

Coronavirus Pandemic

COVID-19 imported cases and severity: expected information from genomic characterization of SARS-CoV-2 strains in Mozambique

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Abstract

Introduction: The novel coronavirus, severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), etiological agent of coronavirus disease 2019 (COVID-19) was first reported in China in December 2019 and spread worldwide. As of March 6th, 2021, there have been 116,670,105 million confirmed cases globally including 2,592,085 deaths. COVID-19 cases have been reported in 219 countries and territories, creating global panic. Mozambique has witnessed the evolution of COVID-19 epidemic associated with the weakness of health system, mostly in terms of laboratory diagnosis capacity, concerns on compliance to effective public health measures including physical distancing, use of masks in crowded indoor areas, hand hygiene, isolation and quarantine of people.

Methodology: The data included in this study were collected from published articles regarding COVID-19 imported cases and severity in Africa, especially in Mozambique. Additionally, official documents of COVID-19 epidemiology from Minister of Health and National Institute of Health of Mozambique from 22nd of March 2020 to 1st of August 2020 were included.

Results: The SARS-CoV-2 strains imported mainly from South Africa and European countries might have been playing an important role on COVID-19 epidemic evolution in Mozambique.

Conclusions: These circulating strains in the country, might be similar enough to the strains found in other countries, yet the genomic characterization is needed particularly during the phase of borders reopening through understanding the source of infections and guiding the implementation of containment and mitigation measures in the country.

Key words: COVID-19 imported cases; severity; genomic characterization; SARS-CoV-2; Mozambique.

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Introduction

The novel coronavirus, severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), emerged in Wuhan, Hubei Province (China) in December 2019 and in less than three months spread throughout the globe causing a highly contagious disease called coronavirus disease 2019 (COVID-19) [1-3].

The World Health Organization (WHO) officially declared the outbreak a pandemic on March 11st, 2020 [4]. To date (March 6th, 2021), COVID-19 has spread to 219 countries and territories, including 57 African countries. According to Worldometer, 03:32 GMT (a reference website that provides real-time worldwide statistics), 3,975,048 COVID-19 cases have been reported in Africa as the last continent to be hit by the pandemic with 105,405 deaths, mostly in South Africa, Egypt, Morocco, Tunisia, Algeria, Ethiopia and and Libya [5].

The first COVID-19 cases have been travel-related (imported cases) in several countries. The first SARS-

CoV-2 case in Africa was reported on February 14th, 2020 in Egypt, which was from a contact of a person with a history of travel to China. In the sub-Saharan region, the first COVID-19 case was reported in Nigeria on February 27th, 2020 from an Italian citizen who worked in Nigeria [6], and the first case in Southern Africa was reported on March 5th, 2020, in South Africa from a citizen returning from Italy [7]; whilst in Mozambique the first COVID-19 case, was reported on March 22nd, 2020 from a 75-year-old Mozambican man, who returned from United Kingdom [8].

The tracking and analyses of demographic, clinical patient as well as genomic information have been accomplished worldwide to understand the transmissibility and COVID-19 severity. The COVID-19 severity has been associated with several factors including people with underlying comorbidities, such as chronic lung disease, serious heart conditions, high blood pressure, obesity and diabetes and age, where individuals older ≥ 65 years are at higher risk [9-11].

For instance, fatality case of 1.38 % was reported from China, with substantially higher ratios in older age groups; 0.32 % in those aged < 60 years vs. 6.4 % in those aged \geq 60 years, up to 13.4 % in those aged 80 years or older [12]. In addition to this, genomic variation of virus has medical and biological impacts on the prevention, diagnosis, and therapy of the diseases [13].

The current emergence of newer SARS-CoV-2 variants in many countries underlines the significance of enhancing efforts to sequence the genome of the virus from across the globe including Mozambique [14]. In the present study the COVID-19 imported cases and severity were analyzed to understand the epidemiology of the disease and to highlight the future information that might be obtained through genomic characterization of SARS-CoV-2 strains in Mozambique.

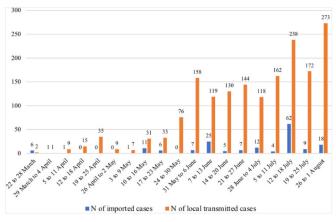
COVID-19 epidemic in Mozambique, from March 22nd to August 1st, 2020

COVID-19 imported cases

COVID-19 epidemic was firstly related to imported cases like in other countries, where the first case was reported on March 22nd 2020, from a 75-year-old Mozambican man, who returned from United Kingdom [8].

Within the analyzed 19 epidemic weeks the COVID-19 cases raised steadily in the country. On August 1st, 2020, 1,907 cases were reported, of which,

Figure 1. Local and imported in Mozambique, from 22nd of March 2020 to 1st of August 2020.



175 (9 %) imported and 1,732 (91 %) locally transmitted (Figure 1 and Table 1). In the first epidemic week (March 22nd to March 28th, 2020), the COVID-19 disease was dominated by imported cases (in total 6), from the UK, South Africa, Portugal and France. From April 5th to April 11st, 2020 the imported cases started to decrease, where from April 12nd to May 2nd no imported cases were reported, whilst the local transmitted cases increased.

Notably, in five epidemic weeks, May 10th to May 16th; June 7th to June 13th; June 28th to July 4th; July 12nd to July 18th; and July 26th to August 1st, 2020; 11, 25, 12, 62 and 18 COVID-19 imported cases, respectively, were reported.

Table	1. Evolution	of COVID-1	9 epidemic and in	iported in Mozan	nbique.

Epidemic week	N of tested cases	N of reported cases	N of imported cases	N of local transmitted cases	Countries
22 to 28 March	174	8	6	2	United Kingdom, South Africa, Portugal, France and England
29 March to 4 April	136	2	1	1	Portugal
5 to 11 April	210	10	1	9	Portugal
12 to 18 April	299	15	0	15	-
19 to 25 April	619	35	0	35	-
26 April to 2 May	751	9	0	9	-
3 to 9 May	1,402	8	1	7	Portugal
10 to 16 May	1,964	42	11	31	South Africa*
17 to 23 May	2,203	39	6	33	South Africa*
24 to 30 May	2,312	76	0	76	-
31 May to 6 June	3,133	165	7	158	South Africa*
7 to 13 June	4,647	144	25	119	South Africa*
14 to 20 June	5,043	135	5	130	South Africa*
21 to 27 June	4,852	151	7	144	Malawi*
28 June to 4 July	4,543	130	12	118	South Africa*
5 to 11 July	6,593	166	4	162	South Africa*
12 to 18 July	6,098	300	62	238	Eswatini and South Africa*
19 to 25 July	6,255	181	9	172	South Africa and Malawi*
26 to 1 August	7,547	291	18	273	Zimbabwe and South Africa*
Total	58,871	1,907	175 (9 %)	1,732 (91 %)	-

* Other countries might be involved.

From May 10th to August 1st, 2020, COVID-19 imported cases were mainly from African countries including South Africa, Malawi, Eswatini and Zimbabwe. These countries share borders with Mozambique.

The analyzed period shows that from March 22nd to May 9th, 2020, the imported cases were originated from European countries and from May 10th to August 1st are tracked to African countries. However, there is a paucity of published data related to the profile of COVID-19 imported cases, so there might have been involvement of other countries [8].

The number of COVID-19 positive tests were considerably higher from May to August 1st, 2020 following the increased testing capacity. In total 58,871 COVID-19 tests were done during the analyzed period as an essential step in fighting COVID-19 (Table 1).

By July 26th, 2020, 51.7 per 1 million of habitants were positive against the 11.3 registered on June 5th that might be related to increased testing capacity in Mozambique [8].

COVID-19 severity

Individuals of all ages are at risk for infection and severe COVID-19 disease, but it has been noticed that serious COVID-19 disease is higher in people aged \geq 60 years, and in those with chronic medical conditions. On August 1st, 2020, 1907 confirmed COVID-19 cases were reported in Mozambique, with 645 patient (34 %) recovered and 12 (0,6 %) died. Death rate was 0.4 % per 1 million of habitants by July 26th, 2020 [8].

Table 2. COVID-19 severity in Mozambique.

Most of recovered patients were observed in the last two analyzed epidemic weeks, July 19^{th} to July 25^{th} and July 26^{th} to August 1^{st} , with 135 and 102 cases, respectively (Table 2). In addition, 49 patients were hospitalized and only 10 (20 %) remained in hospital by August 1^{st} , 2020.

The COVID-19 fatalities included children (4) and adults (8), the majority were male and occurred in Nampula followed by Maputo city provinces (both provinces having community transmission) and were associated mainly with comorbidities including hypertension, pulmonary and cardiac diseases (Table 3).

Expected information and role of genomic characterization

Strains imported from Europe and African countries might have been playing important role in the evolution of COVID-19 in the country. It is expected that these strains of SARS-CoV-2 from these countries are evolving in Mozambican population and a typical profile could emerge. The rapid spread of SARS-CoV-2 associated with non-compliance of COVID-19 measures, and also regional or international travels that contribute to the importation of SARS-CoV-2 might be important factors in the emergence of a newer strains in Mozambique. Several efforts with the aim to slow down the transmission of COVID-19 have been implemented in the country including the improvement of laboratory diagnosis capacity and monitoring the compliance to preventive measures.

Epidemic week	N of reported cases	N of recovered patients*	N of deaths**
22 to 28 March	8	0	0
29 March to 4 April	2	1	0
5 to 11 April	10	1	0
12 to 18 April	15	2	0
19 to 25 April	35	5	0
26 April to 2 May	9	10	0
3 to 9 May	8	16	0
10 to 16 May	42	9	0
17 to 23 May	39	8	0
24 to 30 May	76	39	2
31 May to 6 June	165	36	0
7 to 13 June	144	25	0
14 to 20 June	135	25	2
21 to 27 June	151	48	1
27 June to 4 July	130	31	2
5 to 11 July	166	93	2
12 to 18 July	300	59	1
19 to 25 July	181	135	1
26 to 1 August	291	102	1
Total	1,907	645	12

Limited information is available regarding the SARS-CoV-2 strains characterized by Whole Genome Sequencing (WGS) in Mozambique according to our knowledge. Thus after borders reopening and allowing the international travel, the genomic characterization of SARS-CoV-2 strains could be very important tool to better understand and to monitor the COVID-19 epidemiology in the country. This is a very important tool to monitor the emergence of new pathogenic strains including SARS-CoV-2 strains [14,15].

Genome tools such as WGS provide highest resolution information about an organism with accurate identification of virulence factors, path of disease transmission within a population and provide information on the probable source thereby facilitating infectious disease management [15,16].

SARS-CoV-2 has been spreading worldwide, allowing the emergence of distinct lineages of viruses circulating in different regions. The rapid genomic surveillance by WGS is helpful in comparing sequences in order to quickly rule out possible lines of transmission of SARS-CoV-2 infections. This powerful tool is also useful in monitoring the spread and identifying the source of some cases, where contact tracing fails and when international travel resumes [15,17].

Despite the fact that WGS could provide plenty of data on SARS-CoV-2 infections, it is more important to include the antigenic sequencing approach, since in some cases the virus escapes due to the viral load in the earlier period of the disease or during recovery stage [18].

The antigenic sequencing can help to perform antigen tests to detect the viral presence in symptomatic or asymptomatic individuals. Immunoassays mostly through antigen tests can be used as a complementary method of genomic surveillance due to its advantages that include simplicity of utilisation, lower costs and rapidity of the result which allow an increased volume of testing and faster isolation of people who test positive. The isolation of positive cases plays important role in breaking chains of transmission.

In summary, data on genetic features of the virus could save lives by forming strategies for public health and clinical care, as well as helping the design of therapies and vaccines to combat the virus. In addition, this tool can enhance surveillance of the virus and provide better understanding of transmission patterns. Next-generation sequencing has been considered an important role to tackle COVID-19.

Discussion

The findings from this study are congruent with current analyses considering that in Africa most of the first COVID-19 cases were imported from Europe rather than from China where the virus emerged [19,20] (Table 4). It is, however, believed that under-reporting is widespread in several African countries due to the less developed healthcare systems associated with lower capacity of COVID-19 testing [21].

In 2020, nine African countries such as Algeria, Cameroon, Egypt, Morocco, Nigeria, Senegal, South Africa, Togo and Tunisia reported over 40 cases showing the spreading of the disease by the end of the first week of March and most index cases originated in Europe [21].

European countries played an important role for early spread of the pandemic on the African continent since Europe was the epicenter by March 13rd, 2020 [22].

The African continent has been preparing to deal with imported cases of COVID-19, led by the Africa CDC, Nigerian CDC, African Union, PANDORA-ID-NET and other research and capacity development and training consortia [21]. For instance, the early implementation of measures to tackle COVID-19, such as travel bans to most affected Asian and European countries and mandatory quarantine periods for most

Table 3. COVID-19 Fatalities in Mozambique

	Date	Age	Sex	City	Region	Comorbidities
1	25 May	13	unknown	Nampula	Nothern	+
2	28 May	45	F	Pemba	Nothern	+
3	15 June	84	М	Nampula	Nothern	+
4	16 June	6	М	Nampula	Nothern	?
5	18 June	38	М	Maputo	Central	+
6	26 June	37	М	Nampula	Nothern	+
7	2 June	58	М	Tete	Central	+
8	4 July	17 days	F	Maputo	Southern	+
9	9 June	54	М	Quelimane	Central	?
10	18 July	54	М	Xai-Xai	Southern	+
11	20 July	26	F	Tete	Central	?
12	1 August	12	М	Maputo	Southern	+

travelers [23] played an important role in decreasing the imported and locally transmitted cases as well as the fatalities in Mozambique.

Currently, most of COVID-19 imported cases are from other African countries that share borders with Mozambique. This situation might be influenced by repatriation of Mozambican citizens and clandestine entry and trade market with neighboring African countries. For instance, 589 Mozambican citizens were repatriated from South Africa on May 11st, 2020, during the second period of the state emergency [24].

The early limitation of travel through the state emergency declared on March 30th, 2020, (that was implemented from April 1st to April 30th, 2020 and extended to May 30th, 2020), contributed to decrease the number of imported COVID-19 cases in some weeks during the analyzed period, such as: April 12nd to April 18th, April 19th to April 25th, April 26th to May 2nd, May 3rd to May 9th, April 19th to April 25th, and April 26th to May 2nd (Table 1), showing the role of this measure in tackling COVID-19. The issuance of entry visas to Mozambique were suspended during the state emergency period and the control of land, sea and air borders were strengthened by Mozambican authorities. Data to analyze COVID-19 severity still lacks in Mozambique. However, the emerging data suggests that subjects with comorbidities are at higher risk, that is consistent with previous studies. Higher rates of comorbidity conditions (*e.g.*, cardiac disease, diabetes, hypertension, obesity, pulmonary, chronic lymphocytic leukemia disease) and more advanced age (\geq 65 years), increase the risk for symptom manifestations and COVID-19 severity [25,26] and this has been observed also in Mozambique; although, the fact that most of fatalities in adults ranged from 26 to 58 years of age highlights the major role of comorbidities.

Additionally, most of the patient remained asymptomatic (58%) or experienced few and mild symptoms (34%) [8], that is of particular concern based on an increasing number of studies describing that asymptomatic individuals can transmit SARS- CoV-2 [27-29], even though the mechanism remains unknown. However, this type of transmission may be contributing to a substantial amount of community transmission. Maputo city, Nampula and Pemba reported this type of COVID-19 transmission [8,30]. Therefore, physical distancing, face coverings and frequent handwashing are still effective preventive measures in reducing SARS-CoV-2 infections.

 Table 4. Origin of the first COVID-19 cases (imported cases) in some African countries.

African country	Country of importation**	Continent	Confirmation date
Algeria	Italy	Europe	25 February
Angola*	Portugal	Europe	21 March
Botswana*	United Kingdom and Thailand	Europe/Asia	30 March
Cameroon	France	Europe	6 March
Comoros*	France	Europe	30 April
Djibouti	Spain	Europe	18 March
Eswatini*	United States	America	14 March
Ivory Coast	Italy	Europe	11 March
Gabon	France	Europe	12 March
Kenya	United States or other	America	12 March
Lesotho*	Saudi Arabia	Asia	13 May
Malawi*	India	Asia	2 April
Madagascar*	France	Europe	20 March
Mali	France	Europe	25 March
Mauritius*	United Kingdom and other	Europe	19 March
Moroco	Italy	Europe	2 March
Mozambique*	United Kingdom	Europe	22 March
Namibia*	Spain	Europe	14 March
Nigeria	Italy	Europe	27 February
Republic of the Congo*	France	Europe	14 March
Sierra Leone	France	Europe	31 March
Senegal	France	Europe	2 March
Seychelles*	Italy	Europe	14 March
South Africa*	Italy	Europe	5 March
Tunisia	Italy	Europe	2 March
United republic of Tanzania*	Belgium	Europe	16 March
Zambia*	Italy	Europe	18 March
Zimbabwe*	Italy	Europe	21 March

*Member state of Southern African Development Community (SADC); **Data was taken from World Organization Health (WHO) Africa (2020). External Situation Report 2 to 7 [50].

COVID-19 fatality rate in Mozambique is 0.4 by one million inhabitants, which is lower than other African countries including Botswana, Tanzania, Angola, Zimbabwe, Namibia, Malawi, Lesotho, Eswatini, Zambia and South Africa. The latter country was the most affected in the Southern African Development Community (SADC) with 137.5 fatalities in each one million of inhabitants [31,32].

Notwithstanding the rapid spread of COVID-19 in developing countries worldwide, many African countries including Mozambique, having a weak health systems and poor testing capacity, have been largely spared by this pandemic disease. The global death toll remains highly concentrated in few high-income, middle income or upper-middle countries [22], such as the United States, Brazil, Russia, Spain, and Kazakhstan, and South Africa on the African continent that has reported 8,366 deaths, although the deaths decreased in the past 7 days [33]. In some European high-income countries hit by COVID-19 pandemic, such as Luxembourg, Spain, Belgium, and San Marino, 110.23, 139.62, 175.59, and 942.90 fatalities per million, respectively were reported [34].

Demography (youthful population) and the variant of SARS-CoV-2 strains that circulated in Mozambique by August 1st, 2020, as well as other factors may contribute to the current COVID-19 severity in Mozambique. The number of older adults is lower as people > 60 years of age make up 4.6 % of the population, followed by ages 15-45 years accounting for 38.5%, and ages 0-15 years for 46.7% [35]. Most COVID-19 fatalities (7/12, 58%) affected people \geq 37 years of age [31] thus suggesting that apart from age, other factors including comorbidities may increase the risk of severity. However, it is still insufficient data to understand the severity and proportion of deaths and the dynamics of COVID-19 [34].

Mozambique registered lower infections and deaths by SARS-CoV-2 per 1 million of habitants in the analyzed period when compared to the majority of African countries belonging to the SADC region or member states [8,36]. This situation can be associated with the fact that Mozambique was one of the last countries affected by COVID-19 in the region and related to the type of SARS-CoV-2 strains that circulated.

COVID-19 community transmission could be an important factor in emerging of new virus strains due to the rapid spread of SARS-CoV-2 in the population associated with reduced compliance to COVID-19 preventive measures. Additionally, the delay in patient recovering from COVID-19, which makes Mozambique as one of African countries with lowest rate [8] might engender novel mutations in the virus [37,38].

Recent studies have shown that a large number of mutations in SARS-CoV-2 may have arisen through intra-host evolution in one or more individuals with prolonged viral replication or infectious over 20 weeks [39,40]. Although this phenomenon of viral evolution has been observed in the context of human immunodeficiency virus (HIV) infection, other mechanisms can be associated with multiple mutations in SARS-CoV-2 or evolution [41-43]. However, further studies are needed for better understanding the mechanisms of emergence of new SARS-CoV-2 strains.

Currently, the circulation of the new South African COVID-19 strain (SARS-CoV-2 lineage 501Y.V2) characterized by eight lineage-defining mutations in the spike protein, including three at important residues in the receptor-binding domain (K417N, E484K and N501Y) [43,44], might play an important role in emerging of new variants in the country.

The SARS-CoV-2 lineage 501Y.V2 and other new variants have shown the trend to replace the wild type in some countries due to its rapid spread and dissemination [45]. The South African lineages have been detected in Botswana, UK, Scotland, France, Sweden, Switzerland, South Korea and Australia [45,46].

The spread of SARS-CoV-2 in Mozambique is of particular concern due to the weakness of the health system, non-compliance of preventive measures and probably due to the circulation of new SARS-CoV-2 strains mainly of the South African lineages 501Y.V2 already confirmed.

Apart from the circulation of South African lineages, other new variants such as clade 20I/501Y.V1, VOC 202012/01 or B.1.1.7 (initially identified in UK) and clade P.1 (initially identified in Brazil) [46-48], might be circulating due to international travel to Mozambique.

Like in other countries, SARS-CoV-2 mutations might arise in Mozambique with effects on human disease prevalence and health outcomes, thus genetic monitoring and biological characterization of new mutations is a high priority in research. Additionally, systematic clinicopathological, genomic and other socio-economic data, together with implementation of preventive measures are important factors to effectively fight against COVID-19.

The new variants are emerging probably due to environmental pressures including vaccine-induced immunity, antiviral therapies, and public health intervention strategies that could promote virus survival and escape. The selective pressures may drive antigenic variation, promote virus stability and transmissibility, alter virus virulence and pathogenesis of SARS-CoV-2 [49], making WGS including antigenic sequencing very important tools to be used as control and prevention measures.

It is expected that future project for SARS-CoV-2 strains characterization offer insights into the viral dissemination and severity in Mozambique.

Conclusions

The COVID-19 imported cases from European countries might have been playing an important role in Mozambique. Due to the epidemic COVID-19 evolution, the country is currently characterized by an increasing number of confirmed cases, hospitalizations and deaths; genomic surveillance of SARS-CoV-2 including the antigenic sequencing approach might be useful tools in designing new control and prevention measures through understanding the epidemiologic, immunologic, and evolutionary processes in the country and to guide the global pandemic response.

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References

- Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, Zhao X, Huang B, Shi W, Lu R, Niu P, Zhan F, Ma X, Wang D, Xu W, Wu G, Gao GF, Tan W (2020) A Novel Coronavirus from patients with pneumonia in China, 2019. N Engl J Med 382: 727–733.
- Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei -Y, Yuan ML, Zhang YL, Dai FH, Liu Y, Wang QM, Zheng JJ, Xu L, Holmes EC, Zhang YZ (2020) A new coronavirus associated with human respiratory disease in China. Nature 579: 265–269.
- 3. Kumar D (2020) Corona virus: a review of COVID-19. EJMO 4: 8–25.
- BBC World News (2020) Coronavirus confirmed as pandemic by World Health Organization. https://www.bbc.com/news/world. Accessed: 1 August 2020.
- 5. Worldometers (2020) Coronavirus updates. Available: https://www.worldometers.info/. Accessed: 5 August 2020.
- BBC Africa News (2020) Coronavirus: Nigeria confirms first case in sub-Saharan Africa. Available: https://www.bbc.com/news/world/africa. Accessed: 1 August 2020.
- The National Institute for Communicable Diseases (NICD) (2020) First case of COVID-19 Coronavirus reported in SA. Available: https://www.nicd.ac.za/. Accessed: 1 August 2020.

- National Institute of Health of Mozambique (INS) (2020) COVID-19. Be attentive. Available: https://covid19.ins.gov.mz/. Accessed: 1 August 2020. [Available in Portuguese].
- 9. Richardson S, Hirsch JS, Narasimhan M, Crawford JM, McGinn T, Davidson KW, and the Northwell COVID-19 Research Consortium, Barnaby DP, Becker LB, Chelico JD, Cohen SL, Cookingham J, Coppa K, Diefenbach MA, Dominello AJ, Duer-Hefele J, Falzon L, Gitlin J, Hajizadeh N, Harvin TG, Hirschwerk DA, Kim EJ, Kozel ZM, Marrast LM, Mogavero JN, Osorio GA, Qiu M, Zanos TP (2020) Presenting characteristics, comorbidities, and outcomes among 5700 patients hospitalized with COVID-19 in the New York City area. JAMA 323: 2052-2059.
- Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, Qiu Y, Wang J, Liu Y, Wei Y, Xia J, Yu T, Zhang X, Zhang L (2020) Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. Lancet 395: 507–513.
- Liu K, Chen Y, Lin R, Han K (2020) Clinical features of COVID-19 in elderly patients: A comparison with young and middle-aged patients. J Infect 80: e14–e18.
- 12. Verity R, Okell LC, Dorigatti I, Winskill P, Whittaker C, Imai N, Cuomo-Dannenburg G, Thompson H, Walker PGT, Fu H, Dighe A, Griffin JT, Baguelin M, Bhatia S, Boonyasiri A, Cori A, Cucunubá Z, FitzJohn R, Gaythorpe K, Green W, Hamlet A, Hinsley W, Laydon D, Nedjati-Gilani G, Riley S, van Elsland S, Volz E, Wang H, Wang Y, Xi X, Donnelly CA, Ghani AC, Ferguson NM (2020) Estimates of the severity of coronavirus disease 2019: a model-based analysis. Lancet Infect Dis 20: 669–677.
- Khailany RA, Safdar M, Ozaslan M (2020) Genomic characterization of a novel SARS-CoV-2. Gene Rep 19: 100682.
- Desai S, Rane A, Joshi A, Dutt A (2021) Evolving Insights from *SARS-CoV-2* Genome from 200K COVID-19 Patients. BioRXiv Preprint 2021.01.21.427574.
- Janus J (2020) Using whole genome sequencing to help combat COVID-19. Available: https://www.phgfoundation.org/blog/wgs-to-combat-COVID-19. Accessed: 3 August 2020.
- Gilchrist CA, Turner SD, Riley MF, Petri WA, Hewlett EL (2015) Whole-genome sequencing in outbreak analysis. Clin Microbiol Rev 28: 541–563.
- 17. Pillay S, Giandhari J, Tegally H, Wilkinson E, Chimukangara B, Lessells R, Moosa Y, Mattison S, Gazy I, Fish M, Singh L, Khanyile KS, San JE, Fonseca V, Giovanetti M, Alcantara LC, de Oliveira T (2020) Whole genome sequencing of SARS-CoV-2: adapting illumina protocols for quick and accurate outbreak investigation during a pandemic. Genes (Basel) 11: 949.
- Alpdagtas S, Ilhan E, Uysal E, Sengor M, Ustundag CB (2020) Evaluation of current diagnostic methods forCOVID-19. APL Bioeng 4: 041506.
- Nextstrain (2020) Genomic epidemiology of novel coronavirus

 Africa-focused subsampling. Available: https://nextstrain.org/ncov/africa?l=clock&p=grid. Accessed: 10 April 2020.
- World Health Organization (WHO) Africa (2020) More than 15 countries in Africa report COVID-19 cases. Available: https://www.afro.who.int/. Accessed: 3 August 2020.
- 21. Gaye B, Khoury S, Cene CW, Kingue S, N'Guetta R, Lassale C, Baldé D, Diop IB, Dowd JB, Mills MC, Jouven X (2020)

Socio-demographic and epidemiological consideration of Africa's COVID-19 response: what is the possible pandemic course? Nat Med 26: 996–999.

- World Health Organization (WHO) (2020) Briefing on COVID-19. Available: https://www.who.int/dg/speeches/detail/who-director-generals-opening-remarks-at-the-mission (2020). Accessed: 15 March 2020.
- Presidency of the Republic of Mozambique (2020) Comunication to the Nation COVID-19, 29 March 2020. Available: https://www.presidencia.gov.mz/por/Informacao/Imprensa/Di scursos/Comunicacao-de-Sua-Excelencia-Filipe-Jacinto-Nyusi-Presidente-da-Republica-de-Mocambique-a-Nacaosobre-a-situacao-da-Pandemia-do-Corona-Virus-COVID-19. Accessed: 1 May 2020. [Available in Portuguese].
- O País (2020) After all repatriated Mozambicans were serving sentences in South Africa. Available: http://opais.sapo.mz/. Accessed 5 May 2020. [Available in Portuguese].
- 25. Scarfò L, Chatzikonstantinou T, Rigolin GM, Quaresmini G, Motta M, Vitale C, Garcia-Marco JA, Hernández-Rivas JÁ, Mirás F, Baile M, Marquet J, Niemann CU, Reda G, Munir T, Gimeno E, Marchetti M, Quaglia FM, Varettoni M, Delgado J, Iyengar S, Janssens A, Marasca R, Ferrari A, Cuéllar-García C, Itchaki G, Špaček M, De Paoli L, Laurenti L, Levin M-D, Lista E, Mauro FR, Šimkovič M, Van Der Spek E, Vandenberghe E, Trentin L, Wasik-Szczepanek E, Ruchlemer R, Bron D, De Paolis MR, Del Poeta G, Farina L, Foglietta M, Gentile M, Herishanu Y, Herold T, Jaksic O, Kater AP, Kersting S, Malerba L, Orsucci L, Popov VM, Sportoletti P, Yassin M, Pocali B, Barna G, Chiarenza A, dos Santos G, Nikitin E, Andres M, Dimou M, Doubek M, Enrico A, Hakobyan Y, Kalashnikova O, Ortiz Pareja M, Papaioannou M, Rossi D, Shah N, Shrestha A, Stanca O, Stavroyianni N, Strugov V, Tam C, Zdrenghea M, Coscia M, Stamatopoulos K, Rossi G, Rambaldi A, Montserrat E, Foà R, Cuneo A, Ghia P (2020) COVID-19 severity and mortality in patients with chronic lymphocytic leukemia: a joint study by ERIC, the European Research Initiative on CLL, and CLL Campus. Leukemia 34: 2354-2363.
- Price-Haywood EG, Burton J, Fort D, Seoane L (2020) Hospitalization and mortality among black patients and white patients with Covid-19. N Engl J Med 382: 2534–2543.
- 27. Kapata N, Ihekweazu C, Ntoumi F, Raji T, Chanda-Kapata P, Mwaba P, Mukonka V, Bates M, Tembo J, Corman V, Mfinanga S, Asogun D, Elton L, Arruda LB, Thomason MJ, Mboera L, Yavlinsky A, Haider N, Simons D, Hollmann L, Lule SA, Veas F, Abdel Hamid MM, Dar O, Edwards S, Vairo F, McHugh TD, Drosten C, Kock R, Ippolito G, Zumla A (2020) Is Africa prepared for tackling the COVID-19 (SARS-CoV-2) epidemic. Lessons from past outbreaks, ongoing pan-African public health efforts, and implications for the future. Int J Infect Dis 93: 233–236.
- Rothe C, Schunk M, Sothmann P, Bretzel G, Froeschl G, Wallrauch C, Zimmer T, Thiel V, Janke C, Guggemos W, Seilmaier M, Drosten C, Vollmar P, Zwirglmaier K, Zange S, Wölfel R, Hoelscher M (2020) Transmission of 2019-nCoV infection from an asymptomatic contact in Germany. N Engl J Med 382: 970–971.
- 29. Yu P, Zhu J, Zhang Z, Han Y (2020) A familial cluster of infection associated with the 2019 novel Coronavirus indicating possible person-to-person transmission during the incubation period. J Infect Dis 221: 1757–1761.

- Ministry of Health (MISAU) (2020) Pemba declared area of community COVID-19 transmission. Available: http://www.misau.gov.mz/. Accessed 4 August 2020. [Available in Portuguese].
- National Institute of Health of Mozambique (INS) (2020) COVID-19. Be attentive. Analyses of the SARS-CoV-2/COVID-19 epidemiological Situation, 3 August 2020. Available: https://covid19.ins.gov.mz/. Accessed: 5 August 2020. [Available in Portuguese].
- WHO Africa region (2020) External Situation Report 20. Available: https://reliefweb.int/sites/reliefweb.int/files/resources/SITREP _COVID-19_WHOAFRO_20200722-eng.pdf. Accessed: 22 July 2020.
- World Health Organization (WHO) (2020) COVID-19 Situation report – 196. Available: https://www.who.int/. Accessed 4 August 2020.
- 34. Hallal PC (2020) Worldwide differences in COVID-19-related mortality. Cien Saude Colet 25 Suppl 1: 2403–2410.
- National Statistics Institute (INE) (2019) 2017 census brochure of definitive results of National IV General Population and Housing Census. Available: http://www.ine.gov.mz/iv-rgph-2017/mocambique/censo-2017-brochura-dos-resultadosdefinitivos-do-iv-rgph-nacional. Accessed 11 April 2020. [Available in Portuguese].
- 36. Southern African Development Community (SADC) (2020). SADC Regional Response to COVID-19 Pandemic Bulletin 8: Global and SADC regional outlook of COVID-19 Pandemic; interactions between COVID-19, HIV/AIDS and TB, and its Impact on Economic, Energy and Natural Resources Sectors. Available: https://reliefweb.int/report/angola/sadc-regionalresponse-covid-19-pandemic-bulletin-no-8. Accessed: 10 July 2020.
- Sanjuán R, Domingo-Calap P (2016) Mechanisms of viral mutation. Cell Mol Life Sci 73: 4433–4448.
- Koyama T, Platt D, Parida L (2020) Variant analysis of SARS-CoV-2 genomes. Bull World Health Organ 98: 495–504.
- Avanzato VA, Matson MJ, Seifert SN, Pryce R, Williamson BN, Anzick SL, Barbian K, Judson SD, Fischer ER, Martens C, Bowden TA, de Wit E, Riedo FX, Munster VJ (2020) Case study: prolonged infectious SARS-CoV-2 shedding from an asymptomatic immunocompromised individual with cancer. Cell 183: 1901-1912.e9.
- 40. Choi B, Choudhary MC, Regan J, Sparks JA, Padera RF, Qiu X, Solomon IH, Kuo H-H, Boucau J, Bowman K, Adhikari UD, Winkler ML, Mueller AA, Hsu TY-T, Desjardins M, Baden LR, Chan BT, Walker BD, Lichterfeld M, Brigl M, Kwon DS, Kanjilal S, Richardson ET, Jonsson AH, Alter G, Barczak AK, Hanage WP, Yu XG, Gaiha GD, Seaman MS, Cernadas M, Li JZ (2020) Persistence and Evolution of SARS-CoV-2 in an Immunocompromised Host. N Engl J Med 383: 2291–2293.
- 41. Karim F, Gazy I, Cele S, Zungu Y, Krause R, Bernstein M, Ganga Y, Rodel H, Mthabela N, Mazibuko M, Khan K, Muema D, Ramjit D, Lustig G, Ndung'u T, Hanekom W, Gosnell BI, COMMIT-KZN Team, Wong E, de Oliveira T, Moosa M-YS, Leslie A, Kløverpris H, Sigal A (2020) HIV status alters disease severity and immune cell responses in β variant SARS-CoV-2 infection wave. MedRxiv Preprint 2020.11.23.20236828.
- Salemi M (2013) The intra-host evolutionary and population dynamics of human immunodeficiency virus type 1: a phylogenetic perspective. Infect Dis Rep 5: e3.

- 43. Tegally H, Wilkinson E, Giovanetti M, Iranzadeh A, Fonseca V, Giandhari J, Doolabh D, Pillay S, San EJ, Msomi N, Mlisana K, von Gottberg A, Walaza S, Allam M, Ismail A, Mohale T, Glass AJ, Engelbrecht S, Van Zyl G, Preiser W, Petruccione F, Sigal A, Hardie D, Marais G, Hsiao M, Korsman S, Davies M-A, Tyers L, Mudau I, York D, Maslo C, Goedhals D, Abrahams S, Laguda-Akingba O, Alisoltani-Dehkordi A, Godzik A, Wibmer CK, Sewell BT, Lourenço J, Alcantara LCJ, Pond SLK, Weaver S, Martin D, Lessells RJ, Bhiman JN, Williamson C, de Oliveira T (2020) Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. MedRxiv Preprint 2020.12.21.20248640.
- 44. Jornal Notícias (2020). Mozambican minister says South African variant has been circulating in the country since November. Available: https://www.oseculoonline.com/ministro-mocambicano-dizque-variante-sul-africana-circula-no-pais-desde-novembro/. Accessed: 1 February 2021. [Available in Portuguese].
- 45. Tang JW, Toovey OTR, Harvey KN, Hui DDS (2021) Introduction of the South African SARS-CoV-2 variant 501Y.V2 into the UK. J Infect 82: e8-e10.
- Galloway SE, Paul P, MacCannell DR, Johansson MA, Brooks JT, MacNeil A, Slayton RB, Tong S, Silk BJ, Armstrong GL, Biggerstaff M, Dugan VG (2021) Emergence of SARS-CoV-2

B.1.1.7 Lineage — United States, December 29, 2020–January 12, 2021. MMWR Morb Mortal Wkly Rep 70: 95–99.

- 47. Center for Disease and Control Prevention (CDC) 2021 Science Brief: Emerging SARS-CoV-2 Variants. Available: https://www.cdc.gov/coronavirus/2019-ncov/more/scienceand-research/scientific-brief-emerging-variants.html. Accessed: 28 January 2021.
- 48. Burki T (2021) Understanding variants of SARS-CoV-2. Lancet 397: 462.
- 49. Baric RS (2020) Emergence of a Highly Fit SARS-CoV-2 Variant. N Engl J Med 383: 2684–2686.
- World Health Organization (WHO) Africa (2020) External situation report 2 to 7. Available: https://www.afro.who.int/. Accessed: 3 August 2020.

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