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COVID-19: evolution of the pandemic in Russia. Report II: dynamics of the circulation of SARS-CoV-2 genetic variants

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Abstract

Background. The ongoing pandemic of the novel coronavirus infection (COVID-19) draws attention to the significance of molecular and genetic monitoring of the SARS-CoV-2 spread among the population of the Russian Federation.

The **aim** of the study was to analyze the dynamics of circulation of SARS-CoV-2 genetic variants in Russia.

Materials and methods. The analysis of the circulation dynamics for SARS-CoV-2 genetic variants in Russia was carried out, covering the period from 28/12/2020 to 26/6/2022. The analysis included the data from Rospotrebnadzor Report No. 970 "Information about Infectious Diseases in Individuals with Suspected Novel Coronavirus Infection" and the Virus Genome Aggregator of Russia (VGARus). The presence of SARS-CoV-2 RNA was confirmed by the real-time reverse transcription polymerase chain reaction. The primer panels developed at the Central Research Institute of Epidemiology were used for amplification of genomic fragments and the subsequent sequencing.

Results and discussion. Using the Russian VGARus platform developed by the Central Research Institute of Epidemiology, we received the data on mutational variability of SARS-CoV-2. By monitoring the circulation of SARS-CoV-2 genetic variants in Russia from 28/12/2020 to 26/6/2022, we found that Delta and Omicron genetic variants prevailed at different stages of the epidemic.

Conclusion. The data of molecular and genetic studies are an essential component of epidemiological surveillance, being critically important for making executive decisions aimed at prevention of further spread of SARS-CoV-2 and laying the groundwork for creating new vaccines.

Keywords: *COVID-19, incidence, epidemic process, SARS-CoV-2, sequencing, genetic variant*

Ethics approval. The study was conducted with the informed consent of the patients. The research protocol was approved by the Ethics Committee of the Central Research Institute for Epidemiology (protocol No. 3, March 27, 2020).

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Научная статья
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COVID-19: эволюция пандемии в России. Сообщение II: динамика циркуляции геновариантов вируса SARS-CoV-2

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Аннотация

Актуальность. Продолжающаяся пандемия новой коронавирусной инфекции (COVID-19) определяет актуальность проведения молекулярного-генетического мониторинга распространения SARS-CoV-2 среди населения Российской Федерации.

Цель работы — анализ динамики циркуляции геновариантов вируса SARS-CoV-2 на территории России.

Материалы и методы. Проведён анализ динамики циркуляции геновариантов вируса SARS-CoV-2 с 28.12.2020 по 26.06.2022 на территории России. Использованы материалы отчёта Роспотребнадзора № 970 «Информация о случаях инфекционных заболеваний у лиц с подозрением на новую коронавирусную инфекцию», Российской платформы агрегации информации о геномах вирусов (VGARus). Наличие РНК SARS-CoV-2 было подтверждено методом полимеразной цепной реакции в режиме реального времени с обратной транскрипцией. Для проведения амплификации фрагментов генома и последующего секвенирования использовались разработанные в ЦНИИ Эпидемиологии праймерные панели.

Результаты и обсуждение. С помощью российской платформы VGARus, развёрнутой на базе ЦНИИ Эпидемиологии, получены данные о мутационной изменчивости SARS-CoV-2. Мониторинг циркуляции геновариантов SARS-CoV-2 на территории России с 28.12.2020 по 26.06.2022 выявил доминирование геновариантов Delta и Omicron на различных этапах эпидемии.

Заключение. Данные молекулярно-генетических исследований являются важнейшим компонентом эпидемиологического надзора для принятия управленческих решений по предотвращению дальнейшего распространения SARS-CoV-2 и формируют основу для создания новых вакцинных препаратов.

Ключевые слова: *COVID-19, заболеваемость, эпидемический процесс, SARS-CoV-2, секвенирование, геновариант*

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Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

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Introduction

The rapid development of the epidemic process of the novel COVID-19 infection (Corona Virus Disease 2019), which is etiologically related to the SARS-CoV-2 coronavirus (Severe acute respiratory syndrome-related coronavirus 2), has created favorable evolutionary conditions worldwide for emerging genetic variants of the pathogen, which acquire new pathogenic properties. This evolutionary trend of SARS-CoV-2, on the one hand, is supported by the advantages of the virus variants that are actively transmitted from human to human and, on the other hand, it is driven by the constraining of the spread of the virus variants that can cause severe disease and, consequently, result in hospitalization of patients and fewer numbers of effective contacts. It should be noted that at present, the global COVID-19 epidemic process is in unstable dynamic equilibrium; even a slight increase in the transmissibility of the pathogen, other things being equal, can cause a rise in the incidence [1–7].

Like other RNA viruses, SARS-CoV-2, adapting to its new hosts – humans, undergoes genetic evolution, which, consequently, results in mutations in the viral genome, and these mutations can alter the pathogenic potential of the virus. Addressing the problem of the growing number of SARS-CoV-2 variants, the U.S. Center for Disease Control and Prevention and the World Health Organization (WHO), independently of each other, have developed classification systems to divide emerging mutations of the virus into several subgroups based on their impact on transmissibility, fatality, and response to treatment.

Although there are differences between these two classifications, the first group of variants of concern (VOCs) can also include variants with proven characteristics such as enhanced transmissibility, severe disease, the increased number of fatal outcomes, and a significant decrease in neutralization by antibodies generated in response to the previous infection or vaccination. Currently, according to the WHO classification, the above category includes Delta (B.1.617.2) and Omicron (B.1.1.529) variants[1]. The second group is composed of variants of interest (VOIs) and includes variants with specific genetic markers associated with changes in receptor binding, reduced neutralization by antibodies, increased transmissibility, reduced efficacy of treatment, and the predicted increase in disease severity. The third group is represented by variants under monitoring (VUM), which are described as having potential effect on the virus transmission rate and treatment efficacy; however, over time, their percentage decreased almost to zero. The classification offered by the U.S. Center for Disease Control and Prevention has one more category – variants of high consequence (VOHC), which have clear evidence that the existing strategies of diagnosis, prevention, and treatment are significantly less effective for them than for previously circulating variants. In the meantime, currently there are no strains falling into the VOHC category[2]. The above abbreviations have become commonly used terms to define variants of the coronavirus causing COVID-19.

The analysis of the dynamics of the spread of the known and new genetic variants of SARS-CoV-2 circulating in Russia is of critical importance. In accordance with RF Government Decree No. 448 "On Approval of the Temporary Procedure for Provision of Decoded Genome Data for the Novel Coronavirus Infection (COVID-19)" dated 23/3/2021, the Central Research Institute of Epidemiology has developed and launched the Virus Genome Aggregator of Russia (VGARus)[3]. The VGARus database contains information about nucleotide sequences of SARS-CoV-2 viruses and their mutations prevailing in different regions of Russia and can be used for storage, systematization, and retrieval of data for detection of mutations and identification of virus strains.

VGARus offers the possibility for continuous monitoring of mutational variability of SARS-CoV-2, providing critically important data for detection of new genetic variants and tracing their prevalence in Russia. Molecular and genetic studies are essentially important for making executive decisions on preventive and epidemic control measures aimed to prevent the further spread of SARS-CoV-2 and create the platform for development of new vaccines [8–10].

The **aim** is to analyze the dynamics of circulation of SARS-CoV-2 genetic variants in Russia.

Materials and methods

The study was performed at the Central Research Institute of Epidemiology of Rospotrebnadzor. The dynamics of circulation of SARS-CoV-2 genetic variants in Russia was analyzed, covering the period from 28/12/2020 to 24/4/2022. The information about patients was retrieved from the database incorporating data from Rospotrebnadzor Report No. 970 "Information about Infectious Diseases in Individuals with Suspected Novel Coronavirus Infection". The ICD-10 U07.1 "COVID-19, identified virus" code was assigned to the above patients: COVID-19 was confirmed by laboratory tests, regardless of the severity of clinical manifestations or symptoms. The study included materials from VGARus, the national platform for aggregated data on SARS-CoV-2 genomes, the centralized data-

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[1] WHO. Tracking SARS-CoV-2 variants. 2021.
URL: https://www.who.int/ru/activities/tracking-SARS-CoV-2-variants/tracking-SARS-CoV-2-variants

[2] CDC. SARS-CoV-2 Variant Classifications and Definitions; 2022.
URL: https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html

[3] VGARus (Virus Genome Aggregator of Russia) Project.
URL: https://genome.crie.ru/app/index

base for epidemiological analysis on the novel coronavirus infection (COVID-19) and software "Epidemiological Analytics for the Novel Coronavirus Infection (COVID-19)" [11, 12].

The laboratory tests were performed in compliance with Guidelines MR 3.1.0169-20 "Laboratory Diagnostics of COVID-19" and other regulatory documents. The biological material used in the study included nasal, nasopharyngeal, and/or throat swabs, bronchial washings collected during fibrobronchoscopy (bronchoalveolar lavage), (endo)tracheal and nasopharyngeal aspirate, sputum, biopsy or autopsy material of the respiratory tract.

The presence of SARS-CoV-2 RNA was confirmed by using the real-time reverse transcription polymerase chain reaction together with AmpliSens® Cov-Bat-FL (No. RZN 2014/1987 of 7/4/2020) and LAMP AmpliSens® SARS-CoV-2 (No. RZN 2021/13357 of 3/2/2021) test systems. The AmpliSens® COVID-19-FL (No. RZN 2021/14026 of 09.04.2021) reagent kit was used to quantify SARS-CoV-2 RNA during RT-PCR. The sequencing was performed at the Central Research Institute of Epidemiology using the Illumina MiSeq platform and MiSeq Reagent Kit v2 (PE 150+150 or PE 250+250 cycles) or MiSeq Reagent Kit v3 (PE 300+300 cycles) as well as Illumina NextSeq 2000 and NextSeq 1000/2000 P2 reagents (300 cycles) v3. All sequences obtained during the study were deposited to the VGARus database. In addition to the above techniques, other organizations participating in building the VGARus database used other methods of amplification of nucleic acids and high-throughput sequencing techniques.

The statistical analysis was conducted using standard methods of descriptive statistics in Microsoft Excel and Statistica v.12.0 (StatSoft).

Results

The implementation of RF Government Decree No. 448 of 23/3/2021 resulted in establishment of the Consortium made up of scientific organizations of Rospotrebnadzor and scientific organizations of other agencies. Currently, it combines 131 organizations, 40 of them are engaged in sequencing [13].

The implementation of the decree produced the resource that is unique in the territorial coverage and completeness of supporting information including data required for epidemiological analysis. The operation algorithm used for VGARus data can be effectively used for real-time and retrospective analysis of prevalence of SARS-CoV-2 genetic variants, taking advantage of the latest information about the genetic diversity of the COVID-19 pathogen.

At present, the evolution of the virus is continuously monitored to provide prompt response to its emerging and potentially dangerous variants as well as to revise and adopt measures aimed at prevention of COVID-19. The compulsory registration is performed in accordance with RF Government Decree No. 448 "On Approval of the Temporary Procedure for Provision of Decoded Genome Data for the Novel Coronavirus Infection (COVID-19)".

Scientists from the Central Research Institute of Epidemiology have designed bioinformatical analytical tools for detection of mutations and identification their affinity to epidemiologically significant strains. Sequencing data, including metadata, are steadily being deposited.

Clinical specimens registered in the database automatically receive registration numbers; the information about specimens includes the data obtained by sequencing of the nucleotide sequence of the SARS-CoV-2 variant. The algorithms used in the database automatically analyze mutations and identify the SARS-CoV-2 variant in each specimen. After the nucleotide sequence of the virus is downloaded, the system automatically launches the process of sequence validation, analyzing the identity with the specific genetic variant and (in case of a whole genome) identifying the genetic variant in accordance with the PANGOLIN nomenclature. The platform collects information from different sources: VGARus, epidemiological data from Rospotrebnadzor, data from the StopCoronavirus portal, WHO, demographic and social data for Russia (statistical data, reference materials). In addition, the VGARus platform provides the software program "Epidemiological Analytics for Novel Coronavirus Infection", which offers real-time analysis of data downloaded to the VGARus database.

The dynamic monitoring of mutation changes in coronaviruses detected in Russia, has been conducted since December 2020 when the first case of Alpha genetic variant (B.1.1.7) importation (28/12/2020) was detected.

Based on the data from the national VGARus database, a total of 130,355 sequences of SARS-CoV-2 have been registered, including 67,451 (51.7%) whole-genome sequences and 62,904 (48.3%) partial sequences.

Among the sequences deposited to the VGARus database, 112,344 (86.2%) belong to VOC variants according to the WHO classification (the revised version of 26/11/2021). Each of these variants differs from the Wuhan variant by a specific set of mutations; 1,217 (0.9%) sequences belong to the Alpha variant; 94 (< 1%) belong to the Beta variant; 26 (< 1%) – to the Gamma variant; 58,530 (44.9%) and 52, 477 (40.2%) are classified as Delta and Omicron variants, respectively. 18,011 (13.8%) of the deposited sequences do not belong to VOC variants.

The Alpha genetic variant circulated in Russia in winter 2021. The Beta and Gamma genetic variants also occurred at the beginning of 2021; however, their occurrence was limited. The Delta genetic variant started spreading in Russia during the second half of April 2021 and prevailed till January 2022. The Omicron genetic variant was detected in Russia in December 2021, and since January 2022 it has been dominant in Russia. The dynamics of detected genetic variants of SARS-CoV-2 during 2020-2022 and the COVID-19 incidence rates (per 100,000 population) in Russia are presented in **Fig. 1**.

After the whole-genome sequencing performed from 30/3/2020 to 26/6/2022, a total of 67,451 identified specimens were deposited to the VGARus database. 724 (1.07%) specimens were classified as the B.1.1.523 genetic variant; 1,329 (1.97%) were classified as B.1.1.317, 3,903 (5,79%) as B.1.1, 802 (1.19%) as Alpha (B.1.1.7), 3,678 (5.45%) as other genetic variants, 22,818 (33.83%) were classified as Omicron (B.1.1.529+BA*), 34,197 (50.69%) specimens were classified as Delta (B.1.617.2+AY*) (**Fig. 2**).

The distribution of SARS-CoV-2 genetic variants by periods of the epidemic increase in the COVID-19 incidence rates in Russia during 2020-2022 as the evidence of dominance of Delta (B.1.617.2+AY*) and Omicron (B.1.1.529+BA*) genetic variants is shown in **Table 1.**

From May to December 2021, the Delta genetic variant (B.1.617.2 + AY.*) prevailed in Russia, reaching 100% occurrence among the detected variants. The variant, which was named AY.122 by the PANGOLIN nomenclature on 26/11/2021, has been dominant (83.3%) during all months of monitoring since the Delta genetic variant was registered.

In addition to AY.122, the most frequently occurred Delta subvariants were represented by the "parental" B.1.617.2 (9.1%), AY.126 (3,0%), and others. Other subvariants were of rare occurrence, accounting for 4.6% of the total Delta sequences (**Fig. 3**).

A total of 30 sublineages of the Delta genetic variant were isolated in Russia; 5% of the analyzed whole genomes of the Delta lineage (B.1.617.2 + AY.*) are presented in **Fig. 4.**

The analysis of the dynamics of subvariants of the Delta lineage (B.1.617.2 + AY.*), which were iso-

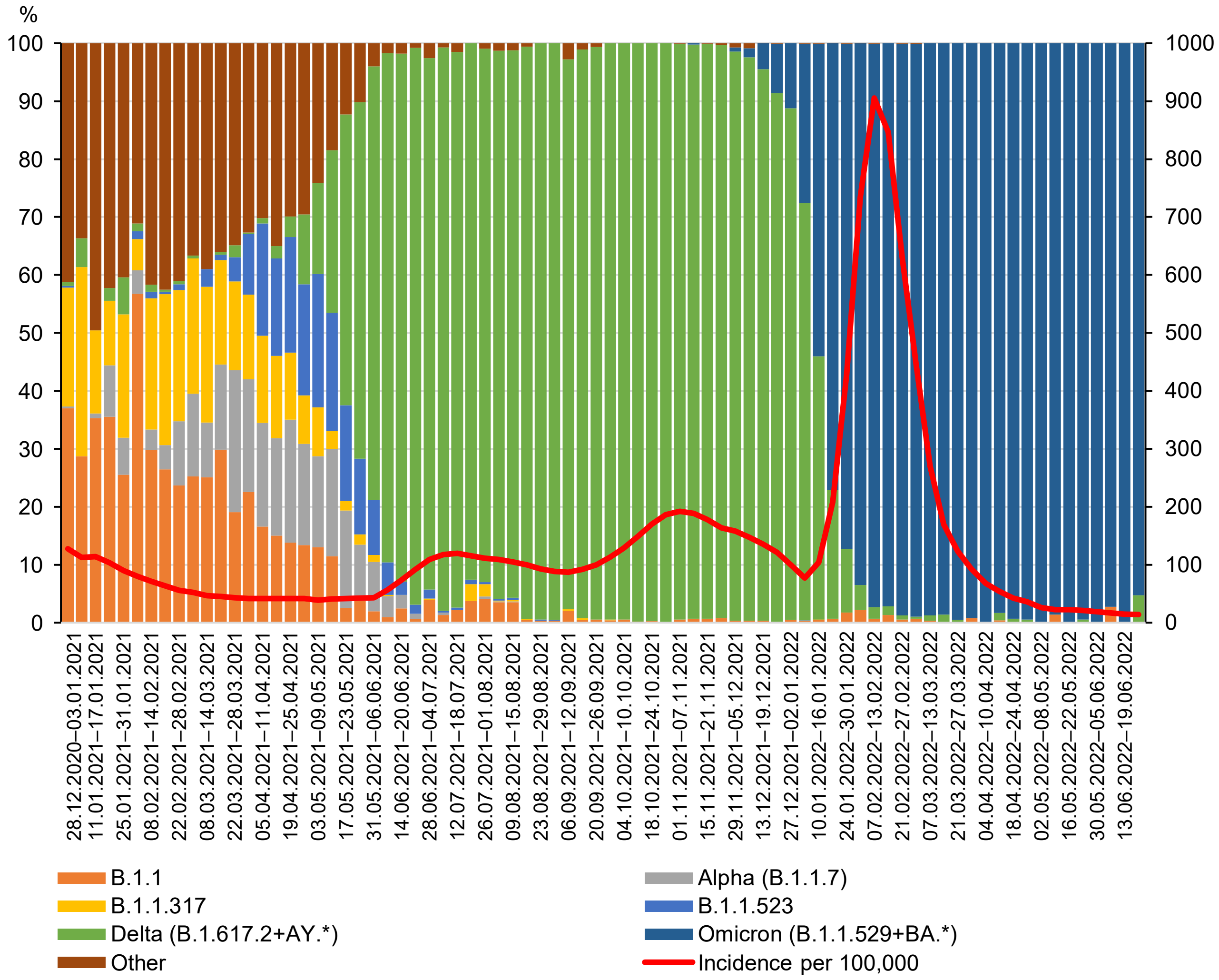

Fig. 1. Dynamics of genetic variants of SARS-CoV-2 and COVID-19 incidence rates (per 100,000 population) in Russia (2020–2022).

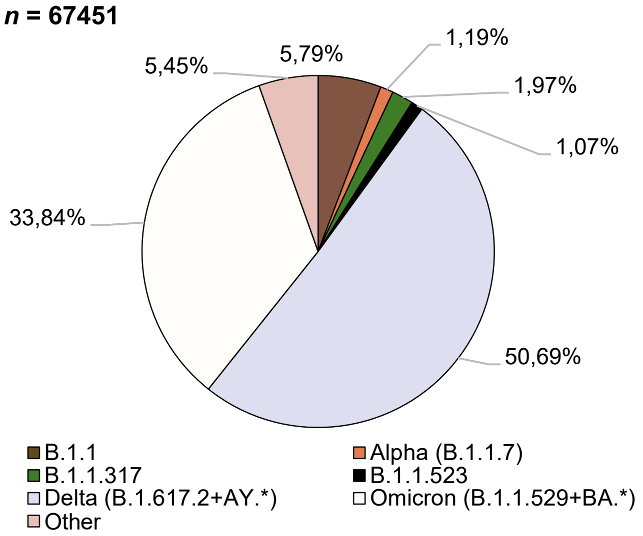

Fig. 2. The distribution of genetic variants in biomaterial specimens collected from 28/12/2020 to 26/6/2022.

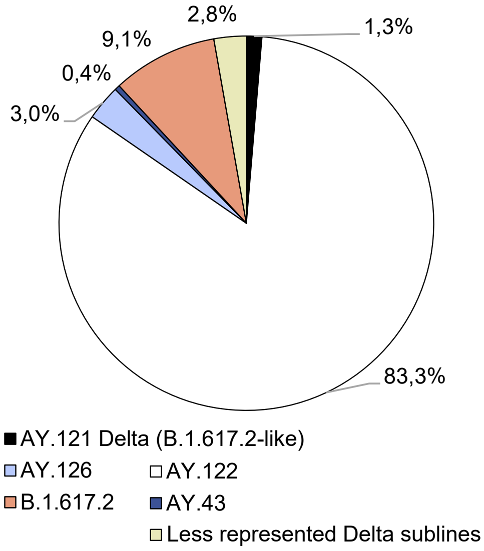

Fig. 3. Subvariants of the Delta lineage (B.1.617.2+AY.*) isolated in Russia.

lated in Russia, showed that in May 2021, the Delta lineage was mainly represented by B.1.617.2 (38.7%) and AY.122 (33.8%) sublineages and less frequently occurring sublineages; after their dissociation, the AY.122 sublineage accounted for 80% of the total population (**Fig. 5**).

The Omicron variant has been rapidly spreading since December 2021; currently, it is the dominant variant in Russia (100% of all the studies specimens). The analysis of the data from the national VGARus database helped reveal the dissociation of the gentic Omicron lineage in Russia with the most frequently circulating subvariants BA.1 (54.5%), BA.1.1 (21.7%), and BA.2 (23.8%). Subvariant BA.3 was of rare occurrence and currently accounts for less than 0.1% of the total Omicron population (**Fig. 6**).

It should be noted that since 1/3/2022 subvariant BA.2 has been dominating in the Omicron lineage (B.1.1.529 + BA.*); its dominance coincided with the decrease in the COVID-19 incidence. It accounts for more than 80% of the total population of subvariants (**Fig. 7**).

Thus, having analyzed the structure of the dominant genetic variants of the Delta lineage (B.1.617.2 + AY.*) and the Omicron lineage (B.1.1.529 + BA.*), we can conclude that heterogeneity and rapid changes

Table 1. Distribution of SARS-CoV-2 genetic variants by periods of the epidemic increase in the COVID-19 incidence in Russia (2020–2022)

Period	Number of samples	Genovariants, abs. (%)						
		B.1.1	B.1.1.317	B.1.1.523	Alpha (B.1.1.7)	Delta (B.1.617.2+AY.*)	Omicron (B.1.1.529+BA.*)	other
I period 30.03.2020–30.08.2020	1701	1056 (62,08)	55 (3,28)	–	–	–	–	590 (34,69)
II period 31.08.2020–09.05.2021	7417	2497 (33,67)	1202 (16,21)	378 (5,10)	536 (7,23)	121 (1,63)	–	2683 (36,17)
III period 10.05.2021–12.09.2021	10 602	126 (1,19)	67 (0,63)	345 (3,25)	266 (2,51)	9502 (89,62)	–	296 (2,79)
IV period 19.09.2021–09.01.2022	23 315	21 (0,09)	2 (0,009)	1 (0,004)	–	21 795 (93,48)	1420 (6,09)	76 (0,33)
V period 10.01.2022–26.06.2022	24 416	203 (0,83)	3 (0,012)	–	–	2779 (11,38)	21 398 (87,64)	33 (0,14)
Total	67 451	3903 (5,79)	1329 (1,97)	724 (1,07)	802 (1,19)	34 197 (50,69)	22 818 (33,83)	3678 (5,45)

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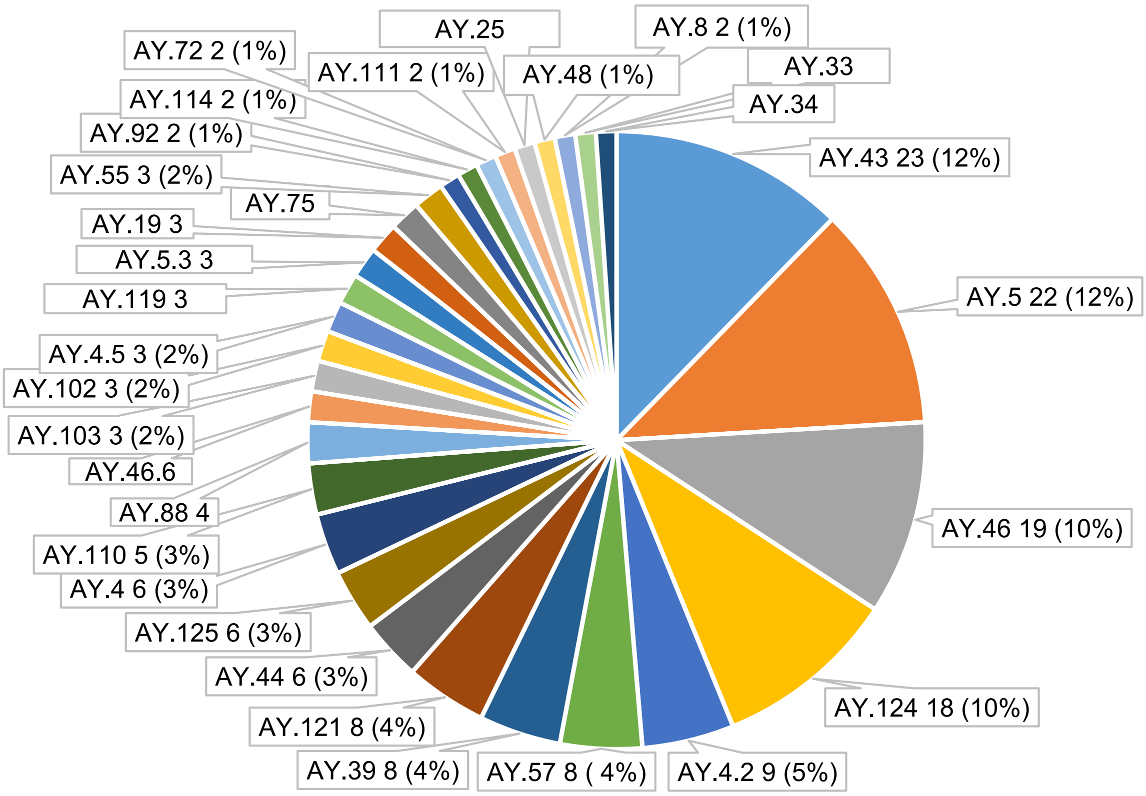

Fig. 4. Subvariants of the B.1.617.2. (Delta) lineage, except for basic variant B.1.617.2 and subvariants AY.122, AY.126, AY.121, AY.43 isolated in Russia.

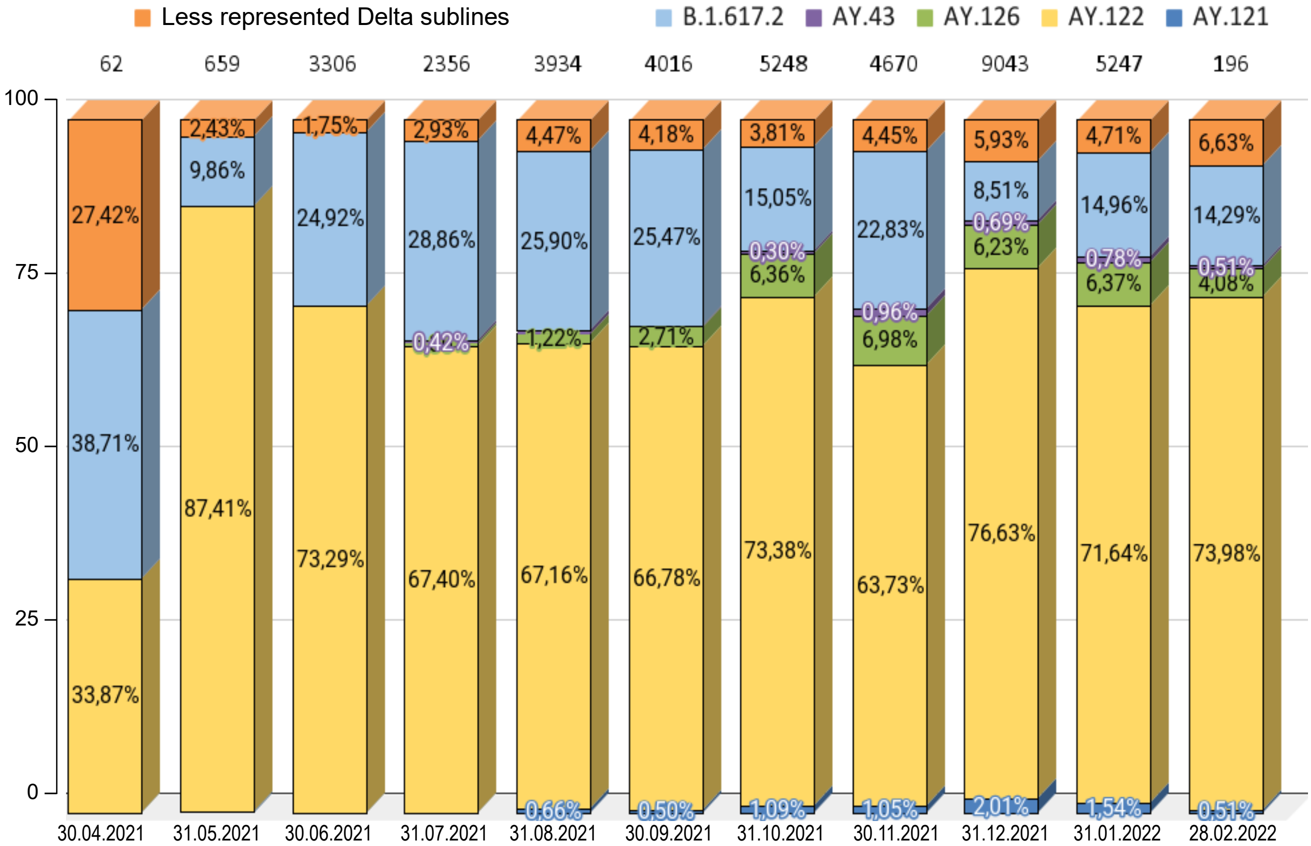

Fig. 5. Dynamics of subvariants of the Delta lineage (B.1.617.2+AY.*), which were isolated in Russia, based on the data from the national VGARus database.

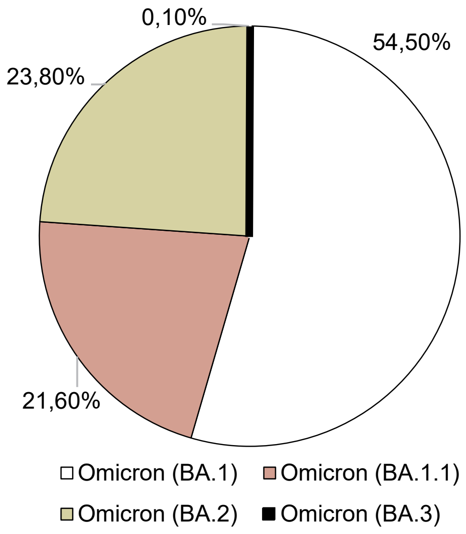

Fig. 6. Subvariants of the Omicron lineage (B.1.1.529+BA.*), which were isolated in Russia, based on the data from the national VGARus database as of 26/6/2022.

in the pathogenic properties and transmissibility of the virus have a clear impact on the development of the epidemic process. This conclusion is supported by the dynamics of the epidemic process manifestations and by severity of the disease (**Table 2**). The highest incidence rate in 2020 (the dominance of the Wuhan strain) was 51.31 (per 100,000 population); the highest incidence rate in 2021 (the dominance of the Delta strain) was 192.45 (per 100,000 population); the highest incidence rate in 2022 (the dominance of the Omicron strain) was 905.37 (per 100,000 population).

Discussion

During the first year of SARS-CoV-2 presence in the human population, its genome did not demonstrate any nucleotide substitutions, which could cause noticeable changes in the properties of the pathogen. However, as the survival of the pathogen as a biological species is impossible without evolutionary growth, the range of coronavirus population heterogeneity starts expanding

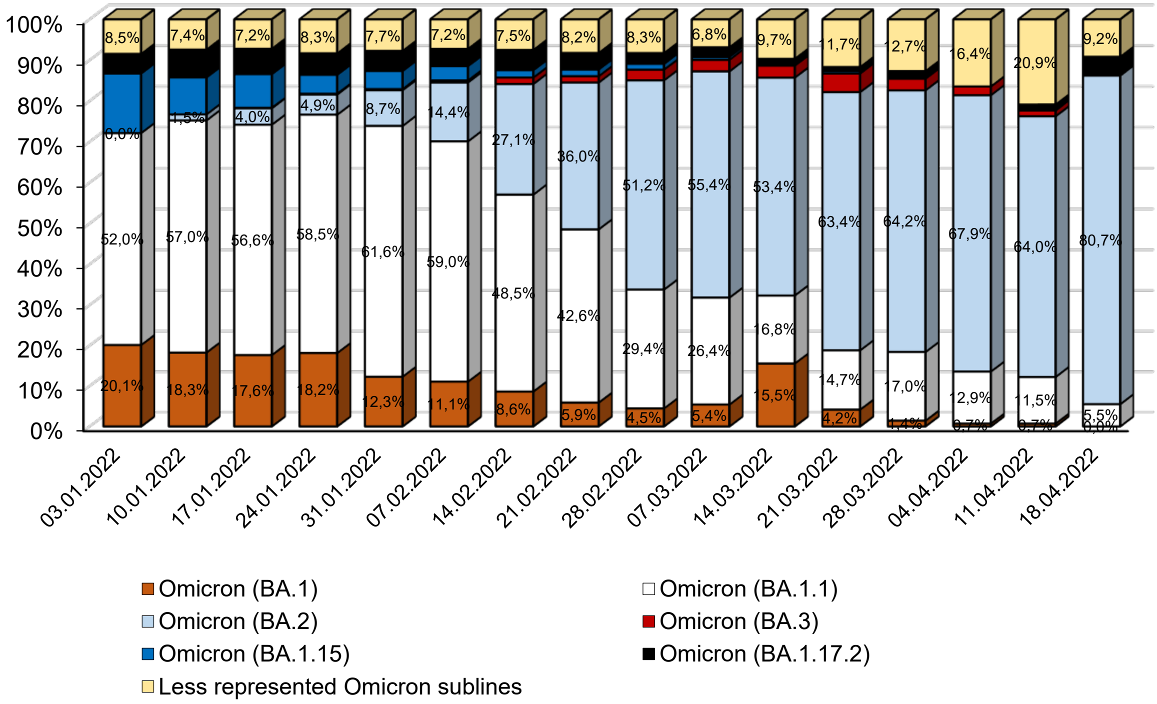

Fig. 7. Dynamics of subvariants of the Omicron lineage (B.1.1.529 + BA.*), which were isolated in Russia, based on the data from the national VGARus database.

Table 2. Comparative analysis (dynamics) of the manifestations of the COVID-19 epidemic process, considering the evolution of the pathogen

Manifestations of the epidemic process	Wuhan genetic variant	Delta genetic variant	Omicron genetic variant
Incidence per 100,000 population	51,31	192,45	905.37 (a 17.6-fold increase; $p < 0.05$)
Percentage of severe cases of infection, %	4,5	2,6	0.4% (a 11.3-fold decrease; $p < 0.05$)
Percentage of circulating coronaviruses among relatively healthy population, %*	10–12	13–16	30–37% (a 3-fold increase; $p < 0.05$)
Percentage of children among affected individuals, %	10	12	18% (a 1.8-fold increase; $p < 0.05$)

Note. *Based on the data for Moscow and Moscow Region (n = 2,366,527).

through circulation of low-virulent and high-virulent variants; the expansion is followed by stabilizing selection and establishment of the epidemic variant of the pathogen. The first significant VOCs were detected at the end of 2020 – at the beginning of 2021: Alpha (B.1.1.7) in Great Britain, Beta (B.1.351) in South Africa, Gamma (P.1) in Brazil, and Delta (B.1.617.2) in India[4]. The emerging mutations altered the amino acid sequence of the spike (S) protein, which binds to the ACE2 receptor and facilitates the entry of the virus into sensitive human host cells, thus becoming the main factor of the COVID-19 pathogenesis. Such mutations raise reasonable concerns, as the aggressiveness of the virus depends on them.

In November 2021, the emergence of the new variant of SARS-CoV-2 coronavirus put an end to cautious optimism and hopes of experts for the soon coming winding-down of the COVID-19 pandemic; the new variant was first identified in Botswana and the Republic of South Africa. The new lineage was designated as BA.2, the main lineage of the recently detected variant of the coronavirus was designated as BA.1, while the umbrella name of the variant remained unchanged — B.1.1.529 according to the PANGO classification. On 26/11/2021, WHO classified the mutated virus as VOC and assigned the Omicron (B.1.1.529 + BA.*) code to it. In the opinion of experts, SARS-COV-2 has undergone evolution, and the genomic changes promoted such characteristics as the ability to cause intensive transmission of the virus, to change the clinical symptoms of the disease, to evade the immune response, diagnostic techniques or therapeutical agents. The existence of multiple COVID-19 cluster on different continents can affect the epidemiological situation, lead to a new source of risk for the health of the global population and to a new wave of infection. Therefore, all countries should improve their epidemiological surveillance; perform genome sequencing for effective monitoring of circulating variants of SARS-CoV-2; deposit whole-genome sequences of the virus and supporting metadata to the publicly accessible database such as GISAID. The global dominance of the Omicron genetic variant calls for exploration of its impact on disease severity, effectiveness of epidemic control measures, immune response, neutralizing activity of antibodies, and other significant parameters[5].

Today, there is a significant amount of data on evolutionary changes in the SARS-CoV-2 genome, including its tendencies to acquire new epidemiological properties. During its circulation in the human population, the SARS-CoV-2 genome, adapting to the new host, has acquired a certain number of nucleotide substitutions.

The COVID-19 pandemic once again confirmed the theory offered by academician V.D. Belyakov who believed that the development of the epidemic process was based on the phase changes in the heterogeneity of biological properties of interacting populations of the pathogen and human, involving the reverse negative relations in the process of self-regulation with an important role played by social and natural factors [14, 15]. In accordance with the theory of self-regulation of parasitic systems, changes are associated not only with genetic variability, but also with other polydeterminant characteristics of the pathogen: With emergence of new genetic variants, SARS-CoV-2 has become less pathogenic, though more contagious for human. This specific characteristic is important not only for theoretical, but also for practical epidemiology, making it possible to predict the pattern of development of the epidemic situation.

Conclusion

The whole-genome sequencing of SARS-CoV-2 genetic variants was performed in Russia from 28/12/2020 to 26/6/2022, using the VGARus database. It confirmed the dominance of Delta and Omicron genetic variants and demonstrated that from May to December 2021, the Delta genetic variant (B.1.617.2 + AY.*) was dominant in Russia, while subvariant AY.122 prevailed (83.3%). The Omicron variant started its rapid spread in December 2021, including dissociation of the Omicron genetic lineage and dominance of subvariants BA.1, BA.1.1, and BA.2. The BA.3 sublineage was of rare occurrence and currently accounts for less than 0.1% of the total Omicron population. The proportion of the BA.2 sublineage is gradually increasing (accounting for 80% of the Omicron sublineages isolated during the 16th–17th week in 2022). In Russia, a few BA.4 and BA.5 genetic variants have been detected; they have not developed into epidemic forms, causing asymptomatic or mild cases of acute respiratory viral infection.

It has been found that with emergence of new genetic variants, SARS-CoV-2 has become less pathogenic, though more contagious for human. This statement is supported by the dynamics of epidemic process manifestations and severity of the disease.

The SARS-CoV-2 virus is going through evolution, thus calling for continuous scientific studies involving advanced methods of the whole genome analysis of its genetic sequences.

Currently, the molecular and genetic monitoring of the SARS-CoV-2 circulation is a high-priority area of the epidemiological surveillance over COVID-19, being of critical importance for development and implementation of epidemic control measures.

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