

New Variant Assessment Platform (NVAP)

Strengthening Genomic surveillance globally

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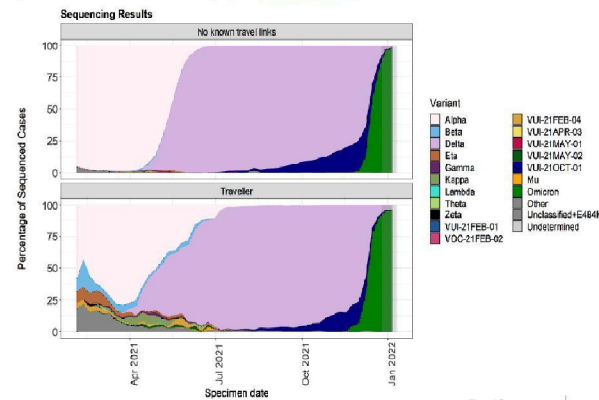
UK Health Security Agency
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Genomic surveillance

Whole genome sequencing increases the sensitivity of our surveillance systems and helps answer questions that otherwise we would not be able to answer on a timely manner.

- Whole Genome Sequencing (WGS) has become the reference microbial typing method of choice and is increasingly applied to national surveillance of infectious diseases.
- Capabilities have been rapidly increased in the context of the COVID response
- Genomics has enabled to a degree global surveillance of SARS-CoV-2
- Development of methods to better integrate and harness the surveillance benefits of WGS

Figure 3. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 10 January 2022 (excluding 1,001 cases where the travel status or specimen date were unknown) (Find accessible data used in this graph in [underlying data](#).)



UKHSA SARS-COV-2 variants of concern and variants under investigation in England, Technical briefing 34; 14 January 2022

Whole Genome Sequencing in England

England established a programme of **whole genome sequencing (WGS) of pathogens in 2012**. It is one of the leading centres implementing the technology worldwide.

Ten years of public health working productively with academic partners has resulted in:

- Delivering **genomics end-to-end solutions** exemplified by **first-in-world service** for tuberculosis
- Delivering **national surveillance and food chain and environmental investigation** of gastrointestinal/food poisoning national system for all hospitalised patients and imported fever cases
- Delivering **targeted outbreak investigation** of serious illnesses

Ground breaking analyses of combined genomics and epidemiological data revealing:

- **Reservoirs** (e.g. Mycobacterium chimera in heater cooler units leading to surgery linked mortalities)
- **Control** of national epidemics (i.e. Clostridium difficile)
- **Outbreak control** (i.e. Candida auris and carbapenem resistant enteric bacteria, interrupting transmission from reusable devices)
- **Reducing the threat of Listeriosis** in hospitals and among vulnerable patients, cases are now more sporadic and with incident rates of less than 30% and rapid investigation and identifying the source of contamination
- Cases of **Shigatoxin producing E.coli 0157 infection and mortality** among under 5 has been reduced to less than 20% of cases in the last decade
- Generating **evidence from winter surveillance of Flu** for annual **vaccine formulation**
- Supporting successful introduction of **new antivirals for Hepatitis C infections**

Challenges to global genomic surveillance

- Lack of diagnostic capabilities
- Lack of standardised case definitions and methods
- Timely communication and data sharing
- Lack of capability and skills in some areas such as bioinformatics
- Sustainability of programmes
- Integration of systems nationally and internationally

UK New Variant Assessment Platform Overview



Flagship initiative launched in April 2021 with £24M budget to deploy UK's unique genomic sequencing capabilities globally to support early detection of variants.



Comprehensive tailored programme of support offered to selected partners to strengthen their genomic sequencing capacity and capability.



Provides access to genomic sequencing capacity in the UK if no capacity in-country and support for in-country and regional hub strengthening to improve their existing capacity.



Builds institutional capacity in countries through training on variant risk assessment, bioinformatics, supplying equipment and reagents and biological assessment of variants.



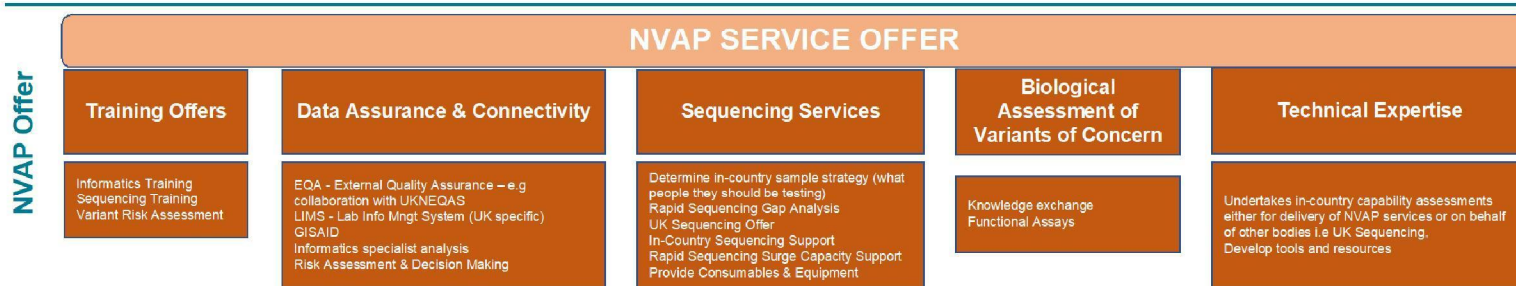
UKHSA led and working cross-HMG with DHSC and FCDO and with WHO, Ministries of Health and philanthropic organisations to coordinate global capacity building.

Sequencing capacity and capability building

NVAP Aims

- Strengthen global health surveillance
- More rapid identification of new variants

<https://www.gov.uk/guidance/new-variant-assessment-platform>



NVAP Achievements



- Strengthened sequencing capability in five countries; agreed sharing ~ 13,000 genomes.
- Sequenced ~1400 genomes in the UK for three countries detecting Delta and Omicron.
- Provided rapid UK sequencing support to Zimbabwe after Omicron and organised scientific exchanges with Zimbabwe, Namibia, Peru and Lithuania on demand.



- Trained 120 participants on variant risk decision-making to improve their variant analysis.
- Negotiated data sharing principles and material transfer agreements for UKHSA.
- Developed tools, protocols and resources on bioinformatics and wet lab sequencing.



- Engaged with over 43 countries and 23 partners & WHO, Gates and Rockefeller to support the vision of establishing a mesh network for genomic surveillance.



- Contributed to cross-HMG global engagements including briefings, roundtable, G7
- Strengthened UKHSA's genomic surveillance and adding valuable data to UKHSA databases.

Strengthening global surveillance through NVAP



Knowledge exchange and developing the science around application of genomic sequencing and surveillance for timely public health action.



Strengthening bioinformatics capability, analytics and data connectivity.



Opportunity to influence global standards, norms and quality assurance on genomic sequencing and surveillance and promoting data sharing.



Creating channels for rapid sharing of intelligence on SARS CoV-2 variants, exchanging biological materials for studies on vaccines, drugs and therapeutics.

Future

- Genomic surveillance has a clear role to play and there is a clear recognition to scale up sequencing.
- In 2021, the International Health Regulations (IHR) Emergency Committee for COVID-19 recommended increasing global sequencing capacities, encouraging the rapid sharing of data including meta-data
- How can countries balance the high cost of genomics in resource-limited settings against the value added benefits to broader public health surveillance?
- Integrated and interoperable systems including genomic surveillance with existing disease control programmes is key.

Thank you

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