



Coronavirus infection in Uzbekistan

DJumaniyazova Z. F.¹

¹ *Candidate of Medical Sciences, Associate Professor
Urgench branch of the Tashkent Medical Academy*

Annotation: The article provides an analysis of the course of the coronavirus infection in Uzbekistan since the beginning of the pandemic.

Introduction. COVID-19 is a new infectious disease caused by a novel coronavirus, SARS-CoV-2, not previously seen in humans. In the word COVID-19, "CO" stands for "corona", "VI" for "virus", and "D" for disease. The WHO declared the pathology as "2019 novel coronavirus" or "2019-nCoV" [1] following the 2019 outbreak in Wuhan.

Coronaviruses (Coronaviridae, CoVs) are a large family of RNA viruses that cause mild to severe acute respiratory infections in humans such as Middle East Respiratory Syndrome (MERS) and severe acute respiratory syndrome (Severe Acute Respiratory Syndrome). Syndrome, SARS) [2].

They affect the respiratory, gastrointestinal tract, liver and central nervous system of humans and many other animal species, including domestic animals, livestock, birds, and bats. Prior to the SARS epidemic in 2002 and MERS in 2012 [8], coronaviruses were not considered highly pathogenic for humans, since viruses previously circulating in the human population in immunocompetent individuals mainly caused only mild forms of the disease [6]. Severe, lethal forms of pneumonia that occurred during outbreaks of SARS and MERS in people without immunodeficiency forced a different assessment of the pathogenicity of coronaviruses for humans. On January 7, 2020, the Chinese authorities confirmed the cause of the outbreak as a new strain of coronavirus. January 12, 2020 The World Health Organization (WHO) has proven that CoVs can be transmitted from person to person.

Coronaviruses are enveloped viruses containing single-stranded RNA of positive polarity, they belong to the order Nidovirales, the Coronaviridae family, which includes 2 subfamilies - Orthocoronavirinae and Letovirinae. The subfamily Orthocoronavirinae includes 4 genera: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, Deltacoronavirus. α - and β -coronaviruses infect mammals, while γ - and δ -coronaviruses infect birds [7].

To date, 6 types of coronaviruses are known [1] that can infect humans: Human coronavirus 229E, Human coronavirus NL63 (α -coronaviruses), Betacoronavirus 1, Human coronavirus HKU1, Middle East respiratory syndromerelated coronavirus, Severe Acute Respiratory Syndrome-related coronavirus (β - coronaviruses) [3].

The SARS-CoV-2 coronavirus is a new strain that has not been previously identified in humans. Most cases of the disease are mild, about 15% are severe. In terms of the total number of reported cases and the number of deaths, the SARS-CoV-2 virus epidemic significantly exceeds previous outbreaks of coronavirus infections caused by SARS-CoV and MERS-CoV, which may indicate a serious pandemic



potential of the current infection. As in the case of SARS-CoV and MERS-CoV, bats may be the main reservoir of SARS-CoV-2 infection, while the intermediate host has not been identified [4].

The purpose of the research work is to review information on the new infectious disease COVID-19 caused by the SARS-CoV-2 virus, taking into account previous outbreaks of infections caused by β -coronaviruses MERS-CoV and SARS-CoV, which pose the greatest danger to humans [5] .

Research methods: The work used the statistical data of the Ministry of Health of Uzbekistan.

Research results: In Uzbekistan, according to the results of the analysis of retrospective statistical data, from March 2020 to the present, there are waves of increasing incidence: the first surge occurs in July-August 2020, the second wave of the increase in incidence - in July-August 2021 and III- th growth in January 2022, a slight increase in registration in June-August and November-December 2022 with a decrease in January-February of the current year. These data are directly correlated with the death rates of the disease with an increase from April, June to December 2020, from March 2021 to March 2022 with an annual peak in the month of August. From April 2022 to February 2023, the situation is stable.

During the study period, 251 thousand cases of the disease were registered, 1637 the number of deaths of the disease

An age analysis of registered cases was carried out:

- 0-14 years old - 12.5%
- 15-19 years old - 2.1%
- 20-29 years old - 37.5%
- 30-39 years old - 15.6%
- 40-49 years old - 11.5%
- 50-59 years old - 9.3%
- 60 years and older - 11.5%.

There is a predominance of the occurrence of pathology at a young age.

Discussion: According to the Ministry of Health and the results of the study, a subvariant of the “omicron” strain of coronavirus, BA.5, dominates in Uzbekistan. with a shorter incubation period - 2-3 days, not 5-6 days as in other strains of coronavirus. Among its symptoms it should be noted - sore throat, fever, severe pain in the head and muscles, conjunctivitis, tonsillitis and otitis media.

The number of patients with coronavirus in Uzbekistan has been increasing significantly since November. The dynamics of the increase in the incidence is primarily associated with the cooling of weather conditions, and secondly, people spend most of their time indoors. In addition, an increase in the number of patients is caused by new mutations of COVID-19 with a high level of contagiousness.

Determination of the coronavirus variant in medical samples at the Center for Advanced Technologies under the Ministry of Innovative Development in the Republic in the fall of 2022 showed the predominance of the coronavirus omicron subvariant BA.5 in those hospitalized at the Zangiata Infectious Diseases Hospital No. 1. Its main symptoms are sore throat, hectic body temperature fluctuating up to 41 degrees, severe pain in the head and muscles, weakness, drowsiness, conjunctivitis in 10% of cases, rhinitis and tonsillitis in 40%, otitis media in 10%, diarrhea in 10% of patients. Sometimes patients have a severe cough, chest pain, signs of shortness of breath and lack of air. Damage to the lung tissue is observed in 30-40% of clinical cases. Now in Uzbekistan, the most common strain is "omicron-stealth", a disease that, in the absence of chronic diseases, proceeds favorably.

Conclusions: The observed epidemic situation in the incidence of COVID-19 demonstrates that outbreaks of new human viral infections continue to be an urgent problem of global public health. The epidemic risk of pathology growth depends on the characteristics of the virus, its mutation, the degree of contagiousness, the severity of the emerging disease, and medical or other measures available to control the epidemic situation [10]. Questions remain open about the new coronavirus: its natural reservoir, transmission routes, pandemic potential. It can be assumed that the current outbreak of β -coronavirus infection is not the last. It



should be noted the effectiveness of vaccines and antiviral agents [5]. Risk factors for a severe course of coronavirus infection are reduced immunity, diabetes, hypertension, chronic renal failure, malignant neoplasms, chronic diseases of the heart, lungs, and liver [9]. For COVID-19, comorbidities that worsen illness and outcome include cardiovascular disease, diabetes, chronic respiratory disease, hypertension, and cancer. Vulnerable Populations People with underlying health conditions, smokers, healthcare workers (COVID-19, MERS, SARS), obese people (MERS) and the elderly (COVID-19, MERS) are at increased risk of infection.

When clarifying the sources of the disease, it was found that 35-40% of cases were transmitted from family members, 15-20% - from neighbors or relatives, 7-8% - in public places, 5-8% - at the workplace.

A subline of the omicron strain of the Stealth-Omicron BA.2 coronavirus, known as the "stealth omicron", dominates the number of infections worldwide. The World Health Organization's Working Group on Virus Evolution (TAG-VE) has designated the new subspecies as "Voice of Concern" (VOC). "This strain has been identified in our country, this strain is found in patients with coronavirus infection. Analysis of the virus genome (sequencing) at the Center for Advanced Technologies of the Ministry of Innovative Development revealed the omicron strain in 67% [of those infected], and a new mutation of the omicron strain Stealth-Omicron BA.2 in 33%.

List of used literature:

1. Cheng ZJ, Shan J. 2019 Novel coronavirus: where we are and what we know [published online ahead of print, 2020 Feb 18. *Infection*. 2020;10.1007/s15010-020-01401-y. <https://doi.org/10.1007/s15010-020-01401-y>
2. Cui J, Li F, Shi Z. Origin and evolution of pathogenic coronaviruses. *Nat Rev Microbiol*. 2019;17:181–92. <https://doi.org/10.1038/s41579-018-0118-9>
3. Hui DS, Azhar EI, Madani TA, Ntoumi F, Kock R, Dar O, et al. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health — The latest 2019 novel coronavirus outbreak in Wuhan, China. *Int J Infec Dis*. 2020;91:264–6
4. Li X, Zai J, Wang X, Li Y. Potential of large “first generation” human-to-human transmission of 2019-nCoV [published online ahead of print, 2020 Jan 30. *J Med Virol*. 2020;10.1002/jmv.25693. <https://doi.org/10.1002/jmv.25693>. Hui DS, Zumla A. Severe acute respiratory syndrome. Historical, epidemiologic, and clinical features. *Infect Dis Clin North Am*. 2019;33(4):869–89. <https://doi.org/10.1016/j.idc.2019.07.001>
5. Lu H. Drug treatment options for the 2019-new coronavirus (2019-nCoV) [published online ahead of print, 2020 Jan 28]. *BioSci Trends*. 2020;10.5582/bst.2020.01020. <https://doi.org/10.5582/bst.2020.01020>
6. Song Z, Xu Y, Bao L, Zhang L, Yu P, Qu Y, et al. From SARS to MERS, thrusting coronaviruses into the spotlight. *Viruses*. 2019;11(1):59. <https://doi.org/10.3390/v11010059>
7. Woo PCY, Lau SKP, Lam CSF, Lau CCY, Tsang AKL, Lau JHN, et al. Discovery of seven novel mammalian and avian coronaviruses in the genus deltacoronavirus supports bat coronaviruses as the gene source of alphacoronavirus and betacoronavirus and avian coronaviruses as the gene source of gammacoronavirus and deltacoronavirus. *Virol*. 2012; 86 (7): 3995–4008. <https://doi.org/10.1128/JVI.06540-11>
8. Yin Y, Wunderink RG. MERS, SARS and other coronaviruses as causes of pneumonia. *Respirology*. 2018;23(2):130–7. <https://doi.org/10.1111/resp.13196>.
9. Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin [published online ahead of print, 2020 Feb 03]. *Nature*. 2020. <https://doi.org/10.1038/s41586-020-2012-7>
10. Стовба ЛФ, Лебедев ВН, Петров АА, Ручко ВМ, Кулиш ВС, Борисевич СВ. Новый коронавирус человека, вызывающий заболевание человека. Проблемы особо опасных инфекций. 2015;(2):68–74.

