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Review Article

Insights from Infectious Disease Epidemiology on COVID-19 Response in Ethiopia.

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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. Mathematical and statistical models have played a pivotal role in guiding strategies to combat the virus. These models typically incorporate formulas that account for the number of contacts per unit time, the transmission probability per contact, and the infection duration. 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 example of this is the recent COVID-19 pandemic caused by the novel coronavirus, which has brought the world 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 impact of COVID-19 has led to the 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 the spread of COVID-19.

A transmission model of COVID-19 based 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

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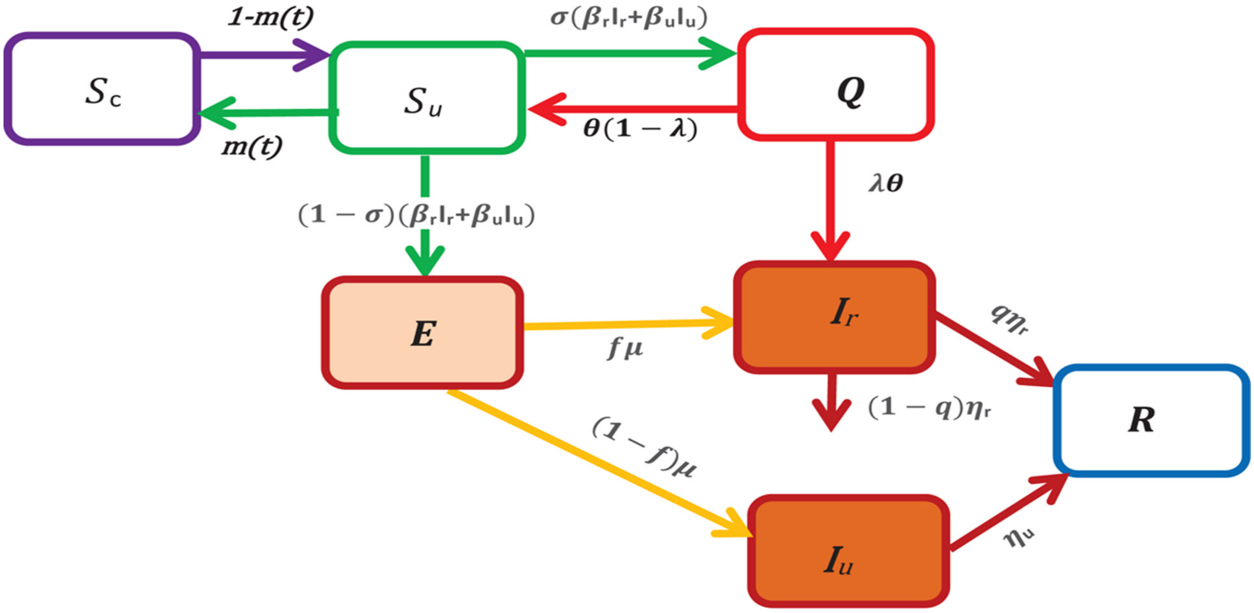
equipment, ICU beds, and trained medical staff are better equipped to handle an outbreak. When a new virus emerges, these countries can quickly test large numbers of people to identify cases, trace contacts, and isolate those infected. The healthcare infrastructure of a nation plays a critical role in mitigating the spread of infectious diseases 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; the number of unconfined susceptible (Su), the number of confined susceptible (Sc), the number of exposed (E), the number of reported infectious (Ir), the number of unreported infectious or silent carriers (Iu), the number of recovered (R), and the number of quarantined (Q) as indicated by the arrow in **figure 1** to show the people moving between the compartments (10). An individual moves to the susceptible unconfined class, Su, either from the confined class at a rate 1 − *m(t)* or from the quarantined class at a constant rate θ (1 − λ).

Figure 1. A schematic of the 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 the fraction of reported individuals that recover from the disease. The remaining fraction, 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) ηr. Let's break this rate down term by term. The first term, 1 − q, captures the fraction of reported cases that do not recover and instead die from the infection. As mentioned, this is equal to the fraction of reported cases resulting in death. The second term, ηr, represents the average length of the infectious period for reported individuals. 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). During the 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 (R0) for COVID-19

R0 defines and indicates the average number of secondary infections that occur when one infected person is introduced into a host population at which all hosts are at potential risk (11). Therefore, the ability to directly quantify R0 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 reduce the risk of secondary infection in the southwestern part of Ethiopia, where we live in the raging COVID-19, which is epidemiologically called targeted reduction of R0. 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. From **Figure 1** above, R_0 illustrates a concept that can be expressed as the product of the number of contacts per unit time, the probability of transmission per contact, and the duration of infection. Therefore, Ro could be calculated from the next generation matrix method and the general classical epidemiological models using

$$Ro = \frac{\mu S0}{\beta + \gamma} = \frac{\mu N}{\beta + \gamma}$$

where $S_0 \simeq N$ is the initial population during the onset of infection and 1/ β+γ is the average infectious period of the disease. The rate of transmission from susceptible to infectious individuals (μ), the rate of recovery from infection (β), and the disease induced death rate (γ), 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

$$\mathrm{R0} = \frac{0.000000000576963 \times 30{,}000{,}000}{0.007176440779023 + 0.0006736792040302\mathrm{a}} = 2.21$$

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

An individual moves to the susceptible unconfined class, Su, either from the confined class at a rate 1 − m(t) or from the quarantined class at a constant rate θ(1 − λ). The fundamental parameter that we have introduced in our model to study the containment measures is the parameter m(t), it can be interpreted as the fraction of confined susceptible individuals at any time t. When the susceptible individuals are exposed to the virus, then the exposition provides either the reported class, Ir or the unreported class, Iu. Without making any distinction about the origin of the infection, we assume that a fraction σ of susceptible unconfined individuals which has been in contact with an infectious individual is quarantined with contact tracing while the other fraction (1 − σ) who was not detected by the contact tracing move to the exposed class E once effectively infected or stay in compartment Su otherwise. Then, the quantities (1 − σ) (βrIr + βuIu) S and σ(βrIr + βuIu)S represent the inflow of new individuals into the exposed class E and quarantined class Q respectively. The parameters βr and βu are the transmission rate of reported and unreported cases, respectively. We assume that reported individuals will participate in the infections with a lower rate than those unreported because they are generally isolated at the hospital or at home. However, they can transmit the infection to caregivers or their entourage. Moreover, they may have first been asymptomatic carriers contributing to the transmission of the virus. The parameter ñ represents the infectivity of the reported cases and for ñ = 1, the reported and unreported have the same level of infectivity. Among the quarantined individuals, a fraction λ of individuals are effectively infected and moves in the reported infectious class, Ir, after an average duration of isolation, 1/θ, and a fraction 1 − λ returns to the susceptible class without being reported infectious. We assume that only a fraction f of the individuals of exposed class becomes reported infectious and enters to the class Ir at a rate μ where 1/μ represents the average length of the exposed period while the other fraction (1 − f) moves 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 (R_0) 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 proportion of immune to susceptible individuals in a population can determine whether the infection becomes established in a community or rapidly dies out. Herd immunity occurs when a significant proportion of the population (or the herd) have been vaccinated (or are immune by some other mechanism), resulting in protection for susceptible (e.g. unvaccinated) individuals (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. The herd immunity threshold (HIT) is the proportion of a population that needs to be immune in order for an infectious disease to become stable in that

$$\text{HIT} = \frac{R_0 - 1}{R_0} \quad \text{or} \quad 1 - \frac{1}{R_0}$$

community (sometimes called critical proportion) and denoted as $= \frac{2.21 - 1}{2.21} = 55\%$ 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 the effective reproduction number (R) for which the corresponding value is R = 1 or lower from the equation R_0X (where 'X' is the proportion of susceptible population).

Accordingly, the effective reproductive number of COVID-19 in southwestern Ethiopia is $R=R_0$ X susceptable or unimmunized (45%)=2.21X.45≅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 ($Vc=(1-1/R_0)/E$)(14)(11).

In the example above with an R_0 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, the fraction of that must be vaccinated to eliminate 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). Finally, if immunization confers complete and lifelong immunity in all of the immunized individuals for COVID-19 and a fraction 'f' is immunized before the age of the first infection, then '1-f' would be the maximum fraction of the population of susceptible, and expressed as the basic reproductive number under vaccination (R0p), which refers to the basic reproductive number under vaccination (the number of secondary cases caused by one primary case introduced into a population in which a proportion f has been vaccinated), to eliminate 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 caused by one primary case.

CONCLUSION AND RECOMMENDATION

Infectious disease epidemiology plays a crucial role in understanding and controlling the spread of diseases such as 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 (R_0) 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.

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