20200604 - Frederico Santos
20200613 - Tiago Ramos
20200994 - Rupesh Baradi

WHAT IS A SARS-COV-2 VARIANT OF CONCERN?

INTRODUCTION

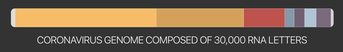
Conversations surrounding the concern for emerging variants of SARS-CoV-2, the virus that causes COVID-19, have been increasing rampantly since the turn of the year 2021.

This infographic explores the terminology, understanding, and general knowledge of this emerging subject, tracking and visualizing the global growth, spread, and probable impact of the three current variants of concern (VOC).

WHAT IS A MUTATION, VARIANT, STRAIN?

Confusion regarding these terms is commonplace.

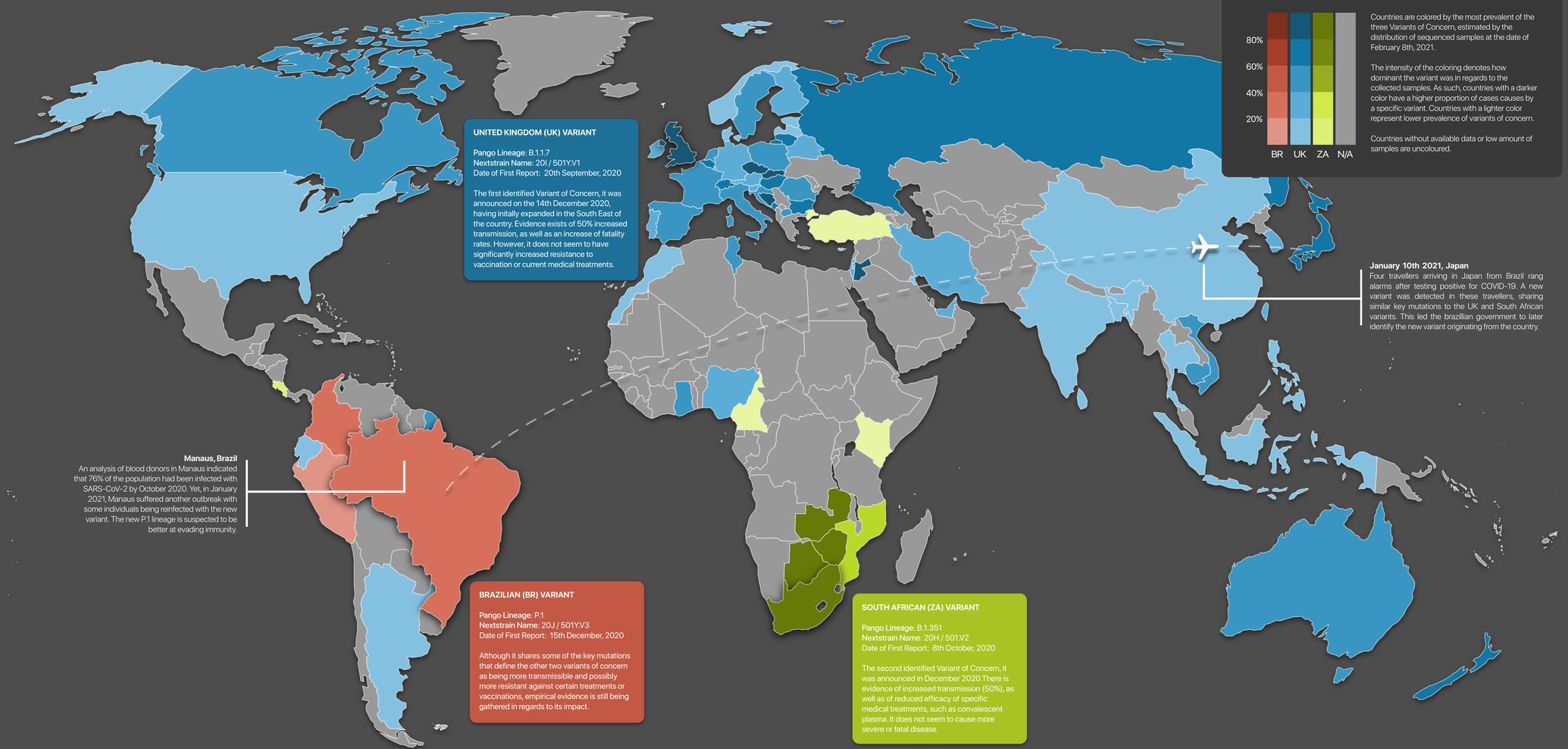
The genetic material of SARS-CoV-2 is called ribonucleic acid (RNA). Instructions for the virus to replicate are encoded in 30,000 "letters" of RNA — a, c, g and u — which the infected cell reads and translates into many kinds of virus proteins.



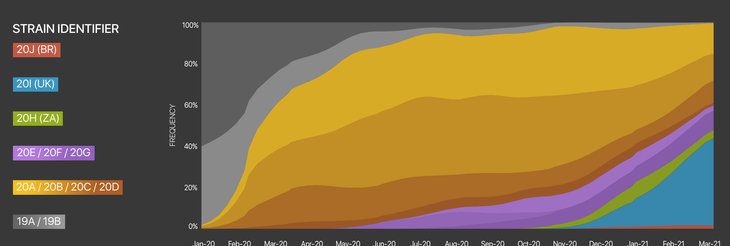
CORONAVIRUS GENOME COMPOSED OF 30,000 RNA LETTERS

Small errors originate in the process of duplicating RNA, generating a non-exact copy of the sequence. These are the so-called mutations, characterized by the different letters in the sequence. Despite this, viruses with mutations can still retain the parent's properties and behave exactly like the original virus - these are called silent mutations.
As time passes, the genome for the virus acquires many documented mutations. Some such mutations significantly alter the virus' properties or behavior, originating a new strain of the virus. Some of these altered properties may translate to higher transmissability, altered resistance to medical treatment, or even an increased severity of the disease. This has been the case with some recently detected strains (named Variants of Concern).

Because of these threats, sequencing, closely monitoring, and documenting these mutations is paramount to combat the ongoing pandemic, including preparing and containing potentially dangerous strains.



FREQUENCIES BY LINEAGE



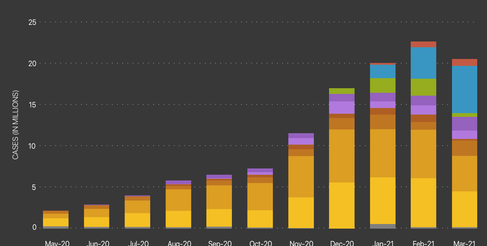
VARIANT 19A / 19B

The initial strains mutated quickly, giving way to the more stable and dominant 20A and 20B strains which accounted for about of 60% of all collected sequences in 2020. This is aligned of the observation of slower rate of mutation of the SARS-CoV2 virus when compared to other flu-like virus.

VARIANT 20A / 20B / 20C / 20D

The virus remained relatively stable during 2020, with no new major variants being detected. Moreover, they did not significantly alter key characteristics of the disease such as vaccine immunity, transmissability, or lethality.

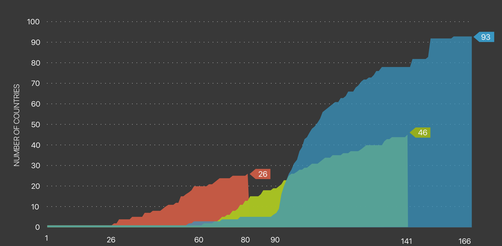
ESTIMATED DISTRIBUTION OF VARIANTS ON ACTIVE GLOBAL CASES



VARIANT 20I (UK)

After being first detected, the UK strain spread unlike any other so far. By March 1st, sequences of the UK variant accounted for an estimed 44% of active cases, signalling an extreme growth not characteristic of the virus' pattern of stable and slow mutation.

GLOBAL SPREAD OF VARIANTS OF CONCERN



The growth and spread of these variants seems linked to the severity of lockdown measures. After weeks of contained spread, the UK variant's worldwide presence exploded, increasing its presence sevenfold over the course of late December. This is indicative of the increased travel and exposure during this time, but is also a consequence of the increased transmissability of this strain. The Brazillian and South African variants show similar growth to each other (roughly 3.5 new countries per week), despite the Brazillian strain spreading earlier.

sources