



Graphic detail

Feb 27th 2021 edition

It's a family affair

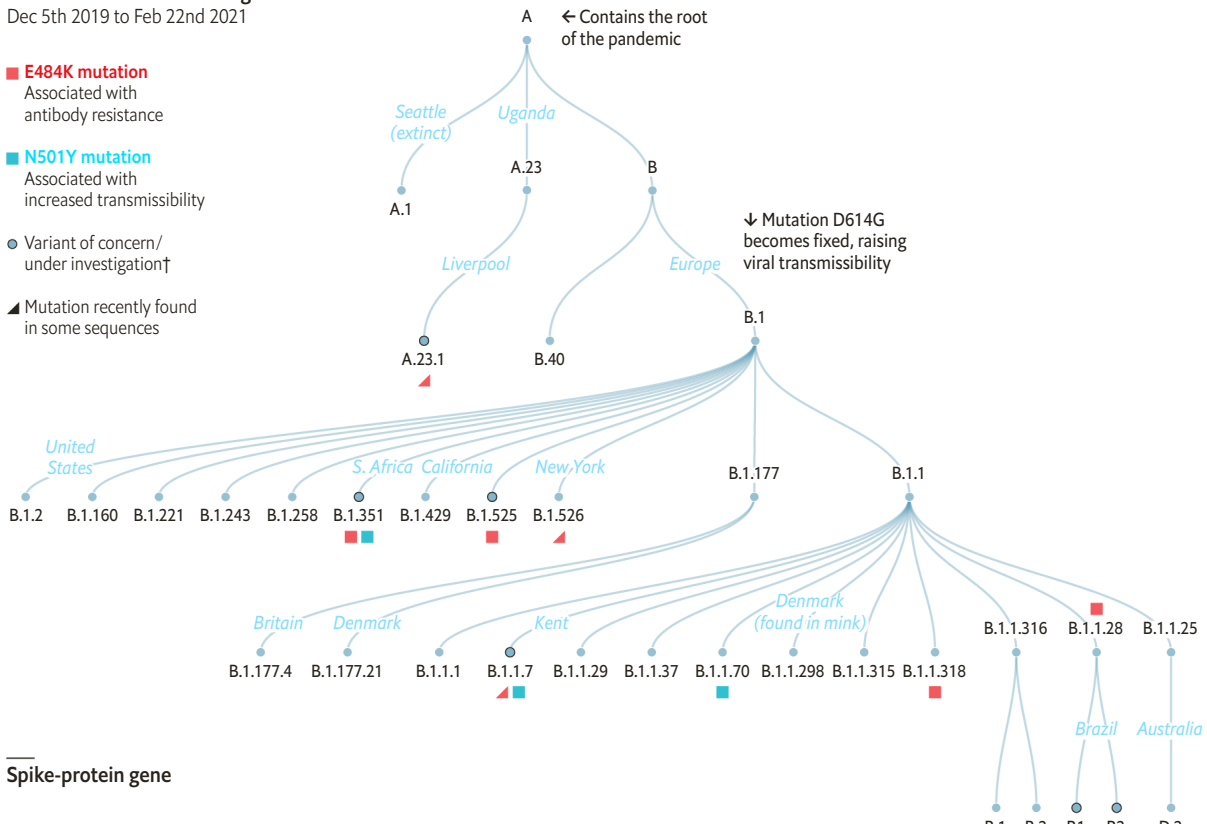
The same covid-19 mutations are appearing in different places

Convergent evolution may make travel restrictions redundant

FEB 27TH 2021

Selected SARS-CoV-2 lineages*
Dec 5th 2019 to Feb 22nd 2021

- **E484K mutation**
Associated with antibody resistance
- **N501Y mutation**
Associated with increased transmissibility
- Variant of concern/under investigation†
- ▲ Mutation recently found in some sequences



Spike-protein gene

Original ⁴⁸²GGU⁴⁸³GUU⁴⁸⁴GAA⁴⁸⁵GGU⁴⁸⁶UUU
Code for glutamic acid (E)

E484K GGU⁴⁸³GUU⁴⁸⁴AAA⁴⁸⁵GGU⁴⁸⁶UUU
Code for lysine (K)

K.1 K.2 P.1 P.2 D.2
■ ■ ■ ■ ■

*36 of 880 lineages containing 68% of all 560,000 samples designate
†By Public Health England

THE GENETIC mutations that cause evolution may arise at random. But natural selection often produces creatures that are similar, despite living in different environments. For example birds, bats, pterodactyls and insects all developed wings independently, because they were a nifty way to travel. This process is known as convergent evolution.

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Viruses evolve, too. SARS-COV-2, which causes covid-19, replicates while infecting its host. As it does, the virus's genetic information—a sequence of 30,000 RNA letters—is sometimes corrupted. These mutations can make SARS-COV-2 more dangerous in several ways. They can increase transmissibility, evade detection by tests, avoid immune responses (including from vaccines) and cause more severe illness.

This makes tracking the evolution of SARS-COV-2 crucial. Of the 110m covid-19 cases found worldwide, scientists have sequenced and published the genomes of 600,000. By comparing these sequences and other viral characteristics, evolutionary biologists create phylogenetic trees—a set of hypothetical relationships between sequences which show how the virus has evolved over time.

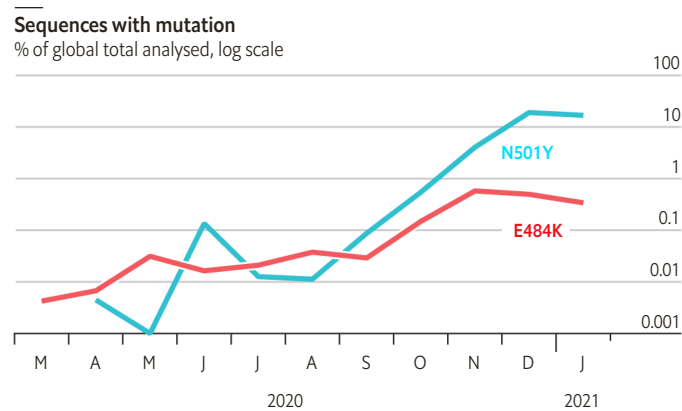
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All trees begin with an initial sample from Wuhan sequenced in January 2020, with subsequent samples as descendants. Sequences with similar new features are grouped into “lineages”, using criteria and a nomenclature developed by

researchers at the universities of Edinburgh and Oxford. So far 41,000 mutations have been documented, falling into 880 lineages.

Only a handful of these mutations make the virus more dangerous. Most occur within the 3,800 letters used for the virus's spike protein, which helps it bind to its host. Sometimes they can combine to pose several new threats, as they seem to have done in a Californian lineage that is worrying scientists. New studies suggest that this lineage may be more infectious, evade antibodies and cause more severe illness. Sequencing done in the state shows that this variant could already be responsible for a majority of cases there.

Two common mutations have appeared in many other worrying lineages. As with the wings of birds and bats, these familiar foes have evolved independently in different places. The first mutation, known as N501Y, increases transmissibility. It is present in the "Kent" lineage that has run riot in Britain since December, as well as some lineages elsewhere. The second, known as E484K, enables the virus to partially avoid the host's antibodies. It is prevalent in Brazil and South Africa. E484K has also recently been spotted in new lineages in America and Europe, including Britain.



This convergent evolution could eventually render travel bans from South America and Africa redundant. Yet E484K's sudden appearance in many places, regardless of border controls, may hold a silver lining. Far better that the virus produces a few recurrent threats than many different ones. The hope is that drug companies can tweak vaccines to zap these mutants.

More worrying is the world's lack of genetic surveillance. Though Britain has sequenced only 6% of all its cases, that is still nearly as many as the rest of the world combined. With just £32m (\$45m) of funding it can now analyse 30,000 genomes a week. America, which has sequenced just 0.4% of its covid-19 cases, is trying to speed up. The government recently released \$200m, with perhaps another \$2bn to follow. As the new threat in California shows, the world needs

such investment to keep up with natural selection. ■

Sources: "Pangolin: lineage assignment in an emerging pandemic as an epidemiological tool", by A. Rambaut et al., University of Edinburgh; CoV-GLUE, by D. Robertson et al., University of Glasgow; GISAID; *The Economist*

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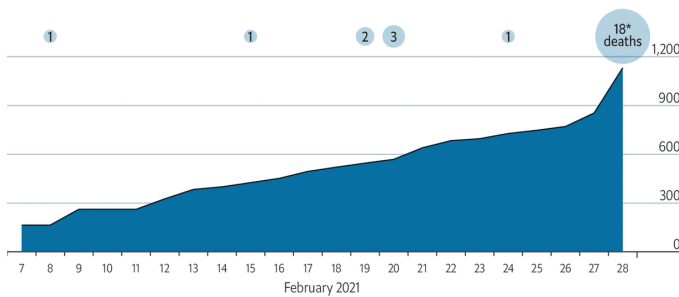
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Source: Assistance Association for Political Prisoners

*UN Human Rights Office estimate

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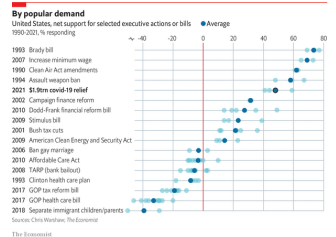
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