**New variant of COVID-19**

**What you need to know**

You may have heard about a new variant of COVID-19 which has been seen in England. It is not unusual for viruses to change and mutate once they are more widespread in the population and it is important that we keep monitoring how the virus is behaving. Here we respond to some common questions about this new development.

**What is a new variant?**

A variant of SARS-COV-2 is a version of the virus that has undergone some genetic changes (mutations). Some mutations may change the characteristics of the virus and how it interacts with humans. We have named this VUI – 202012/01 (the first Variant Under Investigation in December 2020). We are investigating whether one of the mutations found in VUI-202012/01, called N501Y, has a potential impact on the characteristics of the SARS-CoV-2 virus.

**How was this new variant identified?**

We are closely studying the virus all the time to understand how it is behaving. Whilst investigating an increase in cases in the South of England and looking at the scientific detail of the virus, we identified this new variant of SARS-CoV-2. We are closely monitoring the spread of this variant in the UK.

**Is this new strain what caused cases in London and the South East to rise?**

While it is certainly true that we have seen high numbers of the variant virus in some areas where there is also a high incidence of COVID-19, we do not know whether the viral variant is responsible for these increased numbers of cases. It is likely that cases have increased due to changes in people’s behaviour in these areas. It is possible, but not yet proven that the new variant may have made some contribution to these increases.

**Is this new variant more serious?**

There is nothing to suggest that this variant is more likely to cause serious disease. But we’re keeping it up under close review.

**Given this is change in the spike protein, does this mean the vaccines are unlikely to protect against it?**

It is considered unlikely at this stage that the vaccine will prove to be ineffective against this variant. However, we are looking closely at this variant and will know more in the coming weeks.

**How can I protect myself against this new variant?**

Keep following all the existing advice as this spreads in the same way as the original virus - reduce your number of contacts, keep your distance from others, wear a face mask in enclosed settings, regularly wash your hands and keep areas well ventilated.

**How many cases have there been?**

We have identified over 1,000 cases with this variant, predominantly in the South of England.

**Are there other variants / mutations you are concerned about?**

The virus is under constant review and we are currently not aware of any other variants of concerns in the UK. However viruses like this one mutate regularly and most of these are of no clinical consequence.

**Is this related to the mink strain?**

No, this is a separate strain unrelated to the strain from Denmark.

**Does this virus transmit faster than other strains?**

This variant is increasing faster than some other variants that are circulating which may mean it is more transmissible but we cannot say that definitively – our investigations continue and we are working with partners including public health teams in the regions. However, the main things we all can do are to stick to the rules.

**Do the tests we use pick this variant up or is it harder to detect?**

The PCR tests use a number of gene targets. The ‘S’ gene appears to be lacking in the new variant. Labs have been instructed to avoid using assays that use S gene as a single target and replace with assays that look for at least 2 or 3 gene targets.

**Has this mutation been seen before?**

Globally, only a very small proportion (around 0.3% of confirmed cases) have a viral genome sequenced. The UK has contributed 48% of all sequences to the global database. The mutation at position 501 has been seen before in small numbers of cases in other countries. The mutation has also been seen to have arisen multiple times, in multiple places and with different mutations.

**Has it been seen anywhere else in the world?**

The global genome database, GISAID, has four reported genomes that are very similar to this variant; three of these are reported from Denmark and one in Australia. Our understanding of this globally depends on countries undertaking genomic testing and then reporting to GISAID

**What will happen next?**

This virus variant will be investigated in the laboratory to determine whether it shows increased infectivity, and whether it behaves differently in response to antibodies from people who have had prior infection or been vaccinated; this will take approximately 14 days.