Global meeting on sustaining gains in genomics for managing pandemic and epidemic threats

Istanbul, Türkiye
14–15 December 2023
Report
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Report
Abstract
WHO held the Global meeting on sustaining gains in genomics for managing pandemic and epidemic threats on 14–15 December 2023 in Istanbul, Türkiye.

This meeting was organised to support countries into stabilizing genomic surveillance systems and formulate future action plans based on the global strategy, regional initiatives and latest tools and guidance including the Step-by-Step Guide to establish strategies at the country level and using the Genomics Costing Tool to inform investments. Countries and other stakeholders shared experiences, discussed key use cases and shared good practices that ensure readiness for future pandemics and epidemics.

KEYWORDS
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PANDEMICS
EMERGENCIES
COVID-19
EUROPE

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<tr>
<td>Africa CDC</td>
<td>Africa Centres for Disease Control and Prevention</td>
</tr>
<tr>
<td>COP</td>
<td>communities of practice</td>
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<td>COVID-19</td>
<td>coronavirus disease</td>
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<td>COVIGEN</td>
<td>COVID-19 Genomic Surveillance Regional Network</td>
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<td>GCT</td>
<td>genomics costing tool</td>
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<td>IPSN</td>
<td>International Pathogen Surveillance Network</td>
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<td>NGS</td>
<td>next-generation sequencing</td>
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<td>PAHO</td>
<td>Pan American Health Organization</td>
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<td>PAHOGen</td>
<td>PAHO Genomic Surveillance Regional Networks</td>
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<td>SARS-CoV-2</td>
<td>severe acute respiratory syndrome coronavirus 2</td>
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<td>UKHSA</td>
<td>UK Health Security Agency</td>
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Executive summary

Executive Summary

WHO held a global meeting on sustaining gains in genomics for managing pandemic and epidemic threats on 14–15 December 2023 in Istanbul, Türkiye. In attendance were 103 participants, inclusive of representatives of Member States, partner agencies and WHO staff.

The meeting aimed to facilitate discussions that will support countries in stabilizing genomic surveillance systems and formulate future action plans based on WHO’s Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032. The objectives of the meeting were to:

- reflect on the strategy implementation since its launch and the genomic sequencing public health use cases that are stabilizing capacities and systems post-pandemic;
- launch the genomics costing tool (GCT) and discuss policy support tools that facilitate country implementation of genomics in public health practice; and
- discuss global and regional initiatives and technical partnerships that strengthen genomic surveillance efforts.

Critical, remarkable progress has been made in strengthening genomics capacities, with an increasing use of genomic sequence data globally. However, barriers such as limited access to tools, including reagents and consumables, as well as a shortage of trained workforce, particularly in bioinformatics, hinder equitable and sustainable access to genomics. At the meeting, countries and other stakeholders exchanged experiences, discussed key use cases and shared good practices that ensure the gains made in genomics in recent years are strengthened and sustained.

The meeting provided valuable input and ideas to advance the development and utilization of tools and guidance in genomics. This includes developing simulation exercises, implementing the GCT at the country level (scheduled roll-out beginning in 2024), and developing and implementing a costed national strategy or action plan.

Genomic surveillance should not be viewed as an isolated tool but as an integral part of the broader public health surveillance system. Current genomics use cases for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and influenza provide critical routine opportunities to monitor these pathogens and serve as foundational capacities for monitoring other pathogens and, in due course, “Pathogen X”.
Equity in access to sequencing is challenged in certain settings, including fragile, conflict-affected and vulnerable settings, and remote island settings. Countries are addressing these challenges with novel approaches to using tools, such as portable sequencing devices and international referral mechanisms, when appropriate. To achieve an effective and efficient sequencing target for variant detection and monitoring, minimum sequencing capacity should be based on scientific evidence. Access for all is feasible through innovative approaches and should continue to be strengthened.

Global and regional initiatives and strategies, including the International Pathogen Surveillance Network (IPSN), continued investments from the Global Fund, FIND and research institutions, offer opportunities for equitable and sustainable access to genomics.

Looking forward, based on the utility and demand for genomics, countries will be supported in developing a costed national strategy or action plan for it. A pathogen-agnostic version of the GCT is planned for release in 2024. A laboratory-based tabletop simulation exercise package to review, validate and test essential functions of public health laboratory systems will be developed and rolled out in countries. Global initiatives such as the IPSN will be supporting countries to accelerate progress in genomics and improve public health decision-making.
GLOBAL MEETING ON SUSTAINING GAINS IN GENOMICS FOR MANAGING PANDEMIC AND EPIDEMIC THREATS

Executive summary
Background

Since the coronavirus disease 2019 (COVID-19) pandemic, tremendous gains have been made in the global genomic surveillance landscape. As of December 2022, 84% (163 of 194) of countries have sequencing capability for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This represents a 58% increase (from 103 to 163) in the proportion of Member States with sequencing capability between February 2021 and December 2022. This achievement has been accompanied by gains in workforce and infrastructure strengthening through training, procurement, coordination and implementation across many countries.

There is significant momentum and political impetus for strengthening genomic surveillance through implementation of the WHO Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032 (1). Since the launch of the strategy, countries, partners and WHO have collectively worked together to strengthen genomic surveillance for pandemic and epidemic threats to global health security.

Concerted efforts are now needed to stabilize and strengthen the gains made during the COVID-19 pandemic. This includes national policy development and costing for sustainability, and expansion of genomic surveillance capacities for preparedness, prevention, detection and response to other pandemic and epidemic threats beyond COVID-19 (2).

In light of the work ahead, WHO hosted this multidisciplinary stakeholder meeting to foster sustained and improved local-to-global coherence for stronger genomic surveillance for pandemic and epidemic threats.

Objectives of the meeting

The meeting aimed to:

- reflect on the strategy implementation since its launch and the genomic sequencing public health use cases that are stabilizing capacities and systems post-pandemic;
- launch the GCT and discuss policy support tools that facilitate country implementation of genomics in public health practice; and
- discuss global and regional initiatives, and technical partnerships that strengthen genomic surveillance efforts.

This report summarizes discussions from the meeting.

The full programme for this event can be found in Annex 1 of this report, and the list of participants, in Annex 2.
Global overview of genomics for pathogens with epidemic and pandemic potential – Maria van Kerkhove, WHO headquarters, Geneva, Switzerland

Genomics is important in the context of global emergency preparedness and response. As part of collaborative surveillance, it is one of the capacities required by countries to strengthen the global architecture for health emergency preparedness, response and resilience. There has been a steady increase in genomic sequencing capacities, particularly since the beginning of the COVID-19 pandemic. Between February 2021 and December 2022, the number of WHO Member States with the capacity to sequence SARS-CoV-2 increased 58%. By December 2022, 163 Member States had the capacity to perform SARS-CoV-2 in-country sequencing.

Recognizing that challenges exist, sustainable and equitable access to genomic surveillance globally must be ensured. The Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032 was developed with this need in mind. It is a high-level framework with a goal to strengthen and scale genomic surveillance for quality, timely and appropriate public health action within local to global surveillance systems.

There are many use cases for genomics, and countries are using the capacities they have built since the COVID-19 pandemic to expand to other pathogens. Genomic surveillance is part of the broader surveillance and laboratory system, and its implementation should reinforce end-to-end capacities, including sample collection, diagnostics, data sharing and analysis.

To date, sustained investment in both public health intelligence gathering and bioinformatics has proven to be a significant limiting factor. Systems need to be set up with efficient workflows to ensure that the correct samples arrive at the right laboratories on a timely basis, using spillover maps to inform of the disease risk across regions and countries.

Support needs to be given to Member States to integrate genomic surveillance into national and regional strategies. Overall, more advocacy is required in the genomics space in the face of pandemic potential and other, numerous global challenges.
In the Americas, several networks have long supported viral disease surveillance and response. These networks include RELDA (the Arbovirus Diagnosis Laboratory Network of the Americas) and SARInet plus (which includes national influenza centres and other national public health laboratories in charge of surveillance of respiratory pathogens). In March 2020, the COVID-19 Genomic Surveillance Regional Network (COVIGEN) was established, enabling provision of protocols, reagents, training and support in data analysis to countries with already established sequencing capacity.

COVIGEN also facilitated sample shipment from countries with limited or no sequencing capacity to one of eight reference laboratories distributed across the Americas. In parallel, COVIGEN supported these countries in establishing sequencing platforms at their national public health laboratories.

This capacity is now being utilized to tackle other public health problems, including endemic diseases like dengue and foodborne pathogens, as well as outbreak response, including the resurgence of cholera in Haiti and the outbreak of chikungunya in Paraguay.

This work is carried out within the framework of PAHO’s strategy on regional genomic surveillance for epidemic and pandemic preparedness and response (3), approved in September 2022 by Member States and which is aligned with the WHO global genomic surveillance strategy. In this context, the PAHO Genomic Surveillance Regional Networks (PAHOGen) was established in 2023 as a network of genomic networks working not only on arboviruses (ViGenDA) and respiratory viruses (RESVIGEN, an expansion of COVIGEN) but also foodborne pathogens (PulseNet Latin America and Caribbean) and antimicrobial threats (ReLAVRA+). PAHOGen aims to promote integration and sustainability by enhancing collaboration of existing surveillance networks and sharing equipment, reagents, servers and other tools.

It is important to highlight that genomic surveillance is not synonymous with sequencing, and requires clear context – and pathogen-specific objectives defined and implemented in close coordination with epidemiological surveillance, clinical management and laboratory systems. Other important challenges going forward include the availability and roll-out of external quality assessment programmes, bioinformatics capacity and overall sustainability of genomic surveillance.
The COVID-19 pandemic put next-generation sequencing (NGS) and genomic surveillance on the map. NGS is critical to monitoring the evolution of SARS-CoV-2 and its variants, as well as to informing public health action and medical interventions. However, NGS resources are not equitably distributed worldwide, and public databases are needed to store data to make them freely available.

SARS-CoV-2 genomic sequencing remains important as the virus continues to evolve; it is now in its endemic stage, and there are now even more regional variants than before. Surveillance needs to continue and to be increased in order to reach geographically representative numbers of sequencing.

Yet, genomic surveillance activities and data sharing have actually decreased, impairing the visibility and characterization of variants. Conversely, turnaround time from collection of samples to entry in a database is increasing – from single-digit days in January 2020 to as many as triple digits reported in 2023. This increased turnaround time is a true hindrance to effective real-time surveillance.

WHO is currently recalibrating its SARS-CoV-2 variant genomics surveillance systems. This includes transitioning the SARS-CoV-2 reference laboratory network, which was set up in the early days of the pandemic to support countries without capacity, into a coronavirus-wide network. This is being carried out using a One Health approach, while leveraging existing systems such as expanded Global Influenza Surveillance and Response System and WHO collaborating centres with expertise in environmental and wastewater surveillance.
Netherlands (Kingdom of the) was comparatively well prepared for the pandemic. Amplicon-based sequencing protocols were set up immediately. On 27 February 2020, the Netherlands detected its first case of SARS-CoV-2, and the entire genome generated just 24 hours later. Hundreds of genomes were produced within the first month.

The sequencing data set was used to determine geographic signals, identify significant variations in the virus and conduct outbreak investigations in hospitals, nursing homes, gyms, schools, the food industry and zoos.

Investigations were also carried out on mink farms, where increased mortality was reported starting in April 2020. On the first two mink farms reporting, 2.4% and 1.2% of mink died, respectively. By the end of 2020, 69 out of 110 mink farms had been affected. Genomic sequencing of livestock on these farms showed human-to-mink transmission followed by mink-to-mink and occasional mink-to-human transmission. Five disease clusters were identified based on phylogenetic clustering and epidemiological data, indicative of mink farm to mink farm transmission. There was also collaboration with the mink farming industry in Poland.

It is essential to monitor the role animals play in the circulation of disease and to assess the level of such surveillance as well as whether it should be centralized or otherwise. However, the sequencing of pathogens needs to be combined with existing disease surveillance strategies both in human and animal reservoirs. The constant collection of genomes needs to be balanced with the understanding of phenotypic consequences, which is not always the case.
Panel discussion with the following panelists:
Gerald Mboowa, Africa Centres for Disease Control and Prevention (Africa CDC), Ethiopia
Bas Munnink, Erasmus MC, Netherlands (Kingdom of the)
Biran Musul, WHO Country Office in Türkiye

WHO Country Office in Türkiye
In Türkiye, sequencing across several pathogens was already being implemented before COVID-19. Nonetheless, the pandemic itself highlighted the importance of strengthening genomic surveillance for infectious disease agents to inform public health actions. It also identified the need for a more systematic, comprehensive and integrated approach to genomic surveillance. To consolidate and expand capacities built through investments during the pandemic, a national genomic surveillance strategy was developed for Türkiye, which incorporates different areas of infectious disease genomic surveillance.

As a result of Türkiye’s surveillance strategy for high-threat pathogens post-COVID-19, resources are being used more efficiently by the Ministry of Health. Advocacy plays a key role, and comprehensive documentation systems help all stakeholders to understand exactly what is being implemented in the country, how and why. The strategy has been developed to build on strengths and existing capacities, overcome weaknesses and utilize opportunities.

The Türkiye strategy – setting priorities
In May 2022, a scientific meeting was held to share experiences on developing and implementing genomic surveillance strategies. Countries with longer-term experience as well as those that had benefited from the process were invited. A separate meeting was organized specifically to discuss antimicrobial resistance (AMR) from a One Health perspective as well as the use of sequencing for AMR.

A task force that included the heads of respective laboratories, and surveillance, disease control and epidemiology staff was formed to develop the national genomic surveillance strategy through monthly meetings. The team of experts identified and addressed high-threat pathogens to develop pathogen-specific annexes, including individual sequencing objectives. This is a living document to enable adaptation to the ever-shifting landscape of new, emerging and re-emerging threats.

Independent sampling strategies for individual pathogens are also being considered, including the number of samples required, which laboratories will deal with those samples and the workflow required. All of this work is intended to guide the decision on which pathogens to include and the level of sequencing required for each pathogen for genomic surveillance so as to inform public health actions.
To improve and implement genomic capacity, Africa CDC and WHO developed a tiered structure of regional, national and specialized laboratories to work with across the African Region. Almost 40 national public health laboratories now have in-country sequencing capabilities.

The region served by Africa CDC faces challenges when it comes to capacity building and equipment. Regarding the sharing of sequencing data, reliable and fast connectivity has been a particular issue which has been greatly alleviated via investment in Starlink satellite internet provision. Equally challenging is the frequent lack of access to a reliable supply chain of reagents.

Efforts are being put to work with countries on integrating genomic surveillance into public health programmes to ensure more sustainable government funding, and the national pathogen surveillance strategy is helping to enable long-term reliable access to reagents. Although Africa CDC has been procuring reagents for Member States for over 3 years, a viable longer-term strategy is needed which includes local ministries of health having their own procurement plans.

**Erasmus MC, Netherlands (Kingdom of the)**

A lack of consistent testing is a challenge in Netherlands (Kingdom of the) as are the difficulties involved in assessing and determining the precise level of surveillance needed to identify the next variant of concern.

Netherlands (Kingdom of the) is one of the countries with a system already in place to randomly test respiratory samples, although it is essential to survey wastewater as part of monitoring pathogens throughout communities.

SARS-CoV-2 highlighted the importance of genomic surveillance. In addition, climate change and the ever-shifting viral landscape are enabling pathogens to spread in new ways (such as Mpox). Significant money has already been invested in any case, so it would make sense to use available funds to leverage surveillance capacity.

The benefits of investing in genomic surveillance are obvious compared with the potentially disastrous costs of locking down an economy in the case of a disease outbreak, epidemic or pandemic. WHO’s new genomic costing tool will be invaluable in demonstrating the benefits of investing in genomic surveillance.
Drug resistance in tuberculosis is a serious issue. Currently, 20 different drugs are being used to treat the disease, and the pathogen has developed a resistance to nearly all of them. Targeted sequencing is therefore a key diagnostic tool to effectively and rapidly identify mutations as they occur in a community.

Traditional phenotypic drug susceptibility testing can take weeks to perform, whereas targeted sequencing on clinical samples can be carried out within just 2–3 days to detect resistance to almost any drug, which will inevitably improve treatment of the disease.

Homa Attar Cohen, WHO Hub for Pandemic and Epidemic Intelligence, Germany
The IPSN is a global network of pathogen genomic actors, brought together by the WHO Hub for Pandemic and Epidemic Intelligence, to accelerate progress in pathogen genomics and to improve public health decision-making.

Recognizing the different use cases of pathogen genomics, the IPSN is developing a framework to visualize different pathogen surveillance objectives that can be informed by genomic information. This framework would help countries see the range of use cases for genomics and support their planning and prioritization processes. It would also help to inform better and faster decision-making. In addition, the framework can be used to advocate for investments in genomic surveillance.
Session 2: Looking ahead: Opportunities for building and sustaining gains in genomics. Moderator: Gina Saaman

“Exercise DNA” - a simulation to reflect on connectivity during a future emergency presented by Oluwatosin Akande, WHO headquarters, Geneva, Switzerland

Exercise participants:
Leena Inamdar, UK Health Security Agency (UKHSA), United Kingdom of Great Britain and Northern Ireland
Francis Inbanathan, WHO Viet Nam Country Office
Bas Munnink, Erasmus MC, Netherlands (Kingdom of the)
Hicham Oumzil, Mohamed V University, Morocco

Exercise DNA was a tabletop simulation exercise based on a fictional scenario involving a national laboratory officer, a national public health officer, a national animal health officer and an international health officer (WHO). The objective of the exercise was to test the connectivity and interdependencies between actors during an event focusing on genomics.

Exercise DNA began with a notification of the public health system of an atypical family cluster of severe pneumonia in a national hospital, resulting in two deaths. Initial testing using polymerase chain reaction (PCR) did not identify the pathogen.

The evolution of the situation is addressed in four injects, with accompanying questions asking exercise participants how they would function as the scenario evolves.

In inject two, public health investigation links the index cluster to a national zoo and a massive power surge destroys the sequencer in the national laboratory before the results are available.

In inject three, there is sustained community transmission and a novel adenovirus is confirmed. It has now been declared a public health emergency of international concern, following its detection in 15 countries.

In inject four, cases are detected in three highly remote island countries with no in-country sequencing capacity, very low human population but dense forests and large chimpanzee populations.
Global Meeting on Sustaining Gains in Genomics for Managing Pandemic and Epidemic Threats

Session 2: Looking ahead: Opportunities for building and sustaining gains in genomics. Moderator: Gina Saaman

The panelists:
Oumzil Hicham, Mohamed V University, Morocco
Leena Inamdar, UK Health Security Agency, UK
Francis Inbanathan, WHO Vietnam Country Office
Bas Minnink, Erasmus, Netherlands (Kingdom of the)

This session started with a practical demonstration of a simulation exercise (SimEx). The panelists were presented with a theoretical health emergency scenario. As the scenario developed, panelists were presented with several questions to be answered from the perspective of a national laboratory, public health, WHO/international, and animal health representative.

Following the demonstration, a hotwash debrief took place to discuss the following issues:

- Keeping genomic systems warm – defining needs for simulation exercise packages for genomics
  Lisa Carter, WHO Lyon Office, France

A short presentation was given explaining how a simulation exercise (SimEx) reproduces aspects of a real situation, to test existing procedures and awareness of actions and needs of preparedness and response. The WHO SimEx manual was then presented as part of the project for developing simulation exercises for public health laboratories.

The manual contains simulation exercise packages for the following scenarios:
- Scenario 1 – exercising surge laboratory capacity
- Scenario 2 – sample transport and referral mechanism
- Scenario 3 – detection and characterization of a novel pathogen

All three scenarios, their scope, and specific objectives are fully adaptable based on the country context. It is now planned to initially target three to four countries to pilot the implementation of SimEx material.

The exercise was followed by a hotwash to reflect on the exercise and discuss opportunities for improvement, based on four themes: connectivity, timely access, data sharing and utility, and test and surge (Fig. 1).

Fig. 1. Thematic framework for sustaining and strengthening gains in genomics

- **Connectivity**
  Connectivity between stakeholders in genomics

- **Timely Access**
  Timely access to sequencing for better geographical representation

- **Data Sharing & Utility**
  Data sharing and data utility from local to global genomic surveillance systems during an emergency response

- **Test and Surge**
  Test the surge and stretch of systems to be ready for emergencies
Simulation exercises are used to test laboratory readiness for emergencies. This aligns with Objective 5 of the global strategy, which is to maintain a readiness posture for emergencies. Simulation exercises could be tabletop, functional or field exercises, and could include testing the following components of genomic surveillance: coordination mechanisms, national and international referral mechanisms, troubleshooting lab and data analysis, and identifying and characterizing an unknown pathogen.

The Public Health Laboratory Strengthening unit is developing laboratory-based tabletop simulation exercises and drills to review, validate and test essential functions of public health laboratory systems in a safe environment. Currently, there are three proposed scenarios:

- Scenario 1 – exercising surge laboratory capacity,
- Scenario 2 – sample transport and referral mechanism, and
- Scenario 3 – detecting and characterizing a novel pathogen.

Looking forward, WHO plans to identify three to four countries to pilot implementation of simulation exercise materials, make exercise materials publicly accessible for wider-scale roll-out, identify countries and partners to champion the roll-out of these projects and leverage country and stakeholder experience to carefully articulate needs to develop simulation exercises in the area of genomic surveillance.
The purpose of the breakout session was to get feedback from countries, partners and other stakeholders on specific needs for simulation exercises.

Participants were divided into 12 groups, each with an assignment to design a simulation exercise based on one of the five following topics:

- sequencing
- bioinformatics and data analysis
- communication and information sharing
- plans and policies
- development of sequencing strategy.

Each group developed simulation exercise objectives, scenarios and injects. The breakout session was followed by a discussion session where participants presented key ideas across the groups.
Equity in access to sequencing for public health action – plenary discussion
Moderator: Tuyet Hoang, University of Melbourne, Australia

Panelists:
Askar Abdaliyev – Ministry of Health of the Republic of Kazakhstan
Amal Barakat – WHO Regional Office for the Eastern Mediterranean
Eka Buadromo – The Pacific Community
Edyth Parker – African Centre of Excellence for Genomics of Infectious Diseases (ACEGID)

It is important for all countries to have equitable access to sequencing capacities for timely response to public health threats. However, there are many barriers to equitable access. These include: inadequate funding, poor access to high-precision technology, inadequate skilled workforce, delays in procuring supplies, challenges related to long-term maintenance of sequencing equipment and suboptimal knowledge in interpreting and using sequencing data.

Countries have taken different steps towards ensuring equitable access to sequencing technology. In Pacific countries, a two-tiered network of new laboratories was developed. Two reference laboratories perform NGS, with another six laboratories responsible for PCR. Sequencing was also introduced in the six already existing regional laboratories.

In the Eastern Mediterranean Region, three groups of countries have been identified and appropriate support is being given to these countries:

- Group 1 – countries with timely sequencing and bioinformatics capacities;
- Group 2 – countries with some sequencing and bioinformatics capacities but that require additional support; and
- Group 3 – countries with limited sequencing and bioinformatics capacities and challenges regarding referral to international laboratories.

Located in Nigeria, ACEGID is an institution that conducts genomics research and training for infectious diseases in Africa. To increase the availability of skilled workforce, the institution trains scientists from across many African countries on NGS and bioinformatics.

The Global Fund employs a bottom-up method of funding, where funds are disbursed at the country level. The organization supports sustainable genomic surveillance by facilitating access to equipment, reagents and consumables and supporting workforce development through sequencing and bioinformatics training.
Greater coordination among donors could help understand the precise needs of countries and budget priorities. When procuring equipment, thought needs to be given to its realistic lifespan, likely date of obsolescence, the budget for its ongoing maintenance and whether training will be needed to operate it correctly.
The IPSN (4) is hosted by the WHO Hub for Pandemic and Epidemic Intelligence and brings together the pathogen genomics community to accelerate progress on deploying pathogen genomic surveillance and to improve public health decision-making. The IPSN vision is that every country have equitable access to sustained capacity for genomic sequencing and analytics as part of its public health surveillance system. IPSN’s mission is to create a mutually supportive global network of pathogen genomic surveillance actors that amplifies and accelerates the work of its members to improve access and equity. Members of the IPSN include government agencies, academic institutions, philanthropic foundations, multilateral organizations, civil society and private-sector business associations.

At present, the IPSN is engaging in five main areas of work:

- Communities of practice (COP) to solve common challenges. The COP on genomic data aims to build trust among data producers, users and policy-makers, support the interoperability of data and analytics across databases and advocate for “data for decision-making”. The COP on environmental and vector genomic surveillance aims to support the development of standards and guidance, define use cases for public health and encourage intersectoral (e.g., One Health) work.

- The country scale-up accelerator (CSUA) to enable exchange and amplify country voices. The CSUA is developing a country capacity framework and defining use cases for PGS as planning tools for countries.

- Catalytic grant funding to support projects led by IPSN members from low- and middle-income countries. Two calls for proposals are planned for 2024.

- Advocacy and communications to keep pathogen genomics high on the agenda.

- Convening partners to share progress and innovations.

The first annual IPSN Global Partners Forum took place in October 2023 in Berlin, Germany. The event was held alongside the World Health Summit to bring together country, regional and global partners involved in pathogen genomic surveillance. The event will provide a platform for public health practitioners, academics, policy-makers and financial institutions to build partnerships, and introduce innovations and ideas.
Opportunities for strengthening genomics and fostering greater collaborations – panel discussion
Moderator: Colin Russell, University of Amsterdam, Netherlands (Kingdom of the)

Panelists:
Laura Hughes-Baker – Centers for Disease Control and Prevention, USA
Khoo Yoong Khean – Asia Pathogen Genomics Initiative, Singapore
Anita Suresh – FIND, Switzerland

Partners provide support in assessing capacities, building and strengthening technical capacities, providing implementation guidance, strengthening legal regulation and data analysis.

Communication was identified as a key challenge, as was the need to shift from pathogen-specific thinking to a more comprehensive approach. The collective advice was to engage with collaborators, coordinate between partners, monitor and support mapping of investments, identify sequencing and genomic surveillance objectives and increase genomics literacy and advocacy.
The GCT – Joanna Salvi Le Garrec (Zwetyenga), WHO Regional Office for Europe, and Oluwatosin Akande, WHO headquarters

The GCT (5) is the result of a multiagency collaboration between the following five agencies: the Association of Public Health Laboratories, FIND, the Global Fund, the UKHSA and WHO.

The GCT facilitates budgeting and resource mobilization for infrastructure, workforce, biosafety and quality assurance associated with SARS-CoV-2 genomic surveillance. The tool will be useful to country, regional and global policy-makers, health administrators and economists, laboratory directors, quality managers, donor institutions and other stakeholders engaged in genomic surveillance for priority pathogens. The GCT is a Microsoft Excel-based tool accompanied by a user manual to guide its users.

The tool was validated through pilot exercises conducted in three laboratories with varying throughput capacities and sequencing and bioinformatics infrastructure in Ghana, Kyrgyzstan and Oman. The tool and its user manual were finalized following this validation process. Early experiences in rolling out the tool in Georgia and Namibia are extremely positive. Looking ahead, the team plans to develop a pathogen-agnostic version of the tool in 2024.
Oman was the first country in the Eastern Mediterranean Region to use the costing tool. With 41 attendees including representatives of diverse disease programmes, and procurement and administrative officers, there is a lot of interest and support for developing a well-costed policy for integrated genomic surveillance. The tool is comprehensive, covering many areas that are not traditionally incorporated into funding plans. Procurement in Oman is centralized but controlled by different ministries, ensuring transparency of orders. Careful planning must be done in advance and on an annual basis.

The costing exercise was immediately followed by a workshop on developing a national strategy, using WHO’s step-by-step guide (6). The results from the costing exercise were incorporated into the strategy development efforts. The workshop was attended by representatives from academia, and from the public health veterinary, agriculture and forensic sectors. The costing exercise was a driver for the multisectoral collaborative nature of this workshop.

The presentation was followed by shared experience of costing:

Training on the costing tool in Georgia was done in November 2023 by the technical team that developed the GCT. Technical personnel, including representatives from the procurement and logistics teams, participated in the training. The tool clearly showed that the true cost of sequencing is much higher than previously estimated. The tool demonstrated the need to consider many factors that are not usually considered and factored into costing. There are now plans to start using the tool. It would be valuable to have this tool expanded to other pathogens outside of SARS-CoV-2.

The Centre for Pathogen Genomics, University of Melbourne, Australia, recently published a systematic review showing the economic evaluations of whole-genome sequencing for pathogen identification in public health surveillance and health-care-associated infections.

The costs and effectiveness of sequencing for infectious disease surveillance vary widely, and are largely setting- and pathogen-specific. Economic evaluations are limited to high-income countries and are centred on health-care-associated infections and foodborne pathogens. Until now, there has been no standard method for costing genomics; the tool will be invaluable for the future.
A lens on efficiency in genomic surveillance –
Alvin Han, University of Amsterdam, Netherlands (Kingdom of the)

This presentation looked at identifying effective and efficient routine sequencing targets to monitor the emergence and prevalence of new variants of acute respiratory viruses (e.g., SARS-CoV-2, influenza viruses, respiratory syncytial viruses).

Mathematical models show that increasing sequencing output at low sequencing rates (i.e., < 1 sequence per million people per week) can meaningfully speed up variant detection by weeks to months. However, once sequencing rates reach > 10 sequences per million per week, any further increase in sequencing output will result in little to no change in time-to-variant detection.

A minimum sequencing capacity of two sequences per million people per week with a 2-week turnaround time can be an effective and efficient sequencing target for variant detection and monitoring.

Country comments on the sequencing target of 2–30 sequences per million people per week for COVID-19:
Shipping and receiving samples from all over poses significant challenges for some countries. To reduce the turnaround time, they would need decentralized sequencing, with laboratories working on smaller numbers of samples and exploring the need for different sequencing platforms with different throughputs. These issues must be carefully considered when comparing cost-effectiveness versus sequencing.
Roundtable discussion on promoting the tool and identifying its training needs
Moderator: Joanna Salvi Le Garrec (Zwetyenga), WHO Regional Office for Europe

Panelists:
Teodora Buzarova – Institute for Public Health, North Macedonia
Timothy John Dizon – Research Institute for Tropical Medicine, Philippines
Aigul Dzumakanova – Ministry of Health, Kyrgyzstan
Aude Wilhelm – UKHSA, United Kingdom

The following questions were posed to the panel:

“Will you use the tool?”

“Do you foresee the need for training to use the tool? How easy is it to use?”

“In the implementation phase of genomics sequencing, have you identified any training requirements apart from the tool?”

“What are your suggestions for securing financial support for implementation?”

Some countries have the experience of using the laboratory test costing tool (7) and will be using the GCT. For countries working on their national genomics strategies, the tool will be useful in evaluating plans, justifying costs and analysing cost-effectiveness. Moreover, the tool will allow transparency that will facilitate discussion with high-level stakeholders in ministries of health, finance and so forth to justify costs and investments in genomics. In addition, countries are interested in using the tool for a range of pathogens beyond SARS-CoV-2.

Though the tool is accompanied by a user manual and is intuitive, using it requires training workshops. A platform for online consultations on the tool should also be considered. Aside from instruction on the tool itself, training should be expanded to sequencing and bioinformation as workforce demand continues to grow.

Buy-in from all relevant key stakeholders is needed to secure investments in genomics. Genomics is a specialized field, and technical personnel should be able to clearly communicate to these stakeholders the usefulness of genomics in preparing and responding to pandemics. It is helpful to have coherent objectives and a clear, realistic budget; the GCT and the step-by-step guide for developing a national strategy will be useful in this process.

Sequencing was initially mainstream in academia/research institutions. With the increasing use of sequencing in national public health laboratories, collaboration with academia/research institutions should be encouraged and supported. The New Variant Assessment Programme (NVAP) of the UKHSA supports many public health laboratories in optimizing and building genomics. As one of the institutions involved in developing the tool and
with its experience in delivering training in genomics, the NVAP will use the tool in supporting countries and incorporating lessons learnt into development of the second version of the GCT.

**Interactive session to train participants in use of the tool**

An interactive session to train participants in using the GCT was conducted. This session was facilitated by the GCT working group.
Conclusions and next steps

Over the last 3 years, there have been significant gains in genomic surveillance capacities globally. As of December 2022, 84% (163 of 194) of countries have sequencing capability for SARS-CoV-2, representing a 58% increase (from 103 to 163 Member States) between February 2021 and December 2022. This achievement has been accompanied by gains in workforce and infrastructure strengthening through training, procurement, coordination and implementation.

On 14–15 December 2023, WHO hosted a global meeting on sustaining gains in genomics for managing pandemic and epidemic threats to facilitate discussions to foster sustained and improved local-to-global coherence for stronger genomics, in line with the Global Genomic Surveillance Strategy for Pathogens with Pandemic and Epidemic Potential, 2022–2032 (1). At the meeting, countries and other stakeholders shared experiences, discussed key use cases and shared good practices that ensure the gains made in genomics in recent years are strengthened and sustained.

The meeting provided valuable input and ideas to advance the development and utilization of tools and guidance in genomics. This includes developing simulation exercises, implementing the GCT at the country level (scheduled roll-out beginning in 2024), and developing and implementing a costed national strategy or action plan.

Current genomics use cases for SARS-CoV-2 and influenza provide critical routine opportunities to monitor these pathogens and serve as foundational capacities for monitoring other pathogens. These include those with the potential to trigger a severe global epidemic (‘pathogen X’). Using a One Health lens, it is important that all stakeholders across relevant sectors and disease programmes work together to foster efficiency and effectiveness.

Equity in access to sequencing is challenged in certain settings, including fragile, conflict-affected and vulnerable settings, and remote island settings. Countries are addressing these challenges employing novel approaches to use of tools such as portable sequencing devices and international referral mechanisms, when appropriate. To achieve an effective and efficient sequencing target for variant detection and monitoring, minimum sequencing capacity should be based on scientific evidence. Access for all is feasible through innovative approaches and should continue to be strengthened.

Countries articulated the need to establish a costed national strategy, tailored to their needs, to strengthen and sustain capacity for sequencing priority pathogens, including pathogen X. Global and regional initiatives and strategies, including the IPSN, the Global Fund, FIND and research institutions, offer opportunities to continually strengthen and sustain access to genomics.
Looking forward, based on demand and demonstrated utility of the costing tool, countries will be supported in developing a costed national strategy or action plan for genomics. This will facilitate investment, planning and implementation of sustainable genomics for pathogens with pandemic and epidemic potential. In addition, a broader, pathogen-agnostic version of the GCT will be developed in 2024. Feedback from participants on the current version of the tool will be incorporated. Likewise, feedback from participants helps inform development of simulation exercise packages.
References


Annex 1. Programme

<table>
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<tr>
<td>08:30 – 09:00</td>
<td>Registration and coffee</td>
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<tr>
<td>09:00 – 09:30</td>
<td><strong>Introduction and housekeeping</strong></td>
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<tr>
<td></td>
<td>Oluwatosin Akande, WHO</td>
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<td></td>
<td><em>Welcome remarks</em></td>
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<tr>
<td></td>
<td>Nhu Nguyen Tran Minh, WHO</td>
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<td>Ayse Hande Turk, Ministry of Health Turkiye</td>
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<td>Lucas de Toca, Government of Australia</td>
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<td></td>
<td>Gina Samaan, WHO</td>
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<td></td>
<td><em>Meeting agenda, objectives and expected results</em></td>
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<tr>
<td></td>
<td>Joanna Salvi Le Garrec (Zwetyenga), WHO</td>
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<tr>
<td><strong>Session 1</strong></td>
<td>Where are we now? Genomic surveillance gains since COVID-19</td>
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<tr>
<td>09:30 – 09:40</td>
<td>Global overview of genomics for pathogens with pandemic and epidemic</td>
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<td>Maria Van Kerkhove, WHO</td>
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<td>09:40 – 10:00</td>
<td>**Genomic surveillance of epidemic-prone pathogens: PAHO's regional</td>
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<td>strategy and genomic networks</td>
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<td></td>
<td>Lionel Gresh, PAHO/WHO</td>
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<td></td>
<td><em>Sustaining and integrating SARS-CoV-2 variant surveillance</em></td>
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<td>Jane Cunningham, WHO</td>
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<td><em>Whole genome sequencing during the SARS-CoV-2 pandemic and the way</em></td>
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<td>Bas Munnink, Erasmus University Medical Center</td>
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<td>10:00 – 10:30</td>
<td>**Eye on the horizon - genomics for a subset of pandemic- and</td>
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<td>epidemic-prone pathogens, and integration with other priority use</td>
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<td>Panel discussion</td>
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<tr>
<td>10:30 – 11:00</td>
<td>Group photo and coffee</td>
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<tr>
<td><strong>Session 2</strong></td>
<td>Looking ahead: Opportunities for building and sustaining gains in</td>
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<td>genomics</td>
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<tr>
<td>11:00 – 12:30</td>
<td>**“Exercise DNA” - a simulation to reflect on connectivity during</td>
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<td>a future emergency</td>
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<td>Host: Lisa Carter, WHO</td>
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<tr>
<td>12:30 – 13:30</td>
<td>Lunch</td>
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<tr>
<td>13:30 – 14:45</td>
<td>**Keeping genomic systems warm – defining needs for simulation</td>
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<td>exercise packages for genomics</td>
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<td>Breakout sessions</td>
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<tr>
<td>14:45 – 15:45</td>
<td>Equity in access to sequencing for public health action</td>
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<td>Plenary discussion</td>
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<tr>
<td>15:45 – 16:15</td>
<td>Coffee</td>
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<tr>
<td>16:15 – 17:30</td>
<td>**Opportunities for strengthening genomics and fostering greater</td>
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<td>collaborations**</td>
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<td>Moderator: Colin Russel, University of Amsterdam</td>
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**Annex 1. Programme**

**International Pathogen Surveillance Network**
Josefina Campos
Panel discussion

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<tr>
<td>17:30</td>
<td><strong>Day 1 wrap-up</strong></td>
<td>Oluwatosin Akande, WHO</td>
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<tr>
<td>17:30 - 19:00</td>
<td><strong>Networking reception</strong></td>
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**Day 2: 15 December 2023**

**Session 3**
An Introduction to the Genomics Costing Tool

<table>
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<tr>
<td>09:00 – 09:25</td>
<td><strong>Presentation on the Genomics Costing Tool</strong></td>
<td>Joanna Salvi Le Garrec (Zwetyenga), WHO &amp; Oluwatosin Akande, WHO</td>
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<tr>
<td>09:25 – 09:45</td>
<td><strong>Costing tool: The Omani experience</strong></td>
<td>Luke Meredith, WHO Questions and answers</td>
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<tr>
<td>09:45 – 09:55</td>
<td><strong>A lens on efficiency in genomic surveillance</strong></td>
<td>Alvin Han, University of Amsterdam</td>
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<tr>
<td>09:55 – 11:00</td>
<td><strong>Roundtable discussion on promoting the tool and identifying its training needs</strong></td>
<td>Panel discussion</td>
<td>Moderator: Joanna Salvi Le Garrec (Zwetyenga), WHO</td>
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<tr>
<td>11:00 – 11:30</td>
<td><strong>Coffee break</strong></td>
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<tr>
<td>11:30 – 11:40</td>
<td><strong>Closing reflections on Strategy rollout and transition into the interactive session on the Genomics Costing Tool</strong></td>
<td>Nedret Emiroglu, WHO Joanna Salvi Le Garrec (Zwetyenga), WHO</td>
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**Session 4**
Interacting with the Genomics Costing Tool

<table>
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<th>Time</th>
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<th>Presenters</th>
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<tbody>
<tr>
<td>11:40 – 13:30</td>
<td><strong>Interactive session to train participants on the use of the tool</strong></td>
<td>Facilitators: Alex Jaguparov, WHO; Marco Marklewitz, FIND; Biran Musul, WHO; Joanna Salvi Le Garrec (Zwetyenga), WHO; Swapna Uplekar, FIND; Aude Wilhelm, UKHSA</td>
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<tr>
<td>13:30 – 14:30</td>
<td><strong>Lunch</strong> (note: those who do not join the interactive session may go to lunch earlier, as from 12:30 onwards)</td>
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</table>

**Moderator:**
- Nicksy Gumede-Moeletsi, WHO
- Joanna Salvi Le Garrec (Zwetyenga), WHO
- Nicksy, WHO
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- Alvin Han, University of Amsterdam
- Nedret Emiroglu, WHO
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Nurgul Seitkazieva  
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Tina Kusumaningrum
National Professional Officer (Laboratories), WHO Country Office in Indonesia, Jakarta

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Sri Lestari
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