COVID-19 REPRODUCTION RATE: Relevance in the Mozambican Context

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A ser publicado na: Rev. cient. UEM: Sér. ciênc. bioméd. saúde pública - ISBN 2307-3896

Data de submissão: 11/06/2020

Data de aceitação: 20/06/2020

Data de publicação: xx/xx/xxxx

Como citar este artigo: CHONGO, A. E. *et al.* COVID-19 reproduction rate: relevance in the Mozambican context. **Rev. cient. UEM: Sér. ciênc. bioméd. saúde pública.** *Pre-print*, 2020.

Pre-print - Rev. cient. UEM: Sér. ciênc. bioméd. saúde pública - ISBN 2307-3896

Artigo de revisão

COVID-19 REPRODUCTION RATE: Relevance in the Mozambican Context

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ABSTRACT: Coronavirus disease 2019 (COVID-19), caused by Severe Acute Respiratory Syndrome CoronaVirus 2 (SARS-CoV-2), has been swamping health-care systems and devastating societies and economies worldwide. Mathematical models havepredictedthe numbers of infections and deathsrelated to the outbreak of COVID-19 on the African continent. In this article we discuss the approach of the models published by the London School of Hygiene &Tropical Medicine (LSHTM) and Imperial College London in relation to the outcomes predicted for COVID-19 in Mozambique. We also analyse the reproduction rate of COVID-19 and its relevance in the context of Mozambique. The results predicted for Mozambique by the aforementioned models have not been observed; this may be related to several factors that affect the reproduction rate (Re), such aspeople's behaviour and some of the socio-economic and cultural realities of the country. Therefore, tracking the Re through increasing the capacity for COVID-19 testing is crucial in order to assess the impacts of the possible relaxation of social distancing measures.

Keywords: COVID-19, Mozambique, Reproduction rate, SARS-CoV-2.

TAXA DE REPRODUÇÃO DA COVID-19: relevância no contexto moçambicano

RESUMO: A doença coronavírus 2019 (COVID-19) causada pela Síndrome Respiratória Aguda Grave CoronaVírus 2 (SARS-CoV-2), vemsaturando os sistemas de saúde, devastando sociedades e economias em todo o mundo. Foram propostos modelos matemáticos para prever o número de infecções e mortes relacionadas com o surto da COVID-19 no continente africano. Neste artigo, discutimos a abordagem dos modelos publicados pela London School of Hygiene & Tropical Medicine (LSHTM) e pelo Imperial College London em relação aos resultados previstos para a COVID-19 em Moçambique. Analisamos também a taxa de reprodução da COVID-19 e sua relevância no contexto de Moçambique. Os resultados previstos pelos modelos acima mencionados para Moçambique não foram observados. Istopode estar relacionado com vários factores que afectam a taxa de reprodução (Re), principalmente, o comportamento das pessoas e os factoressocioeconómico e culturais do país. Portanto, rastrear o Re é crucial para decidir sobre o possível relaxamento das medidas de distanciamento social.

Palavras-chave: COVID-19, Moçambique, Taxa de reprodução, SARS-CoV-2.

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INTRODUCTION

Since the outbreak of COVID-19 to date (6th June 2020), 6.869.136 COVID-19 positive cases were reported worldwide, with 179.657fromAfrica (JOHNS HOPKINS CORONAVIRUS RESOURCE CENTER, 2020). In Mozambique, 409 positive cases were confirmed from 13.398 tests(INS, 2020). Modellers have been attempting to predict the scale and impact of the disease across the globe. Results predicted by the mathematical model published by the London School of Hygiene & Tropical Medicine (LSHTM), on the 25th of March (PEARSON and VAN SCHALKWYK, 2020), estimated that the number of infections for Mozambique would reach 1.000 somewhere between the 21st of April and the 3rd of May, and 10.000 between the 11th and 23rd of May. However, as of the 6th of June, only 409 cases of COVID-19 have been confirmed. So how do we assess these predictions?

Firstly, there are many unanswered questions and a lack of data: in fact, we do not know whether the LSHTM model, for example, has failed to predict the scale of infection in Mozambique or not, because only 13.398 samples have been analysed from a selected and targeted group. The models are not predicting the number of cases that would be detected by the National Health systems of each country, but the number of infections in each country, whether they were detected or not. The National Institute of Health reported that 47%(INS, 2020) of the positive cases in Mozambique have been asymptomatic, so it is possible that the outbreak is more significant, but has gone unnoticed.

Secondly, all mathematical models have limitations. Both the LSHTM and Imperial College London(WALKER, WHITTAKER and WATSON, 2020) models assumed a basic reproduction number (or reproductive ratio) of the virus, referred to as R_0 (R-naught). This is the number of cases that are "expected to occur on average in a homogeneous population as a result of infection by a single individual, when the population is susceptible at the start of an epidemic, before widespread immunity starts to develop and before any attempt has been made at immunization" (BRASSEY, ARONSON and MAHTANI,2020). The R_0 where one infected person passes it on to two others is 2; it is 3 where that person infects three others. It is calculated from the cases that are diagnosed. But the zero in "R zero" refers to the fact that it presumes *zero immunity* in the population. So with a completely new virus, such as SARS-CoV-2, the earlier in the outbreak that the measurements are made, the closer the calculated value will be to the 'true value' of R_0. There are many estimates of the R_0 of SARS-CoV-2, but they vary widely. One systematic review(ALIMOHAMADI, TAGHDIR and SEPANDI,2020) reported that the mean of 29 reported values of R_0 from 21 studies was 3.3, but with a range of 1.9 to 6.5; all the included studies were from China. In a statement on 23rd January 2020 about the outbreak of COVID-19 the World Health Organization (WHO) gave a preliminary R_0 estimate of 1.4–2.5.

It is more useful, however, to refer to the transmissibility of a virus at the time that it is measured, which is known as the effective reproduction number, or Re. This represents the number of people infected by a single carrier at any particular time. Over time, the Re for a virus changes, reducing as the population becomes increasingly immunized, either by individual immunity following infection or because a vaccine becomes available. Importantly, though, the Re is also affected by the number of infected people and the number of susceptible people that they are in contact with. Therefore, people's behaviour (including social distancing, for example) can also affect Re.

The fact that the effective reproduction number can change according to behaviour may help explain the slower transmission rates in Mozambique. The different socioeconomic and cultural realities of Mozambique, compared to the northern hemisphere countries that suffered such rapid and widespread outbreaks of SARS-CoV-2, might have served to slow the initial spread of the disease. International air travel, which was behind the initial spread, is generally the preserve of the Mozambican upper and the middle classes, who also have private cars for their domestic transport needs. The imported cases might have been in people that were already 'socially distanced', not because there were rules and regulations at that time, but because this was a feature of their lifestyles (Chongo *et al*, 2020).

In rural areas, where 65% of the population resides(INE, 2019), the dispersed settlement patterns and low population densities, may have also slowed the spread of infection, variables that could have been factored into the modelling.[1]Archaeological evidence shows that the dispersion of settlements in Sub Saharan Africa was in fact an adaptive response by rural communities to mitigate the threat of infectious diseases(CHIRIKURE, 2020). Mozambican socio-economic and cultural realities may, therefore, have worked in favour of reducing the Re at that time and the spread of those imported infections.

The second transmission chain to be identified was at the Afungi Gas Exploration Project Facilities in Cabo Delgado province, where the largest number of cases (19) were reported on April 24, 2020. However, the location and nature of life in this camp, with little interaction between the occupants and the surrounding populations, and the rapid response from health authorities, may have contributed to the lower Re initially in Cabo Delgado.

Thirdly, the LSHTM modelling was based on the absence of any measures to reduce the spread, whereas the Imperial College London model was designed instead to predict the impact that strict social distancing measures would have, depending on when they were introduced. The model applied several variables to different countries (GDP, household, contact patterns between age-groups, healthcare capacity with focus on intensive care units, and capacity for mitigation and suppression, including surveillance to test and isolate all cases and their close contacts) and incorporated varying values for R_0 (from 2.4 to 3.3). A central focus of the study was the comparison of the outcomes predicted from two different approaches for containing transmission: 'suppression', where the intention is to bring the infection rate to below 1, and 'mitigation', aimed at reducing the impact of the epidemic, but not interrupting transmission completely. It was this study that was the basis for the UK government's change in its policy towards tackling coronavirus. In the absence of any control measures and with an R_0 of 2.7, the model suggested that 81% of the UK population would become infected, with over half a million deaths. The UK changed course, but at a point where there was already widespread community transmission. In Mozambique, by contrast, the authorities introduced strict social distancing on the day after the first case was detected.

All this may mean that the government's strategy of aggressive contact tracing, and the early introduction of measures to enforce social distancing, have in fact resulted in a different infection curve in Mozambique. But, whilst Mozambican socio-economic and cultural realities and the measures to date may have worked in favour of reducing the initial spread of imported infections, recent data suggests the possibility of an exponential growth of COVID-19 cases in the future. On 17th May, the INS announced that in accordance with the WHO criteria (INS, 2020), the outbreak had passed from being sporadic cases to an epidemic with clusters of transmission. By the 28th May the disease had been identified in each province across the country and on 2nd of June a record number of 53 new positive cases were confirmed, mainly from Nampula province (47 cases). Nampula was subsequently declared as being the first region with community transmission on the 6th of June, when 28 new cases were registered.

Based on this reality, the efforts to contain and avoid community transmission across the rest of the country must continue. Since the Re value for SARS-CoV-2 may vary, we need to be able to track it as far as possible in different settings, ideally at regular and frequent intervals (for example, weekly, included in epidemiological reports). It will vary according to the extent to which social distancing measures are imposed and adhered to. For Mozambique to mount an effective response to the outbreak of SARS-CoV-2 we must be able to track the Re and for that, we must be able to scale up the testing at national level.

CONCLUSION

An Re above 1 would mean that the number of cases will increase exponentially, but if it is below 1, the disease will tend to disappear, by reducing new infections that could sustain the outbreak(BRASSEY, ARONSON and MAHTANI, 2020). Tracking the Re will be crucial for deciding how and where the measurements can be lifted, depending on the transmission rates in each province.

Since 47% of COVID-19 detected cases to date were asymptomatic, and there has been no significant demand on health care facilities associated with COVID-19, it is necessary to carefully evaluate any possible relaxation of social distancing measures. Whilst there are studies (LIU *et al.*,2020;GOLD *et al.*, 2020, ZHOU *et al.*, 2020)that have shown that the disease can be mild for younger and healthy individuals, it is a much larger threat to immunocompromised individuals.

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[1] Note that the data used in the models to incorporate the contact patterns of all African populations were based on a single study from Zimbabwe.