



Mathematical Modeling of COVID-19 Transmission and Intervention in South Korea: A Review of Literature

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South Korea implemented interventions to curb the spread of the novel coronavirus disease 2019 (COVID-19) pandemic with discovery of the first case in early 2020. Mathematical modeling designed to reflect the dynamics of disease transmission has been shown to be an important tool for responding to COVID-19. This study aimed to review publications on the structure, method, and role of mathematical models focusing on COVID-19 transmission dynamics in Korea. In total, 42 papers published between August 7, 2020 and August 21, 2022 were studied and reviewed. This study highlights the construction and utilization of mathematical models to help craft strategies for predicting the course of an epidemic and evaluating the effectiveness of control strategies. Despite the limitations caused by a lack of available epidemiological and surveillance data, modeling studies could contribute to providing scientific evidence for policymaking by simulating various scenarios.

Key Words: COVID-19, mathematical modeling, transmission dynamics, intervention, South Korea

INTRODUCTION

The novel coronavirus disease 2019 (COVID-19), which began in December 2019, has spread rapidly worldwide. On March 11, 2020, the World Health Organization declared COVID-19 a pandemic, a public health emergency of international concern. Non-pharmaceutical interventions (NPIs) have been implemented to control the COVID-19 pandemic, which are crucial when an effective vaccine is unavailable. Social distancing, mask wearing, school closures, reducing social activities, and introducing restrictions were among the common NPI measures implemented. The first case of COVID-19 in Korea was diagnosed on January 20, 2020, after which the Korean government implemented NPIs that limited or prohibited many social activities and required schools to frequently close. In Ko-

rea, vaccination has been implemented since February 26, 2021; however, mutation of the disease-causing virus continues to place a burden on the public health system.

In the early phase of the outbreak, the epidemiological characteristics of COVID-19 were unclear, and clinical features were unavailable because it was a newly emerging infectious disease. In these circumstances, various studies were conducted using mathematical models to predict the transmission dynamics of infectious diseases and evaluate the impact of intervention measures. Consequently, models have played an important role in designing strategies for effectively controlling and responding to the spread of infectious diseases.

The increasing capacity of modeling in support of responses to the pandemic motivated us to perform this descriptive review of published literature on the mathematical modeling of COVID-19 transmission dynamics and control interventions in South Korea. Fig. 1 depicts a summary of the present research landscape on COVID-19 modeling. Our analysis covers model structure characterization, modeling methods, and the modeling role.

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SEARCH METHOD AND CRITERIA

A review of articles published between August 7, 2020 and Au-

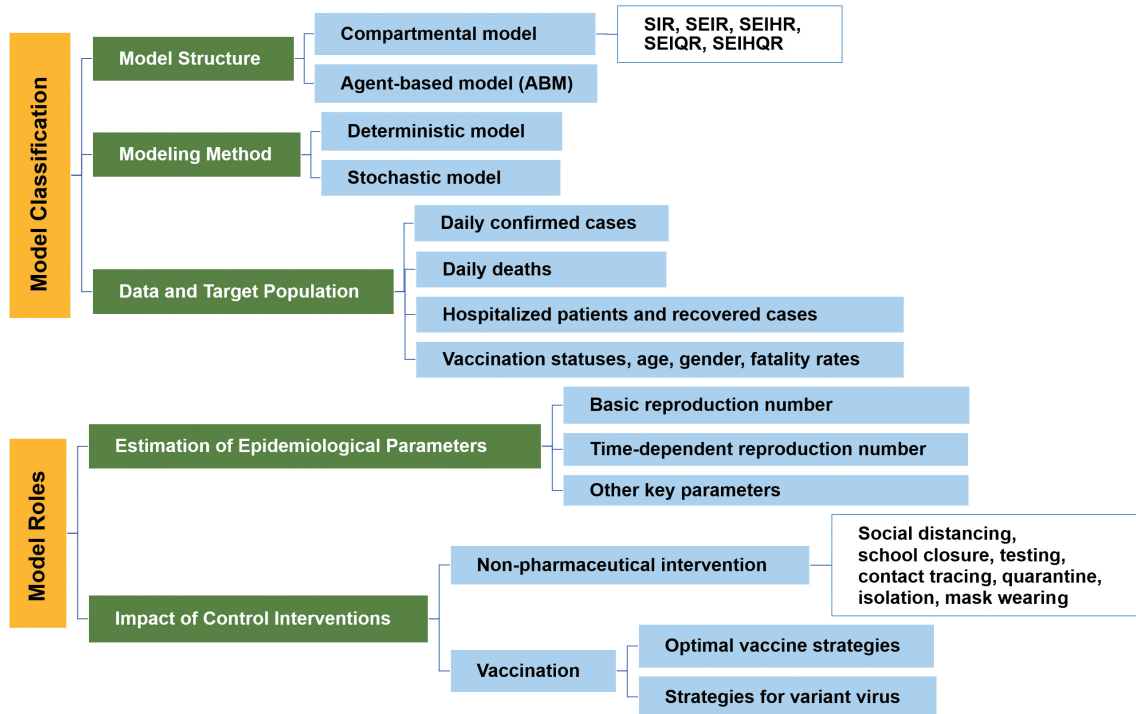


Fig. 1. Diagram outlining the research landscape of COVID-19 modeling.

gust 21, 2022 was performed to characterize mathematical models relevant to COVID-19 transmission in Korea. The publications to be reviewed were searched using Web of Science, Scopus, Google Scholar, and PubMed. The search strategy aimed to return relevant publications using the following keywords in each category: 1) country: in Korea, in South Korea, in Republic of Korea, or Korean; 2) disease: SARS-CoV-2, COVID-19, or corona; 3) model type: compartment*, stochastic model, agent-based or individual-based, statistical model, mathematical model*, deterministic model, SIR, SEIR*, SEIR, or SEIQR; and 4) purpose: predict*, forecast*, assess*, control*, intervent*, NPIs, vaccin*, impact*, effect*, or estimat*.

The search yielded 92 papers, and the abstracts of all returned studies were evaluated for suitability. Full-text articles were excluded if the study was not on a mathematical model. For example, studies that used statistical methods or machine learning to analyze clinical data were excluded. We also excluded cases that were not directly related, such as those studying the impact of the COVID-19 pandemic on other diseases. In total, 42 published papers were selected for the final analysis through a full-text assessment of the remaining papers.

MODEL CLASSIFICATION

Different modeling approaches can be applied to solve a variety of problems and modeling goals. Table 1 summarizes the associated modeling structures, methods, target population, and modeling objectives.

MODEL STRUCTURE

Mathematical models are often classified into two types according to their structure: compartmental and agent-based models (ABMs). Of the papers reviewed, 35 used compartmental models, and four used ABMs to reflect individual attributes or perform individual-level analyses. Exceptions that are not in either category are used to estimate disease-related characteristics, such as incubation periods, serial intervals, and asymptomatic proportions, by applying statistical and probability formulas.¹⁻³

In compartmental models, a population is categorized into several compartments according to disease status. Compartmental models under a homogeneous assumption indicate that the interaction is constant between individuals because of well-mixed properties.⁴⁻²⁰ SEIR is a simple example of a compartmental model with common infection categories consisting of S, E, I, and R, where waning immunity is not considered. S denotes individuals susceptible to the disease, that is, those who are not infected. E denotes individuals who are within the exposure period after infection transmission; these individuals are assumed to remain uninfected. I denotes infectious individuals who can spread the disease by contact with susceptible individuals. R denotes individuals who have been infected and then removed from the possibility of spreading the infection.

Most homogeneous compartmental models are based on the SIR^{7,15,16,21} or SEIR structures,²¹ or their variations.^{13,14,18,20} The infectious compartment is typically subdivided according to various criteria, such as detection, symptoms, and isolation.^{13,14,18} Some studies have expanded the models by adding

compartments required to address particular research questions. SEIHR,^{4,5,9,11} SEIQR,⁸ and SEIHRQ models were constructed to analyze the effects of isolation and quarantine, in which

hospitalization (H) and quarantine (Q) were introduced. A death compartment was added to the SEIR model to assess mortality rate.^{10,21} Behavior-changed, vaccinated, and quaran-

Table 1. Summary of Approaches and Objectives of COVID-19 Modeling

Ref	Modeling approaches		Objectives		Target populations
	Structures	Methods	Values estimated	Intervention evaluated	
1	Statistical approach (maximum likelihood estimation)		R_0 , others (incubation period, serial interval)		Korea
2	Statistical approach (renewal equation)		R_0 , $R(t)$		Korea
3	Statistical approach (probabilistic model)		Others (undetected asymptomatic patients)		Korea
4	SEIHR	Deterministic		Social distancing	Korea
5	SEIHR	Deterministic	R_0		Daegu/Gyeongbuk
6	SS _r EIQR	Deterministic	R_0	Behavior change	Daegu/Gyeongbuk
7	SIR	Deterministic	$R(t)$		Korea
8	SEIQR	Deterministic		Quarantine	Seoul/Gyeonggi
9	SEIHR	Deterministic	$R(t)$	Social distancing	Seoul/Gyeonggi
10	SEIRD	Deterministic	Others		Daegu/Gyeongbuk
11	SEIHR	Stochastic	$R(t)$	Social distancing	Korea (cities)
12	SS _r EIHR	Deterministic	$R(t)$	Social distancing, behavior changes	Korea
13	SADR	Deterministic	R_0 , others		Korea
14	SUC	Deterministic	Others	Testing	Korea
15	SIR	Deterministic		Social distancing, school closure, mask wearing, quarantine	Korea
16	SIR	Stochastic		Social distancing, isolation	Korea
17	$S_r, S_q, V, V_q, E, E_q, I, I_q, R$	Deterministic	Others	Vaccination	Korea
18	SEP, P ₂ , M ₁ , M ₂ , G ₁ , I ₂ , R	Deterministic	$R(t)$	Social distancing, contact tracing, testing	Korea
19	SEIHRQ	Deterministic	R_0 , $R(t)$, others	Social distancing, testing	Korea
20	SI	Stochastic	R_0		Korea
21	SIR, SEIR	Deterministic	Others	Testing, health facility expansion, contact tracing	Korea
22	SEIHR+age	Deterministic	$R(t)$, $R(\text{age})$, others	Social distancing	Seoul/Gyeonggi
23	SEAIHVR+age	Deterministic	$R(\text{age})$	Vaccination	Korea
24	SEIQR+age, job	Deterministic	$R(t)$, $R(\text{age})$	Vaccination	Korea
25	V-SLIR+age	Deterministic		Vaccination	Korea
26	SEIQH+age	Deterministic	$R(\text{age})$	Social distancing, school closure, contact tracing, testing	Korea
27	SEAPR+age	Deterministic	$R(\text{age})$	Vaccination	Korea
28	SEAPMIR+age	Deterministic		Vaccination	Korea
29	SS _r EIQR+age	Deterministic	$R(\text{age})$	Social distancing, school closure	Seoul/Gyeonggi
30	SQ _s EQ _e I _q R+age	Deterministic	Others	Social distancing, school closure, quarantine, isolation	Korea
31	SVEPAIH ^M H ^R RD+age	Deterministic	$R(t)$, $R(\text{age})$	Vaccination	Korea
32	SEI _p I _s Q+age	Stochastic	Others		Korea
33	SEI _a I _{ad} I _s VRD+age	Deterministic	$R(t)$, others	Vaccination	Korea
34	SEIQRUVP+age	Deterministic	$R(t)$, $R(\text{age})$	Vaccination	Korea
35	SEIR+job	Deterministic		Testing, quarantine	Tertiary hospital
36	ABM	Stochastic	Others	Social distancing, school closure	Daegu/Gyeongbuk
37	ABM	Stochastic		Isolation	Korea
38	ABM	Stochastic	Others	Mask wearing	Sarang Jeil church
39	ABM	Stochastic	Others	Contact tracing, quarantine, isolation	Korea
40	XE _s E _o I _s I _o Q _s Q _o M _s M _o C _s C _o R+age	Deterministic	Others	Vaccination	Korea
41	SEIQR+region	Deterministic	Others	Social distancing, testing	Korea
42	SEPIACR+region	Stochastic	R_0 , others		Daegu/Gyeongbuk

ted statuses have also been used as compartments in models to evaluate their impact.^{6,12,17}

In a simple compartmental model that divides people into groups based on disease status alone, each group is represented by one representative variable. Therefore, all other characteristics of everyone belonging to a group are considered to be the identical. However, individual compartments of the model can be further subdivided according to additional characteristics to become a structured model in order to better describe a phenomenon or answer a question of interest. In the reviewed studies, age was the most considered characteristic other than disease status,²²⁻³⁴ and an age-structured model was established to evaluate vaccine policy²²⁻³⁴ and examine school-related policy.^{26,29,30} Several studies have used structured models that subdivide groups into occupational categories for analysis, taking into account the roles and risks of healthcare workers.^{24,35} By adding the characteristics of each individual in this way to subdivide the groups, we ultimately arrive at an ABM.

ABM is the most heterogeneous methodology for predicting phenomena or determining strategies. In ABM, individuals interact within the network as unique and autonomous entities and act by adapting to the situation of the system including themselves, other entities, and the surrounding environment. This enables the prediction of transmission dynamics that reflect desired factors by depicting the characteristics of each individual and their behavioral patterns similar to real situations. In addition, ABM is known to be very suitable for individual-level policy development and evaluating individual strategies, since it can represent the actual location where control measures are taken to reduce transmission of the disease. On the other hand, simulations are time-consuming because the models are complex and computationally intensive, and mathematical theories and tools to support problem solving are lacking. In practice, we often do not take full advantage of ABM because it requires a wealth of input information to provide detailed results.

ABMs have also been used to describe infection processes for each individual in a population and to provide an opportunity to determine whether individuals become infected and develop the disease over time, in most cases.³⁶⁻³⁹ These models were used in Korea to predict the incidence and analyze the effect of intervention measures, reflecting the special circumstances of the Sarang Jeil church that led the initial spread of COVID-19.^{36,38} The effectiveness of tracing and isolation was evaluated by building a network-based ABM in which connections between individuals affect whether they are infected.^{37,39}

MODELING METHOD

Mathematical models can be developed using deterministic and stochastic approaches. In deterministic models, we assume that the epidemic process is deterministic; that is, the

behavior of a population is determined completely by its history and rules. However, stochastic models incorporate possible variations in the transmission process with the randomness of possible behaviors.

Numerous models in the reviewed literature are deterministic because they are relatively easy to implement, and predicting events on average is sufficient for many purposes.^{4-10,12-15,17-19,21-31,33-35,40,41} Most compartmental models are deterministic models in which transitions between categories are described by applying averaging transition rates. Deterministic compartmental models are formulated in the form of differential equations. Key parameter values were obtained by fitting model on actual data, except for some studies that extracted all parameter values from previous studies.^{8,18,28}

Stochastic models incorporate chance into whether events occur to predict variation in outcomes that may occur. Given fixed input values, deterministic models provide the same results, whereas stochastic models provide a range of possible outcomes. Stochastic models may be preferred in many instances, as the chance of fluctuations may have a major role in governing disease dynamics, and variation in outcomes may be as important as the average behavior. A discrete-time stochastic model was used to simulate the spread of COVID-19 within the Sarang Jeil Church because chance may significantly influence the epidemiological patterns that emerge in small populations.³⁸ Events by chance at the beginning of an epidemic can lead to completely different consequences in the future, such as the amount of cases that occur throughout an outbreak or whether an outbreak occurs. Several studies applied stochastic models to investigate the spread in the Daegu and Gyeongbuk regions, which correspond to the early stages of the COVID-19 outbreak in Korea.^{36,38,39,42} Other studies implemented stochastic models to provide a range of possible outcomes or account for uncertainty in the parameters.^{11,16,20,32}

DATA SOURCE

The Ministry of Health and Welfare (MOHW) and its affiliated agency, the Korea Disease Control and Prevention Agency (KDCA), have released various pieces of information related to COVID-19. The data provided by these agencies included the number of daily confirmed cases, number of daily deaths, number of hospitalized patients and those who recovered, vaccination statuses, and age and sex fatality rates. Most studies referenced the KDCA and MOHW for data.^{1-7,9-17,19-34,36,39-42} Several studies that considered regional characteristics in transmission dynamics utilized the number of quarantined and released people and the number of daily confirmed cases in the region, yielded by each local government. The data were primarily used to estimate key parameters, such as the reproduction number and transmission rate.

Some studies employed data confined to specific circum-

stances or sources other than the public data mentioned above to answer their research questions. A model was calibrated to the cluster infection events of Sarang Jeil Church to assess the effectiveness of mask wearing.³⁸ In a study comparing the impact of different intervention strategies in a tertiary hospital, data from the hospital were referenced.³⁵ In addition, data from the International Airport Corporation, as well as Korea, were used to evaluate the risk of transmission considering importation.² Moreover, some studies extracted all parameters from previous studies without using data.^{8,18,37}

MODELING OBJECTIVES

Estimation of epidemiological parameters

Estimating parameters using mathematical modeling addresses four main topics: the basic reproduction number (R_0), time-dependent reproduction number, age-dependent transmission rate, and several epidemiologically important parameters. Of the 42 papers reviewed, 14 estimated the basic reproduction number in the early stage of the COVID-19 outbreak in Korea by fitting data to a model. Estimating the basic reproduction number by fitting data involves two primary approaches: the transmission rate from the next-generation matrix and the renewal equation.

Basic reproduction number

Several papers have described a method of estimating the basic reproduction number using the transmission rate of a compartmental model.^{5,6,19,20} Kim, et al.⁶ approximated the number of susceptible and behavior-changed susceptible individuals by estimating the transmission rates of COVID-19 and awareness or fear of the disease. Feng, et al.¹⁹ employed an adaptive Metropolis-Hastings algorithm to estimate the transmission rate and effective control reproduction number using the SEI-HQR model and obtained an expression for R_0 by applying a next-generation matrix. Park, et al.²⁰ analyzed the basic reproduction number in South Korea, which enabled the identification of the level of vaccines required to achieve herd immunity. Kim, et al.⁴² calculated R_0 by applying the approximate Bayesian computation sequential Monte Carlo method based on the two-patch model to account for the COVID-19 outbreak in the Shincheonji community and Daegu city under a super-spreading event (SSE). Both studies determined differences in the basic reproduction number between church members and the remainder of the population in Daegu.

Time-dependent reproduction number

Other studies obtained time-dependent and effective reproduction numbers rather than the basic reproduction number.^{2,9,11,12,18,19,22,31,33,34} Ko, et al.²⁴ applied maximum likelihood estimation to calculate reproduction number in consideration of the transmission matrix and used this to determine optimal

vaccination priority. To explore different intervention scenarios for COVID-19 strategies, Jo, et al.³³ estimated a time-varying reproduction number based on case notification data and serial interval distributions. Memarbashi, et al.¹³ defined direct and indirect basic reproduction numbers using the virus transmission probability through direct contact and the probability of infection from touching contaminated objects.

Studies have been conducted on the age-dependent transmission rate to describe the observed phenomenon well or analyze intervention strategies related to age characteristics.^{22-24,26,27,29,31,34} Kim, et al.²³ estimated age-specific transmission probability for corresponding NPI levels to evaluate the effectiveness of age-specific vaccination prioritization strategies to minimize morbidity and mortality. Shim²⁷ calculated an age-specific susceptibility to account for relative incidence by age group. Kim, et al.²⁹ estimated the transmission rate by age group based on reported data and quantified the impact of school closures on the spread of COVID-19.

Other key parameters

In addition to reproduction numbers and age-dependent transmission rates, several key parameters have been estimated using mathematical models.^{1,12-14,17,19,21,22,30,32,33,38-42} Son³⁶ approximated the probability of infection through contact with infected individuals in the household to analyze the impact of school openings. Choi, et al.²² estimated the period from symptom onset to confirmation, the transmission rate, and the infection probability of a person in each age group to investigate the potential impact of social distancing under various scenarios. Kim, et al.⁴² estimated the parameters of the SEICR model, epidemic doubling time, and epidemic growth rate to quantify the rapid spread of COVID-19 in Daegu City, driven by a community of Shincheonji members.

Impact of control interventions

NPI

The Korean government has implemented various NPI strategies and vaccinations to prevent the spread of COVID-19. Twenty-three papers analyzed the impact of NPIs on the COVID-19 epidemic in Korea, including social distancing, school closures, testing, contact tracing, quarantine, isolation, and mandatory mask wearing. Most papers that analyzed the effect of social distancing to control COVID-19 adopted deterministic compartmental models.^{4,9,11,12,15,18,19,22,26,30,41} Feng, et al.¹⁹ used a deterministic compartment model to analyze the impact of interventions on new infection cases according to contact rates. Cho and Kim¹⁶ employed a stochastic compartment model based on the Bayesian approach to explore how social distancing affected the reduction of SSEs. A statistical model was applied to assess the country-specific importation risk of COVID-19 and to investigate its impact on local transmission of the disease.² In addition to social distancing, school closures were considered

major intervention measures.^{15,26,29,30,36} A stochastic ABM was used to simulate different scenarios to predict future spread and to analyze the impact of school openings.³⁶ Several work compared the effectiveness of testing^{14,18,19,21,26,35,41} and contact tracing.^{18,26,39} Others have incorporated quarantine^{8,15,30,35,39} and isolation factors into the models to assess their impact.^{30,35,37,39} In addition, studies have targeted mask wearing, health facility expansions, and behavior changes.^{6,12,15,21,38}

Vaccination

Since February 2021, when the vaccine was introduced to Korea in earnest, studies analyzing vaccines have been conducted with different purposes, depending on the publication period. Literature in 2020–2021 primarily investigated vaccine strategies and policies. Based on the scenarios, studies searched for optimal vaccine strategies or policy priorities to reduce confirmed cases and deaths and to reach herd immunity.^{24,25,27,28,31,34} Several studies published from February to September 2021 analyzed vaccine prioritization strategies.^{24,27,31,34} Wang, et al.¹⁷ analyzed the vaccination impact on mutated COVID-19 transmission. Jo, et al.³³ investigated the effect of vaccination on the cumulative incidence and intensive care unit (ICU) capacity according to social distancing level.

Moreover, some studies have examined the impact of control interventions in consideration of both NPI and vaccination.^{17,23,33,34,40} Kim, et al.²³ described the effects of social distancing, quarantine, and contact tracing, and evaluated the strategies of vaccine and booster shots. Ko, et al.⁴⁰ analyzed how NPIs, antiviral drugs, and vaccination affect the spread of the omicron variant and number of severe cases by investigating vaccination and booster shot effects on omicron. Social distancing and screening for overseas travelers were confirmed to have played an important role in reducing transmission.

Summary of selected papers by topic for modeling role

Reproduction number in the early outbreak period

We summarized several representative papers that considered the diversity of the structure, method, and role of modeling. The first study estimated the reproduction number using a compartmental model at the early stage of the outbreak in Korea.⁵ In the second study, the impact of vaccination was analyzed using a deterministic age-structured model.²⁷ Finally, the last study employed ABM to investigate the effectiveness of case isolation and contact tracing.³⁹

Choi and Ki⁵ estimated the basic reproduction number to evaluate the effectiveness of NPIs in the early stages of an outbreak in Korea using data on the number of confirmed cases from January 20, 2020 to March 4, 2020 provided by the KDCA. A deterministic compartmental model was proposed that included susceptible, exposed, symptomatic infectious, hospitalized, recovered, and death compartments. The basic reproduc-

tion number from January 20, 2020 to February 17, 2020 was estimated to be 0.55, indicating that the control intervention was effective in mitigating the COVID-19 outbreak. However, from February 18, 2020 to March 4, 2020, the reproduction number was estimated to be between 3.472 and 3.543. Therefore, to implement effective control interventions, isolating patients quickly proved to be important to reducing both the probability of transmission when coming into contact with an infected case and duration of transmission.

Optimal vaccination strategy with heterogeneity

Shim²⁷ developed optimal vaccination strategies to maximize the benefits of vaccines for individuals and communities under different supply and efficacy scenarios. The deterministic age-structured model provided an optimal vaccine allocation scheme to minimize three goals: infections, deaths, and loss of life years, by considering demographic factors such as country-specific age distribution and contact structure. The individuals were categorized into 16 age groups: 0–4, 5–9, ..., ≥75 years. The unvaccinated population was divided into susceptible, exposed, asymptomatic, symptomatic, and recovered compartments, and the vaccinated population was divided into five compartments by age. The scenarios of partial protection for all vaccinated persons were assumed by reducing the probability of contracting the SARS-CoV-2 disease. In particular, the study determined that transmission-blocking vaccines should be prioritized in adults aged 20–49 years to minimize the cumulative incidence and in adults aged 50 years and older to minimize mortality. Moreover, administering vaccines with low efficacy to teenagers and adults aged 50–59 years can be suggested.

Impact of isolation and contact tracing using ABM

The spread of COVID-19 in South Korea experienced two outbreak waves related to SSEs in Daegu and Gyeongbuk (the first) and Seoul and Gyeonggi (the second). Owing to the occurrence of an SSEs in Korea in the early stages of COVID-19 in 2020, SSEs are recognized as an important factor. Ryu, et al.³⁹ developed an ABM, focusing on the early epidemiology of COVID-19 in Korea to capture the intrinsic nature of heterogeneous transmission dynamics, which involves the social and behavioral features and epidemiological characteristics of different levels of infectivity. An ABM can analyze essential individual variability by incorporating NPIs by varying the transmission rate and reproduction number of the index case. An ABM was utilized to evaluate the effectiveness of case isolation and contact tracing under various scenarios, and the simulation results indicated that isolating SSEs reduced the outbreaks size. Case isolation combined with effective contact tracing was also determined to play a critical role in mitigating larger outbreaks.

DISCUSSION

A descriptive review of 42 articles published between August 7, 2020 and August 21, 2022 was performed to characterize mathematical models relevant to COVID-19 transmission in Korea. In the classification of models according to structure, the compartmental model was dominant. However, many compartmental models used heterogeneous structures of age and region to better explain phenomena or answer questions of interest. The compartmental model has several advantages in that it is relatively easy to implement and because predicting events on average as quickly as possible is important during a pandemic. On the other hand, ABM is known to be very suitable for predicting specific transmission dynamics and developing control measures by depicting characteristics, behavioral patterns, and locations of individuals similar to real-life situations.

Many studies have applied deterministic approaches, especially when using compartmental models. Stochastic models have been used in applications where the chance of fluctuations may have a major role in dynamics and where the variation in outcomes may be important. A representative case in which chance of fluctuations may have a major role in dynamics is when the population to be modeled is small. Examples include modeling small outbreaks at an early stage or predicting eradication of an epidemic at the end.

One role of modeling is to estimate key indicators, such as the basic reproduction number, time-dependent reproduction number, age-dependent transmission rate, and other epidemiologically important parameters. Models can also be used to predict the transmission process of diseases and quantify the impact of various interventions by comparing estimated transmission rates and reproduction numbers. In addition, numerous studies have primarily focused on evaluating the effects of intervention strategies, such as social distancing and school attendance policies, quarantine and isolation, and vaccination.

The results have helped us understand the epidemiology of the disease, such as how far COVID-19 will spread and when the epidemic will end. In addition, the results have contributed to improving policies by analyzing the impact of intervention measures according to several scenarios. In summary, mathematical modeling has been found to be a useful tool for providing scientific evidence for predictions and policymaking. For example, an expert in mathematical modeling for infectious disease was selected as a member of the National Advisory Committee on Infectious Disease Crisis Response starting from June 2022 in Korea.⁴³ Also, reports for the estimation of COVID-19 cases in Korea using mathematical modeling have been provided by the National Institute for Mathematical Sciences.^{44,45} However, each government department has its own advisory committee as needed, and the procedure and scope of utilizing the models are different. Accordingly, it would be nice if a systematic process was introduced to determine where

modelers participate in committees and how models are considered and reflected in policy.

We would like to point out the limitations of modeling research during the COVID-19 pandemic and suggest further research required in the future. The diversity of studies, with different groups implementing their own models, allows us to look at different aspects of epidemics. However, we observed that model selection in general tends to be biased in terms of structure, method, and study topic. For example, compared with ABM, the compartmental model was overwhelmingly used, and few studies have addressed economic value. This appears to be partly because of the availability of the data required to build the model. During the COVID-19 pandemic, governments provided well-organized data; however, because the data have been processed, they are often unsuitable for use in certain studies. Obtaining data in a timely manner was almost impossible because different institutions handle the necessary data, such as severe cases, deaths, number of ICU beds, and disease-related costs, and the process of obtaining the data was difficult. Therefore, it is necessary to establish a system that allows easy and quick access to necessary data and to conduct research using various types of models.

Modeling studies have rarely investigated the economic impact of the COVID-19 pandemic in Korea, whereas some studies have explored the economic impact in other countries such as Europe and the United States.⁴⁶⁻⁵⁰ Chen, et al.⁴⁸ explored the relationships between COVID-19 infected cases and economic cost, including mobility trends and stock prices in the early stages of the COVID-19 epidemic using a stochastic SIRD model. The model could provide financial implications related to COVID-19 by estimating the impact of social distancing in the United States. As pandemics of infectious diseases pose large social and economic impacts, as well as the burden of disease itself, research in this field will be helpful.

Approaches have been developed to reflect the key factors of COVID-19 transmission using various model structures and parameters. Examples of these factors include heterogeneous contact patterns, behavioral changes according to disease spread and intervention strategy, and the transmission risk of exposed, age-dependent characteristics related to disease. Some studies have analyzed the effect of contact tracing despite a lack of accessible close contact information.⁵¹⁻⁵⁴ To overcome these limitations, most of the simulations were based on scenarios set under a certain level of assumptions, limiting quantitative analysis results. The quantification of contact patterns is important for describing the transmission of infection through contact. For example, for the question "By how much will the number of cases increase if social distancing is relaxed?", changes in terms of contact levels as intervention strategies can be estimated using contact surveys.^{44,55-63} Jo, et al.⁵² estimated a COVID-19 infection network from actual data. However, the data used did not identify individuals who infected the patient, as no regional information was available on the route of infection

via contact tracing. It is recommended to conduct research that prepares evidence for key factors in infectious disease modeling that can greatly improve the reliability of research results, such as contact patterns.

Another limitation of most studies is that they do not reflect asymptomatic and unreported cases due to the lack of supporting information. Chun, et al.³² identified the need to estimate the rate of asymptomatic infection more accurately, particularly in children and adolescents who frequently experience asymptomatic infection, and emphasized the importance of age-specific susceptibility. Shakiba, et al.⁶⁴ described the population seropositive prevalence of the COVID-19 virus infection, indicating that asymptomatic infections are much higher than the number of confirmed cases. In addition, the asymptomatic rate has been estimated by comparing the symptoms of seropositive individuals.⁶⁵ Evidently, estimating asymptomatic cases can be improved if seropositive data are available, as shown in several studies. Improving models by analyzing asymptomatic and unreported cases based on seroprevalence data is warranted in future research.

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