£12.2 million boost for genomic surveillance to help stop transmission of COVID-19

- £12.2 million to expand whole genome sequencing to see how COVID-19 spreads and evolves
- Viral genome sequencing data increases our understanding of outbreaks and help to track patterns of infection
- This research is essential for monitoring the evolution of COVID-19 for mutations which may impact the efficacy of vaccines

The public will be better protected from COVID-19 with £12.2 million of funding awarded to potentially life-saving research into how the virus spreads and evolves through genome sequencing.

The COVID-19 Genomics UK (COG-UK) Consortium will use the funding to expand whole genome sequencing of the SARS-CoV-2 virus, the cause of COVID-19. Whole genome sequencing uses scientific techniques to read the virus’s genetic code, aiding our understanding of how the virus spreads and evolves through the study of DNA.

This means any changes to the genetic code, or mutations, can be picked up in samples from people and the environment. Tracking these changes to the genetic code helps us understand the spread of the virus which causes COVID-19.

The rising number of COVID-19 cases in the UK requires an expansion of the national SARS-CoV-2 genome sequencing capacity, to ensure that the benefits of using genome sequence data can be realised in a rapid and robust manner. The funding will facilitate the genome sequencing capacity needed to meet the increasing numbers of COVID-19 cases expected in the UK this winter.

The viral genome sequencing data will be integrated within Public Health England (PHE) and NHS Test and Trace to help understand outbreaks and strengthen infection control measures across the country to help protect the public and break chains of transmission.

Health Minister Lord Bethell said:

> This virus is the biggest public health challenge we have faced in a century. We have responded with one of the greatest collective efforts this nation has seen in peacetime. As each day passes, we are learning more and there have already been incredible advancements in science.
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> As we pull together to tackle this, it’s imperative we are on the front foot with our research. This funding is a big step forward in going further to advance our understanding of COVID-19, and help us

> protect the most vulnerable – ultimately saving lives across the world.

Linking the data from viral genome sequencing with health data of those who test positive for COVID-19 allows us to better understand how the virus may become more or less infective, or more or less harmful to those who catch it.

This vital research will also assist in developing potential vaccines in the future. Some vaccines work by targeting part of a virus’s genetic code, and by tracking changes in the genetic code, we are able to identify any changes which may affect a vaccines ability to provide protection.

This additional investment will enable COG-UK to grow and strengthen current genomic surveillance efforts spearheaded by the Wellcome Sanger Institute, PHE, and other COG-UK partners, with the aim of increasing sequencing capacity across the national network and reducing turnaround time from patient sample to genome sequence.

Professor Sharon Peacock, Director of the COVID-19 Genomics UK (COG-UK) Consortium, Professor of Public Health and Microbiology at the University of Cambridge and a Director Of Science (Pathogen Genomics) at PHE, said:

> To fully understand the spread and evolution of the SARS-CoV-2 virus, we must sequence and analyse the viral genomes. The pattern of accumulation of mutations in the genomes enables us to determine the relatedness of virus samples and define viral lineages in order to understand whether local outbreaks are caused by transmission of single or multiple viral lineages.
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> Analysis of viral genome sequences also allow us to monitor the evolution of SARS-CoV-2 and assess whether specific mutations influence transmission, disease severity, or the impact of interventions such as vaccines.

Since its launch in March 2020, COG-UK has generated and made publicly available more than 100,000 SARS-CoV-2 genomes, making up over 45 per cent of the global total. This unprecedented effort has not been achieved previously for any pathogen, anywhere in the world.

COG-UK researchers have built a central database and developed cutting-edge analytical methodology and data pipelines for SARS-CoV-2 genomics. COG-UK has led the development of analytical software to define viral lineages and shares methods globally.

Collectively, these data and tools have provided important scientific insights into the spread and evolution of the virus, at local, regional, national and international scales.

The 4 UK public health agencies and COG-UK are working to link SARS-CoV-2 genome data with epidemiological, clinical and contact tracing records nationally.

This will help establish a comprehensive national dataset linking viral sequencing with host genomics, immunology, clinical outcomes and risk factors.