

## Wellcome Genome Campus | Variant Hunters COG-Train Edit1

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Genomics is the study of an organism's complete genetic code, how it's structured, and how it functions. It can help us understand what happens to viruses like the SARS-COV-2 coronavirus and its variants. As the virus replicates, it picks up genetic changes. Genomics can be used to track these changes helping us understand how and where the virus is spreading allowing us to fight back against diseases such as COVID-19, which can threaten human lives and world economies.

I think there is a general feeling amongst those of us who are virologists and sequencing virologists that this was our time and that we needed to put everything else down and respond for a pandemic which was causing deaths in our country.

COG-UK is a consortium of people made up of the four public health agencies of the United Kingdom, numerous academic institutions across the United Kingdom together with the Wellcome Sanger Institute. We first became aware of the Alpha variant in around November 2020. If we look back in our records, we'd sequenced the first Alpha variant in September. But they were in the country in very, very low levels.

Most of the time, mutations in the viral genome are not important. Certainly, they usually don't give any advantage to the virus. But there are changes that have been emerging in SARS-COV-2 which do give the virus a distinct advantage.

We know that certain very successful viruses such as HIV and now SARS-COV-2 have higher mutation rates than you would otherwise expect in such viruses, and this causes major problems.

Genomic surveillance is important because it enables us to look at the genetic code of the virus over time. We take samples of the virus ideally over a wide geographical area, and then when we take the virus and put it into the sequencing machine, we can look at the genetic code and see what parts of the virus are changing.

So our expertise is really in interpreting the genetic data that's coming out from COG-UK sequencing centres. So we, first of all, make some of these interesting mutations or new mutations in artificial virus systems and then test the effect on the virus and its behaviour. Well, we discovered the blueprint for how variants of concern actually occur because we had the opportunity to study an individual who was infected with SARS-COV-2 for a period of about three months.

One of the unique mutations we found in the patient was a deletion of two missing amino acids in the spike protein. And we were intrigued by this so we started looking in the genome database that was curated by COG-UK. And we found huge numbers of this deletion in the UK. And then when we looked more closely at the spike sequences, they were very, very different from anything that had gone before. In other words, there was a new variant that had emerged.