Journal of Life Sciences & Biomedicine, vol. 2(75), No 2, p. 113-118 (2020)

A time-dependent *SIR* model for COVID-19 in Azerbaijan

R.I. Khalilov[1*], G.A. Aslanova[2]

[1] Department of Biophysics and Biochemistry, Baku State University, 23 academician Z.Khalilov Str., Baku AZ1148, Azerbaijan
[2] Department of Molecular Biology and Biotechnologies, Baku State University, 23 academician Z.Khalilov Str., Baku AZ1148, Azerbaijan
**For correspondence: hrovshan@hotmail.com*

Received 03 Novembe 2020; Received in revised form 18 November 2020; Accepted 23 Novembe 2020

A novel coronavirus named ''2019-nCoV'', has been causing the deadliest pandemic in late 2019 and early 2020. This novel virus was defined as the coronavirus disease 2019 (COVID-19) by the World Health Organization (WHO). Diseases have afflicted humans ever since there have been human beings. From AD 541 to 542, the global pandemic known as "the Plague of Justinian" is one of the worst pandemics in the world and is estimated to have killed 15–25% of the world's 200 million population. Today we are battling to control and prevent the spread of COVID-19. Coronavirus has the potential to cause the deadliest pandemic in human history. The number of cases of COVID-19 outside China has drastically grown up since 16th March, 2020. On 28 February, 2020 Azerbaijan has confirmed first positive case of COVID-19 within its border. The patient, a Russian national, had traveled from Iran to Azerbaijan. On 31 October, 2020 the total number of confirmed coronavirus cases is 55.269 in Azerbaijan. In this paper, we conduct mathematical and numerical analyses of COVID-19. We have applied the SIR model considering data from Azerbaijan. Assuming the published data are reliable, the SIR model can be applied to assess the spread of the COVID-19 disease and predict the number of infected, removed and recovered populations and deaths in the communities, accommodating at the same time possible surges in the number of susceptible individuals.

Keywords: *COVID-19, SIR, mathematical model, simulation, susceptible, infected, recovered*

INTRODUCTION

Due to the comparable transmissibility as severe acute respiratory syndrome coronavirus (SARS-CoV) in 2003, since the first case of corona virus disease 2019 (COVID-19) was reported in Wuhan city of China in late December 2019, it quickly spread to 24 countries in 4 continents around the world in less than two months. On January 30, the World Health Organization (WHO) declared this fast-growing outbreak of COVID-19 as a Public Health Emergency of International Concern (PHEIC) (Tang et al., 2020).

COVID-19 has spread rapidly worldwide, and World Health Organization (WHO) has increased the assessment of the risk of spread and risk of impact of COVID-19 to very high at the global level and has labeled it as a "pandemic". Therefore, it becomes necessary to develop and use the mathematical approach to study the pathogenesis of this virus in humans.

Daily updated data of COVID-19 in countries outside China were collected from the coronavirus disease (COVID-2019) situation reports released by WHO (Wu et al., 2020a).

Due to the continuous public health interventions adopted in China and other countries outside China, the transmission model of COVID-19 would change all the time until it arrived at a relatively stable status (Wu et al., 2020b). Therefore, the time-varying SIR models were developed based on the daily increased case number and were used to calculate the infection parameters of the COVID-19.

doi.org/10.29228/jlsb.70
Available online 25 December 2020

MATERIALS AND METHODS

In the typical mathematical model of infectious disease, one often simplify the virus-host interaction and the evolution of an epidemic into a few basic disease states. One of the simplest mathematical models of disease spread is SIR (Susceptibles, Infectives, Removed) model (Tang et al., 2020). It splits the population into three basic categories according to disease status.

People who have not yet had the disease are labelled "susceptibles". Everyone is assumed to be born susceptible and they capable of being infected.

Those who have infected the disease and are capable of passing it to susceptibles are the "infectives". The third group are euphemistically referred to as the "removed" class. These are the people who have had the disease and recovered or those who have died. This is referred to as the SIR model. SIR model can provide information for how to prevent diseases spreading.

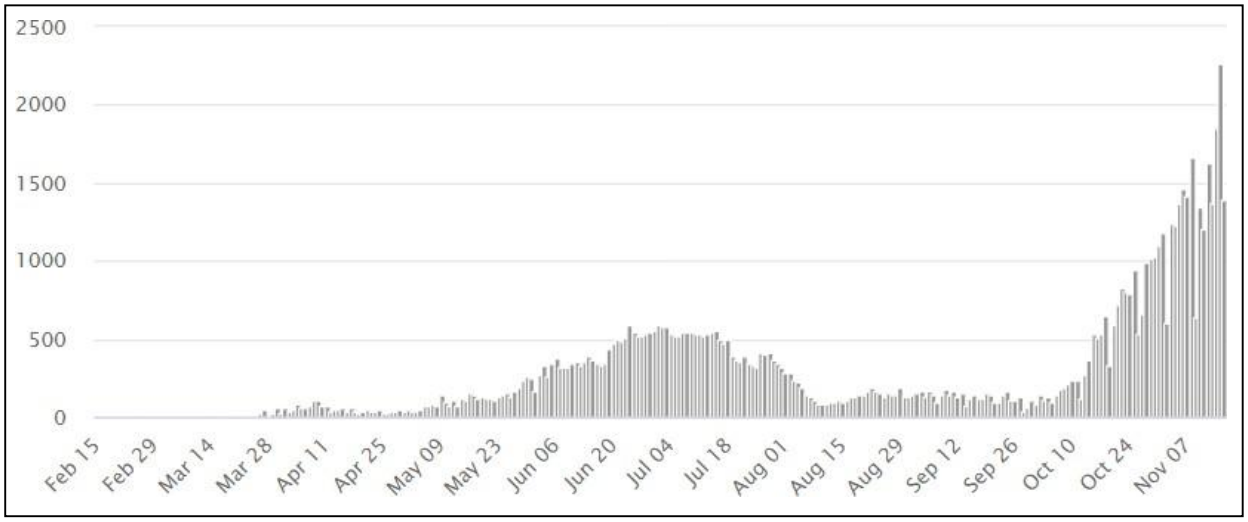

Fig. 1. Daily new cases in Azerbaijan.

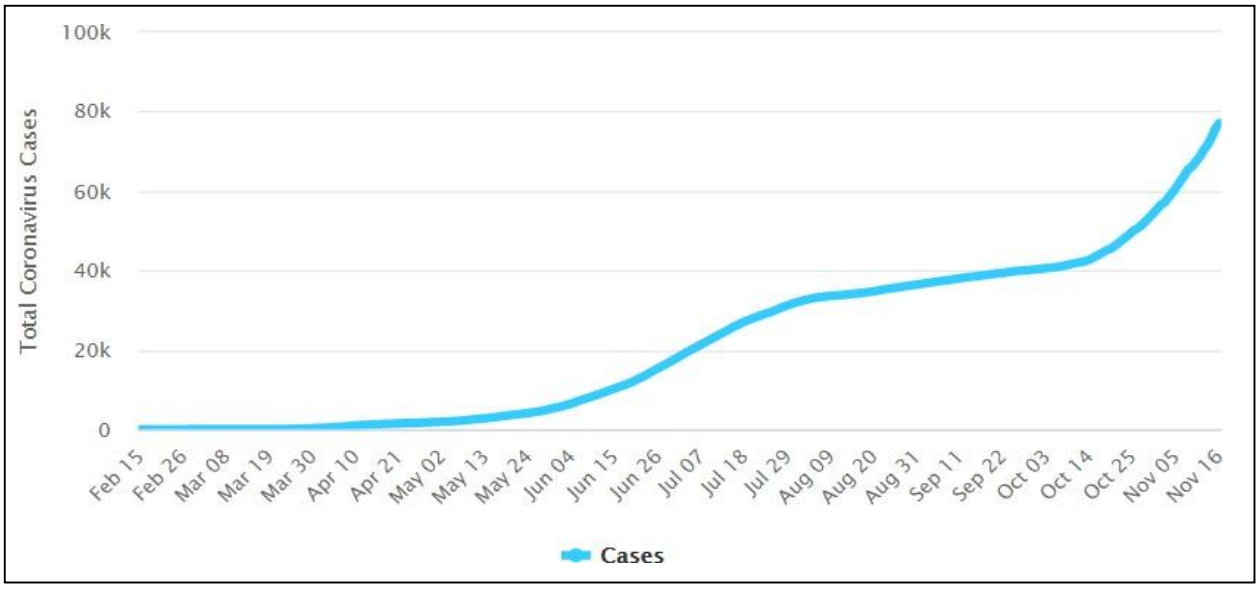

Fig. 2. Total coronavirus cases in Azerbaijan.

In the traditional SIR model, it has two time-invariant variables: the transmission rate and the recovering rate (Kraemer et al., 2020). The transmission rate means that each individual has on average contacts with randomly chosen others per unit time (Nishiura et al., 2020). On the other hand, the recovering rate indicates that individuals in the infected state get recovered or die at a fixed average rate. This assumption is too simple to precisely and effectively predict the trend of the disease.

$$\frac{dS}{dt} = -\beta IS \quad \textbf{(1)}$$

$$\frac{dI}{dt} = \beta IS - \gamma I \quad \textbf{(2)}$$

$$\frac{dR}{dt} = \gamma I \quad \textbf{(3)}$$

Therefore, we propose the time-dependent SIR model, where both the transmission rate and the recovering rate are functions of time t (Wangping et al., 2020). Such a time-dependent SIR model is much better to track the disease spread, control, and predict the future trend (Tang et al., 2020).

As in the classical SIR model, S(t), I(t), R(t) represented the number of susceptible, infectious, and recovered people respectively at time t in the population size of N (Scarpino and Petri, 2019). To model the dynamics of the outbreak we need three differential equations, one for the change in each group, where β and γ represented the probability of a susceptible-infected contact resulting in a new infection and the probability of an infected case recovering and moving into the resistant phase, respectively (Chinazzi et al., 2020).

In these equations, the parameters β (the infection rate) and γ (the recovery or removal rate of infectives) (Wu et al., 2020) are constants: β controls the transition between S and I, equation (1), while γ controls the transition between I and R, equation (3) (Rüdiger et al., 2020). From a dimensional point of view, assigning no units to S, I, R, and N the parameters β and γ have units of inverse of time (measured typically in days, weeks or months in epidemiological records) (Kucharski et al., 2020).

Notice that equation (1) expresses the interaction between S and I (at time t) as the product SI and that a fraction of this product are the individuals that at time t becomes infected and removed from S (which, because of the negative sign in equation (1), decreases as time increases from zero) (Yang et al., 2020). This interaction in the form of the product SI makes difficult to determine the parameter β from observed epidemiological data. On the other hand, from equation (3), the inverse of the parameter (γ) gives a measure of the time spent by individuals in the infectious state (Fanelli and Piazza, 2020). Consequently, by carefully observing the development of an infectious disease, the parameter γ can be estimated relatively precisely by epidemiologists from epidemiological records (as the inverse of the recovered or infectious period) (Hethcote, 2009).

Beta is the infection rate of the pathogen, and gamma is the recovery rate. They are real, positive, parameters of the initial exponential growth and final exponential decay of the infected population *I* (Giordano et al., 2020). Together, these two values give the basic reproduction number R_0. Basic reproduction number (R_0) is avarage number of people who will catch the disease from single infected person. If the R_0 value is greater than one, the infection rate is greater than the recovery rate, and thus the infection will grow throughout the population (Jung et al., 2020). If R_0 is less than one, the infection quickly will die out since people are healing faster than they are spreading it. Basic reproduction number (R_0) for COVID-19 is 1.4-5.7.

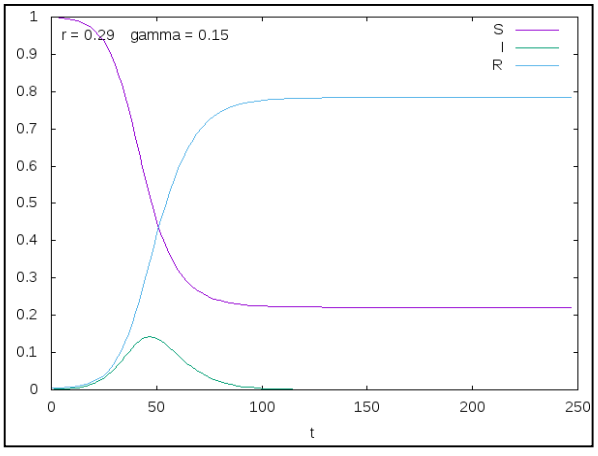

Fig. 3. Simulation of the SIR model of the spread of a disease in Azerbaijan.

Based on these assumptions and concepts, the rates of change of the three populations are governed by the following equation of SIR, what constitutes the SIR model used in this study (Backer et al., 2020).

From the simulation of the SIR model, the first day starts with only one infected person then the infection rate in the simulation increases exponentially with the increasing number of new infected people.

CONCLUSION

The rate of increase in the number of infections depends on the product of the number of infected and susceptible individuals. An understanding of the SIR simulation explains the staggering increase in the infection rate in the Azerbaijan. Infected people traveling different parts of the Azerbaijan and has led to the increase in infected numbers and this results in a further increase in the susceptible population. This gives rise to a positive feedback loop leading to a very rapid rise in the number of active infected cases.

Thus, during this period, the number of susceptible individuals increases and as a result, the number of infected individuals increases as well. For example, as of 19 May, 2020, there were 3518 infected individuals and by 31 October, 2020, this number had grown to a staggering 55,269.

Here, we have applied the SIR model considering data from Azerbaijan. Assuming the published data are reliable, the SIR model can be applied to assess the spread of the COVID-19 disease and predict the number of infected, removed and recovered populations and deaths in the communities, accommodating at the same time possible surges in the number of susceptible individuals.

The countries in the world took extreme actions with closures, confinement, social distancing, and people wearing masks. This type of action produces a decline in the number of infections and susceptible individuals. If the number of susceptible individuals does not decrease, then the number of infections just gets increased rapidly.

As at this moment, there is no effective vaccine developed, the only way to reduce the number of infections is to reduce the number of individuals that are susceptible to the disease. Consequently, the rate of infection tends to zero only if the susceptible population goes to zero.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

REFERENCES

Backer J., Klinkenberg D., Wallinga J. (2020) Incubation period of 2019 novel coronavirus (2019-nCov) infections among travellers from Wuhan, China, 20-28 January. *Eurosurveillance*, **25(5):** Article ID 2000062, 6 p.

Chinazzi M., Davis J.T., Ajelli M., Gioannini C., Litvinova M., Merler S., Viboud C. (2020) The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak. *Science*, **368(6489):** 395-400.

Cowling B.J., Muller M.P., Wong I.O.L., Ho L.-M., Louie M., McGeer A., Leung G.M. (2007) Alternative methods of estimating an incubation distribution: examples from severe acute respiratory syndrome. *Eurosurveillance*, **18(2):** 253-259.

Fanelli D., Piazza F. (2020) Analysis and forecast of COVID-19 spreading in China, Italy and France. *Chaos, Solitons & Fractals*, **134:** Article ID 109761, 5 p.

Giordano G., Blanchini F., Bruno R., Colaneri P., Di Filippo A., Di Matteo A., Colaneri M. (2020) Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy. *Nature Medicine*, **26:** 855-860.

Hethcote H.W. (2009) The basic epidemiology models: models, expressions for R_0, parameter estimation, and applications. In: *Mathematical understanding of infectious disease dynamics*, **16:** 1–61.

Jung S., Akhmetzhanov A.R., Hayashi K., Linton N., Yang Y., Yuan B., Kobayashi T., Kinoshita R., Nishiura H. (2020) Real-time estimation of the risk of death from novel coronavirus (COVID-19). Inference using exported cases. *J. Clin. Med.*, **9(2):** Aericle ID 523, 10 p.

Kraemer M.U., Yang C.H., Gutierrez B., Wu C.H., Klein B., Pigott D.M., Brownstein J.S. (2020) The effect of human mobility and control measures on the COVID-19 epidemic in china. *Science*, **368(6490):** 493-497.

Kucharski A.J., Russell T.W., Diamond C., Liu Y., Edmunds J., Funk S., Davies N. (2020) Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *The Lancet Infectious Diseases*, **20(5):** 553-558.

Nishiura H., Jung S.M., Linton N.M., Kinoshia R., Yang Y., Hayashi K., Kobayashi T., Yuan B., Akhmetzhanov A.R. (2020) The extent of transmission of novel coronavirus in Wuhan, China, 2020. *Journal of Clinical Medicine*, **9(2):** 330.

Rüdiger S., Plietzsch A., Sagués F., Sokolov I.M., Kurths J. (2020) Epidemics with mutating infectivity on small-world networks. *Scientific Reports*, **10(1):** 1–11.

Scarpino S.V., Petri G. (2019) On the predictability of infectious disease outbreaks. Nature communications. **10(1):** 1–8.

Song P., Wang L., Zhou Y., He J., Zhu B., Wang F., Eisenberg M. (2020) An epidemiological forecast model and software assessing interventions on COVID-19 epidemic in China. *MedRxiv*, **Epub.**: 35 p; *Journal of Data Science*, **18:** 409-432.

Tang B., Bragazzi N.L., Li Q., Tang S., Xiao Y., Wu J. (2020) An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov). *Infect. Dis. Model.*, **5:** 248- 255.

Tang B., Wang X., Li Q., Bragazzi N.L., Tang S., Xiao Y., Wu J. (2020) Estimation of the transmission risk of the 2019-ncov and its implication for public health interventions. Journal of clinical medicine. **9(2):** 462.

Wangping J., Ke H., Yang S., Wenzhe C., Shengshu W., Shanshan Y., Miao L. (2020) Extended SIR prediction of the epidemics trend of COVID-19 in italy and compared with hunan, China. *Frontiers in Medicine (Lausanne)*, **7:** Article 169, 7 p.

Wu J.T., Leung K., Bushman M., Kishore N., Niehus R., de Salazar P.M., Cowling B.J., Lipsitch M., Leung G.M. (2020a). Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China. *Nature Medicine*, **26:** 506-510.

Wu J.T., Leung K., Leung G.M. (2020b) Nowcasting and forecasting the potential domestic and international spread of the 2019-ncov outbreak originating in Wuhan, China: a modelling study. *The Lancet*, **395:** 689–697.

Yang Z., Zeng Z., Wang K., Wong S.S., Liang W., Zanin M., Liang J. (2020) Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions. *Journal of Thoracic Disease*, **12(3):** 165-174.

COVID-19-un Azərbaycanda zamandan asılı SİR modeli

R.İ. Xəlilov [1], G.Ə. Aslanova [2]

[1] Bakı Dövlət Universitetinin Biofizika və biokimya kafedrası, Bakı, Azərbaycan
[2] Bakı Dövlət Universitetinin Molekulyar biologiya və biotexnologiyalar kafedrası Bakı, Azərbaycan

"2019-nCoV" adlanan yeni bir koronavirus 2019-cu ilin sonu və 2020-ci ilin əvvəllərində ən ölümcül pandemiyaya səbəb olur. Eramızdan əvvəl 541-542 arasında "Justinianın taunu" olaraq bilinən qlobal pandemiya dünyanın ən pis pandemiyasından biridir və dünyanın 200 milyon əhalisinin 15-25% -ni öldürdüyü təxmin edilir. Bu gün COVID-19-un yayılmasının qarşısını almaq üçün mübarizə aparırıq. Koronavirus insanlıq tarixində ən ölümcül pandemiyaya səbəb ola bilər. Çin xaricində COVID-19 hadisələrinin sayı 16 Mart 2020-ci ildən bəri kəskin şəkildə artmışdır. 28 fevral 2020-ci ildə Azərbaycan, sərhədində ilk müsbət COVID-19 hadisəsini təsdiqlədi. Rusiya vətəndaşı olan xəstə İrandan Azərbaycana səyahət etmişdi. 31 oktyabr 2020-ci il tarixdə Azərbaycanda təsdiqlənmiş koronavirüs hadisələrinin ümumi sayı 55269-dur. Bu məqalədə COVID-19-un riyazi və ədədi analizlərini aparırıq. Azərbaycandan alınan məlumatları nəzərə alaraq SIR modelini tətbiq etdik. Nəşr olunan məlumatların etibarlı olduğunu düşündükdə, SIR modeli COVID-19 xəstəliyinin yayılmasını proqnozlaşdırmaq üçün tətbiq oluna bilər.

Açar sözlər: *COVID-19, SİR, riyazi model, simulyasiya, həssaslar, yoluxmuşlar, bərpa olunmuşlar*

Времязависимая модель *SIR* COVID-19 в Азербайджане

Р.И. Халилов[1] , Г.А. Асланова[2]

[1] Кафедра биофизики и биохимии Бакинского государственного университета , Баку, Азербайджан
[2] Кафедра молекулярной биологии и биотехнологий Бакинского государственного университета, Баку, Азербайджан

Новый коронавирус, названный «2019-nCoV», вызвал самую смертоносную пандемию в конце 2019 - начале 2020 года. Этот новый вирус определен Всемирной организацией здравоохранения (ВОЗ) как коронавирусное заболевание 2019 года (COVID-19). Болезни поражают людей со времен их появления. С 541 по 542 годы нашей эры глобальная пандемия, известная как «Чума Юстиниана», была одной из самых страшных пандемий и, по оценкам, унесла жизни 15–25% 200-миллионного населения мира. Сегодня мы ведем борьбу за контроль и предотвращение распространения COVID-19. Коронавирус может вызвать самую смертоносную пандемию в истории человечества. Число случаев COVID-19 за пределами Китая резко выросло с 16 марта 2020 года. 28 февраля 2020 года на территории Азербайджане был выявлен и подтвержден первый положительный случай COVID-19. Пациентом оказался гражданин России, приехавший из Ирана в Азербайджан. На 31 октября 2020 года общее число подтвержденных случаев коронавируса в Азербайджане составило 55269 человек. В этой статье мы проводим математический и численный анализ распространения COVID-19. Мы применили модель SIR с учетом данных из Азербайджана. Предполагая, что опубликованные данные надежны, модель SIR может быть применена для оценки распространения болезни COVID-19 и прогнозирования результата.

Ключевые слова: *COVID-19, SIR, математическая модель, симуляция, чувствительный, инфицированный, восстановленный*