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Estimating R_0 Of The COVID-19 Virus Outbreak in Malawi: Opportunities and Challenges

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Abstract

COVID-19 remains a global concern such that social distancing, wearing of face masks and hand washing remain key prevention measures. Additionally, various types of vaccines have been developed and put to use. On the other hand, epidemiologists continue to monitor published COVID-19 data to analyse the dynamics of the disease including estimation of the reproduction number (R_0). However, lack of continuous authenticated data defines a daunting task of estimating R_0 both locally and globally. This paper aimed at assessing the scope of COVID-19 in Malawi and extent of estimating R_0, existing challenges and opportunities. The assessment showed that for the past one year, COVID-19 data showed some cyclic pattern with a probable occurrence of third wave. But no traceable reasons of curve flattening were clearly met. In addition, we observed missing of some data which present an obstacle to the process of deriving various disease parameters including R_0. Nevertheless, based on the available dataset, a preliminary estimate of R_0=1.05 was obtained using method of generation interval. Thus, more effort should be spent on gathering and publishing clean and continuous data. Nonetheless, the available COVID-19 data, openly published by relevant authorities, sets a benchmark for possible estimation of R_0 in Malawi.

Keywords: *COVID-19, Data, Reproduction number, Challenges, Opportunities, Malawi.*

1. BACKGROUND

Originating in Wuhan, China in December 2019 (Huang et al., 2020; WHO, 2020a; Zavascki et al., 2020), the Corona Virus Disease 2019 (COVID-19) is an infectious disease caused by a newly discovered novel strain of coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and is a fundamentally global crisis (Xu & Kraemer, 2020). The pandemic has presented a unique challenge, threatening the lives and livelihoods of millions of people around the world, in particular the elderly and women (Liu et al., 2020a; Yan et al., 2020). Being a novel virus, the coronavirus has raised innumerable questions and speculations about its nature, function, and effects on human beings (Wang et al., 2020; Komesaroff & Kerridge, 2020). This situation has ignited more scientific research on the virus including that of developing COVID-19 vaccines (WHO, 2021).

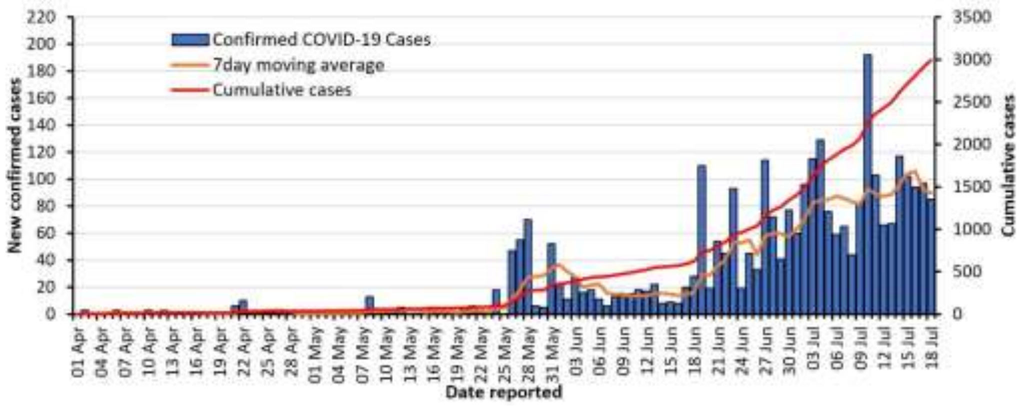

Figure 1: New and cumulative confirmed COVID-19 cases in Malawi for April to July 2020, Source: PHIM COVID-19 situation report.

The COVID-19 situation in Malawi has been unique because the first records of cases (Montsho, 2020) had coincided with an unstable political environment, following the nullified May 2019 presidential elections results which had polarised the country along regional, ethnic and political partisanship lines (Chitete, 2020). During the three months of April, May and June 2020, the political situation had further weakened the mandate of the then governing regime. Despite daily record and publication of cases (e.g. Figure 1), people/politicians went about attending and holding political mass rallies with very minimal social distancing and wearing of masks measures up until the voting day of 23 June 2020. Further, the Taskforce Committee on COVID-19 was not fully embraced by the general public, weakening further the authority of the information from the committee, even when measures of controlling further spread of the disease were proposed. For example, an injunction against government's proposed 21 day-lockdown was granted by the courts to minimize the economic impacts it would have brought on the people (Gatenby, 2020).

As such, willingness of the people to observe social distance, wash hands with soap, and wear face masks in public as COVID-19's first safety measures (WHO, 2020b) was eventually reduced. Due to such laxity, evidently, the potential impact was a steady rise of reported cumulative COVID-19 cases and deaths with an increase in community transmission up until July 2020 (Figure 1). However, the trend flattened between July and December 2020 (Figure 2). At this point, the disease reached an endemic equilibrium, with R_0 almost equal to one (Li, 2018; Eisenberg, 2020).

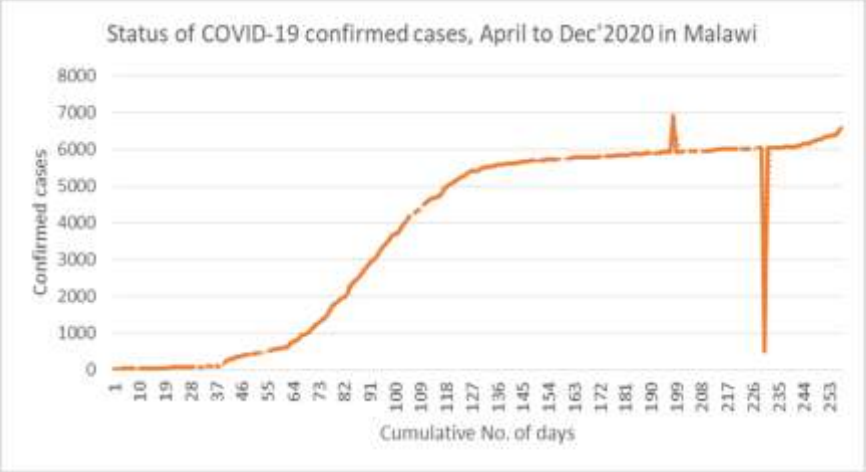

Figure 2: Data distribution of confirmed cases, April to Dec 2020.

Also known as the basic reproductive number, Eisenberg (2020) defines R_0 as "the average number of secondary infections that a single infected individual could produce in a totally susceptible population during the entire duration of infectiousness". Epidemiologically, R_0 is a threshold value that often determines the ***extinction*** or ***persistence*** of the disease. $R_0 < 1$ means that a single infectious individual is very likely infecting less than one susceptible individual in some given population and hence the disease gradually dies out (Liu et al., 2020b). This situation is called flattening the curve and it is what every COVID-19 infected country strives to achieve by means of proposing all precautionary measures such as social distancing, wearing of face masks, and avoiding touch. On the other hand, $R_0 > 1$ means that one infectious individual is very likely to infect more than one susceptible individual and therefore, the disease invades more of the susceptible communities and therefore persists (Liu et al., 2020b).

Lack of continuous authenticated COVID-19 data from most countries in sub-Saharan Africa including Malawi presents a daunting task of estimating of R_0 both at local and global level (Liu et al., 2020b; Olanrewaju et al., 2021). With no encountered traceable reasons of the curve flattening of COVID-19 in Malawi, this paper aims to assess the scope of COVID-19 in Malawi and identify any existing challenges and opportunities towards estimation of the disease reproduction number R_0.

2. DATA AND METHODS

First, COVID-19 cumulative data published between April 2020 and April 2021 on the Website and Facebook page of the Malawi Ministry of Health (MoH) was collected and documented in a self-designed Excel database. This was followed by graphical analyses which were done to establish the scope of COVID-19 in Malawi for the past one year. Thereafter, different epidemiological techniques for estimating R_0 of a disease were reviewed and discussed in the context of the existing data set to identify existing challenges and opportunities to estimation of COVID-19 disease parameters including R_0. All data analyses were done in Excel at 95 % confidence interval (α=0.05).

3. RESULTS AND DISCUSSIONS

3.1 COVID-19 in Malawi from April 2020 to April 2021

For the period from April 2020 to April 2021, the results show that a cyclic pattern (Figure 3) of COVID-19 cases occurred in Malawi, with a record of first wave (April-July 2020) and second wave (January-February 2021). Overall, the trend shows a general increase in the number of confirmed cases with unclear reasons for flattening despite others citing government’s early enforcement of COVID-19 measures (Masina, 2020b). To the contrary, the drop of recorded cases could also be explained by shortage of testing kits such that only those that showed COVID-19 symptoms were tested (Munharo et al., 2020). Further, the occurrence of two identified waves could be linked to two possible occasions when hundreds of people returned from South Africa in May 2020 (Huaxia, 2020; Masina, 2020a) and January 2021 (Masina, 2021), respectively.

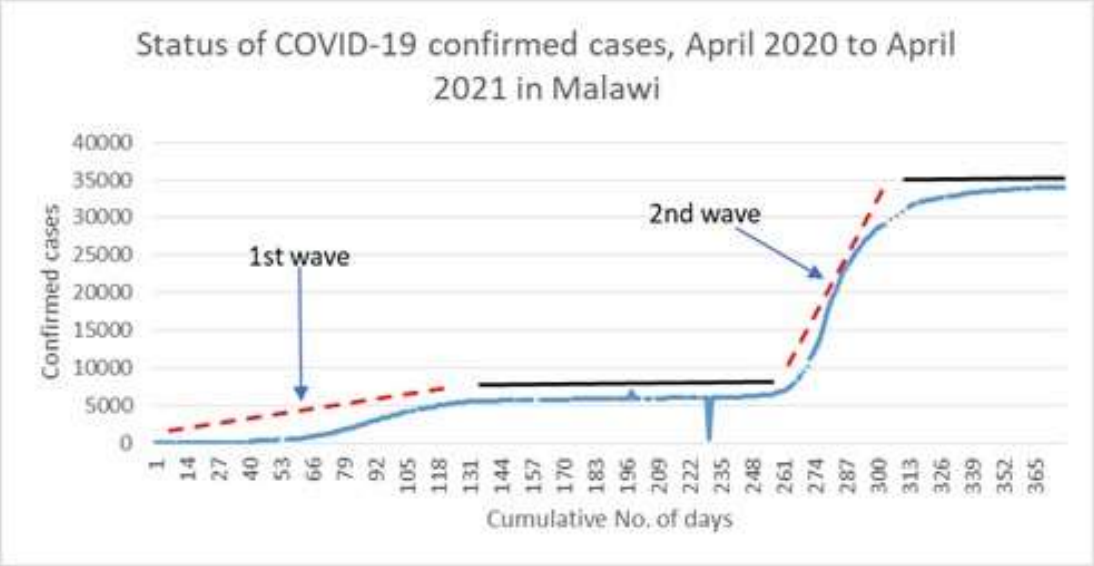

Figure 3: A 365 days trend of COVID-19 cases in Malawi, April 2020 to April 2021

An increase in number of confirmed COVID-19 cases (Figure 3) positively correlated ($r = 0.56$) with the increase in the number of active cases (Figure 4), following a similar trend when the curve of the latter decreased. Thus, the curve flattens at the time when the number of active cases begin to drop (Garba et al., 2020).

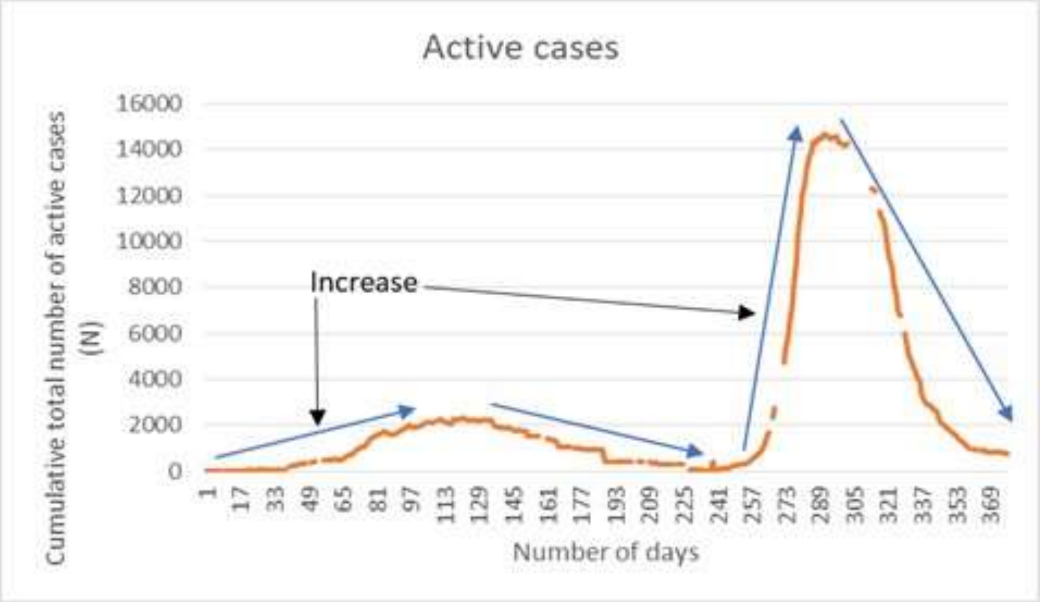

Figure 4: Number of active cases for the first 365 days.

3.2 Opportunities and Challenges towards estimation of $\boldsymbol{R_0}$ in Malawi

As a country, Malawi is endowed with 24-hourly COVID-19 data published by Public Health Institute of Malawi (PHIM), either on https://covid19.health.gov.mw/ or https://thandizo.mw through COVID-19 Helpdesks. This data can of course be validated against World Health Organization (WHO) data sources. Though limited by its accessibility, an attempt can be done to deduce a preliminary estimate of R_0 from such data. This is possible for both first and second wave (Figure 6) data sets by determining the disease growth rate k from an assumed exponential growth function $y = y_0 b^k$ for $k \geq 0$ and the ***base*** $b > 0$. An assumption for the exponential model is valid based on the 7 day-moving average (MA) curve of Figure 1.

The growth pattern of infection, assuming one person has an infection can be modelled as a recurrence relation $a_k = ba_{k-1}$, for $k \geq 1$ where $a_0 = 1$ and solved by method of generating function to obtain the solution $a_k = a_0 b^k$. Taking the limit as $k \rightarrow \infty$ results into an exponential growth of infected people. Then, from the deduced $y(t) = y_0 b^{kt}$ where k describes how fast the disease is progressing, one can estimate R_0 using method of generation interval (Wallinga & Lipsitch, 2007) where R_0 is related to k by the equation:

$$R_0 = {}^{1}\Big/_{\int_0^{\infty} e^{-k\tau} w(\tau) d\tau}.$$

The generation interval $w(\tau)$, "waiting time from being infected to secondary infection", can be empirically estimated (Park et al., 2019; Ganyani et al., 2020) from contact tracing data. Such information is not captured in the PHIM database, however. This is the first challenge we encounter towards estimation of R_0. Alternatively, using a mechanistic model such as **SIR**[1] or **SEIR**[2] (Li, 2018) to respectively deduce R_0 from:

$$R_0 = 1 - {}^{k}/_{\gamma} \quad \text{or} \quad R_0 = 1 + k\left(\frac{k}{\sigma\gamma} + \frac{1}{\gamma} + \frac{1}{\sigma}\right)$$

where γ and σ are recovery and disease death rates, respectively.

Lack of data to estimate γ presents a second challenge when one decides to consider R_0 deduced by either SIR or SEIR models. Nonetheless, since available COVID-19 data at PHIM website is presented cumulatively, one would perhaps consider estimating R_0 via more sophisticated phenomenological models such as Logistic or Richards models (Wu et al., 2020). Assuming an average infection waiting time $\tilde{w}(\tau) = 7$ days, we found $R_0 = 1.05479$ for the first wave (Figure 5) using method of generation interval. Although R_0 was nearly one, increasing decimals provided a *signal* of growth of the pandemic if measures of minimizing contact rates were not seriously followed. Such induction has been confirmed by continued growth of the disease (Figure 3).

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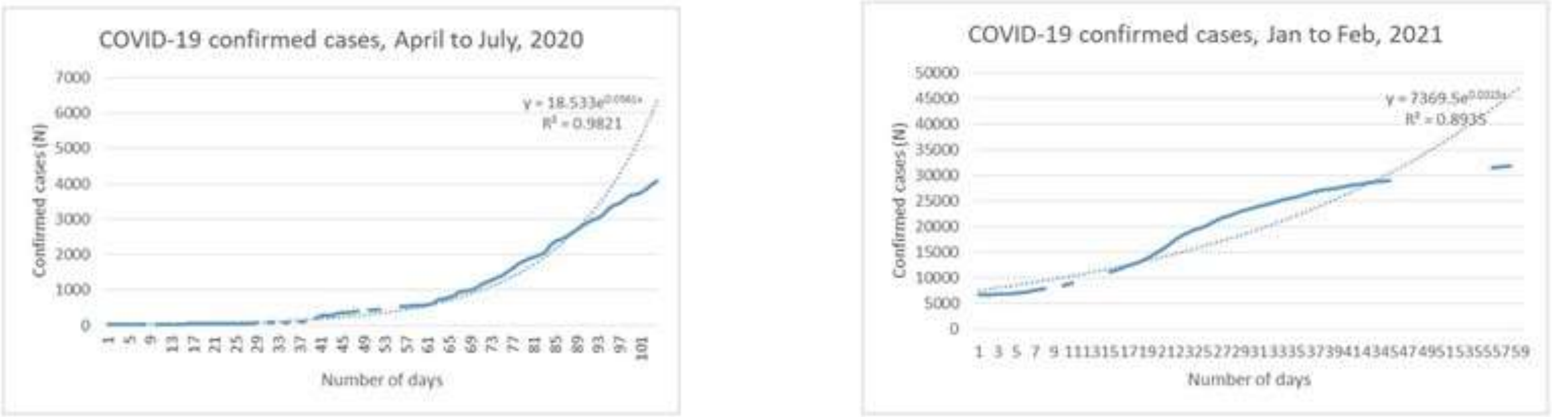
[1] SIR – Susceptible, Infected, Recovered compartmental model based on a set of ordinary differential equations

[2] SEIR –Another compartmental model which extends SIR by inclusion of "Exposure" compartment for a population



First wave

Second wave

Figure 5: Exponentially distributed data of confirmed cases showing first and second waves.

Comparably, we observed that the exponential growth rate decreased during the second wave than it was during the first wave (Figure). While this might seem unsound, considering that more deaths were recorded in the second wave than the first wave (Figure), the decrease in the exponential growth rate could have resulted from depletion of the susceptible.

Further, the positive correlation ($r = 0.56$) between cumulative number of confirmed cases and number of active cases we found means a lot. First, despite misconception about COVID-19 being politically motivated, the probability of data falsification or fabrication during both recording and reporting could therefore be very negligible. Otherwise, we could have observed much discrepancy between the presented Figure 3, Figure 4, and Figure 6. However, PHIM through MoH and other designated clusters must ensure that we do not have cases of missing data on certain cumulative number of days as this may raise serious eye-brows to the public. Secondly, the trend observed so far, may have serious implications over the predictive power of what may happen next. By moving from high to low, then low to high may imply a possible repeat of the pattern such that now, from low, we might again go higher than before in recording number of COVID-19 cases. This pattern has also been observed elsewhere, such as in Kenya which has already suffered from the third wave (Mutambo, 2021).

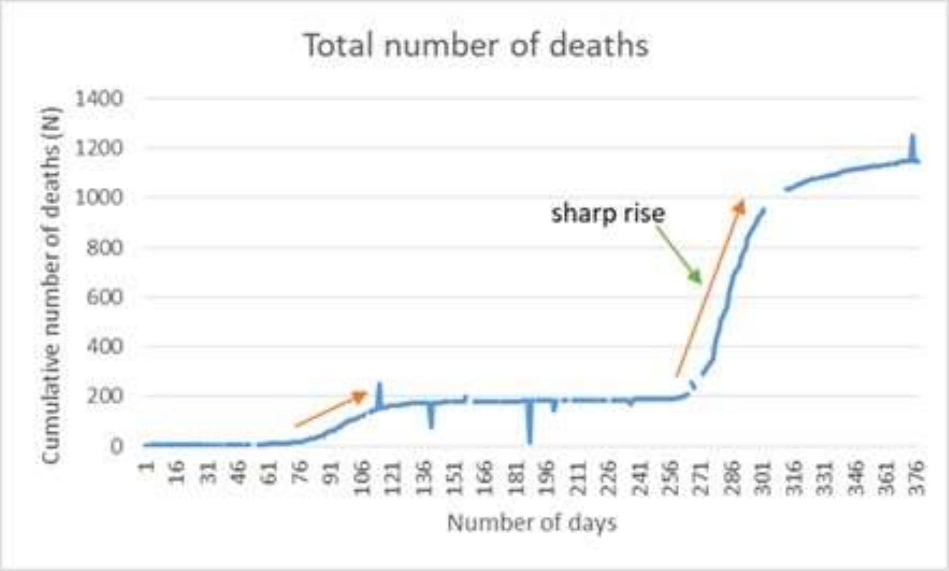


Figure 6: Distribution of number of recorded deaths due to COVID-19.

It may not be an exceptional case for Malawi as well. We must therefore seriously watch this pattern and take all necessary precautionary measures to prevent it from repeat. Should this pattern repeat, not predicting doom though, Malawi may move out of the flattened curve for another wave (third) with R_0 much greater than one.

4 CONCLUSION(S) AND FURTHER RESEARCH

Based on the preliminary estimate of $R_0 > 1$, the COVID-19 pandemic is likely to continue in Malawi for long if not all the necessary safety measures are strictly followed (Covid-19.gov, 2020). To better establish a more realistic measure of R_0, however, we are currently working on an SEIR Disease Model in order to fully understand the COVID-19 transmission rates and determine the influence of socio-demographic factors on the disease dynamics (Li, 2018).

There are also other several directions for further research. While working on a proposed SEIR Disease Model, it is also possible to consider developing a stochastic epidemic model (Julie & Lauren, 2018) to predict the probability of disease extinction and foretell the duration of the pandemic in Malawi. Thus, a continuous-time Markov chain model could be considered in this case with usage of the Branching process (Li, 2018). As we continuously watch the COVID-19 pattern, in future, we may consider using chain sized data approach (Blumberg & Lloyd-Smith, 2013) in predicting R_0 should the disease exhibit subcritical transmission (i.e. $0 < R_0 < 1$) in our SEIR or Markov chain-based models. Lastly, based on the cumulative data set, real-time prediction of COVID-19 severity in Malawi using a simple model such as Logistic or Richards (Wu et al., 2020) should be possible as well.

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