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High acceptability of a national platform for public health genomic data sharing and surveillance in Australia: a mixed methods study

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Abstract

Background Pathogen genomics has increasingly been integrated into infectious disease surveillance, outbreak detection, and response globally. However, formal evaluation of pathogen genomic surveillance systems has been a major gap. In Australia, the AusTrakka platform was established and deployed nationally to address barriers to genomic data sharing across jurisdictions, enhance interoperability and usability, and improve governance of public health genomic data. Here we present our evaluation of AusTrakka and examine how its utilisation and impact shifted throughout the COVID-19 pandemic.

Methods We utilised the US Centers for Disease Control (CDC) Updated Guidelines for Evaluating Public Health Surveillance Systems to guide assessment of the AusTrakka platform. The evaluation used a mixed-methods approach consisting of a quantitative analysis of AusTrakka utilisation data throughout the COVID-19 pandemic and a qualitative component comprised key informant interviews and analysis of investigation reports produced by the AusTrakka National Analysis Team. Quantitative and qualitative data were collected concurrently between June 2020 and October 2022. Semi-structured individual and group interviews were held with key informants ($n = 63$) representing all jurisdictions across Australia and New Zealand. These included individuals representing public health laboratories and health departments, infectious disease physicians, genomic epidemiologists, and bioinformaticians.

Results AusTrakka users reported that the platform had a very high degree of usefulness as a centralised platform to enable sharing sequence data across jurisdictions, facilitate multijurisdictional outbreak investigations, and clarify transmission chains. *Acceptability* was a key system that contributed to the usefulness of the platform, enhanced through collective design of data governance frameworks. Integration of epidemiological data with the pathogen genomic data was an ongoing challenge in data completeness.

Conclusions Robust evaluation of pathogen genomics surveillance systems is critical to identify contextual and system elements that impact the capacity of these systems to accomplish their objectives. Our findings demonstrate the importance of strong stakeholder engagement in developing data governance mechanisms for pathogen genomics in ultimately ensuring the capacity of surveillance systems to detect outbreaks and support public health utility, and reinforce the value of a nationally developed, purpose-built approach in Australia.

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Keywords Pathogen genomics, Surveillance, Public health, Evaluation, COVID-19

Background

Pathogen genomics is increasingly being integrated into public health surveillance and outbreak investigations around the world in the detection, prevention, and control of infectious diseases [1]. The US Food and Drug Administration established GenomeTrakr in 2012 as the first laboratory network to utilise whole genome sequencing (WGS) in tracing bacterial foodborne contamination and pathogen identification [2]. Soon after, in 2014, Public Health England began using pathogen genomics in *Salmonella* surveillance [3] and by 2016, 26 European countries reported routine use of WGS in public health practice [4]. In 2020, the COVID-19 pandemic brought into focus the necessity of national and international surveillance systems that are adequately equipped to understand and respond to emerging and previously unknown pathogens. Australia was also an early adopter of pathogen genomics for public health surveillance and response activities with national genomic surveillance of listeriosis as an example [5].

Rigorous and systematic evaluation of surveillance systems that integrate pathogen genomics is important for making explicit the expected contribution of pathogen genomics; understanding how well such surveillance systems are meeting their objectives; and clarifying the processes by which they do so, or areas requiring further strengthening. Evaluation contributes to the body of evidence available for the development of genomics-informed public health practice and supports identification of needed investment, infrastructure, and training [6]. Despite substantial investment into the integration of pathogen genomics in public health surveillance, evaluation of genomics-informed surveillance systems has been limited. Where evaluation has taken place, the focus has been on economic evaluation [7–9], rather than the surveillance system's usefulness, or the attributes that contribute to the system attaining its objectives. This may be because there are limited systems globally that have been fully implemented.

The US Centers for Disease Control (CDC) published the *Updated Guidelines for Evaluating Public Health Surveillance Systems* in 2001 to support integration of surveillance and health information and address changes in public health surveillance to respond to emerging health threats including new diseases [10]. The updated guidelines aim to help organise the evaluation of a public health surveillance system for assessment of how well the system meets its purpose and objectives. These guidelines also underpin the elements of surveillance quality

in WHO's 2006 *Communicable disease surveillance and response systems: Guide to monitoring and evaluating* [11].

At the time of this evaluation, despite the strong and increasing investment in public health pathogen genomics and the integration of pathogen genomics into surveillance systems, a systematic evaluation of attributes contributing to the usefulness of such systems was not available. We therefore applied the CDC Updated Guidelines for Evaluating Public Health Surveillance Systems to evaluate the usefulness of the Australian national platform for public health pathogen genomics, AusTrakka [12]. This represents an early opportunity to evaluate one of the first national platforms for data integration in pathogen genomics globally and identify strengths and opportunities for enhancements of such systems. The updated guidelines were selected to underpin the evaluation as they have been widely used to evaluate surveillance systems in diverse contexts [13–15] and provide a useful framework for understanding the key components in the functionality and utility of all surveillance systems.

At the start of the COVID-19 pandemic in Australia, there were no established mechanisms for rapid and consistent sharing, analysis, and reporting of SARS-CoV-2 genomic data. AusTrakka was established as the Australian national platform for interjurisdictional sharing of SARS-CoV-2 genomic data and is operationalised under the Communicable Disease Genomics Network (CDGN) by the AusTrakka Advisory Group and a National Analysis Team (NAT). The CDGN includes representatives from public health laboratories across all jurisdictions in Australia and New Zealand. While the AusTrakka platform commenced development in 2017 with intended use for established pathogens, the pandemic accelerated its development and deployment, with the platform becoming active in May 2020 specifically for SARS-CoV-2.

Here we report on our evaluation of AusTrakka and examine how its utilisation and impact shifted throughout the pandemic to demonstrate the public health utility of pathogen genomics and the merit of integrated national platforms to support its implementation.

Methods

Setting

AusTrakka was established to address barriers to genomic data sharing across jurisdictions in Australia and New Zealand, enhance the interoperability and usability of genomic data, and coordinate governance of genomic data. Both countries have a decentralised structure, with

A number of analyses can be undertaken through AusTrakka, including routine phylogenetic analysis. Requests for multijurisdictional analyses, where sequence data may need to be shared between jurisdictions, or requests for interjurisdictional data are governed through established approval processes. The AusTrakka NAT, comprised

Relevant components of the Guidelines included in the evaluation were:

- **Usefulness:** Contributes to the prevention and control of adverse health-related events, including an improved understanding of the public health implications of such events
- **Acceptability:** Willingness of persons and organisations to participate in the system

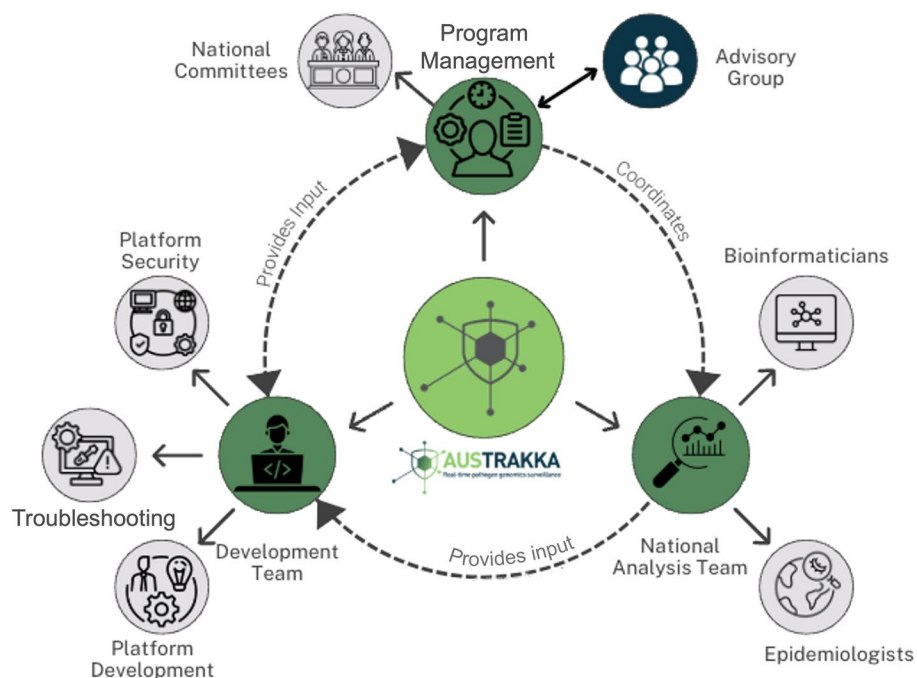


Fig. 1 AusTrakka ecosystem during the COVID-19 pandemic representing its structure and governance

- **Representativeness:** Describes the occurrence of a health-related event over time and its distribution in the population by place and person
- **Sensitivity:** Proportion of cases of a disease detected and the ability of the system to detect outbreaks and monitor changes in the number of cases over time
- **Timeliness:** The speed between steps in a public health surveillance system
- **Data quality:** The completeness and validity of the data recorded in the public health surveillance system
- **Flexibility:** Ability to adapt to changing information needs or operating conditions with little additional time, personnel, or allocated funds [10]

Given the evaluation's focus on the contribution of AusTrakka to public health surveillance and response to COVID-19, the technical attributes of the system were not assessed. The elements of *Simplicity* (the simplicity of the surveillance system's structure and ease of operations) and *Stability* (a system's ability to collect, manage, and provide data properly without failure and ability to be operational when needed) were therefore not included. *Predictive Positive Value* (the proportion of reported cases that actually have the health-related event under surveillance) is not relevant to pathogen genomics and was also excluded.

Quantitative and qualitative data were collected concurrently between June 2020 and October 2022.

Quantitative data

Quantitative data from AusTrakka was analysed to examine changes in utilisation of AusTrakka over time. Upload and user data are available from the launch of AusTrakka and all utilisation data are available from April 2021. This includes:

- Total number and role of users
- Uploads of sequences to AusTrakka from each PHL
- Number of user sessions to view phylogenetic trees
- VoC summary table views

These variables were selected to provide an overview of platform users, how the characteristics of users changed over the study period (numbers and roles of users by jurisdiction), how users were providing data (uploads of sequences), and how they were obtaining data from the platform (sessions to view phylogenetic trees and VoC summary table views). These variables are relevant to the *Usefulness*, *Acceptability*, and *Representativeness and sensitivity* attributes of the Guidelines.

Descriptive analysis was undertaken across each of these variables. To determine the relationship between

reported weekly COVID-19 cases and weekly sequence uploads to AusTrakka, a Spearman's correlation test was run using Python [16]. Weekly COVID-19 cases were drawn from Australian Government weekly COVID-19 trends reporting between January 2020 and October 2022 [17].

Qualitative data

Semi-structured individual and group interviews were held with key informants ($n=63$) representing all jurisdictions across Australia and New Zealand between June 2020 and October 2022. Key informants included:

- Representatives from the CDGN
- PHL staff (bioinformaticians, genomic scientists, genomic epidemiologists)
- AusTrakka team members (NAT, Development Team)
- AusTrakka stakeholders (user groups, end users (government, public health units (PHUs), clinicians))

These categories are not mutually exclusive as individuals may fulfil multiple roles simultaneously. For this reason, it is also not possible to identify the number of individuals interviewed in each subgroup.

In 2020, 24 interviews were conducted with key informants in Victoria given the impact of the pandemic primarily in Victoria at the time. In 2021, 24 individual interviews and 3 group interviews (with 31 participants in total) were held across seven Australian jurisdictions and New Zealand. In 2022, 5 interviews and 5 group interviews (with 18 participants in total) were held. Some 2021 and 2022 interviews included follow-up discussions from previous years. Group interviews were organised with people that requested to be interviewed together and that formed part of a distinct group (e.g. a team that worked together in a particular organisation). Individual interviews were always offered if preferred.

Two authors (ASF and DE) conducted the interviews. ASF (PhD, female) is the lead researcher and holds an Academic Specialist position. DE (MPH, female) conducted interviews in the role of Research Assistant. Both interviewers have had training and extensive experience in conducting interviews and qualitative research. The interviewers did not have knowledge or relationships with the interviewees prior to study commencement.

Key informants were approached due to their positions held, their interaction with the AusTrakka platform, and their involvement in the COVID-19 response. Participants were also asked to identify any additional relevant key informants. Initial contact was via email. Interviews lasted between 45 min and 1 h 15 min. Interviews were audio recorded using Zoom [18] and notes taken during

the interviews. Participants were given the opportunity to review their transcripts to ensure completeness and accuracy, and were able to provide corrections or additional information. Transcripts were pseudonymised following transcription and review.

While the majority of key informants agreed to participate in the research, there were some that were not available due to the intensity of competing demands on their time during the research period. Recruitment continued until key informants in relevant positions were identified across all jurisdictions.

Interview guides and analysis were underpinned by the relevant attributes outlined in the US CDC's Guidelines. Interview themes (provided in Supplementary material 1) were structured to assess the perspectives of key informants regarding the acceptability, usefulness, and sustainability of the AusTrakka platform, as well as broader themes around how pathogen genomics informed the COVID-19 response.

In 2020 and 2021, upon request, the AusTrakka NAT provided ongoing monthly national reports and weekly SARS-CoV-2 VoC reports to support multijurisdictional outbreak investigations. These reports were examined with regard to intended audience, application, and information included.

Deductive qualitative coding was undertaken by ASF using NVivo13 [19]. Codes were developed a priori based on the structure of the relevant attributes from the Guidelines (provided in Supplementary material 2) [20]. Qualitative data were reported according to the consolidated criteria for reporting qualitative research (provided in Supplementary material 3) [21].

Results

Usefulness

In 2021, the majority of end users from PHLs indicated that they used AusTrakka regularly to situate their own local sequences within the national context and highlighted the utility of centralising jurisdictional data.

...it's important to have the national sort of samples because initially at the time when the first COVID happened [Australia] only ha[d]... 200 cases and they're all from all sorts of different places, or different areas. So in order to trace particular cases or clusters is a bit tricky ... So it's always important to consolidate everything that we have into a single repository, and that's where AusTrakka comes in...

When end users were asked about the reason for their AusTrakka use over 2020 and 2021, the most common response across a number of settings was for confirming or rejecting a hypothesis regarding transmission

that had been developed from the epidemiological data or providing additional clarity about transmission where there was limited epidemiological information available.

In 2022, the utilisation of AusTrakka focused on VoC surveillance in response to the public health demand at the time. While to date, the direct public health impacts of VoC surveillance are uncertain, this was particularly important for communication and understanding the distribution of variants in the population, as well as monitoring the possibility of emerging strains that may exhibit increased public health risks.

The first fear was, you know, a new variant of concern... suddenly another variant starts to take over there's this worry, is this going to be worse? ... Will it be resistant to drugs? Will it ... be a more severe disease?

A key use of AusTrakka in the COVID-19 pandemic was in providing access to data and reports which increased confidence in public health approaches. The interviewee below reflects a frequent theme, demonstrating that lockdowns were effective in preventing transmission, which led to increased confidence in continuing to use this strategy to control outbreaks.

By the time [the state Health Department] get[s] to that point we don't need that link – it's not going to change anything we do, it just provides a bit of reassurance...

In addition, the genomic findings had value in being able to provide accurate advice regarding VoCs to national bodies and provide context for data interpretation with regard to jurisdictional sequencing strategies.

So it's been a very invaluable process to be able to see what is going on, particularly because [Public Health Laboratories] have to provide a lot of advice higher up...and it's helped the confidence of the advice in that we do actually understand what is going on nationally.

In addition to individual users within jurisdictions using AusTrakka to identify interjurisdictional transmission, the AusTrakka NAT regularly produced national-level reports, including monthly Communicable Diseases Intelligence reports for COVID-19 and monthly AusTrakka SARS-CoV-2 national genomics surveillance reports. AusTrakka reports were helpful in providing up-to-date data used in briefings and public-facing sessions, facilitating appropriate public communication both internally and externally, nationally and internationally.

Acceptability

As the interviewee below outlines, developing the three elements of AusTrakka was shown to be central to the acceptability of the platform.

I think it's fair to say AusTrakka is kind of three different things, it's... the data sharing philosophy... there's the web platform...itself which enables the interaction sharing of the data, and then there's sort of the governance and all the agreements behind it. And although the platform only exists now, the philosophy was there, and then quite a few years were spent getting this data sharing agreement up over many years...the philosophy was always there, the data sharing took years of groundwork...

Open Science principles around data sharing were central to the design and implementation of AusTrakka. Underpinning this philosophy of open data sharing was the presence of established governance between all stakeholders and a governance framework to ensure responsible data-sharing practices.

...I think that if [AusTrakka] had had a team that wasn't as conscious of their legal responsibilities, if data breaches had occurred, or if there had been any leakage, it would've posed a problem. So I think the information security side has been good, that's provided a sense of trust.

Quantitative analysis supports the above quotes, indicating an increased willingness to participate by an increase in the number of users and contributing jurisdictions over time. As of October 2022, there were 76 active

users across 12 individual organisations with access to the AusTrakka platform. Within 2 months of the launch of AusTrakka, there were active users from each of Australia's jurisdictions and New Zealand, showing that the platform was adopted quickly. Over the initial 3 months, the numbers of users grew at an average of 10 new users per month (Fig. 2) and by the end of 2020 most jurisdictions had at least four end users.

The next section describes in more detail the willingness of users to contribute sequence data to the system.

Representativeness and sensitivity

The representativeness and sensitivity of AusTrakka relies on the consistent generation and contribution of sequences from across jurisdictions. As of October 2022, a total of 166,083 SARS-CoV-2 sequences from Australia and New Zealand were available through AusTrakka. In this time, 1735 phylogenetic trees were made available to end users. The total number of sequences uploaded mirrored growing case totals in Australia and New Zealand throughout the second wave in Victoria in July 2020, the Delta outbreak in New South Wales (NSW) and Victoria from July/August 2021, and the start of the Omicron outbreak in December 2021. Following this, we see the number of uploaded sequences remaining high throughout 2022 with peaks in April and July where over 2500 sequences were uploaded in a single week. Each of these peaks was primarily driven by a large number of uploads from an individual organisation and jurisdiction (Fig. 3). A Spearman's correlation test was run to determine the relationship between reported weekly COVID-19 cases and weekly sequence uploads to AusTrakka.

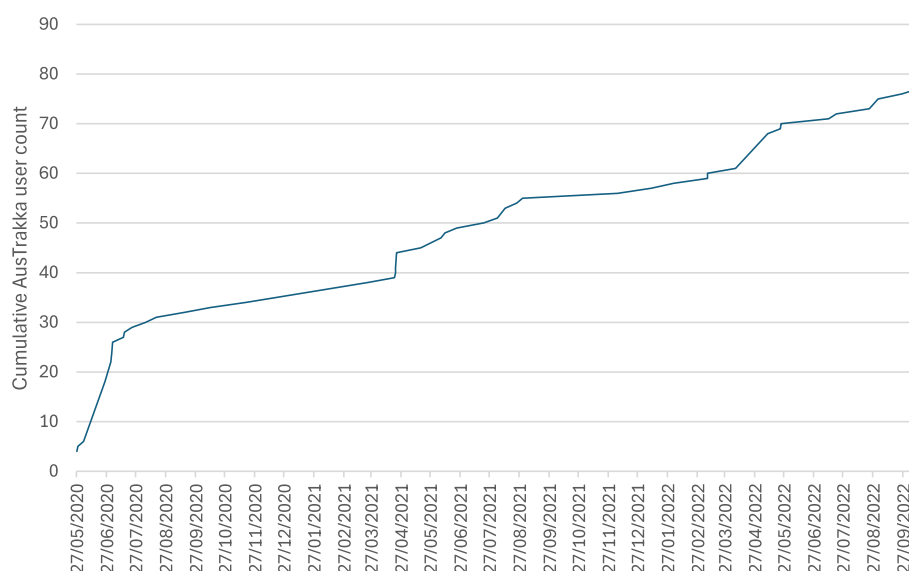


Fig. 2 Cumulative AusTrakka user count, May 2020 to October 2022

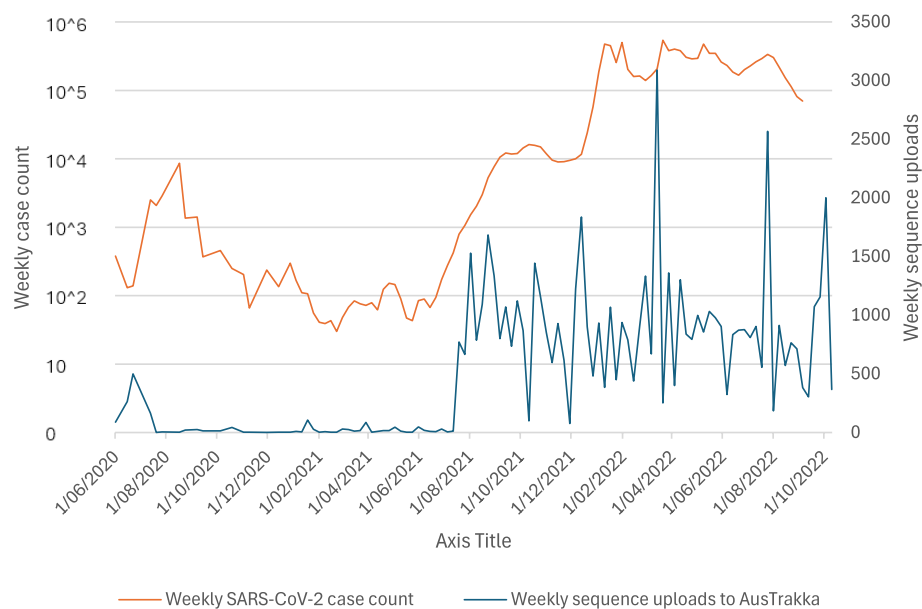


Fig. 3 Weekly COVID-19 cases versus AusTrakka sequence uploads, June 2020 to October 2022

The test showed a strong, positive monotonic correlation and association between COVID-19 case numbers and sequence uploads ($R=0.697$, 95% CI (0.604–0.772), $p<0.001$).

By the end of 2021, a total of 53,285 SARS-CoV-2 sequences were uploaded to AusTrakka by PHLs, at an average rate of 500 sequences uploaded per week. Additionally, 535 phylogenetic trees were made available to users—174 between June 2020 and June 2021 and 361 between July and December 2021. In the first 10 months alone of 2022, 112,798 sequences were uploaded to

AusTrakka at an average rate of 2700 sequences uploaded per week. During this time, 1200 phylogenetic trees were made available at an average rate of 30 tree accesses per week (Fig. 4).

Figure 5 shows a clear peak of tree image loads in June and July 2021 of 60–87 weekly loads respectively, which correlates with rising cases at this time. In total, there are 1204 tree data loads recorded in 2021 with an average of approximately 38 loads per week in this time. Utilisation begins to increase again towards the end of 2021 as case totals related to the Omicron variant surge.

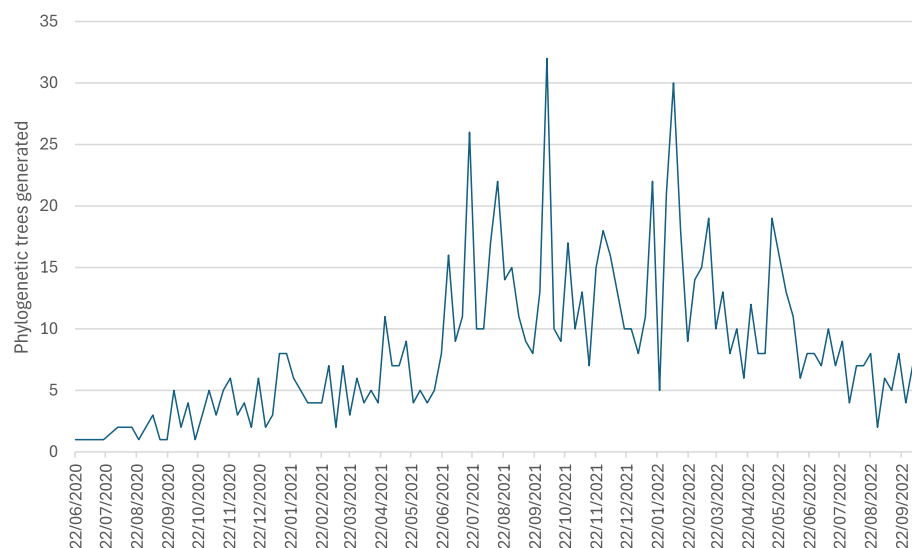


Fig. 4 Weekly counts of phylogenetic trees generated, June 2020 to October 2022

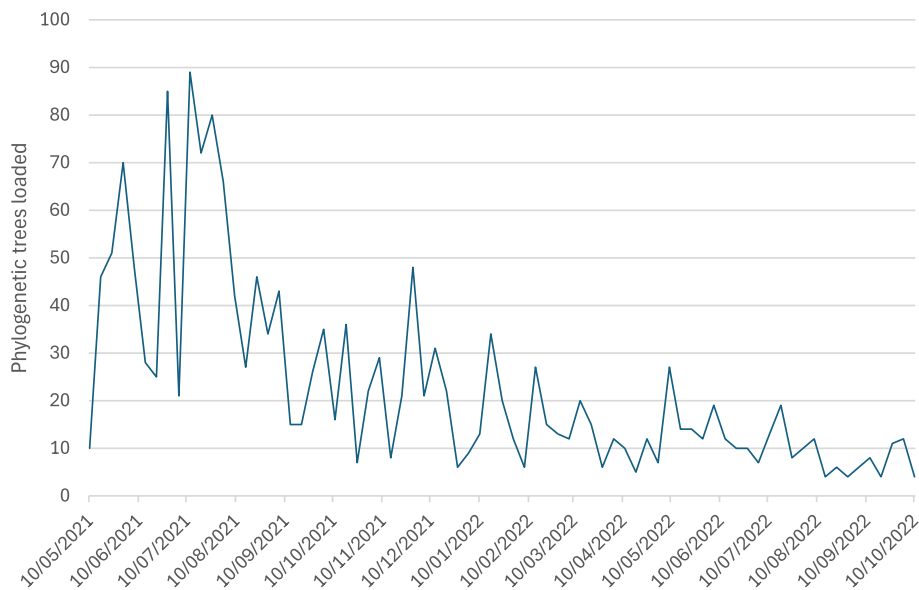


Fig. 5 Weekly counts of phylogenetic trees loaded, May 2020 to October 2022

Throughout 2022, the number of tree data loads declines despite rising case numbers as contact tracing efforts and social restrictions begin to be rolled back in multiple jurisdictions.

Similarly to the tree uploads, there is a peak of use in June 2021 of 22 VoC weekly loads. From May 2021 until December 2021, there are 230 VoC summary table views which is approximately eight views per week throughout the year. However, unlike the number of tree loads, which declines over 2022, VoC table views remain high, indicating continued use (Fig. 6).

Qualitative data helps to contextualise the decrease in tree image loads and VoC summary table views over time. From early 2022, with the opening of the international borders and the increasing use of rapid antigen testing (RAT), there was a shift in how AusTrakka was utilised in the public health response to SARS-CoV-2.

With the sheer number of COVID cases now, AusTrakka is less representative through no fault of its own just the sheer number of cases and the prevalence of ... RATs which you can't sequence from and a shift in the ... sequencing priorities from the jurisdictions ...

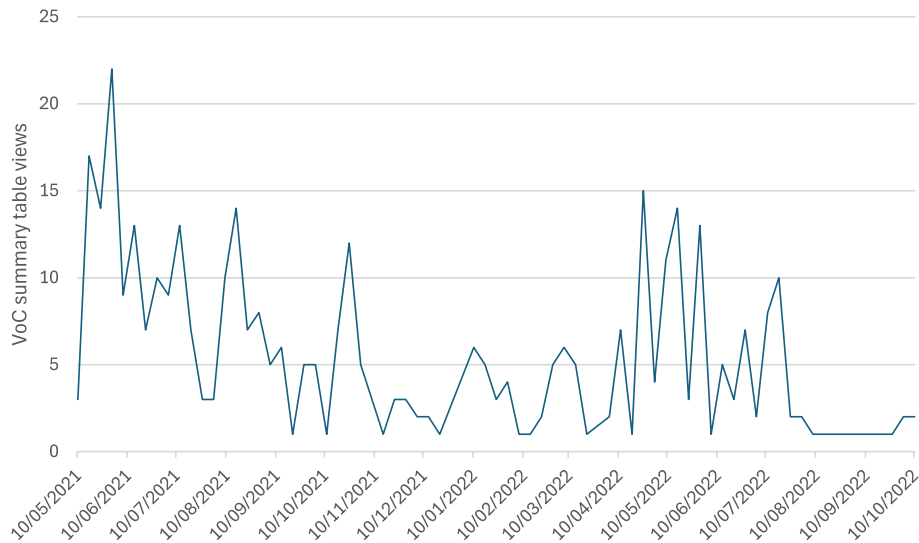


Fig. 6 Weekly counts of VoC summary table views, May 2020 to October 2022

and so the focus of AusTrakka has shifted to more of a variant surveillance platform.

This shift in priorities throughout the pandemic led to lowered rates of direct user engagement with AusTrakka alongside a continued high level of interest in and utilisation of AusTrakka reports, particularly in relation to VoC identification.

At the moment [the AusTrakka National Analysis Team] are providing...a really great graphic in the VOC report that actually goes up to the health minister weekly so that's on the variants ... and then of course the information does filter through to the weekly surveillance reports that get developed at the national level.

Timeliness

While interviewees generally agreed that having access to genomic data through AusTrakka was useful in confirming or discarding these hypotheses, the majority also indicated that genomic data was typically not available quickly enough to inform the day-to-day response to COVID-19.

...on a day-to-day basis it doesn't actually make a huge impact, we're responding very rapidly as you would understand and need to respond rapidly within 24 hours of identifying a case in terms of managing the case, and identifying their close contacts, so obviously in relation to those close contacts it has no impact, but and also in relation to outbreaks when our outbreak management is very much based on epidemiological data...

Data quality

The importance of the relationships between PHLs and PHUs in relation to ensuring pathogen genomic data quality and the articulation between epidemiological and genomic data was a recurring theme in the interviews. There was an understanding that the power of genomic data lies in its use alongside epidemiological data, and interviewees were consistent in expressing a need for routine articulation to derive the most benefit from genomic data.

But I think the other really important thing that I have learnt is that you do have to line it up with the epidemiology and what you get from basic interviewing, you know like with the ICU people had [the Infection Prevention and Control team] not known that they were married we would've said they were separate, completely separate subtypes. So yeah I think correlating it with your epi is really important.

While some interviewees indicated that this was normally done well, others expressed concern that there were times that incorrect conclusions were drawn due to insufficient contextualisation from epidemiological data.

The collaborative nature of the work also brought with it significant challenges in managing data across organisations, which was repeatedly mentioned throughout the research. While the following quote comes from the earlier days of the pandemic, subsequent interviews indicated that there have been minimal improvements to data management.

And I think one of the hardest things has actually been data management... we're getting information from at least six different sources... a lot of privacy issues means it's hard to match things up...trying to coordinate that has been a bit of a nightmare.

Some interviewees indicated that the COVID-19 epidemic presented a unique opportunity to create viable structures to enable stronger integration.

...the main thing I would like to see coming out of this is an extension to the way genomic and epidemiological data are integrated and speed and efficiency with which intelligence can be gathered by their integration. That's what I'd really love to come out of this. And we've got that opportunity now.

Flexibility

While AusTrakka was rapidly developed during the COVID-19 pandemic and focused on SARS-CoV-2, interviewees indicated that the genomics infrastructure developed in response to COVID-19 was largely applicable to other pathogens. A key development to facilitate and simplify data-sharing moving forward has been a shift towards 'pathogen agnostic' governance frameworks which support the broader application of pathogen genomics.

What has changed is...[AusTrakka] had pathogen-specific data governance but now because we were working with COVID mainly and we had started branching out to some other pathogens but now that [AusTrakka is] starting to take a lot more pathogens and... we have now shifted to a pathogen agnostic framework which has the same principles it's just that it covers all of the pathogens.

While there has been a move towards data-sharing agreements that cover all pathogens, participants also indicated that elements such as minimum metadata requirements would need to be established on a per-pathogen basis. In line with this approach, 'AusTrakka 2' has been developed to be pathogen agnostic.

AusTrakka 1 really was set up in a hurry for COVIDAusTrakka 2 is set up in a much more generic way, so [the AusTrakka Development Team] can put in different proformas for different fields are expected and they're validated and we have to supply that metadata if you are putting it in through that system, all the metadata can be kind of checked against one another in a consistent way and the permissions can be set up and done properly.

There are several possible and developing applications where capacity could be strengthened to increase the benefit of pathogen genomics in the control of COVID-19 and future preparedness. While still in the early stages, there is scope for AusTrakka to potentially be used more broadly to enable access to genomic data across a variety of organisations in human health.

I think well there will be two main potential clients – one would be hospitals and the other ones would be labs more generally. So in the hospital a lot of it will come through the micro lab, but I think we're kind of viewing this as a pilot for how AusTrakka or a similar platform can be used to communicate genomic data to hospitals and health systems and labs....

Interviewees consistently referred to other communicable diseases and a small number mentioned the potential benefits of the AusTrakka platform evolving as a One Health tool.

We also now see that outside of the context of COVID-19, the AusTrakka model is going to be useful for so many other communicable diseases. So currently Monkeypox, but also Japanese Encephalitis, and the really important thing about Japanese Encephalitis is that we have an opportunity for AusTrakka to bridge the boundaries of human health and to evolve into a One Health tool.

A summary of the components of the Guidelines included in the evaluation, performance of the AusTrakka platform against these, and the impact of the element are provided in Table 1.

Discussion

WGS has proven to be a revolutionary technology, and one that has been increasingly embedded into public health responses to current communicable disease threats and planning for future epidemic and pandemic preparedness [1–4]. With sequencing capacity continuing to increase, there is a need for ongoing evaluation of pathogen genomics surveillance systems both to ensure functionality and to understand and incorporate

elements of pathogen genomics-informed surveillance systems that contribute to public health outcomes [6].

The development and implementation of AusTrakka in the early stages of the COVID-19 pandemic in Australia allowed for centralised and efficient interjurisdictional sharing of sequences, as well as epidemiological and sequence metadata, which previously did not exist. This facilitated jurisdictional and national understanding of transmission events and outbreaks, and informed population-level public health responses [12]. Over the period 2020 to 2022, data from user interactions with the platform and interviews indicate that the use of AusTrakka in the public health response shifted with changes in the COVID-19 pandemic.

Previous research has found that the surveillance system attributes of acceptability and representativeness are highly correlated [13]. This is reflected in the AusTrakka data, where the high *Acceptability* (willingness of persons and organisations to participate) of AusTrakka was predicated on the governance mechanisms which were collectively established by stakeholders across Australian jurisdictions. Interviewees consistently indicated that having national-level coordination and governance of AusTrakka was an important factor both in facilitating the development of the platform and in ensuring continued trust and buy-in. This finding is reinforced by the emphasis placed on national leadership, ownership, and commitment by the *WHO guidance for developing national genomic surveillance* [22], and reflected in the experiences of other countries, where structures to facilitate partnerships and collaboration were found to be key to successful integration of genomic surveillance [23]. However, this engagement must be multi-level, rather than resting solely at the national level, and include representation from subnational and organisational levels that generate and use pathogen genomic data. This includes PHLs, policymakers, PHUs, donors, and implementing partners. The central role played by end users in the design led to rapid adoption across jurisdictions, which then supported robust sequence uploads and increased *Representativeness* (ability to accurately describe the occurrence of a health-related event over time) and *Sensitivity* (proportion of cases detected by a surveillance system and the ability to detect outbreaks). Given the ongoing evolution in application of pathogen genomics, this ongoing coordination and engagement is also necessary to support adaptability and sustainability of the system.

Sequence data must be appropriately contextualised in order to be useful for public health purposes [1]. This necessitates the harmonisation of data from different sources; however, integration between epidemiological and genomic data was identified by interviewees as an

Table 1 AusTrakka performance against elements of public health surveillance system quality

Elements of surveillance quality	AusTrakka performance	Impact of element
Usefulness: contributes to the prevention and control of adverse health-related events, including an improved understanding of the public health implications of such events	• Provided a centralised platform to enable interjurisdictional data sharing • Shift over the course of the pandemic from identifying transmission networks towards VoC surveillance • Provided centralised access to jurisdictional and national-level data and reports • Provided advice to national bodies and context for data interpretation • End users used centralised data to situate their own local sequences within the national context • Provided up-to-date data used in briefings and public-facing sessions	• Shared sequence and metadata were used to facilitate investigation of outbreaks and clarify transmission chains to inform prevention of interjurisdictional transmission • Availability of data and reports increased confidence in public health approaches, including large-scale lockdowns to prevent transmission • Improved communication and understanding distribution of variants in the population and contributed to monitoring emerging strains that may increase public health risks • Facilitated appropriate public communication both internally and externally, nationally and internationally
Acceptability: willingness of persons and organisations to participate in the surveillance system	• AusTrakka is underpinned by established governance between all stakeholders and a framework to ensure responsible data-sharing practices	• Established data governance by stakeholders was shown to be central to the acceptability of AusTrakka • Quick uptake across jurisdictions at the beginning of the pandemic • Steady increase in number of users and organisations contributing to AusTrakka from mid-2020 to 2022 • Tree image views correlate with rising cases
Representativeness: ability to accurately describe the occurrence of a condition over time and its distribution in the population Sensitivity: at the level of case reporting, the proportion of cases of a disease detected by the surveillance system; also, the ability to detect outbreaks and monitor changes in the number of cases over time Timeliness: the speed between steps in a surveillance system	• Strong positive correlation and association between COVID-19 case numbers and sequence uploads • Shift in priorities throughout the pandemic led to lower rates of direct user engagement with AusTrakka alongside a continued high level of interest in and utilisation of AusTrakka reports, particularly in relation to VoC identification • Genomic data generally not available within a timeframe to inform day-to-day decision-making or case management • AusTrakka supported access to data that was used to confirm or discard hypotheses regarding transmission	• Genomic data was used to support broader outbreak management and clarify transmission chains • Availability of data and reports increased confidence in public health approaches, including large-scale lockdowns to prevent transmission • Facilitated appropriate public communication both internally and externally, nationally and internationally • Concern regarding incorrect conclusions due to insufficient contextualisation from epidemiological data
Data quality: completeness and validity of the data recorded in the public health surveillance system Flexibility: able to adapt to changing information needs or operating conditions	• Relationships between PHUs and PHUs crucial to ensuring pathogen genomic data quality and articulation between epidemiological and genomic data • Challenges in managing data across organisations • AusTrakka was limited to SARS-CoV-2 data, but infrastructure is largely applicable to other pathogens • AusTrakka 2 has been developed to be pathogen agnostic	• The establishment of AusTrakka facilitated a shift towards 'pathogen agnostic' governance frameworks which support the broader application of pathogen genomics • Scope for AusTrakka to enable access to genomic data across a variety of health organisations • Potential of AusTrakka evolving as a One Health tool

ongoing challenge to the *Data quality* system attribute as laboratories, public repositories, hospitals, and other data sources use different standards, formats, and methods for collection and organisation of data. Tools to support data harmonisation and visualisation are being developed to support stronger pathogen genomics integration [24] and approaches such as the Public Health Alliance for Genomic Epidemiology (PHA4GE) contextual data standard aim to address the attendant challenges [25]. Development of the AusTrakka COVID-19 pro forma was based on the PHA4GE data standards for international consistency. Within Australia, programs such as AusPathoGen (a translational research program funded by the Medical Research Future Fund) are now providing evidence towards a best-practice national approach and strengthening capacity to coordinating the genomics experts across Australia to harmonise the implementation of pathogen genomics within Australia's health system [26].

Data harmonisation may also be facilitated through the development of a centralised approach to data management and sharing [22] and establishment of a centralised platform for data sharing such as AusTrakka can facilitate and be an impetus for coordinated data harmonisation at multiple levels. In developing the future iterations of AusTrakka, a focus on consistency and alignment with both national and international data standards will be required to ensure ease of use of the platform. Furthermore, interoperability or harmonisation of the platform to existing surveillance systems at both a subnational and national level will assist with potential issues in resourcing or capacity that may arise in a post-pandemic environment where investment in pathogen genomics will not be at the same scale.

The evaluation of AusTrakka makes clear how supporting criteria of surveillance quality facilitates system use and impact. Ongoing monitoring and evaluation is essential to ensure that the fundamental changes to surveillance systems enacted by the introduction of pathogen genomics (e.g. changes in data generation, governance, and sharing; reporting and communication; and use of genomic data in public health implementation) are undertaken in ways that provide increased utility to users and contribute to public health outcomes [22, 27]. Consideration of these factors and how to ensure they are represented in the system should be undertaken in the early stages of planning, establishment, and integration of public health pathogen genomics. Frameworks to support evaluation of pathogen genomics-informed surveillance systems have been adapted from established guidelines to evaluate surveillance systems [6]; use of these frameworks to guide development and implementation will support in-depth understanding of how well

the system is functioning, identification of expected and unexpected impacts, and early and ongoing identification of appropriate targets for system strengthening. This will be particularly relevant as use of pathogen genomics continues to expand and be used in novel approaches, such as in the development of One Health surveillance systems and integration of metagenomics.

Conclusions

WGS is a transformative technology that has been increasingly integrated into public health responses to communicable diseases. The development and implementation of AusTrakka in the early stages of the COVID-19 pandemic in Australia allowed for centralised and efficient interjurisdictional sharing of sequences, as well as epidemiological and sequence metadata. The experience of AusTrakka highlights the importance of robust governance on the willingness of persons and organisations to contribute and participate. This engagement and adoption is fundamental to the effectiveness, representativeness, and sensitivity of the system. With public health sequencing capacity continuing to increase, there is a need for ongoing evaluation of pathogen genomics surveillance systems both to ensure functionality and to understand and incorporate elements of pathogen genomics-informed surveillance systems that contribute to public health outcomes.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s44263-026-00265-y>.

Supplementary Material 1: Interview themes.

Supplementary Material 2: Coding framework.

Supplementary Material 3: The completed COREQ (Consolidated criteria for REporting Qualitative research) checklist.

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Authors' contributions

ASF conceptualised the research. ASF and CME drafted the initial manuscript. All authors participated in data collection and analysis and all authors read and approved the final manuscript.

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Data availability

The interview data generated and analysed during the current study are not publicly available due to reasons of confidentiality and privacy. System-level data from the AusTrakka platform is included in this published article. Weekly

SARS-CoV-2 case counts are publicly available from the Australian Government Department of Health and Aged Care and can be found at <https://www.health.gov.au/news/new-weekly-covid-19-trends-reporting>.

Declarations

Ethics approval and consent to participate

This study adhered to all elements of the Helsinki Declaration. Ethical approval to conduct this study was obtained from the University of Melbourne Biomedical Sciences Human Ethics Advisory Group (HEAG) (Application ID: 2056426.1). Written informed consent to participate was obtained from all interviewees.

Consent for publication

Consent for publication was obtained from all participants in line with ethical approval from the University of Melbourne HEAG.

Competing interests

All authors are employed at the organisation that has received funding for development of the AusTrakka platform (Microbiological Diagnostic Unit Public Health Laboratory). The authors are not directly involved in this work. ASF is an editorial board member of BMC Global and Public Health.

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