

SARS-CoV-2
Genomic
Variation -
African
perspective

Sep 26, 2020

SARS-CoV-2 Genomic Variation - African perspective

Olabode Omotoso¹

¹University of Ibadan

1 Works for me dx.doi.org/10.17504/protocols.io.bmpfk5jn

Cancer Research and Molecular Biology Laboratories, University of Ibadan

Olabode Omotoso

ABSTRACT

This protocol outlines the methodology for the acquisition and analysis of SARS-CoV-2 genomic sequences.

ATTACHMENTS

[SARS-CoV-2 Genomic
Variation - African
Perspective.pdf](#)

DOI

dx.doi.org/10.17504/protocols.io.bmpfk5jn

PROTOCOL CITATION

Olabode Omotoso 2020. SARS-CoV-2 Genomic Variation - African perspective. **protocols.io**
<https://dx.doi.org/10.17504/protocols.io.bmpfk5jn>

KEYWORDS

SARS-CoV-2 , genomic variation

LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Sep 24, 2020

LAST MODIFIED

Sep 26, 2020

OWNERSHIP HISTORY

Sep 24, 2020  Emily Hasser  Cornell University

Sep 26, 2020  Olabode Omotoso

PROTOCOL INTEGER ID

42439

Data Acquisition

1 

Mine and analyze SARS-CoV-2 genomic sequences from the Global Initiative on Sharing All Influenza Data (GISAID) database ([epicov.org](https://www.gisaid.org/)). Use sequences filtered as “high coverage only, Homo sapiens, complete, all clades and low coverage excl”, with patient’s status, “Africa”.

2 

Obtain the patient's age of all the sequences to determine the age distribution of the infected patients.

3 

Obtain country data of the number of confirmed cases, recoveries, reported deaths due to COVID-19 from Worldometer (worldometers.info) and WHO database (covid19.who.int).


4 

Obtain the number of tests done per country and each nation's population from the Worldometer database.


5 

Obtain the age distribution of countries with the highest prevalence of COVID-19 cases from the World Factbook (www.cia.gov).

Sequence and Mutational Analysis

6 

Use the mined SARS-CoV-2 viral sequences to analyze the genomic variability since the index case of the COVID-19 pandemic in Africa in February 2020 to identify the frequency and spread of mutations in the African population.

7 

Assess and evaluate the evolution of the COVID-19 outbreak with respect to the transmission in the mutational hotspots on the GISAID web interface (www.epicov.org). Focus on recurrent mutations observed as they are likely to confer viral-host structure-function relationship promoting higher transmission rate.

Determination of Testing, Fatality and Recovery Rate

8 

Determine the testing rate for each African country as a percentage of the total test done from the country's population.



Testing Rate (%) =
(Total COVID-19 tests done/Country's population) x 100

9 

Determine the fatality rate as a percentage of total reported deaths due to COVID-19 from each country's number of confirmed cases.



Fatality Rate (%) =
(Total number of COVID-19 deaths reported/Number of confirmed cases) x 100

10



Determine the recovery rate as a percentage of the number of infectious patients who recovered from all reported confirmed cases in each country.



Recovery Rate (%) =
(Total number of COVID-19 infected patients who recovered/Number of confirmed cases) x 100