

# UNDERSTANDING THE SARS-COV-2 VARIANT (B.1.1.7) IDENTIFIED IN THE U.K.

Several SARS-CoV-2 variants of concern have now been identified, including **B.1.1.7** (first identified in the U.K.), **B.1.351** (first identified in South Africa) and **P.1** (first identified in Brazil).

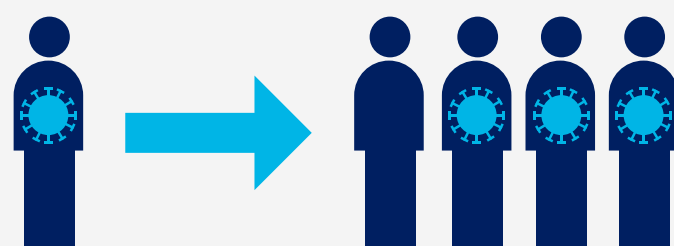
**IDENTIFYING AND CHARACTERIZING ALL NEW VARIANTS IS KEY TO INFECTION PREVENTION AND CONTROL.**

## LEARN MORE BY EXPLORING THE CASE OF THE B.1.1.7 VARIANT

### Viral genome



- **Mutations** occur occasionally when a virus infects a host and copies itself many times.
- Mutations change the genetic code (genome) of the virus.
- A **variant** or **lineage** of a virus contains a group of mutations in its genome so that it differs from that of the originally described virus.
- **Over 1000** variants of SARS-CoV-2 have been described.



This new variant is estimated to be 50-70 per cent more transmissible than pre-existing variants.



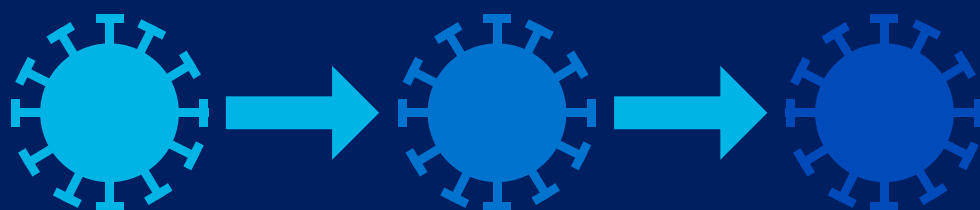
**December 2020, United Kingdom:**  
A surprising number of cases caused by the same variant are identified.



VirusSeq identification and genome sequencing results in rapid health policy decisions and strategies to minimize spread and ensure ongoing tracking across the nation.



**Mid-January 2021:**  
The variant has been detected in four provinces.



**VARIANT B.1.1.7 CONTAINS MANY MUTATIONS VS. THE ORIGINALLY DESCRIBED VIRUS AND OTHER LINEAGES CURRENTLY CIRCULATING.**