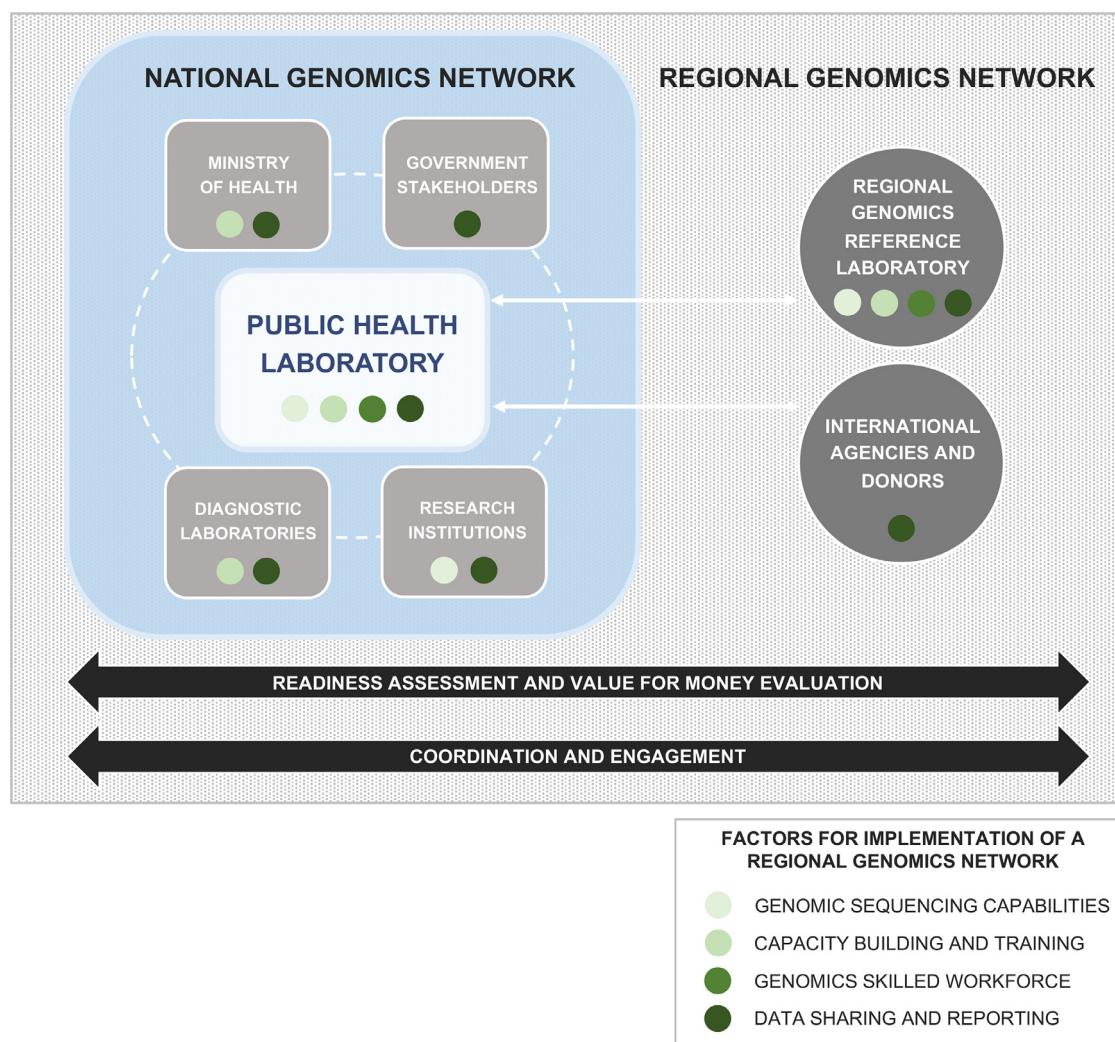


Figure 1. Structure and key components of a regional public health genomics network.

access to the technology without the significant resource investment. Regional networks for genomics provide access to infrastructure and a skilled workforce, through establishment of protocols between laboratories to provide a referral framework and pathway, with appropriate data governance arrangements.

Across both models of access, networking is essential to support capacity building to analyse, interpret and effectively use genomic data to support public health. A networked approach provides an established, accessible system for knowledge transfer across the breadth of specialised expertise required for genomic sequencing, by providing access to molecular scientists to support data generation, bioinformaticians and genomic epidemiologists for data analysis and integration, and genomics-trained medical microbiologists to support interpretation and communication of results.

Underpinned by capacity building, the networking model supports strong collaboration across stakeholders, laboratories and countries, key to sustainable implementation of genomics for public health. Mechanisms for coordination and leadership are critical to provide support for the network.

The utility of establishing national and regional genomics networks has been demonstrated over the course of the COVID-19 pandemic through partnerships established between in-country laboratories and their respective Ministries of Health and policy makers, and regional genomics reference laboratories. For example, through partnerships between in country laboratories and the Microbiological Diagnostic Unit (MDU) public health and genomics reference laboratory at the Doherty Institute, SARS-CoV-2 sequence data from Timor Leste, Papua New Guinea and Fiji has been generated, reported and uploaded to a global, open access

database for SARS-CoV-2 genomic surveillance, GISAID.¹¹ This work has also contributed to the development of an established framework for access to WGS and planning for genomics implementation across Fiji, Timor-Leste and Papua New Guinea.

An opportunity for equitable access

In settings with limited capacity to undertake basic diagnostics and surveillance, implementation of genomics surveillance had previously seemed impossible.² The COVID-19 pandemic has amplified interest in building genomics capacity to support public health responses and provided a roadmap for an equitable approach.

Partnerships between laboratories working at the public health interface during the pandemic have demonstrated the utility of a networked approach for equitable access to genomics, through rapid workforce development in settings without previous genomic expertise, access to technology and guidance on how genomic data can be integrated into public health systems. This approach has been demonstrated through successful COVID-19 genomics networks worldwide, including the COVID-19 Genomics UK Consortium (COG-UK),¹² and the WHO Pan American Health Organisation (PAHO) COVID-19 Genomic Surveillance Regional Network.¹³ Across the Western Pacific region, progress has been made toward establishing a regional laboratory network to support genomics implementation and equitable access to WGS technologies across regional countries, through direct partnerships between public health laboratories, government, industry, or facilitated by international organisations such as the WHO.

The development and success of networks established for COVID-19 has been possible due to the unprecedented investment and interest in genomics, not replicated in other disease control programs. Developments toward improved laboratory capabilities recognise that genomic data should be utilised, along with the opportunity to leverage existing investments to establish genomics as a disease surveillance tool for other infectious diseases.

Development of sustainable genomics surveillance for other disease control programs will require ongoing funding and resources, with assessment of utility and value for money required to support planning for sustainable financing. Opportunities and commitment for funding from global donors to support implementation, and long-term strategy from government to maintain programs need to be secured.

The utility of genomics for other infectious disease has been well documented,^{14–17} and the opportunity to harness progress made toward equitable access to genomics due to COVID-19 will directly impact other public health disease control programs such as the global threat of antimicrobial resistance.

Summary

There is significant momentum in the Western Pacific region to ensure equitable access to genomics as part of the COVID-19 response. Strategic investment to build on this through a network model, using a combination of supported in-country deployment and establishment of referral networks, will provide enhanced surveillance to support public health decision making during the pandemic. This approach will also deliver a genomics-enabled public health network within the region that will address other major threats and rapidly respond to future pandemics.

Declaration of interests

None

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