World Journal of Advance
Pharmaceutical Sciences

Volume 1, Issue 1. Page: 1-5

Review Article

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INSIGHTS FROM INFECTIOUS DISEASE EPIDEMIOLOGY ON COVID-19 RESPONSE IN ETHIOPIA

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How to cite this Article: Daniel Geleta* (2024). INSIGHTS FROM INFECTIOUS DISEASE EPIDEMIOLOGY ON COVID-19 RESPONSE IN ETHIOPIA. World Journal of Advance Pharmaceutical Sciences, 1(1), 1-5.

Article Info

Article Received: 30 October 2024,

Article Revised: 20 November 2024,

Article Accepted: 10 December 2024.

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ABSTRACT

Infectious diseases, caused by living organisms and capable of being transmitted from person to person, have posed a persistent threat throughout human history. These diseases continue to undergo evolution and present challenges to societies in various manifestations. The field of infectious disease epidemiology emerged within human society to address the spread of such diseases. It employs methodologies including surveillance, tracking, statistical analysis, and experimentation to investigate and manage epidemic outbreaks. A prominent contemporary illustration of this is the COVID-19 pandemic, which many have identified as the most significant global challenge since the establishment of the United Nations. COVID-19 is notable for its rapid transmission through human-to-human contact, with varying rates influenced by factors like population density and healthcare system efficacy. Statistical and mathematical models have played a pivotal function in guiding strategies to combat the virus. These models typically incorporate formulas that account for amount of relations per unit time, the transmission probability per contact, and duration of infection. In Ethiopia, such models were utilized to direct governmental initiatives aimed at mitigating the risk of secondary transmission, particularly in the southwestern region of the country.

KEYWORDS: basic reproductive number, COVID-19, Herd immunity, infectious disease.

INTRODUCTION

Infectious diseases caused by living organisms and transmissible diseases have been a longstanding issue and are expected to persist with varying characteristics.[1,2] Infectious disease epidemiology plays a crucial role in addressing these challenges by studying a wide range of infectious disease-related topics. This includes conducting research on epidemic diseases through methods such as supervision, surveillance, statistical inference, analytical research, and experimentation. By understanding the etiological conditions of these diseases, researchers can intervene in their treatment and prevention, leading to broader improvements in health and healthcare services.[3]

In essence, infectious disease epidemiology helps to elucidate the causes of newly emerging infectious diseases, organizes and conducts infectious disease surveillance, identifies sources of outbreaks, and determines transmission routes.[4] A notable instance of this is recent COVID-19 pandemic triggered due to novel coronavirus, which has brought globe to high alert. This pandemic, considered one of the deadliest in history, has tested the world's resilience and response capabilities since the establishment of the United Nations.[3,5] The widespread effect of COVID-19 has led to near-total closure of institutions, creating a human development crisis that extends across all sectors of society.[6]

Unlike other crises, pandemics like COVID-19 initially cause health shocks that can have long-lasting effects on human development and may impact future generations.[7] In light of this, the following text will delve into the role of infectious disease epidemiology in controlling and preventing spreading of COVID-19.

A transmission model of COVID-19 grounded on its potential transmission pattern

The COVID-19 virus has complete human-to-human transmission potential, with high transmission heterogeneity based on demographics and healthcare systems. Countries with well-developed healthcare systems that have adequate resources like hospitals, clinics, testing labs, protective equipment, ICU beds, and trained medical staff are better equipped to handle an outbreak. When a new virus emerges, these countries can quickly test large numbers of people to identify cases, trace contacts, and isolate those infected. The healthcare infrastructure of a nation performs a vital function in mitigating spreading infectious illnesses such as COVID-19. Countries with well-established systems, adequate resources, and trained healthcare professionals are better equipped to conduct efficient testing, contact tracing, and isolation measures, thus reducing the risk of widespread transmission. Conversely, many developing countries struggle with limited infrastructure, resulting in overwhelmed healthcare facilities, resource shortages, and increased vulnerability for healthcare workers. The availability of testing and adherence to public health guidelines are also pivotal in enabling effective virus surveillance and containment. Rural regions face additional obstacles due to limited healthcare access, exacerbating the challenges in controlling disease spread. These various factors collectively influence the speed at which a disease can propagate within a community. Therefore, robust public health systems are indispensable in effectively combating pandemics and preserving public health.[8]

In this regard, mathematical and data-driven modeling aids in providing clues and insights into disease transmission that can easily inform disease-fighting decision-making.[2,9] To support this, the characteristics of population in south-western Ethiopia were divided into seven classes

- Sum of unconfined susceptible (Su)
- Sum of confined susceptible (Sc)
- Sum of exposed (E)
- Sum of reported infectious (Ir)
- Sum of silent carriers (unreported) (Iu)
- Sum of recovered (R)
- Sum of quarantined (Q)

As illustrated by the arrow in figure 1, individuals continue to traverse between the compartments.[10] An individual transits to Su class, either from Q class at a constant rate of $\theta(1-\lambda)$ or from Sc class at a rate of $1-m(t)$.

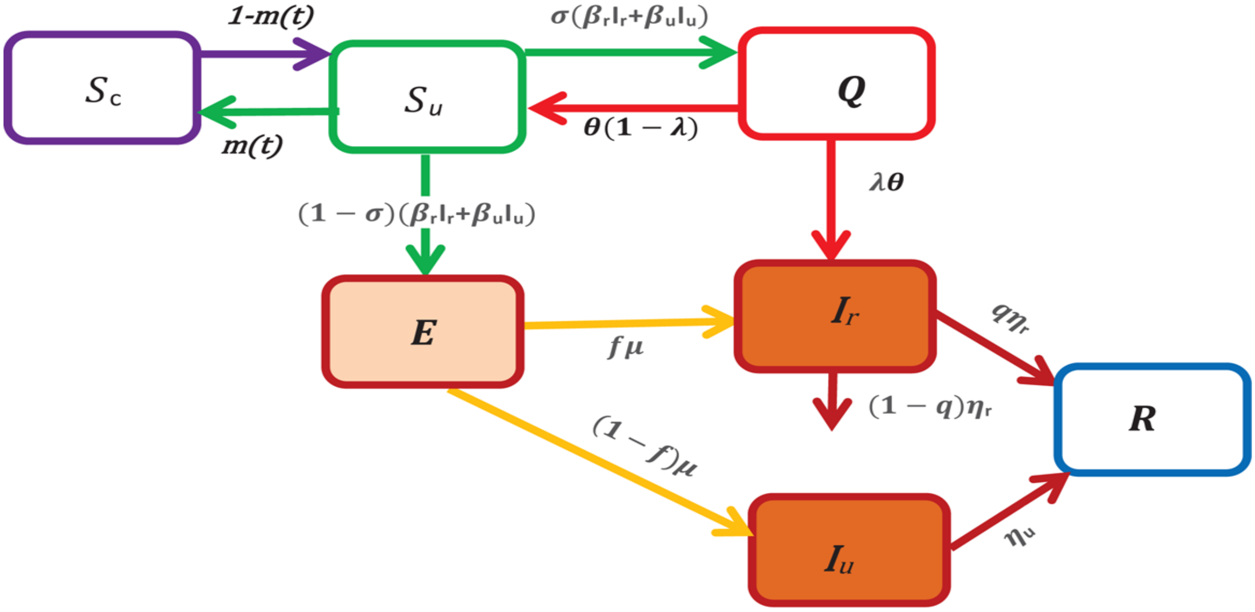

Figure 1: Diagrammatic representation of model for COVID-19 transmission.

In the scenario presented, we are considering what would happen to both reported and unreported individuals infected with the COVID-19. For reported individuals, we can break down their outcomes into recovering or dying from the disease. Not all reported cases will result in death, as some will recover from the infection. We define q as a fraction of reported people that recover from disease. The remaining population, 1-q, represent those reported cases that ultimately result in death.

For those reported individuals that do not recover and unfortunately die from the disease, their rate of death can be represented as $(1-q)\eta r$. Let's break this rate down term by term. The first term, $1-q$, captures fraction of reported cases that do not retrieve and instead die from the infection. As mentioned, this is equal to fraction of reported cases resulting in death. Second term, ηr, represents mean length of the infectious interval for reported population. This can help provide context for how long reported cases on average remain infectious before either recovering or dying. By multiplying these two terms, (1 − q) ηr, we obtain the rate at which reported infectious individuals die from the disease.[10] Throughout COVID-19 pandemic, adherence to these important public health values facilitated crucial clinical studies, epidemiological research, contact tracing efforts, and data sharing. Clinical studies involved monitoring patients with SARS-CoV-2 to understand disease progression and treatment effectiveness. Epidemiologists tracked virus spread based on various factors, aiding in public health recommendations. Contact tracing identified exposures and informed quarantine measures. Regular public health reports provided vital data for trend monitoring and severity assessment. Monitoring variants emphasized the need for ongoing vigilance and tailored response strategies.

Identify the Basic Reproductive Number (R_0) for COVID-19

R_0 defines and indicates the mean figure of secondary infections which appear when an infected individual is introduced into a unifected population at which all hosts are at potential risk.[11] Therefore, the ability to directly quantify R_0 is a useful first step in predicting the emergence or status of the disease. For example, the Ethiopian government is engaged in an ongoing fight to decrease threat of secondary illness in southwestern part of Ethiopia, where we live in the raging COVID-19, which is epidemiologically called targeted reduction of R_0. For a disease to increase, stabilize, or decrease in the host population, a form $R_0 > 1$ (infectious individual must produce at least more than one secondary infectious condition), $R_0 = 1$ (infected individuals must at least replace themselves), or $R_0 < 1$ (fading or disappearing pattern) appears. R0, which can be stated as the product of the sum of interactions per unit time, the likelihood of transmission on each interaction, and the period of infection, is seen in Figure 1 above. Consequently, Ro may be computed using the generic classical epidemiological models and the next generation matrix approach utilizing $Ro = \frac{\mu S0}{\beta+\gamma} = \frac{\mu N}{\beta+\gamma}$, *where the starting population at the beginning of the infection is denoted as* $S_0 \approxeq N$*, and the average infectious time of the disease is represented by* $1/\beta+\gamma$*. The* μ *rate of recovery from infection, the* γ *rate of disease-induced mortality, and the* μ *rate of transmission from susceptible to infected persons with corresponding values being 0.000000000576963, 0.007176440779023, and 0.000673679204030.*[12] *Accordingly, the estimated* R_0 *for nearly 30,000,000 South-west Ethiopian populations at the early stage of COVID-19 will be*

$$R_0 = \frac{0.000000000576963 \ X \ 30{,}000{,}000}{0.007176440779023 + 0.000673679204030 2a} = 2.21.$$

This means that, in southwestern Ethiopia, a single case of COVID-19 will, on average, generate 2 new secondary cases, or the number of persons infected per person infecting is 2.21.

The points of transmission links for potential intervention from the model

Coming from either the confined class or the quarantined class, an individual can transfer to the susceptible unconfined class, Su, at a rate of 1 − m(t) or a constant rate of θ(1 − λ), respectively. We have included the parameter m(t), which represents the fraction of confined susceptible individuals at any given time t, as the central parameter in our model for studying containment techniques. The exposition gives either the reported class, Ir, or the unreported class, Iu, when susceptible individuals are exposed to the virus. It is assumed that, regardless of where the infection originated, a portion σ of susceptible unconfined individuals who have encounter an infectious person are quarantined using contact tracing. On the other hand, a portion (1 − σ) that was not detected by contact tracing either moves to exposed class E once effectively infected or remains in compartment Su otherwise. The new people entering the exposed class E are represented by the quantities (1 − σ) (βrIr + βuIu) S, while the new individuals entering the quarantined class Q are denoted by σ(βrIr + βuIu)S. The reported case transmission rate (βr) and the unreported case transmission rate (βu) are the factors in question. Since most people who report an infection are likely to be in isolation at home or in the hospital, we can safely conclude that the reported infection rate is lower than the unreported infection rate. Nonetheless, they pose a threat of infection to those who care for them or accompany them. Additionally, they might have initially contributed to the spread of the virus as asymptomatic carriers. When the parameter ñ is set to 1, the infectivity level of both reported and unreported cases is equal. After an average length of isolation, 1/θ, a fraction λ of the quarantined individuals become infected and transition to the reported infectious class, Ir, while a percentage 1 − λ returns to the susceptible class without being reported infectious. Assuming that the average length of the exposed period is 1/μ, we find that a fraction (f) of the exposed class's individuals become reported infectious and enter the class Ir at a rate μ, while the other fraction (1 − f) goes to the infectious unreported infectious class Iu at a rate μ.

The fight against COVID-19 in southwest Ethiopia requires strategic public health interventions to reduce the virus's reproduction number (R0) to below 1. This involves reducing social contact, wearing face masks, strengthening quarantine protocols, and contact tracing. Public advisories encourage maintaining at least 6 feet of distance between individuals and restricting gatherings. Large-scale screening using rapid antigen tests helps identify cases early. Contact tracing helps break the chain of transmission by interviewing positive cases and testing those contacts. Comprehensive reporting of confirmed and suspected cases helps assess spread and allocate resources effectively. With continued *community cooperation, the goal of driving the R0 below 1 is within reach.*

The potential herd immunity for COVID-19 through vaccination

For an infection that depends on person-to-person transmission, the ratio of immune to susceptible people in a populace can determine whether the infection becomes established in a community or rapidly dies out. Protecting vulnerable (i.e., unvaccinated) individuals is the goal of herd immunity, which develops when a large percentage of a population or herd is vaccinated or immune to a disease.[13] When enough individuals in a population are immune, the disease has difficulty spreading from person to person. This breaks up the "chain of infection" and lowers the overall amount of transmission in the whole population. In order for an infectious disease to stay stable in a community, a certain proportion of the population must be immune; this proportion is called the herd immunity threshold (HIT). (sometimes called critical proportion) and denoted as

$$\text{HIT} = \frac{R_0 - 1}{R_0} \text{ or } 1 - \frac{1}{R_0} = \frac{2.21-1}{2.21} = 55\%$$

for the scenario in this document.[14]

If 55% of the population is vaccinated against COVID-19, we assume that the infection will stabilize in the population, with each case leading to a new case. Epidemiologically, this assumption can be estimated using effective reproduction number (R) for which corresponding value is R = 1 or lower from the equation R_0X *(where 'X' is ratio of susceptible people).*

Accordingly, applicable reproductive number of COVID-19 in southwestern Ethiopia is

$$R = R0\ X\ \mathit{susceptable\ or\ unimmunized}\ (45\%) = 2.21X.45 \cong 1,$$

the effective reproductive number (R) ≅1 indicating stable COVID-19 spread in South-western Ethiopia.

If for any reason the vaccine fails to be effective, assuming that the vaccine fails in a 1-E fraction of the people who receive it while the E fraction is fully protected, HIT OR critical vaccination coverage level will be divided into the E fraction ($V_c=(1-1/R_0)/E$).[14][11]

In the example above with an R0 of 2.21, a HIT of 55% indicates a need for immunization in at least 55% of the population. However, if there is a failure somewhere along the cold chain required to keep vaccine viable from production to injection and vaccine fail completely assume in 10% of the vaccinated people, fraction of that must be vaccinated to eradicate transmission increases. In this case, the HIT/Vc would again be calculated as 0.55/0.90 = 0.611, which means that 6.1% more vaccination, or 61.1% of the population, needs to be vaccinated (assuming that vaccination takes place at random).

Ultimately, in a scenario where all COVID-19 immunized individuals are completely protected for life and a fraction 'f' of that fraction is vaccinated before the first infection occurs, the highest possible fraction of vulnerable people would be '1-f'. This fraction is represented as the basic reproductive number under vaccination (R0p), which is the sum of secondary cases resulting from one primary case introduced into a community where a proportion 'f' has been immunized, and its goal is to eradicate transmission. Mathematically, it gives R0p = (1-f) R0.[11] *In southwestern Ethiopia, it was assumed that nearly 10,000,000 (33.3%) of the community were immunized before the age of first infection, giving about 66.7% of the susceptible fraction. Consequently, the R0p will be 1-0.333/2.21, which finally provides 0.31. This means that 33.3% of the vaccinated population in southwestern Ethiopia has nearly 0.31 secondary cases triggered due to one primary case.*

CONCLUSION AND RECOMMENDATION

The field of infectious disease epidemiology is vital for comprehending and managing the transmission of diseases like COVID-19. Findings from southwestern Ethiopia highlight the difficulties in managing transmission and underscore the need for targeted public health interventions. Mathematical models indicate that strategies like vaccination can significantly reduce the basic reproduction number (R0) and help achieve herd immunity.

The COVID-19 pandemic has presented not only immediate health challenges but also long-term consequences for human development and societal structures. Effectively tackling these issues requires coordinated efforts among government agencies, healthcare providers, and communities.

To address these challenges, it is essential to increase vaccination coverage, strengthen public health infrastructure, implement community engagement strategies, monitor and evaluate interventions, and promote research and development. These actions will not only help manage current outbreaks but also prepare for potential future pandemics.

ACKNOWLEDGMENT

None to declare.

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