Technical Report 5

Basic Reproduction Number (R_0) of SARS-CoV-2

Nuwan Darshana Wickramasinghe[1*]**, Sumudu Avanthi Hewage**[2]**, Surangi Jayakody**[3]**, Shamini Prathapan**[3]**, Carukshi Arambepola**[4]

[1] Department of Community Medicine, Faculty of Medicine & Allied Sciences, Rajarata University of Sri Lanka; [2] National Program for Tuberculosis Control and Chest Diseases, Ministry of Health and Indigenous Medical Services, Sri Lanka; [3] Department of Community Medicine, Faculty of Medical Sciences, University of Sri Jayewardenepura, Sri Lanka; [4] Department of Community Medicine, Faculty of Medicine, University of Colombo, Sri Lanka

*Correspondence: nuwick74@yahoo.com

https://orcid.org/0000-0001-6025-6022

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Highlights

- Any health crisis is prone to create a lot of misinformation, termed "infodemic" in the current context.

- Current technological advancement facilitates the spread of misinformation much faster.

- Public health community plays a major role in educating media to spread the correct information during a health crisis.

What is Basic Reproduction Number (R_0)?

The basic reproduction number (R_0) is an epidemiologic metric that has been widely used to study the infectious disease dynamics. R_0 is defined as 'the number of secondary cases which one case would produce in a completely susceptible population' (1). Hence, it is considered as a useful metric to describe the contagiousness or transmissibility of infectious agents (2) and it serves as a threshold parameter that predicts whether an outbreak is expected to continue (3).

The main parameters used for the estimation of R_0 are,

- The contact rate

- The duration of the infectious period

- The probability that a contact between an infective and a susceptible individual can lead to an infection, which is a combination of infectivity and susceptibility (1)

Theoretically, even though the actual R value could be possibly measured during an outbreak caused by a novel infectious agent spreading in a completely susceptible population, the issues with accuracy, completeness as well as timeliness of the disease surveillance system make it practically dificult to measure R accurately.

Even though the concept of R and its interpretation is simple, the estimation of the value involves complex mathematical models developed using various sets of assumptions. Thus, interpretation of the estimates of R derived from different models need to take into consideration the underpinning model structures and the data related assumptions.

Public health applications of R_0

The concept of R was initially used in the field of demography and later adopted to the field of epidemiology (4). Initially, the concept was used in studying the disease spread of malaria and at present, R values have been published for a number of infectious diseases such as measles, polio, influenza, Ebola and HIV (2).

R_0 is used to determine the amount of effort necessary to prevent an epidemic as well as to eliminate an infection from a population (1). Considered in the context of other epidemiologically important parameters, the value of R lies in understanding an outbreak and in preparing a public health response (5).

More importantly, using the R the 'hreshold criterion' is determined, which highlights that the outbreak is expected to continue if the R has a value >1 and to end if R is <1 (6).

There are two fundamental strategies used in an outbreak, namely, suppression and mitigation. The main aim of suppression is to reduce the R_0 below 1, using stringent measures ultimately leading the case numbers to decline reversing the epidemic growth, where as the main aim of mitigation is to slow the spread by reducing R_0 not necessarily below 1, reducing peak healthcare demand while protecting those most at risk of severe disease from infection (7).

R_0 of SARS-CoV-2 and gaps in existing knowledge

According to the World Health Organization, the R_0 of SARS-CoV-2 is 1.4-2.5 (8). The R_0 of SARS-CoV-2 has been estimated in a number of studies and a recent review reported the average estimate of R_0 as 3.28 based on the data available for different geographic regions at different stages of the epidemic of COVID-19 (9). Despite the fact that the evidence collated in the review was mainly from studies using data originating from China, the R_0 values of individual studies ranged from 2.2 (95% CI=1.4, 3.9) (10) to 6.49 (95% CI=6.31, 6.66) (11).

The majority of existing evidence on R_0 of SARS-CoV-2 is based on data originating from China and also during the early stages of the epidemic. There is a lack of evidence on estimates of R_0 based on data originating from other countries/regions of the world in parallel with the evolving pandemic of COVID-19.

Applicability of the evidence on R_0 of SARS-CoV-2 to Sri Lanka

Estimation of the R_0 for a particular disease epidemic has limited practical value outside the population from which the disease data originated (5), thus the evidence on estimates of R_0 developed based on data from other countries/regions need to be interpreted and applied to the Sri Lankan context cautiously.

Given that R_0 estimates are based on parameters such as the contact rate, the duration of the infectious period and the probability that a contact between an infective and a susceptible individual leads to an infection, any factor or condition that could potentially influence the above parameters would affect R_0 estimates as well. Hence, a multitude of biological, social, behavioural and environmental factors could affect R_0.

The first local case of COVID-19 was reported in Sri Lanka on 11 March 2020 (12) and since then the Sri Lankan government has taken proactive measures to control COVID-19 outbreak. Considering the limited healthcare capacity to deal with a high caseload, Sri Lanka has taken suppression strategies combined

with mitigation strategies relatively early in the epidemic. Amongst the non-pharmaceutical interventions, government decisions such as imposing island-wide curfew and quarantine procedures have a direct influence on drastically reducing the contact rate. Furthermore, it needs to be appreciated that Sri Lanka has taken such initiatives relatively early in the epidemic, as opposed to many countries from which R_0 data originated.

In addition, differences in factors such as population mixing and contact patterns in Sri Lanka and other countries need to be considered. The government decisions on closure of schools, pre-schools and universities prevented the possibility of homogeneous population mixing, which has resulted in not having widespread community transmission.

An important factor associated with the susceptibility is the underlying population structure and it is noteworthy to observe that the estimates of R_0 have been developed in countries with different population structures to that in Sri Lanka. Furthermore, it is important to note the differences in prevalence of associated comorbidities between populations in other countries/regions and Sri Lanka. Apart from that, the government initiatives on home delivery of medicines for patients suffering from non-communicable diseases further limit the exposure of susceptible populations.

On the other hand, Sri Lanka does not have adequate facilities to perform a large number of diagnostic tests with the aim of early identification of possible cases of COVID-19, which could result in a relatively longer duration of disease spread as opposed to countries with early diagnostic facilities. Furthermore, lack of evidence on asymptomatic cases and withholding travel and contact history linked to COVID-19 (due to various reasons including associated stigma) hinders the possibility of early identification of cases of COVID-19.

In summary, even if the factors such as infectiousness of the agent and the duration of contagiousness remain as biological constants, factors like contact rate and patterns, susceptibility of the population and actual duration of infectivity may vary considerably,

limiting the applicability of R_0 estimates developed in other countries, to Sri Lanka.

Recommendations

Due to the fact that R_0 estimates developed based on the data elsewhere is limited in the Sri Lankan context, developing locally relevant evidence for effective public health response to COVID-19 outbreak in Sri Lanka is highly recommended.

Author Declaration

Author contributions: NW initiated and developed the concept and wrote the draft article. All authors assisted in the interpretation of contents, revised and approved the final draft.

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