Mathematical modelling of the dynamics of the Coronavirus COVID-19 epidemic development in China

P. V. Khrapov, A. A. Loginova

***Abstract*—In this work, mathematical modelling of the dynamics of coronavirus COVID-19 is performed for China. The outbreak of coronavirus in China can be considered as public health emergency of international concern. The number of infected is increasing daily. Cases of COVID-19 virus have been detected in nearly 200 countries. Many sporting events, festivals, exhibitions and tournaments have been canceled or postponed. The pandemic has affected education systems around the world, leading to the massive closure of schools and universities. Viral incubation period of this virus is quite long, it ranges from 1 to 14 days. The danger of a new disease also lies in the fact that it is easily confused with a common cold or flu. Therefore, the spread of coronavirus COVID-19 is a serious threat for international health and economics. A mathematical description of the dynamics of virus allows to study the nature of the disease thoughtfully, to analyze statistical and model data, to make hypotheses concerning the future dynamics of coronavirus and to evaluate the effectiveness of the measures undertaken. For mathematical modelling of coronavirus COVID-19, the authors use a modified system of differential equations constructed according to the SIR compartmental model. The optimal values of the model parameters, that describe the statistical data precisely, were found. The analysis of the current situation of the COVID-19 coronavirus epidemic in China was made, which led to the efficiency mark of the existing measures to struggle against the virus.**

***Keywords*— COVID-19; coronavirus; mathematical modelling; epidemiological modelling; SIR model.**

I. INTRODUCTION

Each new infectious disease is a serious challenge for modern medicine. Rapid environmental changes, global environmental problems – this is only a small part of the factors influencing the emergence of new pathogens [1]. The end of 2019 was notable for a new, rapidly changing and developing phenomenon - the emergence of a new coronovirus. On February 11, 2020, the World Health Organization decided to officially name the virus SARS-CoV-2, and the disease caused by this virus - COVID-19 [2]. On March 11, WHO Director-General Tedros Gebreyesus announced that the spread of coronavirus infection COVID-19 “could be described as a pandemic.” A pandemic is a disease epidemic that has spread across a large region, for instance multiple continents, or worldwide. A widespread endemic disease with a stable number of infected people is not a pandemic. The most affected by the pandemic are such regions as mainland China, Europe (Italy, Spain, Germany, France, Switzerland), the USA, Iran, and the Republic of Korea.

In the general case, Coronaviridae is a family of viruses consisting of pathogens in both humans and animals [3,4]. The family so far includes 40 different types of viruses. The most famous representatives of this group are the SARS-CoV (the causative agent of SARS, the first case of which was registered in 2002) and the MERS-CoV (the causative agent of the Middle Eastern respiratory syndrome, the outbreak of which occurred in 2015) [5]. The name is associated with the structure of the virus: under an electron microscope their shape resembles a corona. Coronavirus is a severe viral disease that is the primary lesion of the respiratory system and the gastrointestinal tract. The severity of the disease in people infected with various viruses of the family is different and varies from a mild illness that resembles a mild cold to a disease with severe clinical symptoms. Fatal outcomes are also possible.

COVID-19 has become the third best known coronavirus [6]. It was first discovered on December 31, 2019 in Wuhan in Hubei Province, China. After that, the spread of the disease was recorded in other provinces of China, as well as in other countries of the world, such as Singapore, Japan, the Republic of Korea, Thailand, the USA, Malaysia, Germany, Vietnam, Australia, France, etc [WHO]. Most of the first patients either worked at the local food market, which sold seafood, birds, snakes, bats and farm animals, in Wuhan, or visited it. Consequently, it was suggested that the virus was spread to humans from animals. There is no precise information, which animal has been carrying the disease. Further, the virus is transmitted from person to person, most likely through contact with discharge from the respiratory tract. Washing your hands regularly is the best way to individually protect yourself from the virus. This measure eliminates possible viral contamination of the hands and avoids infection if a person touches his eyes, mouth or nose. Symptoms of the disease caused by the COVID-19 coronavirus are similar to flu symptoms: fever, dyspnea, and labored breathing. Less common headaches, heart palpitations, dizziness, abdominal pain, nausea and vomiting [7]. Moreover, during a clinical examination it is not possible to distinguish infection with a new coronavirus from other respiratory diseases. With a viral infection of COVID-19, can occur such complications as sinusitis pneumonia, bronchitis, acute respiratory failure, pulmonary edema, sepsis and infectious toxic shock can occur. Diagnosis of the disease is made only through laboratory analysis of discharge from the respiratory tract. For most people the disease ends with recovery, and specific treatment measures are not required. Children and

Manuscript received March 24, 2020.

adolescents are least likely to become infected with coronavirus. Particularly the elderly are at risk, especially those with chronic diseases. In China, the mortality rate among infected under the age of 40 years is 0.2%, at the age of 70-79 years - 8%, and from 80 years old - about 14.8%. Obviously, coronavirus infection with COVID-19 poses a great threat to the elderly. There is no vaccine against the virus so far. Developing a vaccine is being carried out by teams all around the world, but no effective vaccine is expected in the near future [8, 9]. Nevertheless, traditional medicine can help to improve well-being and alleviate the symptoms of COVID-19.

The risk level is determined by the location of the person, or rather the presence or absence of an outbreak in the area. China is the initial focus of the coronavirus spread. From there the virus got into other parts of the world, especially Europe. On March 13, WHO declared Europe the center of a pandemic outbreak. In this region, more infections are recorded daily than at the peak of the epidemic in China. Italy became the leader in the spread of infection. Currently, more than 50 thousand cases are registered in this country. The COVID-19 coronavirus pandemic is especially dangerous in Europe due to the large percentage of older people. That is why there is a large number of deaths now.

Currently, several scientists are trying to predict the behavior of the coronavirus COVID-19 [10,11,12]. At this moment due to lack of statistical data, all works are preliminary. Fortunately, the coronavirus epidemic in China is on the decline. Through research of the spread of COVID-19 in China, scientists can come up with useful insights that will help in combating the pandemic in the future.

II. Mathematical modelling of the dynamics of the Coronavirus COVID-19 epidemic development

In this paper, mathematical model for the coronavirus COVID-19 epidemic development is performed for China on the basis of the epidemiological SIR model [13]. SIR model is widely used in mathematical epidemiology [14]. For example, it is used for modelling Ebola epidemic [15,16] and HIV/ AIDS epidemic [17-19].

The epidemiological SIR model is defined by Cauchy problem for the system of differential equations [20]. Let N be the population of the risk group. The rick group can be divided into three group in each compartment at a particular time:

- $S(t)$ (susceptible) – healthy individuals, who are at the risk group and who can catch the infection;
- $I(t)$ (infected) – infected individuals, who are carries of infection;
- $R(t)$ (removed) – removed individuals, i. e. recovered and dead individuals.

For the above groups the following condition is fulfilled:

$$N = S(t) + I(t) + R(t).$$

Morbidity is proportional to the number of contacts between people of the susceptible $S(t)$ and the infected $I(t)$. Rate at which people leave the infected group $I(t)$, i.e. recover or die, is proportional to the population of this group. Consequently, the development of epidemic can be described by the following system of differential equations:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\alpha S(t)I(t), \\ \dfrac{dI(t)}{dt} = \alpha S(t)I(t) - \beta I(t), \\ \dfrac{dR(t)}{dt} = \beta I(t), \end{cases} \qquad (1)$$

where α and β are the parameters.

The severity of coronavirus COVID-19 disease depends on the characteristics of an individual organism. Both cases of complete recovery and cases of death are known. That is why, it is necessary to divide the removed group $R(t)$ into recovered individuals and dead individuals. For this reason the next groups should be introduced instead of group $R(t)$:

- $\tilde{R}(t)$ (recovered) – recovered individuals and individuals who are immune to this disease;
- $D(t)$ (dead) – dead individuals.

Moreover, it is worth considering that there are certain periods between the onset of the disease, its diagnosis, recovery or death of the patient. Based on the above considerations, the system of differential equations (1) has been modified:

$$\begin{cases} \dfrac{dS(t)}{dt} = -\alpha S(t)I(t-\tau_1), \\ \dfrac{dI(t)}{dt} = \alpha S(t)I(t-\tau_1) - \beta I(t-\tau_2) - \gamma I(t-\tau_3), \\ \dfrac{d\tilde{R}(t)}{dt} = \beta I(t-\tau_2), \\ \dfrac{dD(t)}{dt} = \gamma I(t-\tau_3), \end{cases} \qquad (2)$$

where

α - the average infection rate of an individual,

β - the average recovery rate of an individual,

γ - the average rate of death of an individual,

τ_1 - the average time of the infectious period,

τ_2 - the average recovery time of an individual,

τ_3 - the average time of death of an individual.

By setting the values of α, β, γ, τ_1, τ_2, τ_3, the initial values of N, I, $\tilde{R}$, D, the dynamics of the disease can be calculated. The differential equations system with initial conditions (2) is solved using numerical methods.

Statistical data are taken from the World Health Organization (WHO). In the considered model, the size of the risk group $N = 81500$ people, time shifts $\tau_1 = 2.9$, $\tau_2 = 14$, $\tau_3 = 9$ [WHO],

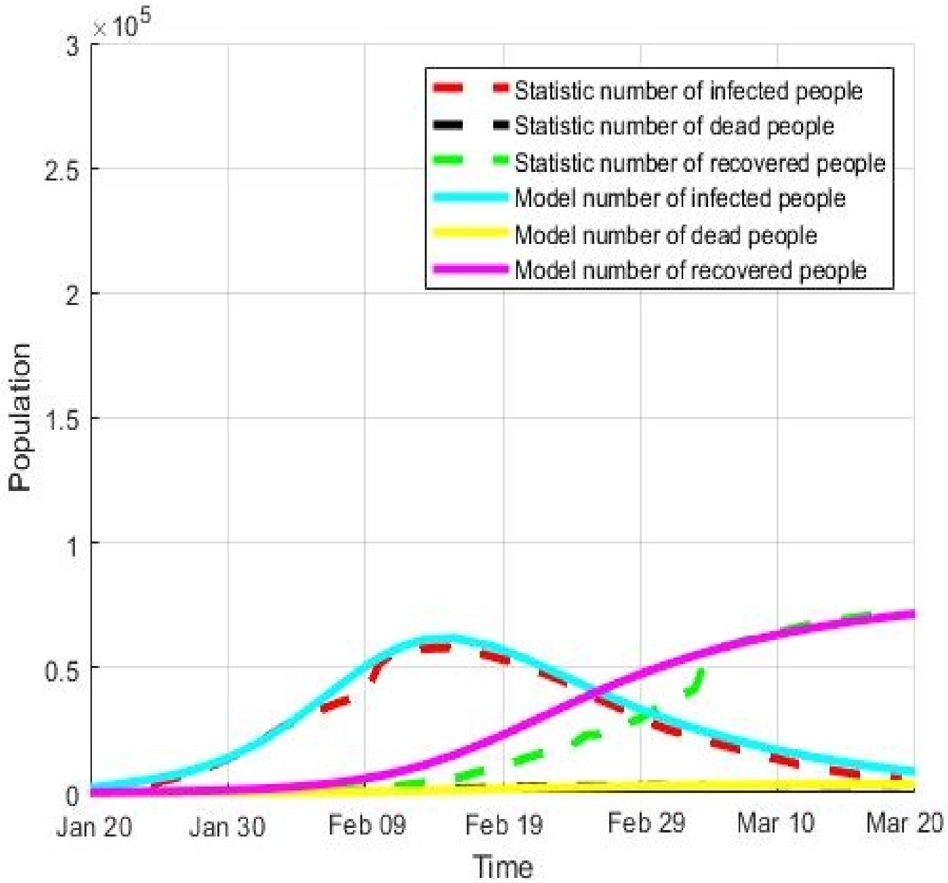

Fig. 1. Dynamics of coronavirus COVID-19 spreading.

parameters $\alpha = 0.4195$, $\beta = 0.0415$, $\gamma = 0.002$ (fig. 1).

We can see a good agreement of the statistical data with the model curves. This indicates the high adequacy of the mathematical model for COVID-19 coronavirus infection. All this suggests that in the future this model can be used to predict the spread of coronavirus in other countries. Based on the statistical and model curves, we can see that the epidemic peaks at the end of February, after which the epidemic declined. This situation can be explained by the national policy of China, aimed at effective struggle against this virus. Moreover, this confirms the effectiveness of the measures introduced. Indeed, in Wuhan, the place where the spread of the virus began, quarantine was implemented at the entry and exit from the city from January 23, 2020. Air traffic, railway transport, public transport, intercity buses were stopped. Similar measures were introduced in other major cities in China.

III. Conclusion

The beginning of 2020 was overshadowed by the outbreak of the pandemic of the new coronavirus COVID-19 [21-23]. This new type of virus spreads extremely quickly. The number of infected has already exceeded 300 thousand cases. The virus poses a great danger to the elderly. The probability of death in case of infection of a person over 65 years old is high enough. Many states have already closed their borders with other countries, implemented quarantine, and banned mass events. The world is in a state of panic and does not know what will happen tomorrow. In addition to obvious threats to international public health, this disease can seriously affect the economies of China, the European Union, the USA, Russia, Australia and other countries [24,25]. Therefore, the development of mathematical models to describe the epidemic of the spread of the COVID-19 coronavirus in China is currently relevant. Now it is very important to investigate this pandemic as much as possible.

This work presents a mathematical model of the spread of the COVID-19 coronavirus epidemic in China. On its base model curves are constructed for the number of infected, recovered and dead (pic. 1). In all cases, the statistics are in good agreement with the model curves, and their behavior indicates that China's national programs to struggle the outbreak are efficient. In this connection, the main peak of the epidemic occurred in mid-February, at the moment the epidemic is in decline, the number of people who have recovered is only increasing. The results obtained during the simulation are consistent with already published works.

Based on the high adequacy of the presented mathematical model, the authors suggest that its use will help in the study of the spread of COVID-19 coronavirus infection in such countries as Italy, Spain, Germany, the USA, Iran, as in the most affected pandemic. Moreover, the authors want to draw attention to the high effectiveness of national measures to combat this disease in China. As the example of China shows, it is in our power to limit the spread of disease outbreaks and stop the transmission of infection. It is important to stay updated on the situation in your area of residence or stay.

The authors of the work show that the epidemic peaks were at the end of February. Further, the disease declined, and the number of recovered people increased. These results can prove the high adequacy of this mathematical model.

REFERENCES

[1] Makarov V.V., Khromov A.V., Guschin V.A., Tkachuk A.P. Emergence of new infections in the 21st century and identification of pathogens using next generation sequencing. Bulletin of Russian State Medical University. 2017; (1): 5-23. DOI: 10.24075/brsmu.2017-01-01 (In Russian)

[2] Notification to the National Health and Health Commission on the preliminary naming of a new coronavirus pneumonia [Online]. Available: http://www.nhc.gov.cn/yzygj/s7653p/202002/18c1bb43965a4492907957875de02ae7.shtml

[3] Bolles, M., Donaldson, E., Baric, R. SARS-CoV and emergent coronaviruses: viral determinants of interspecies transmission. Current opinion in virology. 2011; 1(6): 624-634. DOI: 10.1016/j.coviro.2011.10.012

[4] Shelkanov M. U., Kolobuhina L. V., Lyvov D. K. Men's coronaviruses (Nidovirales, Coronaviridae): increased epidemic hazard. Lechashiy vrach. 2013; (10): 49-54. (In Russian)

[5] Al-Hazmi A. Challenges presented by MERS corona virus and SARS corona virus to global health. Saudi Journal of Biological Sciences. 2016; 23(4): 507-511. DOI: 10.1016/j.sjbs.2016.02.019

[6] Hui D. S., Azhar E. EI, Madani T. A., Ntoumi, F., Kock R.; Dar O., Ippolito G., Mchugh T, D., Memish Z. A. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health — The latest 2019 novel coronavirus outbreak in Wuhan, China. International Journal of Infectious Diseases: journal. 2020, 91: 264-266. DOI: 10.1016/j.ijid.2020.01.009

[7] Wang D., Hu B., Hu C., et al. Clinical characteristics of 138 hospitalized patients with 2019 novel coronavirus–infected pneumonia in Wuhan, China. JAMA. Published online February 07, 2020. DOI: 10.1001/jama.2020.1585

[8] Prevention, Treatment of Novel Coronavirus (2019-nCoV) [Online]. Available: https://www.cdc.gov/coronavirus/2019-ncov/about/prevention-treatment.html

[9] Heymann D. L., Shindo N. COVID-19: what is next for public health? The Lancet. 2020. DOI: 10.1016/S0140-6736(20)30374-3

[10] Read J. M., Bridgen J. RE, Cummings D. AT, Ho A., Jewell C. P. Novel coronavirus 2019-nCoV: early estimation of epidemiological parameters and epidemic predictions. 2020. DOI: 10.1101/2020.01.23.20018549

[11] Kucharski A., Russell T., Diamond C., Liu Y., Edmunds J., Funk S., Eggo R., CMMID nCoV working group. Analysis and projections of transmission dynamics of nCoV in Wuhan [Online]. Available: https://cmmid.github.io/ncov/wuhan_early_dynamics/

[12] Roosa K., Lee Y., Luo R., Kirpich A., R. Rothenberg, Hyman J.M., Yan P., Chowell G. Real-time forecasts of the COVID-19 epidemic in China from February 5th to February 24th, 2020. Infectious Disease Modelling. 2020; 5:256-263. DOI: 10.1016/j.idm.2020.02.002

[13] Kermack W. O., McKendrick A. G. Contributions to the mathematical theory of epidemics. Proceedings of the Royal Society of Edinburgh, Section A. Mathematics. 1927; 115:700–721. DOI: 10.1098/rspa.1927.0118

[14] Martcheva M. An Introduction to Mathematical Epidemiology. Springer. 2015; 453. DOI: 10.1007/978-1-4899-7612-3

[15] Khaleque A. and Sen P. An empirical analysis of the Ebola outbreak in West Africa. Scientific reports. 2017; 7: 42594. DOI: 10.1038/srep42594

[16] Urakova K. A., Khrapov P. V., Mathematical modelling of Ebola hemorrhagic fever epidemiological development in West Africa. Almanakh sovremennoi nauki I obrazovaniya. 2017; 4-5 (118):97-99. Available at: https://elibrary.ru/item.asp?id=29147514 (accessed 10.01.2019). (In Russian)

[17] Huang X. C., Villasana M. An extension of the Kermack–McKendrick model for AIDS epidemic. Journal of the Franklin Institute. 2005; 342.4: 341-351. DOI: 10.1016/j.jfranklin.2004.11.008

[18] Khrapov N. P., Khrapov P. V., Shumilina A. O. Mathematical Model and forecast of AIDS epidemiological development. Almanakh sovremennoi nauki I obrazovaniya, Gramota. 2008; 12(9):218-221. Available at: http://scjournal.ru/articles/issn_1993-5552_2008_12_70.pdf. (In Russian)

[19] Khrapov P. V., Loginova A. A. Mathematical modelling of the dynamics of AIDS epidemics development in the world. International Journal of Open Information Technologies. 2019; 7(6): 13-16. Available at: http://injoit.org/index.php/j1/article/view/755/720.

[20] Arino J. Mathematical epidemiology in a dara-rich world. Infectious Disease Modelling. 2020; 5: 161-188. DOI: 10.1016/j.idm.2019.12.008

[21] Li X., Zeng X., Liu B., Yu Y. COVID-19 infection presenting with CT Halo Sign. Radiology: Cardiothoracic imaging. 2020; 2(1). DOI: 10.1148/ryct.2020200026

[22] Ng M. Y., Lee E. Y., Yang J., Yang F., Li X., Wang H., …, Hui C. K. M. Imaging profile of the COVID-19 infection: radiologic findings and literature review. Cardiothoracic imaging. 2020; 2(1). DOI: 10.1148/ryct.2020200034

[23] Velavan T. P., Meyer C. G. The COVID-19 epidemic. Tropical medicine & international health: TM&IH. 2020. DOI: 10.1111/tmi.13383

[24] Du Z., Wang L., Cauchemez S., Xu X., Wang X., Cowling B. J., Meyers L. A. Risk for transportation of 2019 novel coronavirus (COVID-19) from Wuhan to cities in China. Medrxiv. 2020. DOI: 10.1101/2020.01.28.20019299

[25] Liu Q., Li D., Liu Z., Gao Z., Zhu J., Yang J., Wang Q. Assessing the tendency of 2019-nCoV (COVID-19) outbreak in China. Medrxiv. 2020. DOI: 10.1101/2020.02.09.20021444.

APENDIX

Statistical data sources:

1.WHO. Coronavirus disease (COVID-2019) situation reports. https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/ accessed 22.03.2020.

2. Coronavirus COVID-19 Global Cases by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU). https://gisanddata.maps.arcgis.com/apps/opsdashboard/index.html#/bda7594740fd40299423467b48e9ecf6 accessed 22.03.2020.

3. COVID-19 Global Pandemic Real-time Report. https://ncov.dxy.cn/ncovh5/view/en_pneumonia?from=dxy&source=&link=&share= accessed 22.03.2020.

4. COVID-19 - Situazione in Italia. http://www.salute.gov.it/portale/nuovocoronavirus/dettaglioContenutiNuovoCoronavirus.jsp?lingua=italiano&id=5351&area=nuovoCoronavirus&menu=vuoto accessed 22.03.2020.

5. Coronavirus COVID-19. https://xn--80aesfpebagmfblc0a.xn--p1ai/accessed 22.03.2020.

Authors information

Pavel V. Khrapov, Candidate of Physical-Mathematical Sciences, Associate Professor of the Higher Mathematics Department, Bauman Moscow State Technical University, 5/1 2-nd Baumanskaya, Moscow 105005, Russia,
ORCID: https://orcid.org/0000-0002-6269-0727, e-mail: pvkhrapov@gmail.com , khrapov@bmstu.ru

Anastasia A. Loginova, student at the Higher Mathematics Department, Bauman Moscow State Technical University, 5/1 2-nd Baumanskaya, Moscow 105005, Russia,
ORCID: https://orcid.org/0000-0002-0576-9551, e-mail: loginovaaa@student.bmstu.ru , nastya.loginova@mail.ru.