

# Nigerian scientists have identified seven lineages of SARS-CoV-2: Why it matters

September 7 2020, by Christian Happi

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Nigerian scientists are working to better understand coronavirus. Credit: African Center of Excellence for Genomics of Infectious Disease

By the first week of August 2020 the COVID-19 pandemic had caused about [654,000 deaths](#) worldwide. [In Nigeria](#), as of July 28, there were

38,945 confirmed cases recorded with 813 deaths.

The pandemic hit the [African continent last](#), and the numbers remain comparatively low for most countries. But there is a strong view among scientists that data recorded on the continent are an [underestimate](#) as countries struggle with testing.

As frantic work continues to [find a vaccine](#), countries like Nigeria continue to do all they can to [curb](#) the spread of the [virus](#).

In Nigeria this includes support from both the public and private sector and academia. One example of the work being done is the testing and research being undertaken at the [African Center of Excellence for Genomics of Infectious Diseases](#), Redeemer's University, Ede, Osun State. The center has been focused on infectious disease research including malaria, Lassa fever, Ebola, HIV, yellow fever, and more recently SARS-CoV-2.

Nigeria recorded its [first coronavirus infection](#) on February 27, 2020, through an Italian immigrant whose samples were sent to the African Center of Excellence for Genomics of Infectious Diseases by the Nigerian Center for Disease Control for genome sequencing. As a result of this work, the [first SARS-CoV-2 sequence data](#) on the African continent was published on March 6, 2020.

Genome sequencing helps us understand the virus, its epidemiology and evolution. Globally, there is only one strain of SARS-CoV-2, which is also the same as the strain circulating in Nigeria. However, there are more than [1,000 lineages](#) of this novel virus in circulation around the world.

Lineage classification is based on [mutations](#) or genetic variants that connect the ancestral type to the genetics of the descendants, which do

not change the physiology of the virus.

Basically, viral lineages are formed when mutations occurring do not change the encoded viral protein. However, any mutation that leads to a change in viral pathogenicity, virulence or immunogenicity, will become a new strain.

If a mutation affects the part of a virus that the immune system uses to neutralize the virus, this then becomes a strain that can infect people previously infected or vaccinated. An example of this occurs with the flu virus, which is why a new vaccine is needed for the seasonal flu each year.

We have so far [identified seven](#) of these over 1,000 lineages in Nigeria. Each lineage represents sequences from different countries.

## **The lineages**

Some of the lineages have overlapping sources of origin.

The first lineage represents viral sequences from China and global exports including South East Asia, Japan, South Korea, Australia, the US and Europe.

The second lineage represents a viral sequence from the Italian outbreak. The third represents a new European [lineage](#). The fourth represents sequences from the UK, Iceland and Turkey.

The fifth represents sequences from Netherlands, Turkey, Saudi Arabia, Egypt, Finland and England. The sixth represents a sequence from the Netherlands. The seventh represents sequences from Turkey, Saudi Arabia, Egypt, Finland and England.

The lineages identified in Nigeria are not different from the ones identified in other parts of the world and there are no reports of [strains](#) or lineages unique to Nigeria thus far.

The number of lineages circulating in Nigeria will be updated as we generate more sequence data, taking into consideration the current evidence of community transmission.

It is important to track lineages as they can be very useful for determining how a virus spreads through communities or populations. This means that if a new strain should appear, scientists would have important information needed to contain it. This is especially important for the African region because if the new strain happened to be more virulent, or more transmissible, it would put great pressure on weak health systems.

## **What a mutation in SARS-CoV-2 could mean**

A mutation in SARS-CoV-2 could confer an advantage to the virus. For instance, a virus with an advantageous mutation could affect humans more readily, thereby spreading more easily between people; it could be less recognized by the immune system, or more pathogenic.

[Recent reports](#) suggest that new SARS-CoV-2 "strains" have arisen through mutation that have the potential to increase the severity of the pandemic.

[A study](#) analyzed a set of mutations in the spike protein of SARS-CoV-2, and concluded that a specific mutation had increased in frequency as the virus spread from China into Europe, North America, and Australia. The authors concluded that this increase in frequency arose because the mutation had made the virus more transmissible.

Scientists in Nigeria, as elsewhere, have been tracking these developments very closely. There is a [trend](#) in the increase in the number of this spike protein mutation in Nigeria.

## Why it matters

Continuous monitoring of viral genetic changes or mutations is important as it provides valuable information on the evolution of the virus and its implications.

If a mutation occurs in the region of the virus that was used to develop the vaccine, the vaccine will not be as effective. This is what happens in the case of flu vaccines because the virus keeps mutating into a new strain.

We do not know much about SARS-CoV-2 yet. And we don't know if the virus will mutate into a new strain down the line. If it does happen, it could require the development of a new vaccine.

Nothing can be done to prevent viruses from mutating. They do so naturally as a survival strategy. These mutations happen when the virus makes an error when its DNA or RNA is being replicated, or due to selective pressure.

Currently, researchers are working to determine how many medically relevant strains of SARS-Cov-2 are circulating and what the consequences are for treatment and vaccine development.

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