

As part of the COVID-19 pandemic response, the Public Health Agency Health Protection Surveillance team established a new surveillance system to monitor SARS-CoV-2 genomic variants.

The Surveillance team used reflex assay (genotyping) to screen for variants of concern, and used whole genome sequencing results to monitor the prevalence of genomic lineages, which provided a more detailed view of the genome. The team also used transmission chain analysis to provide predictions on potential transmission events, in order to identify the source of infection and help reduce the chance of more transmission.

During the COVID-19 pandemic, variants in Northern Ireland were identified using genomic surveillance. This information was used to advise public health action in controlling the spread of COVID-19. Screening for variants continues to be important for making informed public health decisions, particularly if we identify a variant shown to cause more severe illness, or if vaccines might not offer as much protection against a new variant.

The latest SARS-CoV-2 genomic variants data for Northern Ireland are presented in the weekly COVID-19 bulletin, which can be accessed here: [COVID-19 Epidemiological Bulletin | HSC Public Health Agency \(hscni.net\)](#)

Further information about SARS-CoV-2 variants can be found in UKHSA's reports here:

[Investigation of SARS-CoV-2 variants: technical briefings - GOV.UK \(www.gov.uk\)](#) and [SARS-CoV-2: genome sequence prevalence and growth rate - GOV.UK \(www.gov.uk\)](#)

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