**Article title:** Life Expectancy and SARS-CoV-2 Genomic Variations Plays Key Role in COVID-19 Transmission and Low Fatality Rate in Africa

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Life Expectancy and SARS-CoV-2 Genomic Variations Plays Key Role in COVID-19 Transmission and Low Fatality Rate in Africa

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Abstract
The novel coronavirus disease (COVID-19) has claimed lots of lives, posing a dire threat to public health and the global economy. The present study determined the severe acute respiratory syndrome-2 (SARS-CoV-2) genomic variability and the contributory factors to the observed low fatality rate in Africa. To assess the SARS-CoV-2 mutational landscape, 924 viral sequences from the Africa region with their sociobiological characteristics mined from the GISAID database were analyzed. The age of infected patients, the number of tests done, confirmed cases, recovery, fatality, and countries' age distribution were obtained to determine the age distribution, testing, recovery, and fatality rate. Mutational analysis of the SARS-CoV-2 sequences revealed highly recurrent mutations in the Spike glycoprotein D614G (97.2%), concurrent R203K, and G204R (65.2% respectively) in the N protein region, and P4715L (97.2%) in the RNA dependent RNA polymerase region. COVID-19 is more severe in older people (> 65 years), Africa has a low percentage of people within this age group (4.36%). The average age of the 924 infected patients in this study is 46 years with only 47 infected patients (5.1%) above 65 years in comparison to 13.12% in countries in other continents with the highest prevalence of COVID-19. Africa's young generation, the late incidence of the disease, and adherence to public health guidelines are important indicators that may have contributed to the observed low COVID-19 deaths in Africa. However, sufficient data is still unavailable due to low testing rate to ascertain the epidemiology, transmission, genomic variation, and the true impact of the pandemic in Africa.

Keywords: Coronavirus, mutations, low fatality, SARS-CoV-2, pandemic, Africa.
**Introduction**

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative pathogen of the novel coronavirus disease 2019 (COVID-19) was first reported in December 2019 in Wuhan, China [1,2]. The highly infectious SARS-CoV-2 has spread globally within 3-months of its first outbreak and has posed dire stress on public health and global economy [1,3].

Globally, as of September 13, 2020, there have been 29,474,968 confirmed cases and 933,423 reported deaths due to COVID-19 [4]. It was predicted that the coronavirus outbreak in the African population would be very lethal and result to economic devastation owing to the prevalence of immune-compromised population (due to HIV/AIDS, tuberculosis, hepatitis virus, malaria etc.), poverty, low lifespan, fragile health care systems, poor economic decisions, and lifestyle factors [3,5]. Africa was the last continent to be hit, and surprisingly boast of about 80% recovery rate as at this stage of the pandemic [6]. Africa accounts for 3.5% of the fatality rate recorded globally with the highest death toll reported in Americas (55.1%) and Europe (25.7%) which are developed regions with high standard of living and healthcare structure [6,7]. In line with public health and World Health Organization guidelines, African governments and policy-makers were quick to institute policies (restrictions such as partial/full-scale lockdowns, physical distancing, accelerated contact tracing, self-isolation and quarantine) and adopt public health measures in light of the index case in the continent [7–9]. Africa’s index case of COVID-19 was on 14th of February, 2020 in Egypt [10], North Africa, and on 27th of February, Nigeria, sub-Saharan Africa reported its index case from an European traveller [11]. As of September 13, 2020 there have been 1,359,569 confirmed cases and 32,678 deaths in Africa, out of which South Africa has the highest toll with 649,793 confirmed cases and 15,447 deaths [4].

Coronaviruses are single-positive-stranded RNA viruses with the largest genome (ranging from 26 to 32 kb) among all RNA viruses consisting of ORF1ab polyprotein (7096 amino
acids), ORF3a (276 aa), ORF6a (62 aa), ORF7a (122 aa), ORF7b (44 aa), ORF8 (64 aa), ORF10 (39 aa) and four structural proteins; nucleocapsid phosphoprotein (N), membrane protein (M), envelope protein (E), and the spike glycoprotein (S) [1,12–14]. Accumulation of mutation is central to viral evolution, transmission and virulence. This gives virus selective advantage for host invasion and adaptation, higher transmissibility of more virulent strains and drug resistance [9,14,15]. Identifying the mutational pattern of coronaviruses and monitoring their spread can be important in guiding drug/vaccine development, and in making decisions to curtail the transmission [16]. The present study aims to gain insight into the mutational landscape of the SARS-CoV-2 genome in African population which may serve as eventual targets for drug design and/or vaccine development. This study also assesses the contributory factors to the low fatality rate due to COVID-19 in the African continent.
Materials and methods

Data acquisition

A total of 924 available SARS-CoV-2 genomic sequences in Global Initiative on Sharing All Influenza Data (GISAID) database as of September 2, 2020 filtered as “high coverage only, Homo sapiens, complete, all clades and low coverage excl”, with patient’s status, Africa were mined from the GISAID web interface (https://www.epicov.org/epi3/frontend) and analyzed. Patient’s age of all the sequences were also obtained to determine the age distribution of the infected patients. The accession numbers and laboratories in Africa that sequenced and deposited complete SARS-CoV-2 genomes on the GISAID database used in this study are provided as Supplementary file S1.

Country data of number of confirmed cases, recoveries, reported deaths due to COVID-19 were obtained from Worldometer and WHO database [4,7]. The number of tests done per country and each nation’s population was obtained from worldometer database [4]. The age distribution of countries with highest prevalence of COVID-19 cases were obtained from the World Fact book [17].

Sequence and mutational analysis

In this study, the mined 924 SARS-CoV-2 viral sequences were used to analyze the genomic variability since the index case of COVID-19 pandemic in Africa in February 2020 to identify the frequency and spread of mutations in the African population. The evolution of COVID-19 outbreak with respect to the transmission in the mutational hotspots was assessed and evaluated on the GISAID web interface (https://www.epicov.org/epi3/frontend). Recurrent mutations observed were focused on as they are likely to confer viral-host structure-function relationship promoting higher transmission rate.
Determination of Testing, Fatality and Recovery Rate

The testing rate was determined for each African country as percentage of total test done from the country’s population. The fatality rate was determined as percentage of total reported deaths due to COVID-19 from each country’s number of confirmed cases. The recovery rate was determined as percentage of number of infectious patients who recovered from all reported confirmed cases in each country.
Results

Genomic variabilities dispersed at various sites in the SARS-CoV-2 sequence were observed, few mutations occurred more frequently (represented as Table 1). Mutational analysis of the 924 SARS-CoV-2 sequences revealed highly recurrent mutations in D614G (898 viral sequences) which falls in the S glycoprotein region, and was observed concurrently with P4715L variant (898 viral sequences) in the ORF1ab polyprotein region. More so, R203K and G204R mutations (602 viral sequences respectively) in the nucleocapsid phosphoprotein region, Q57H (60 viral sequences) in the ORF3a region, L84S (16 viral sequences) in the ORF8 region and L3606F (45 viral sequences), G3278S (73 viral sequences), T265I (26 viral sequences) in ORF1ab polyprotein region were observed. It is worthy of note, 97.3% of viral sequences with the nsp5 G3278S mutation were from South Africa. The distribution of the mutations flags the Spike S1 domain (D614G), N protein R203K and G204R and nsp12 P4715L as SARS-CoV-2 mutational hotspots in the African population. According to mutational pattern, the viral sequences were characterized into the GISAID six (6) clades; GR (598), G (240), GH (57), S (16), O (7), V (4) and L (2).

For the age distribution, the average age of the infected patients is 46 years with only 47 infected patients (5.1%) above 65 years. According to demographic data from world fact book, the percentage of population of Africans ≥ 65 years is 4.36% in comparison to 13.12% in countries in other continents with highest prevalence of COVID-19 (as shown in Figure 1). As at this stage of the pandemic, Africa still face the challenge of low testing as none of the African countries meet up with the 15% testing rate standard, as South Africa has the highest testing rate (6.59%) in Africa. Nevertheless, there is a high recovery rate and low fatality rate observed across the Africa continent. The trend and distribution of confirmed cases, discharged cases, fatality and recovery rate are as shown in Table 2.
| S/N | SARS-CoV-2 region                  | Mutation observed | Occurrence |
|-----|-----------------------------------|-------------------|------------|
| 1   | Spike protein; S1 domain          | L18F              | 2          |
| 2   |                                   | A222V             | 4          |
| 3   |                                   | D614G             | 898        |
| 4   | Spike protein; S2 domain          | E780Q             | 2          |
| 5   | Nucleocapsid phosphoprotein       | P13L              | 2          |
| 6   |                                   | R203K             | 602        |
| 7   |                                   | G204R             | 602        |
| 8   | ORF3                              | Q57H              | 60         |
| 9   |                                   | G251V             | 4          |
| 10  | ORF8                              | L84S              | 16         |
| 11  | ORF1ab; nsp2                      | T265I             | 26         |
| 12  |                                   | D448del*          | 6          |
| 13  |                                   | I739V             | 3          |
| 14  |                                   | P765S             | 3          |
| 15  | ORF1ab; nsp5                      | G3278S            | 73         |
| 16  | ORF1ab; nsp6                      | L3606F            | 45         |
| 17  | ORF1ab; RdRp                      | A4489V            | 3          |
| 18  |                                   | P4715L            | 898        |

Highly recurrent mutations were observed in the spike protein, nucleocapsid phosphoprotein and ORF1ab, flagging these regions as SARS-CoV-2 mutational hotspots.

*Key: RdRp – RNA dependent RNA polymerase. One letter code for corresponding amino acid: A – alanine, D – aspartic acid, G – glycine, E – Glutamate, R – arginine, K – lysine, Q – glutamine, H – histidine, V – valine, L – leucine, S – serine, T – threonine, I – isoleucine, P – proline, and F – phenylalanine.
Table 2. Trend and distribution of confirmed cases, discharged cases and fatality rate across Africa

| S/No | Country      | Confirmed cases | Total deaths | Recovered cases | Total test done | Population     | Testing rate | Fatality rate | Recovery rate |
|------|--------------|-----------------|--------------|-----------------|-----------------|----------------|--------------|---------------|---------------|
| 1    | South Africa | 649,793         | 15,447       | 577,906         | 3,918,478       | 59,461,240     | 6.59%        | 2.38%         | 88.94%        |
| 2    | Egypt        | 101,009         | 5,648        | 84,161          | 135,000         | 102,722,504    | 0.13%        | 5.59%         | 83.32%        |
| 3    | Morocco      | 86,686          | 1,578        | 67,528          | 2,230,069       | 36,999,965     | 6.03%        | 1.82%         | 77.90%        |
| 4    | Ethiopia     | 64,301          | 1,013        | 24,983          | 1,138,012       | 115,528,092    | 0.99%        | 1.58%         | 38.85%        |
| 5    | Nigeria      | 56,256          | 1,082        | 44,152          | 440,248         | 207,152,368    | 0.21%        | 1.92%         | 78.48%        |
| 6    | Algeria      | 48,254          | 1,612        | 34,037          | 44,010,565      | 3.34%          | 70.54%       |               |               |
| 7    | Ghana        | 45,434          | 286          | 44,342          | 450,872         | 31,202,737     | 1.44%        | 0.63%         | 97.60%        |
| 8    | Kenya        | 36,157          | 622          | 23,067          | 481,982         | 54,007,662     | 0.89%        | 1.72%         | 63.80%        |
| 9    | Libya        | 22,781          | 362          | 12,183          | 157,481         | 6,890,311      | 2.29%        | 1.59%         | 53.48%        |
| 10   | Cameroon     | 20,167          | 415          | 18,837          | 149,000         | 26,676,814     | 0.56%        | 2.06%         | 93.41%        |
| 11   | Ivory Coast  | 19,013          | 120          | 18,112          | 142,248         | 26,507,763     | 0.54%        | 0.63%         | 95.26%        |
| 12   | Madagascar   | 15,757          | 211          | 14,368          | 64,174          | 27,831,811     | 0.23%        | 1.34%         | 91.18%        |
| 13   | Senegal      | 14,280          | 297          | 10,520          | 158,751         | 16,831,055     | 0.94%        | 2.08%         | 73.67%        |
| 14   | Zambia       | 13,539          | 312          | 12,260          | 131,034         | 18,485,203     | 0.71%        | 2.30%         | 90.55%        |
| 15   | Sudan        | 13,516          | 835          | 6,757           | 44,052,920      | 49.99%         | 6.18%        |               |               |
| 16   | DRC          | 10,390          | 264          | 9,756           | 90,093,630      | 2.54%          | 93.90%       |               |               |
| 17   | Guinea       | 10,045          | 63           | 9,292           | 28,140          | 13,203,001     | 0.21%        | 0.63%         | 92.50%        |
| 18   | Namibia      | 9,719           | 101          | 6,543           | 80,352          | 2,550,174      | 3.15%        | 1.04%         | 67.32%        |
| 19   | Gabon        | 8,643           | 53           | 7,706           | 135,615         | 2,236,175      | 6.06%        | 0.61%         | 89.16%        |
| 20   | Zimbabwe     | 7,526           | 224          | 5,678           | 154,733         | 14,906,868     | 1.04%        | 2.98%         | 75.45%        |

This shows the countries with highest prevalence of COVID-19 in Africa, the data for all African countries is available as Suppl. file S2. The fatality due to COVID-19 in Africa is 2.4% with 81.21% recovery rate. South Africa has the highest COVID-19 testing rate (6.59%) in Africa.
Figure 1a-e. Age distribution of African countries in comparison with nations from other continents with the highest prevalence of COVID-19. This reveals a high prevalence of younger generations in Africa (0-14 years), with equilibrium at age range 15-54 years when compared to older population (≥55 years) in other regions studied with high COVID-19 prevalence.
Discussion

As of September 5, 2020, over 705 million people in the world live in extreme poverty compared to about 651 million people in 2019 [5]. In 2020, 102,125,917 people are reported to be living in extreme poverty from a total population of 205,323,504 people in Nigeria, the most populous African nation compared to 200,369,248 people, among whom 92,441,550 people lived in extreme poverty in 2019 [5]. The COVID-19 has significantly ravaged economies and posed serious threat to public health and social interaction, spreading across the globe within 3 months of its outbreak [3]. It was hypothesized that low- and middle-income countries, especially African nations would be seriously hit by the pandemic due to her vulnerability to infectious diseases and inadequate health structure. Surprisingly, there have been very low mortality rate due to COVID-19 in African nations when compared to developed nations in the Americas and Europe where the pandemic has had its highest toll of infection and fatality [7]. This study assessed the possible factors that could have accounted for the low mortality rate due to COVID-19 in Africa.

The dataset from infected patients helps to understand the COVID-19 infection rate, risks, epidemiology and spread of the disease. The WHO suggested 10 – 30 tests per confirmed case as an indicator of adequate testing [7]. South Africa has the highest test rate of 3,918,478 people in Africa, representing 6.59 % of its 59,461,240 population, which is still a way long off from the adequate testing indicator. Meanwhile, Nigeria has only tested 440,248 people representing 0.21% of its over 207 million population, this trend holds true for many other African countries. Hence, caution should be taken while interpreting these data as the true number of COVID-19 cases in Africa might still remain undetected. However, with the current data available, though with daily increasing incidence, the mortality rate due to COVID-19 in Africa has been minimal. Other factor such as late incidence of the disease [10,18], which gives an advantage for early preparation before the outbreak by enforcing
regulatory guidelines (active surveillance, isolation, quarantine, contact tracing and social distancing among others) in line with World Health Organization guidelines could have played a key role in managing the pandemic in Africa [7,8]. The APM Research laboratory carried out an extensive study in August, 2020 which identified 88.4 deaths per 100,000 Black Americans compared to 54.4 deaths per 100,000 Latino Americans and 36.4 deaths per 100,000 Asian Americans suggesting higher mortality due to COVID-19 in the latter [19]. This raises a concern to understand why Blacks are dying more due to COVID-19 overseas than in Africa.

The present study also looked into the mutational landscape of SARS-CoV-2 genome in Africa. Highly recurrent mutation (D614G) was observed in the S1 domain of S glycoprotein which facilitates viral entry into host by binding to the human angiotensin-converting enzyme2 (ACE2) receptor. The S2 domain of the S glycoprotein which plays a crucial role in viral-host cell membrane fusion was well conserved; this could serve as an important target for antiviral drug design. The T265I mutation that is prevalent in USA which aids SARS-CoV-2 survival in the host cell [20] was only observed in 26 viral sequences, predominantly in Senegal (69.23 %). P4715L mutation hotspot present in the RNA dependent RNA polymerase (RdRp) region was first observed in Italy during the sporadic increase in incidence and fatality of COVID-19 in Europe [15]. This supports the evidence that most Africa’s index case originates from European and American travellers [3,18], which could have resulted to the vast distribution of these mutations across the infected patients.

The concurrent R203K and G204R mutation are present in the N phosphoprotein region, which plays an important role in viral interaction with the M protein during virion assemblage [21]. Mutations in the nucleocapsid region alter miRNAs binding, which might contribute to the pathogenesis and progression of infection in the patient [22]. The viral ORF3a and ORF10 proteins can synergistically attack heme on the host’s hemoglobin 1-β
chain, thereby disintegrating iron to form porphyrin. This results to reduced hemoglobin carrying oxygen and carbon-dioxide causing extreme poisoning and inflammation of the hepatocytes [23]. Q57H mutation in the ORF3a region was observed to coincide with D614G and P4715L variants. The RdRp P4715L mutation coincides with S protein D614G mutation alongside the concurrent N protein R203K and G204R variants, and in their absence ORF3a Q57H variant. The SARS-CoV-2 membrane, envelope, ORF6, ORF7 and ORF10 proteins were well conserved. These mutational hotspots and conserved domains must be well-considered during drug or vaccine design to avoid vaccine evasion and drug resistance.

Lastly, this study looked at the age distribution of the infected patients as a contributory factor to the low fatality rate. The average life expectancy in Nigeria is 54 years, a reflection of Sub-Saharan Africa (61 years) compared to European union (81 years), China (77 years), and USA (79 years) [24]. Earlier report [3] suggests that COVID-19 have high mortality and severity in older people (>65 years) than the younger population, which have high chances of recovery from the infection. From this study, only 5.1 % of the 924 infected Africans whose age are deposited alongside their viral sequences in the GISAID repository are over 65 years. This could have played a major role in the relatively high recovery rate (81.21 %) and low mortality (2.4 %) due to COVID-19 observed in the African population.

**Conclusion and perspective**

As of now, the highly infectious COVID-19 continues to spread globally, with increasing incidence and mortality. The African continent continues to enjoy the benefit of the swift actions and policies imposed to curtail the pandemic. With the gradual easing of these measures, increasing poverty, poor healthcare structure and a large percentage of immune-compromised population, it is important that the populace adhere to regulatory guidelines. Low life expectancy, low testing rate, late incidence of the disease, adherence to public health
guidelines could be important factors that have contributed to the observed low COVID-19 fatality in Africa. However, sufficient data is still unavailable to ascertain the epidemiology, transmission, genomic variation and the true impact of the pandemic in Africa. Genomic sequences are important in the design and development of antiviral drugs and vaccine. From the over 100,000 complete SARS-CoV-2 sequences available in public repositories, Africa has barely contributed over 2,000 viral sequences (2 %). Collaboration with scientists and research institutes in African nations is highly recommended so as to enhance their delivery capacity.

**Conflict of interest**

None

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**References**

1. Wang H, Li X, Li T, Zhang S, Wang L, Wu X, et al. The genetic sequence, origin, and diagnosis of SARS-CoV-2. Eur J Clin Microbiol Infect Dis. 2020;(China CDC). doi:10.1007/s10096-020-03899-4.

2. WHO. Coronavirus disease (COVID-19) pandemic. 2020.

https://www.who.int/emergencies/diseases/novel-coronavirus-2019. Accessed 13
August 2020.

3. Lone SA, Ahmad A. COVID-19 pandemic – an African perspective. Emerg Microbes Infect. 2020;9:1300–1308.

4. Coronavirus Update (Live): 29,474,968 Cases and 933,423 Deaths from COVID-19 Virus Pandemic - Worldometer. https://www.worldometers.info/coronavirus/. Accessed 12 September 2020.

5. World Poverty Clock. https://worldpoverty.io/headline. Accessed 5 September 2020.

6. Coronavirus Disease 2019 (COVID-19) – Africa CDC. https://africacdc.org/covid-19/. Accessed 5 September 2020.

7. WHO Coronavirus Disease (COVID-19) Dashboard | WHO Coronavirus Disease (COVID-19) Dashboard. https://covid19.who.int/. Accessed 3 September 2020.

8. COVID-19 in Africa: marking six months of response | WHO | Regional Office for Africa. https://www.afro.who.int/covid-19-africa-marking-six-months-response. Accessed 4 September 2020.

9. Omotoso O, Babalola D, Matareek A. Mutational Analysis of SARS-CoV-2 in African Population. bioRxiv. 2020. doi:10.1101/2020.09.07.286088.

10. COVID-19 cases top 10 000 in Africa | WHO | Regional Office for Africa. https://www.afro.who.int/news/covid-19-cases-top-10-000-africa. Accessed 3 September 2020.

11. Nigeria Centre for Disease Control. https://ncdc.gov.ng/news/227/first-case-of-coronavirus-disease-confirmed-in-nigeria. Accessed 3 September 2020.

12. Muhammad TQ, Safar AM, Alamri L-LC. Structural basis of SARS-CoV-2 3CLpro
and anti-COVID-19 drug discovery from medicinal plants. J Pharm Anal. 2020.
doi:10.1016/j.jpha.2020.03.009.

13. GenBank. Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1,
complete genome. NCBI GenBank. 2020;1–28.

14. Koyama T, Platt D, Parida L. Variant analysis of COVID-19 genomes. Bull World
Heal Organ. 2020;(February 24). doi:10.2471/BLT.20.253591.

15. Pachetti M, Marini B, Benedetti F, Giudici F, Mauro E, Storici P, et al. Emerging
SARS-CoV-2 mutation hot spots include a novel RNA-dependent RNA
polymerase variant. J Transl Med. 2020;18:179.

16. Li F. Structure, Function and Evolution of Coronavirus Spike Proteins. Annu Rev
Virol. 2017;3(1):237–261.

17. World — The World Factbook - Central Intelligence Agency.
https://www.cia.gov/library/publications/the-world-factbook/geos/xx.html. Accessed
12 September 2020.

18. Paul O. First African SARS-CoV-2 genome sequence from Nigerian COVID-19 case.
Genome Reports. 2020;(March):1–5.

19. The Color of Coronavirus: COVID-19 Deaths by Race and Ethnicity in the U.S. APM
Research lab. 2020. https://www.apmresearchlab.org/covid/deaths-by-race. Accessed 5
September 2020.

20. Shuvam B, Sohan S, Riju D, Kousik M, Pritha B. Mutational Spectra of SARS-CoV-2
ORF1ab Polyprotein and Signature Mutations in the United States of America.
bioRxiv. 2020. doi:https://doi.org/10.1101/2020.05.01.071654.
21. Malik YA. Properties of Coronavirus and SARS-CoV-2. Malaysian J Pathol. 2020;42(1):3–11.

22. Maitra A, Sarkar MC, Raheja H, Biswas N, Chakraborti S, Singh AK, et al. Mutations in SARS-CoV-2 viral RNA identified in Eastern India: Possible implications for the ongoing outbreak in India and impact on viral structure and host susceptibility. J Biosci. 2020;45(76):1–18.

23. Li C, Wang L, Ren L. Antiviral mechanisms of candidate chemical medicines and traditional Chinese medicines for SARS-CoV-2 infection. Virus Res. 2020;286(May):198073.

24. Life Expectancy. World Bank. https://data.worldbank.org/indicator/SP.DYN.Le00.IN?locations. Accessed 5 September 2020.