Journal of Fundamental and Applied Sciences

Research Article

ISSN 1112-9867

Available online at http://www.jfas.info

COMPARATIVE ANALYSIS OF TRANSMISSIBILITY AND CASE FATALITY RATIO OF SARS, MERS AND COVID-19 VIA A MATHEMATICAL MODELING APPROACH

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Received: 13 October 2020 / Accepted: 28 July 2021 / Published online: 01 September 2021

ABSTRACT

Coronavirus epidemics emerged in the 1960s and the world has witnessed seven coronavirus outbreaks since then. Four of the coronaviruses instigate human influenza while the rest: Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) trigger severe respiratory disorders (SARS, MERS and COVID-19 respectively). The etiology of SARS, MERS and COVID-19 are similar but their epidemiology, in terms of incubation period, infectivity, case fatality ratio and the serial interval differ. In an attempt to compare the infectivity and case fatality ratio of the diseases, a mathematical model was considered for each disease. The key epidemiological quantity, the basic reproduction number, was derived for each model to examine the transmission potential of each disease. The mortality rates for the diseases were also investigated by considering the global report of COVID-19 as of October 1 2020 together with the history of SARS and MERS. Results from the computations showed that COVID-19 had the highest transmission potential and at the same time the lowest case fatality ratio. It was also revealed that COVID-19 would have wrecked more havocs had its case fatality ratio was as high as that of MERS.

Keywords: Coronavirus; incubation period; infectivity; case fatality ratio; reproduction number.

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doi: http://dx.doi.org/10.4314/jfas.v13i3.7

1. INTRODUCTION

Coronavirus is a virus that triggers contagious diseases in birds and mammals. Generally, the virus activates respiratory disorders in man and animals and the first case was reported in the 1960s [1]. The transmission modes of coronavirus are related to the transmission routes of other viruses: through coughing, sneezing, unprotected contact with the infected individuals or contaminated objects [2]. The world has witnessed the epidemics of coronavirus disease that threaten pandemic in 2002-2003 by Severe Acute Respiratory Syndrome (SARS) which emerged in China and also in 2012 by Middle East Respiratory Syndrome (MERS) that emerged in Saudi Arabia [3]. Both SARS and MERS had zoonotic origin and were initiated by SARS-CoV and MERS-CoV respectively [4]. In December 2019, another epidemic of coronavirus that instigates respiratory-related infections erupted in Wuhan, China, a disorder which is now officially recognized as "the coronavirus disease 2019; COVID-19" [5]. COVID-19 is instigated by SARS-CoV-2.

Table 1. Biological characteristics of SARS-CoV, MERS-CoV and SARS-COV-2 [27, 37]

Features	**SARS-CoV**	**MERS-CoV**	**SARS-CoV-2**
Date of Emergence	November 2002	April 2012	December 2019
Country of Emergence	Guangdong, China	Saudi-Arabia	Wuhan, China
Date of Eradication	July 2003	Not yet eradicated	Not yet eradicated
Key hosts	Bats, palm civets and Raccoon dogs	Camels	Bats
Number of countries affected	37	27	213
Signs and symptoms	Fever, malaise, myalgia, headache, diarrhea, shivering, cough and shortness of breath	Fever, chills, generalized myalgia, cough, nausea shortness of breath, diarrhea and vomitting	Cough, fever, shortness of breath
Disease caused	SARS, ARDS	MERS	COVID-19, SARS, ARDS

The outbreak of epidemics is always accompanied with fear given the previous experience of man with pandemics such as the Black Death (1347-1350) that claimed one-third of the total population in Europe, the Great Plague of London (1664-1660) that killed over 75 000 of 460 000 total population and the Spanish flu (1918-1919) that claimed 25 000 000 lives in Europe [https://www.hkumath.hku.hk/~ntw/SCNC1001-2004b.pdf]. The panics that do accompany epidemics outbreaks are shaped by a number of epidemiological factors such as incubation period (the time lag between infection and clinical start of symptoms), transmissibility or contagiousness (spreading potential of a disease), case fatality ratio (CFR) (the ratio of deaths recorded to cases reported) and the serial number (the time lag between commencement of signs of a primary and a secondary case). SARS has come and gone but MERS and COVID-19 are ongoing. While the diseases have common origin, their propensity to spread and claim lives differs. SARS extended to 37 nations [2], MERS has spread to 27 countries [3] but as of 1st October, 2020 (10:31 GMT), COVID-19 has spread to 213 countries worldwide
[32, https://www.woldomter.info/coronavirus/?].

Numerous studies have been conducted to give insights into the transmission dynamics of SARS [6-12], MERS [3, 13, 14] and COVID-19 [15-24]. Besides, efforts have been made to study the epidemiological features of SARS, MERS and COVID-19 [25-28]. However, comparative analysis of transmissibility and CFR of SARS, MERS and COVID-19 through the use of a mathematical modeling approach has not received considerable attentions in the literature. To that end, the present work is motivated to examine the infectivity and fatality rates of the diseases. The literature was searched and a model was considered for each disease to derive the epidemiological parameter that governed the transmission potentials of the diseases. Reports of the incidences of the diseases in terms of cases and mortalities were also obtained up to October 1 2020 to compute the CFR of the diseases.

2. THE MODELS

Three models are considered and used to analyze the infectivity and case fatality rates of SARS, MERS and COVID-19.

2.1 The Model for SARS

The *SIPR* epidemic model was developed in [29] to analyze the transmission dynamics of SARS. In the model, $S(t)$ is used to denote the compartment for the susceptible individuals, $I(t)$ for the

regular infected individuals, *P(t)* for the super-spreading events (i.e. compartment for individuals who have extra-ordinary secondary cases) and *R(t)* for recovered individuals. The dynamics of SARS in the population is governed by the following system of first-order nonlinear ordinary differential equations

$$\frac{dS}{dt} = -\beta(I+P)S \tag{1}$$

$$\frac{dI}{dt} = b\beta(I+P)S - \frac{1}{x}I \tag{2}$$

$$\frac{dP}{dt} = (1-b)\beta(I+P)S - \frac{1}{k}P \tag{3}$$

$$\frac{dR}{dt} = \frac{1}{x}I + \frac{1}{k}P \tag{4}$$

where:

β : effective contact rate,

b : per capita probability that a new infection being a regular infection,

x : average number of days which an individual in *I(t)* spent outside isolation,

k : average number of days which an individual in *P(t)* spent outside isolation.

The reproduction number for the model is derived as

$$R_S = \frac{(1-b)\beta S_0}{\frac{1}{k}} + \frac{b\beta S_0}{\frac{1}{x}} \tag{5}$$

2.2 The Model for MERS

The *SEIJR* epidemic model was formulated in [3] to analyze the dynamics of MERS. In the model, *S(t)* stands for the susceptible compartment, *E(t)* denotes compartment for the exposed individuals, *I(t)* represents the compartment for the infected individuals, *J(t)* is the compartment for the isolated individuals and *R(t)* is used to denote recovered compartment. The following set of first-order nonlinear ordinary differential equations is used to express the transmission dynamics of MERS in the population.

$$\frac{dS}{dt} = P - \frac{S(\beta I + \varepsilon_E \beta E + \varepsilon_J \beta J)}{N} - \mu S, \tag{6}$$

$$\frac{dE}{dt} = P - \frac{S(\beta I + \varepsilon_E \beta E + \varepsilon_J \beta J)}{N} - (k+\mu)E, \tag{7}$$

$$\frac{dI}{dt} = kE - (\gamma + \sigma_1 + d_1 + \mu)I, \tag{8}$$

$$\frac{dJ}{dt} = \gamma I - (\sigma_2 + d_2 + \mu)J, \tag{9}$$

$$\frac{dR}{dt} = \sigma_1 I + \sigma_2 J - \mu R. \tag{10}$$

where:

P : recruitment rate,

β : contact rate,

ε_E : reduction parameter in disease spread by the exposed,

ε_J : reduction parameter in disease spread by the isolated,

k : development rate of symptoms in the exposed,

μ : natural mortality rate,

d_1 : disease-induced mortality for symptomatic individuals,

d_2 : disease-induced mortality for isolated individuals,

σ_1 : recovery rate in symptomatic population,

σ_2 : recovery rate in isolated population,

γ : isolation rate.

Unlike in [3], the present analysis is aimed at determining the transmission potential of MERS in the population without considering any interventions. Therefore, the reproduction number for MERS model is given as

$$R_M = \frac{\beta}{k+\mu} + \frac{k\beta}{(k+\mu)(d_1+\sigma_1+\mu)} \tag{11}$$

2.3 The Model for COVID-19

The *SEIRV* model was designed in [30], to analyze the dynamics of COVID-19. In the model, the susceptible (denoted by *S*), the exposed (represented by *E*), the infected (represented by *I*), and the

recovered (represented by *R*). The dynamics of COVID-19 in the population is governed by the following system of first-order nonlinear ordinary differential equations.

$$\frac{dS}{dt} = \Lambda - \beta_E(E)SE - \beta_I(I)SI - \beta_V(V)SV - \mu S, \tag{12}$$

$$\frac{dE}{dt} = \Lambda + \beta_E(E)SE + \beta_I(I)SI + \beta_V(V)SV - (\alpha + \mu)E, \tag{13}$$

$$\frac{dI}{dt} = \alpha E - (\omega + \gamma + \mu)I, \tag{14}$$

$$\frac{dR}{dt} = \gamma I - \mu R, \tag{15}$$

$$\frac{dV}{dt} = \xi_1 E + \xi_2 I - \sigma V. \tag{16}$$

where:

Λ : recruitment rate,

μ : natural mortality rate,

α : progression rate from asymptomatic phase,

ω : disease-induced mortality rate,

γ : recovery rate,

ξ_1 : rate of contribution to the growth of the pathogen by the exposed,

ξ_2 : rate of contribution to the growth of the pathogen by the infective,

σ : rate of removal of the pathogen from the environment,

$\beta_E(E)$: effective contact rate between asymptomatic and susceptible individuals,

$\beta_I(I)$: effective contact rate between symptomatic and susceptible individuals,

$\beta_V(V)$: effective contact rate between the environment and susceptible individuals.

The reproduction number of the system without taking control measures into consideration is

$$R_C = \frac{\beta_E(0)\Lambda}{\mu(\mu+\alpha)} + \frac{\alpha\beta_I(0)\Lambda}{\mu(\mu+\alpha)(\omega+\gamma+\mu)} + \frac{\beta_V(0)\Lambda[(\omega+\gamma+\mu)\xi_1 + \alpha\xi_2]}{\mu(\mu+\alpha)(\omega+\gamma+\mu)} \tag{17}$$

Having derived theoretical results for the reproduction numbers of SARS, MERS and COVID-19 denoted by R_S, R_M and R_C respectively, simulation is conducted in Section 3 to obtain their numerical values.

3. SIMULATION AND DISCUSSION

The parameters adopted for simulation are displayed in Table 2, Table 3 and Table 4 with some parameters values for the tables taken from [29], [3] and [30] respectively.

Table 2. Definition and values of parameters for SARS model

Parameter	Definition	Value/Unit
β	effective contact rate	0.1 day^{-1}
b	proportion of new infections that is regular infections	0.6 day^{-1}
x	average number of days which an individual in *I(t)* spent outside isolation	0.2 day^{-1}
k	average number of days which an individual in *P(t)* spent outside isolation	0.1 day^{-1}
$S = S_0$	number of people who join susceptible population per day	165 day^{-1}

Table 3. Parameters' definitions and values for COVID-19 model

Parameter	Definition	Value/Unit
P	recruitment rate	170 day^{-1}
β	contact rate	0.101 day^{-1}
ε_E	reduction parameter in disease spread by the exposed	0.2996 day^{-1}
ε_J	reduction parameter in disease spread by the isolated	0.0899 day^{-1}
k	development rate of symptoms in the exposed	0.1926 day^{-1}
μ	natural mortality rate	0.000034 day^{-1}
d_1	disease-induced mortality for symptomatic individuals	0.0294 day^{-1}

d_2	disease-induced mortality for isolated individuals	0.0227 day^{-1}
σ_1	recovery rate in symptomatic population	0.0433 day^{-1}
σ_2	recovery rate in isolated population	0.0475 day^{-1}
γ	isolation rate	0.1501 day^{-1}

Table 4. Parameters' definitions and values for MERS model

Parameter	Definition	Value/Unit
Λ	recruitment rate	150.5 day^{-1}
$\beta_E(0)$	effective contact rate between *S* and *E*	8.8×10^{-8} day^{-1}
$\beta_I(0)$	effective contact rate between *S* and *I*	2×10^{-8} day^{-1}
$\beta_V(0)$	effective contact rate between *S* and *V*	1×10^{-8} day^{-1}
α	progression rate from asymptomatic phase	$\frac{1}{7}$ day^{-1}
μ	natural mortality rate	5.01×10^{-5} day^{-1}
ω	disease-induced mortality rate	0.01 day^{-1}
σ	removal rate of virus	1 day^{-1}
ξ_1	rate of contribution to the growth of the pathogen by the exposed	0.0433 day^{-1}
ξ_2	rate of contribution to the growth of the pathogen by the infective	0.0475 day^{-1}
γ	recovery rate	$\frac{1}{15}$ day^{-1}

3.1 Comparative Result of the Transmission Potentials of SARS, MERS and COVID-19

Using parameter values in Table 2, Table 3 and Table 4 to evaluate Eq. (5), Eq. (11) and Eq. (17) respectively,

$$R_S = 2.64\ ,\quad R_M = 1.91 \quad \text{and} \quad R_C = 2.89\ . \tag{18}$$

The result in Eq. (18) shows that $R_M < R_S < R_C$. That is, the reproduction number of SARS is higher than the reproduction number of MERS but lower than the reproduction number of COVID-19. COVID-19 has the highest transmission potential of the three human coronaviruses. The spreading rate of COVID-19 makes it become pandemic in less than four months of emergence while SARS died out as an epidemic after eight months of emergence. Unlike, COVID-19, MERS has remained endemic since its emergence in 2012. Besides, the result in Eq. (18) reflects the true picture of the reproduction numbers for SARS, MERS and COVID-19. The reproduction number for MERS is within the range of 1 and 2 while the reproduction numbers for SARS and COVID-19 are within the range of 2 and 3 [18, 34, 35].

The SARS outbreak shook the world within 8 months by spreading to 37 countries between November 2002 and July 2003 leading to 8, 096 cases and 744 deaths in Asia, Europe and Africa [27, 31]. The MERS outbreak, on the other hand, has been causing panic particularly in the Middle East beginning from 2012 and has spread to 27 countries resulting in 2, 519 cases and 866 deaths in the process as at January 2020 [36]. However, as of April 20 2020, in less than 4 months of emergence, COVID-19 has infected more than 3 million people and spread to more than 210 countries worldwide [32].

3.2 Comparative Result of the Case Fatality Ratio of SARS, MERS and COVID-19

Case fatality ratio is an epidemiological term that is used to describe the ratio of deaths recorded to cases reported, i.e.,

$$\text{Case fatality ratio (CFR)} = \frac{Deaths\ recorded}{Cases\ reported}$$

Table 5. Reported cases and mortality of SARS, MERS and COVID-19, November 2002 to October 1, 2020

Disease	Reported cases	Deaths	CFR (%)
SARS	8, 096	744	9.19
MERS	2, 519	866	34.3
COVID-19	34, 192, 734	1, 019, 242	2.98

In Table 5, the CFR of SARS is higher than the CFR of COVID-19 but lower than the CFR of MERS. COVID-19 has the least CFR. The result in Table 5 has important implications. The world

population would have been affected more badly had the CFR of COVID-19 was as high as the CFR of MERS. COVID-19 would have claimed almost 11, 967, 457 lives (35% of 34, 192, 734) instead of 1, 019, 242 in Table 5 if it had the CFR of MERS. Even if the CFR of COVID-19 was like the reported CFR of SARS in [29], African continent would have been on the verge of extinction. The reason is that in [29], SARS infected only one person in Africa and the person died of SARS which gave a CFR of 100% for SARS in Africa. As of 9 October 2020, COVID-19 has infected 1, 557, 100 people in Africa [33]. It would have been a serious disaster for Africa if every individual who was infected with COVID-19 died of COVID-19 as it happened during SARS outbreak when a person who was infected with SARS in Africa died of SARS. Table 5 clearly indicates that the severity and fatality rate of COVID-19 are milder than that of SARS and MERS.

4. CONCLUSION

In this study, the transmission and case fatality ratio of SARS, MERS and COVID-19 had been studied via a mathematical modeling approach. A model was considered for each disease and the reproduction numbers were derived. Numerical simulation was carried out to determine the numerical values of the reproduction numbers. Reported cases and mortalities for the diseases were also considered to compute the CFRs of the diseases. Results from the simulation showed that while COVID-19 was more contagious than SARS and MERS, it was less severe and fatal than SARS and MERS. It is therefore concluded that the ongoing COVID-19 pandemic would have instigated more global health crisis had its severity and fatality rates were of the MERS.

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How to cite this article:
Ayoade AA, Latunde T, Folaranmi RO. Comparative analysis of transmissibility and case fatality ratio of sars, mers and covid-19 via a mathematical modeling approach. J. Fundam. Appl. Sci., 2021, *13(3), 1262-1274.*