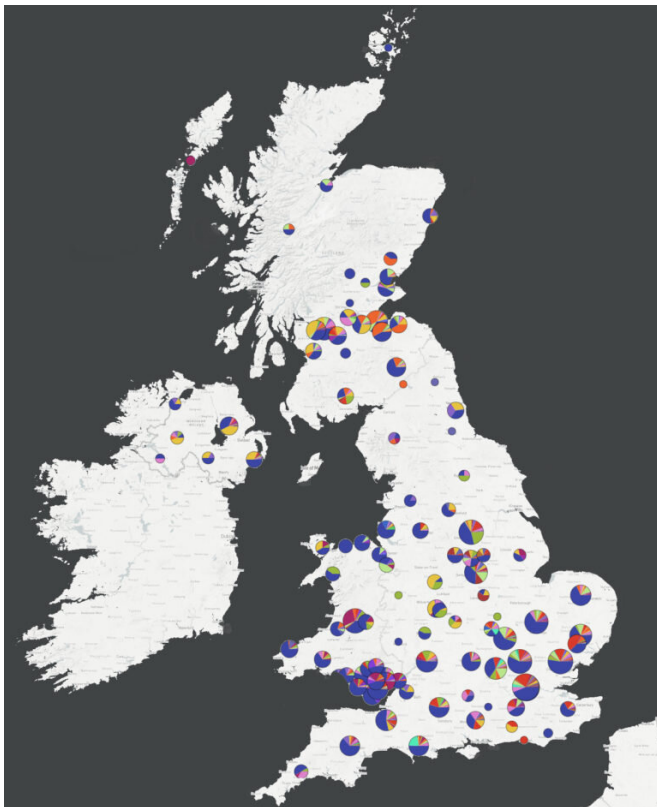


Analysis of COVID-19 genomes reveals large numbers of introductions to the UK in March

25 May 2020



Lineages assigned (using the Pangolin software; developed by University of Edinburgh) can be used to track the spread of lineages across the UK. Data are reported and visualised using Microreact (<http://microreact.org>). The map shows proportions of different lineages at each location where genomes have been sequenced by the 16 centres across the UK. Credit: The Big Data Institute

Approximately 40 lineages of the SARS-CoV-2 virus have been recorded circulating in the UK, some of which have already gone extinct while others thrive. Previously, the different lineages of the single strain of the virus entered the UK through multiple importations from around the

globe, including European countries such as Spain, Italy and France.

Now, fewer international lineages remain in the UK and new cases of COVID-19 arise from local spread rather than importation from other countries. The data reports[§], published by the COVID-19 Genomics UK Consortium (COG-UK), show the value in mapping COVID-19 lineages across the UK to understand how the virus is spreading at national, regional and local levels.

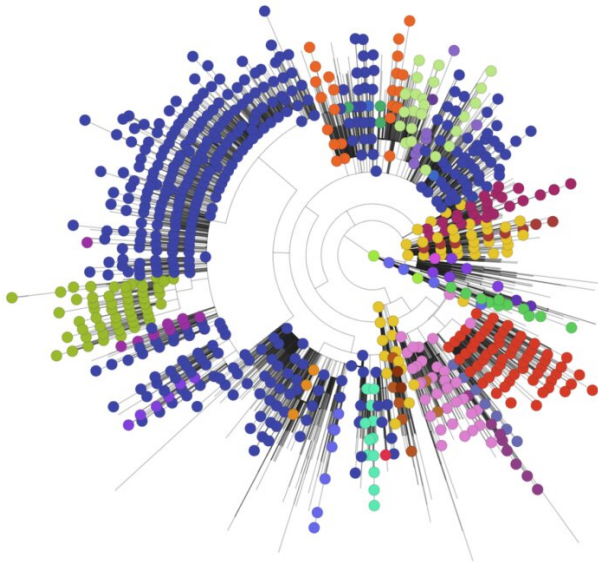
As of 22 May, more than 20,000 viral genomes from positive COVID-19 tests have been sequenced in the UK, which is the largest number of COVID-19 genomes sequenced by any single country affected by the pandemic.

These genome sequences are being generated and utilised by researchers within COG-UK to identify different lineages of the virus circulating in the UK. Despite [recent reports](#), this volume of sequencing confirms the all COVID-19 cases in the UK share a recent common ancestor from China; all cases are closely related. The lineages identified highlight small changes to the virus that enable monitoring and tracking over time, but do not signal the emergence of new strains at this point in the outbreak.

These data will aid the UK government in understanding patterns of spread in the UK to help focus different interventions in particular areas of the UK to control the spread of the virus and ultimately save lives.

The COVID-19 Genomics UK Consortium (COG-UK) – comprised of the NHS, Public Health Agencies and numerous academic and research institutions—is delivering large scale, rapid sequencing of the SARS-CoV-2 virus from positive

COVID-19 samples and sharing intelligence with hospitals, regional NHS centres and the Government.



The phylogenetic tree indicates the position of the UK genomes within a global context. Credit: The Big Data Institute

The latest COG-UK data reports show large numbers of independent introductions of the virus into the UK from around the world, resulting in approximately 40 COVID-19 lineages that are currently, or have been, circulating in the UK. However, recent data suggest new COVID-19 cases in the UK are arising from local spread rather than people travelling to the UK from other countries.

A dynamic [lineage](#) assignment method, developed within the consortium, enables monitoring of SARS-Cov2 dynamics over time within the UK, with data mapped and delivered openly through an interactive web application.

The data generated through COG-UK will be used to provide virus status reports, including estimates for the reproduction number, at the level of cities or local authorities.

"By analysing and comparing the different lineages of the SARS-CoV-2 virus that causes COVID-19 we can see how the virus is spreading through the UK, and determine whether new cases are arising from local spread versus importation from other countries. By ongoing mapping of lineages in space and time we can better understand and react to the changing dynamics of the pandemic," says Professor David Aanensen, Director of the Centre for Genomic Pathogen Surveillance at the University of Oxford Big Data Institute.

"Since starting this project in late March, this consortium has sequenced more than 20,000 viral genomes from positive COVID-19 samples. Undertaking a project of this scale is made possible by an amazing network of collaborators and our staff who have applied their world-class expertise in genomics and surveillance of infectious diseases to tackle COVID-19," says Dr. Cordelia Langford, Director of Scientific Operations at the Wellcome Sanger Institute.

"This [virus](#) is one of the biggest threats our nation has faced in recent times and crucial to helping us fight it is understand how it is spreading. Harnessing innovative genome technologies will help us tease apart the complex picture of coronavirus spread in the UK, and rapidly evaluate ways to reduce the impact of this disease on our society," says Professor Sharon Peacock, Director of the COVID-19 Genomics UK Consortium (COG-UK).

More information: COG-UK data reports for weeks 2 (1 April) and 3 (9 April) are available here: www.cogconsortium.uk/news/

Provided by Wellcome Trust Sanger Institute

APA citation: Analysis of COVID-19 genomes reveals large numbers of introductions to the UK in March (2020, May 25) retrieved 31 July 2022 from <https://medicalxpress.com/news/2020-05-analysis-covid-genomes-reveals-large.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.