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Research article

VIRUS CONTAMINATION OF CENTRALIZED WATER SUPPLY SYSTEMS AS A HEALTH RISK FACTOR: FEATURES OF LONG-TERM DYNAMICS IN THE RUSSIAN FEDERATION

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Despite the fact that high-quality water treatment is currently being carried out, there is a possibility that pathogens of infectious diseases may enter a water supply network. Sanitary and virologic control of water sources and drinking water is currently performed directly by direct detection of viruses, as well as by using indirect indicators of viral contamination, namely, coliphages.

The aim was to study the spectrum of viruses contained in water from a centralized water supply system using laboratory diagnostic methods regulated to determine rated indicators.

Over 2014–2023, water samples were taken from a centralized water supply system (n = 2,847,568). The dynamics and structure of water contamination with hepatitis A (HAV), Rotavirus, Enterovirus, Norovirus, Astrovirus, COVID-19 (SARs-CoV-2) viruses, and Adenovirus in a centralized water supply system were described using classical cultural methods of bacteriology and virology, molecular-genetic and serological methods.

The conducted research found that over 2014–2023, the average proportion of centralized water supply samples that did not meet sanitary and hygienic standards in the Russian Federation was 0.57 % for the presence of viruses and 0.21 % for the presence of coliphages for the period from 2014 to 2023. The proportion of centralized water supply samples per non-conforming Rotavirus contents was 1.41 % (95 % CI: 1.33–1.49) (according to serological studies, 0.08 % of samples (95 % CI: 0.06–0.10); Enterovirus, 0.71 % (95 % CI: 0.57–0.86) (according to PCR studies, 0.37 % (95 % CI: 0.33–0.42); Adenovirus, 0.52 % (95 % CI: 0.38–0.70); Norovirus, 0.20 % (95 % CI: 0.16–0.24); Astrovirus, 0.14 % (95 % CI: 0.11–0.18);

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SARs-CoV-2, 0.09 % (95 % CI: 0.03–0.20); HAV, 0.2 % (95 % CI: 0.01–0.04) (according to serological studies, it was slightly higher (0.09 % (95 % CI: 0.07–0.11). A direct strong correlation was established between the proportion of centralized water supply samples that did not meet sanitary and epidemiological requirements and the presence of coliphages and pathogens of viral infections (r > 0.8); however, determination of nucleic acids in drinking water by molecular genetic methods indicates higher prevalence of viruses as compared to classical coliphage testing.

The structure of virus contamination in water from a centralized water supply system was represented by Rotavirus (52.6 ± 0.3 %), Adenovirus (18.8 ± 0.5 %), Enterovirus (13.9 ± 0.2 %), Norovirus (7.5 ± 0.1 %), Astrovirus (3.8 ± 0.1 %), and SARs-CoV-2 (3.4 ± 0.2 %) over 2020–2023.

Keywords: *water microflora, centralized water supply, water of centralized water supply, viruses, contamination, biological safety, adenovirus, rotavirus, enterovirus, risk factors.*

Providing people with safe water is among the most significant challenges the global community has been facing over the last decades [1, 2]. In the Russian Federation, the state of centralized drinking water supply to the population requires some specific activities aimed at improving the water treatment system [3]. Despite the fact that high-quality water treatment is currently being carried out, there is a possibility that pathogens of infectious diseases may enter a water supply network, for example, due to wear and tear of water distribution systems and / or accidents at water supply networks and wastewater infiltrating them from damaged sewage pipelines [1, 4, 5].

In the Russian Federation, complex investigations of virus species prevalence in drinking water are rather scarce. Some foreign researchers give evidence of three enteric viruses holding the leading place in virus contamination of drinking water, namely *Adenovirus*, *Rotavirus*, and *Enterovirus* [6]. Prevalence of adenoviruses, enteroviruses, and rotaviruses has been shown in samples of treated drinking water taken at water treatment facilities [6–8]. Enterovirus was found in 21 % of treated drinking water samples in China (Wuhan) (5/24) [6]; adenovirus was found in 20 %, enterovirus in 43 % and rotavirus in 23 % of tap water samples in Pakistan [8]; in Brazil, enterovirus was identified in 27.4 % of water samples, adenovirus in 23.3 % and rotavirus in 16.4 % [7]. A review made by C. Mejías-Molina et al. (2024), covered works published over the last five years and reported Norovirus (0.5–6.7 %) and Hepatitis E virus (0.8 %) in water in addition to adenovirus (17–48 %), rotavirus (1,5–44 %) and enterovirus (0.9 %) [9].

Long-term studies confirm the role that belongs to viruses in occurrence of waterborne infections[1] [10]. According to the World Health Organization data (2022), drinking water contamination is among the most significant risk factors of acute enteric infections caused by *Adenovirus*, *Rotavirus*, *Enterovirus*, as well as by other enteric viruses[1]. In some RF regions, additional disease cases are associated with poor drinking water quality including non-conformity with safe standards per microbiological indicators. In 2023, incidence associated with poor drinking water quality was established in 84 regions of the Russian Federation within the range between 18.6 and 4167.7 additional disease cases per 100 thousand people[2].

At present, Rospotrebnadzor makes schedules of planned monitoring examinations aimed at establishing levels of drinking water contamination as a risk factor of enteric viral infections. The main aim is to prevent waterborne infections. The present sanitary and virologic control of water sources and drinking water relies on using indirect indicators of virus contamination such as coliphages and on direct virus identification [5, 11]. Molecular-genetic methods are widely used by sanitary-epidemiological laboratories for direct identification of viruses per their genome (RNA and

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[1] WHO. Guidelines for drinking-water quality: fourth edition incorporating the first and second addenda. *WHO*, 2022, 614 p. Available at: https://www.who.int/publications/i/item/9789240045064 (October 03, 2024).

[2] O sostoyanii sanitarno-epidemiologicheskogo blagopoluchiya naseleniya v Rossiiskoi Federatsii v 2023 godu: Gosudarstvennyi doklad [On sanitary-epidemiological wellbeing of the population in the Russian Federation in 2023: the State Report]. Moscow, Federal Service for Surveillance over Consumer Rights Protection and Human Wellbeing, 2024, 364 p. (in Russian).

DNA). In particular, polymerase chain reaction (PCR) is a common method due to its high sensitivity, availability and a possibility to identify contamination over one day [5, 11]. Parallel PCR use and coliphage identification in water ensure high reliability as regards establishing virus contamination in water since they make it possible to establish epidemiological significance of viruses identified per their RNA and DNA [5]. At present, it is quite relevant to investigate tap water contamination as a health risk factor using up-to-date laboratory diagnostic techniques.

Given all foregoing, **the aim of this study** was to examine the spectrum of viruses contained in water from a centralized water supply system (tap water) using laboratory diagnostic methods regulated to determine rated indicators.

Materials and methods. Over 2014–2023, tap water samples (*n* = 2,847,568) were analyzed in accordance with the valid methodical documents[3] annually within scheduled, unscheduled and industrial control, sanitary-hygienic monitoring conducted in RF regions by Rospotrebnadzor offices. Water samples were taken in sterile containers prior to supply and from distribution networks for centralized water supply in 89 regions of the Russian Federation. The samples were then delivered to laboratories of regional Centers for Hygiene and Epidemiology in conformity with all requirements to sample delivery with preliminary concentration of viruses predominantly using filter membranes[4].

Water samples were analyzed in conformity with the valid documents[4,5] using conventional bacteriological and virologic methods to identify coliphages and enteroviruses *(Enterovirus)*, respectively; molecular-genetic methods to identify RNA of hepatitis A virus *(HAV)*, *Rotavirus, Enterovirus, Norovirus* (since 2018), *Astrovirus* and *SARs-CoV-2* (since 2018 and 2020, respectively); *Adenovirus* DNA (since 2018); serological methods to identify *HAV* and *Rotavirus* antigens. The tests were conducted using tests-systems predominantly manufactured by Rospotrebnadzor's Central Scientific Research Institute for Epidemiology (AmpliSens OKI viro-screen-FL», AmpliSens Cov-Bat), Rospotrebnadzor's Saint Petersburg Scientific Research Institute of

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[3] MUK 4.2.3963-23. Bakteriologicheskie metody issledovaniya vody: metodicheskie ukazaniya, utv. rukovoditelem Federal'noi sluzhby po nadzoru v sfere zashchity prav potrebitelei i blagopoluchiya cheloveka, Glavnym gosudarstvennym sanitarnym vrachom Rossiiskoi Federatsii A.Yu. Popovoi 1 sentyabrya 2023 g. [MUK 4.2.3963-23. Bacteriological methods for water analysis: methodical guidelines, approved by A.Yu. Popova, Head of the Federal Service for Surveillance over Consumer Rights Protection and Human Wellbeing, the RF Chief Sanitary Inspector on September 01, 2023]. *KODEKS: electronic fund for legal and reference documentation.* Available at: https://docs.cntd.ru/document/1304575302 (March 27, 2025) (in Russian); MUK 4.2.1018-01. Sanitarno-mikrobiologicheskii analiz pit'evoi vody: metodicheskie ukazaniya, utv. Glavnym gosudarstvennym sanitarnym vrachom Rossiiskoi Federatsii – Pervym zamestitelem ministra zdravookhraneniya Rossiiskoi Federatsii 9 fevralya 2001 g. [MUK 4.2.1018-01. Sanitary-microbiological analysis of drinking water: methodical guidelines, approved by the RF Chief Sanitary Inspector – the First Deputy to the RF Minister of Health on February 09, 2001]. *KODEKS: electronic fund for legal and reference documentation*. Available at: https://docs.cntd.ru/document/1200029648 (March 27, 2025) (in Russian).

[4] MUK 4.2.2029-05. Sanitarno-virusologicheskii kontrol' vodnykh ob"ektov: metodicheskie ukazaniya, utv. i vved. v deistvie Rukovoditelem Federal'noi sluzhby po nadzoru v sfere zashchity prav potrebitelei i blagopoluchiya cheloveka, Glavnym gosudarstvennym sanitarnym vrachom Rossiiskoi Federatsii G.G. Onishchenko 18 noyabrya 2005 goda [MUK 4.2.2029-05. Sanitary-virologic control of water objects: methodical guidelines, approved and enacted by G.G. Onishchenko, Head of the Federal Service for Surveillance over Consumer Rights Protection and Human Wellbeing, the RF Chief Sanitary Inspector on November 18, 2005]. *KODEKS: electronic fund for legal and reference documentation*. Available at: https://docs.cntd.ru/document/1200042984 (April 16, 2025) (in Russian).

[5] O sostoyanii sanitarno-epidemiologicheskogo blagopoluchiya naseleniya v Rossiiskoi Federatsii v 2023 godu: Gosudarstvennyi doklad [On sanitary-epidemiological wellbeing of the population in the Russian Federation in 2023: the State Report]. Moscow, Federal Service for Surveillance over Consumer Rights Protection and Human Wellbeing, 2024, 364 p. (in Russian); MUK 4.2.2746-10. Poryadok primeneniya molekulyarno-geneticheskikh metodov pri obsledovanii ochagov ostrykh kishechnykh infektsii s gruppovoi zabolevaemost'yu: metodicheskie ukazaniya, utv. Rukovoditelem Federal'noi sluzhby po nadzoru v sfere zashchity prav potrebitelei i blagopoluchiya cheloveka, Glavnym gosudarstvennym sanitarnym vrachom Rossiiskoi Federatsii G.G. Onishchenko 30 sentyabrya 2010 g. [MUK 4.2.2746-10. The Procedure for using molecular-genetic methods when examining foci of acute enteric infections with group incidence: methodical guidelines, approved by G.G. Onishchenko, Head of the Federal Service for Surveillance over Consumer Rights Protection and Human Wellbeing, the RF Chief Sanitary Inspector on September 30, 2010]. *KODEKS: electronic fund for legal and reference documentation.* Available at: https://docs.cntd.ru/document/1200084387 (April 16, 2025) (in Russian).

Epidemiology and Microbiology named after Paster (COVID-2019 Amp), Vector-Best JSC (VGA-antigen-IFA-BEST), BioloT LLC (Igla MEM nutrient medium). The test results were included in the Federal Statistical Report Form No. 18 Data on Sanitary Situation in a region of the Russian Federation and No. 2.14–2.23 Data on Activities Accomplished by Sanitary-Hygienic, Microbiological and Parasitological Laboratories of Centers for Hygiene and Epidemiology. Primary data were collected and obtained from the Rospotrebnadzor's Federal Center for Hygiene and Epidemiology.

Water samples that did not conform to safe standards due to containing coliphages and viruses were denoted as 'non-standard samples' (n/s)[6]. Test results were analyzed using Microsoft Office v.2016. A 95 % confidence interval (CI) for the proportion of detected non-standard samples was calculated with BinomCI function using the Wilson method and DescTools libraries of R software. Trend significance to declining (growing) proportions of tap water samples was estimated per the Mann – Kendall method using Mann Kendall function of R software. A trend was considered significant at $p < 0.05$.

Results and discussion. The accomplished investigation found that the mean specific weight of tap water samples not conforming to safe standards valid in the Russian Federation equaled 0.57 % per viruses and 0.21 % per coliphages over the period between 2014 and 2023. In 2023, a descending trend was established for the specific weight of non-standard samples ($p < 0.05$) (Figure 1). A strong direct correlation was found for the proportion of tap water samples not conforming to sanitary-epidemiological requirements per coliphage and virus occurrence ($r = 0.82$, $p = 0.04$); however, the proportion of non-standard samples per presence of virus nucleic acids was on average 2.7 times higher. This probably indicates that molecular-genetic examinations are more informative for assessing safety of drinking water supply per microbiological indicators.

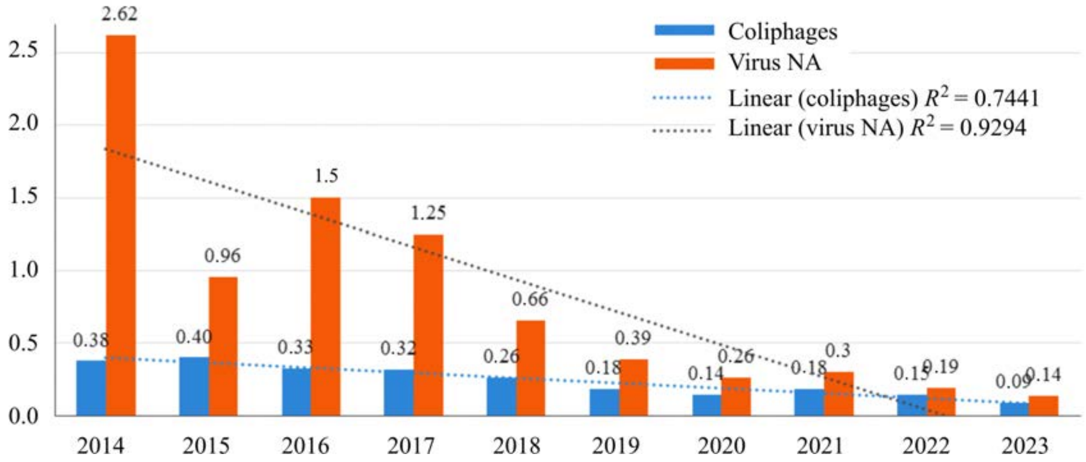

Figure 1. The proportion (%) of tap water samples not conforming to safe standards per occurrence of viruses and coliphages in the RF over 2014–2023

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[6] SanPiN 1.2.3685-21. Gigienicheskie normativy i trebovaniya k obespecheniyu bezopasnosti i (ili) bezvrednosti dlya cheloveka faktorov sredy obitaniya: sanitarnye pravila i normy, utv. postanovleniem Glavnogo gosudarstvennogo sanitarnogo vracha Rossiiskoi Federatsii ot 28 yanvarya 2021 goda № 2 (s izmeneniyami na 30 dekabrya 2022 goda) [SanPiN 1.2.3685-21. Hygienic standards and requirements to providing safety and (or) harmlessness of environmental factors for people: sanitary rules and norms, approved by the Order of the RF Chief Sanitary Inspector on January 28, 2021 No. 2 (last edited as of December 30, 2022)]. *KODEKS: electronic fund for legal and reference documentation*. Available at: https://docs.cntd.ru/document/573500115 (April 16, 2025) (in Russian).

Tests aimed at identifying antigens of enterovirus (*Enterovirus*), rotavirus (*Rotavirus*), and Hepatitis A (*HAV*) infectious agents in drinking water were accomplished using various laboratory diagnostic methods (cultural, serological, and molecular-genetic), Their results are provided in Tables 1–3.

These data over the period 2014–2023 show that *Rotavirus* contamination was more frequently identified by the molecular-genetic method within assessing safety of drinking water supply; *HAV* contamination, by the serological method; *Enterovirus* contamination, by the cultural method. This requires further investigation considering territorial peculiarities of infectious incidence and use of different laboratory testing methods for monitoring in different RF regions.

These data also indicate that the proportion of tap water samples contaminated with *Rotavirus* declined considerably by 2023 ($p = 0.003$). We did not establish any significant decline in the proportion of tap water samples contaminated with *HAV* or *Enterovirus*.

Infectious agents of other virus infections have been monitored in tap water using molecular-biological methods since 2018 (to identify nucleic acids of *Adenovirus*, *Norovirus*, and *Astrovirus*) and 2020 (to identify *SARs-CoV-2* RNA)*;* this allows annual identification of tap water contamination with infectious agents of enteric and respiratory infections (Table 4).

Table 1

Rotavirus contamination in tap water over 2014–2023

Years	PCR				Serological method			
	Total	Of them, positive			Total	Of them, positive		
	n	*n*	% n/s samples	95 % CI	*n*	*n*	% n/s samples	95 % CI
2014	5485	113	2.06	1.70–2.47	9112	11	0.12	0.16–0.22
2015	6962	144	2.07	1.75–2.43	8639	9	0.10	0.05–0.20
2016	7650	260	3.40	3.01–3.83	9463	11	0.12	0.06–0.21
2017	9454	262	2.77	2.45–3.12	8193	11	0.13	0.07–0.24
2018	10,375	188	1.81	1.56–2.09	9406	11	0.12	0.06–0.21
2019	10,816	131	1.21	1.01–1.44	9893	6	0.06	0.02–0.13
2020	6919	55	0.79	0.60–1.03	9169	3	0.03	0.01–0.10
2021	10,684	65	0.61	0.47–0.77	7823	2	0.03	0.00–0.09
2022	10,974	47	0.43	0.31–0.57	7783	2	0.03	0.00–0.09
2023	11,751	19	0.16	0.10–0.25	7241	1	0.01	0.00–0.08
Total (2014–2023)	91,070	1284	1.41	1.33–1.49	86,722	67	0.08	0.06–0.10

Table 2

HAV contamination in tap water over 2014–2023

Years	PCR				Serological method			
	Total	Of them, positive			Total	Of them, positive		
	n	*n*	% n/s samples	95 % CI	*n*	*n*	% n/s samples	95 % CI
2014	1579	0	0.00	0.00–0.23	8844	13	0.15	0.08–0.25
2015	2947	0	0.00	0.00–0.12	9037	19	0.21	0.13–0.33
2016	3160	2	0.06	0.01–0.23	9237	3	0.03	0.01–0.09
2017	3416	1	0.03	0.03–0.16	9490	10	0.11	0.05–0.19
2018	2964	2	0.07	0.01–0.24	9898	3	0.03	0.01–0.09
2019	2819	0	0.00	0.00–0.13	10,512	11	0.10	0.05–0.19
2020	2051	0	0.00	0.00–0.18	8022	12	0.15	0.08–0.26
2021	2770	0	0.00	0.00–0.13	6897	4	0.06	0.02–0.15
2022	3090	0	0.00	0.00–0.12	8446	1	0.01	0.00–0.07
2023	3931	0	0.00	0.00–0.09	8515	4	0.05	0.01–0.12
Total (2014–2023)	28,727	5	0.02	0.01–0.04	88,898	80	0.09	0.07–0.11

Table 3

Enterovirus contamination in tap water over 2014–2023

Years	PCR				Cultural method			
	Total	Of them, positive			Total	Of them, positive		
	n	*n*	% n/s samples	95 % CI	*n*	*n*	% n/s samples	95 % CI
2014	5341	212	3.97	3.46–4.53	1431	6	0.42	0.15–0.91
2015	6629	14	0.21	0.12–0.35	1440	1	0.07	0.00–0.39
2016	7783	17	0.22	0.13–0.35	1867	73	3.91	3.08–4.89
2017	8813	9	0.10	0.05–0.19	2297	1	0.04	0.00–0.24
2018	8632	15	0.17	0.10–0.29	1398	0	0.00	0.00–0.26
2019	10,216	8	0.08	0.03–0.15	1115	1	0.09	0.00–0.50
2020	4586	0	0.00	0.00–0.08	852	0	0.00	0.00–0.43
2021	6768	3	0.04	0.01–0.13	1119	0	0.00	0.00–0.33
2022	8589	8	0.09	0.04–0.18	825	0	0.00	0.00–0.45
2023	10,427	3	0.03	0.01–0.08	1385	15	1.08	0.61–1.78
Total (2014–2023)	77,784	289	0.37	0.33–0.42	13,729	97	0.71	0.57–0.86

Table 4

Viral contamination in tap water in 2018–2023

Name	Indicator	Years						
		2018	2019	2020	2021	2022	2023	Total
Adenovirus	*n*	1014	1639	451	1495	1344	2697	8640
Of them, positive	*n*	17	8	2	2	6	10	45
	% n/s samples	1.68	0.49	0.44	0.13	0.45	0.37	0.52
	95 % CI	0.98–2.67	0.21–0.96	0.05–1.59	0.02–0.48	0.16–0.97	0.18–0.68	0.38–0.70
Norovirus	*n*	8286	8966	6235	9927	10,385	11,033	54,832
Of them, positive	*n*	23	11	11	25	13	27	110
	% n/s samples	0.28	0.12	0.18	0.25	0.13	0.25	0.20
	95 % CI	0.18–0.42	0.06–0.22	0.09–0.32	0.16–0.37	0.07–0.21	0.16–0.36	0.16–0.24
Astrovirus	*n*	6382	8142	5765	8743	9112	9913	48,057
Of them, positive	*n*	4	7	5	28	12	13	69
	% n/s samples	0.06	0.09	0.09	0.32	0.13	0.13	0.14
	95 % CI	0.02–0.16	0.03–0.18	0.03–0.20	0.21–0.46	0.07–0.23	0.07–0.22	0.11–0.18
SARs-CoV-2	*n*	–	–	2019	2084	1375	296	5774
Of them, positive	*n*	–	–	1	4	0	0	5
	% n/s samples	–	–	0.05	0.19	0.00	0.00	0.09
	95 % CI			0.00–0.28	0.05–0.49	0.00–0.27	0.00–1.24	0.03–0.20

Analysis of the test data showed practically no changes in the proportion of tap water samples not conforming to safe standards per *Adenovirus*, *Astrovirus*, *Norovirus*, and *SARs-CoV-2* contents over the analyzed period.

Monitoring data collected by using molecular-biological methods in 2020–2023 were analyzed to show the structure of infection viruses identified in tap water (Figure 2).

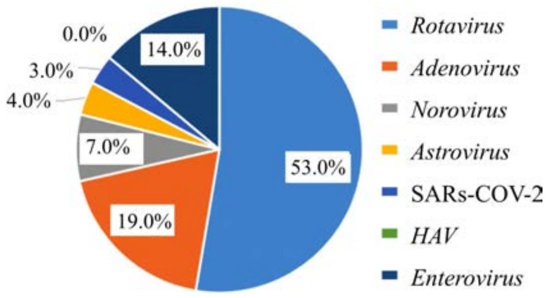

Figure 2. Infectious agents (viruses) identified in tap water in 2020–2023

It is noteworthy that *Rotavirus* prevailed among infection viruses while *Adenovirus* and *Enterovirus* were identified more than twofold less frequently. *Norovirus* and *Astrovirus* had the lowest specific weights. *HAV* was not identified in tap water in 2020–2023; however, it was occasionally detected in water samples between 2014 and 2019. The virus antigen was also annually identified by serological methods (Table 2).

Our findings show that despite the established descending trend, tap water samples did not conform to safe standards in 0.57 % cases per occurring viruses and per a basic indicator (coliphages) in 0.21 % cases on average in Russia over the last decade. This indicates the necessity to continuously monitor safety of drinking water and water sources per microbiological indicators [5, 12, 13] and existing likelihood of virus infections among the population in Russia due to contaminated water intake[8].

Our analysis showed that identification of a basic indicator (coliphages) reflected water contamination with enteric viruses to a certain extent ($r = 0.82$). However, within this study, the proportion of non-standards samples was on average 2.7 times higher per detected virus nucleic acids against coliphages. Bearing this in mind, we can state that coliphage contents as an indicator does not fully reflect virus contamination of water, enteric viruses included. This is consistent with opinions expressed by the authors who do not believe coliphages to be reliable indicators of enteric viruses in water safety assessments[8] [14] and is confirmed by enteric viruses isolated from treated and disinfected drinking water, which was negative in conventional coliphage-detecting tests[8]. Studies did not find any correlation between water contamination with Norovirus, adenoviruses, rotaviruses and coliphages in water objects and tap water [6, 14]. Occurrence of enteric viruses in water samples indicates contamination with wastewaters [15] and a risk of getting infected with enteric viruses for people due to contaminated drinking water intake[8].

Absence of contaminated water samples per coliphage contents as a basic indicator together with present contamination with enteric viruses can also be evidence of molecular-genetic tests being more informative within assessing safety of drinking water supply per microbiological indicators [15, 16].

At the same time, PCR-based methods are usually used for detecting and identifying virus infections in water although PCR alone does not allow the discrimination between infectious and non-infectious viral particles [15]. In addition, water can contain certain inhibitors, which prevent nucleic acids from amplifying by polymerase chain reaction [17]. PCR-based tests aimed at detecting *Enterovirus* identified the virus NA only in 0.37 % of samples, which was almost twofold lower relative to the cultural method, 0.71 % of samples. This can result from PCR inhibitors in water and be explained by virus interference [2, 18, 19]. The review by O.N. Savostikova and others (2021) established that various chemicals could occur in water sources [20], including those potentially able to inhibit PCR. *HAV* RNA and antigen identified in 0.02 % and 0.09 % of water samples respectively can also give evidence of water contamination with infectious and non-infectious virus particles along with various informative values of the molecular-genetic and serologic methods and assumed occurrence of PCR inhibitors in water as well as conditions suitable for virus interference. This requires further investigation considering territorial peculiarities of infection incidence and use of different laboratory testing methods in different regions of Russia.

Given all foregoing, it should be noted that examining water safety with complex laboratory diagnostic methods is becoming more significant for assessing risk factors of enteric virus infections. Foreign researchers emphasize the significance of combining the virologic method relying on using cell cultures

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[1] WHO. Guidelines for drinking-water quality: fourth edition incorporating the first and second addenda. *WHO*, 2022, 614 p. Available at: https://www.who.int/publications/i/item/9789240045064 (October 03, 2024).

with PCR identifying infection viruses, which grow slow or do not produce any cytotoxic effects in a cell culture [15]. Several studies have revealed an association between virus persistence (determined by molecular methods) and infectivity (determined by analyzing cytopathic effects) indicating that degradation of virus nucleic acids has a strong correlation with loss of virus infectivity [16].

Prevalence of virus contamination was considerably lower in Russia in comparison with the data reported by foreign researchers (in this study, *Rotavirus* was detected in 1.41 % of samples; *Enterovirus,* 0.70 %; *Adenovirus,* 0.52 %), which means disinfection activities accomplished within water treatment in the country are quite effective for managing risks of enteric infection incidence. Differences established in discussing the obtained results including those identified in contamination of subterranean and surface water sources require special attention and give grounds for setting new research tasks. Foreign researchers have established the total prevalence of hepatitis E virus to be 4.7 % in drinking water [21], which also requires special attention from Russian researchers.

Overall, over 2014–2023, the proportion of tap water samples that did not conform to basic safe sanitary-microbiological indicators equaled to 0.20 % per *Norovirus*, 0.14 % per *Astrovirus*, 0.09 % per *SARs-CoV-2*, and 0.02 % per *HAV*. Studies with their focus on drinking water contamination with *Astrovirus*, *Norovirus*, *SARs-CoV-2*, and *HAV* have been given very little attention in literature available to us. However, there are some available data on virus prevalence in Thailand in a water reservoir, river water, etc., where various *Astrovirus* genotypes were detected in 4.8 % of the samples with different prevalence (in RF, according to this study, *Astrovirus* was detected in 0.14 % of drinking water samples) [16]. Researchers assert that *Astrovirus* is a prevailing species in the water environment [16], and cases of inter-species transmission have been described for some genotypes [22]. Risk of enteric infections accused by *Astrovirus* due to drinking water intake should be given special attention by researchers.

Virus contamination of drinking water gives evidence of viruses being resistant to disinfectants used in water treatment. The highest virus elimination in water treatment was reported for *Enterovirus* (97 % of viruses are eliminated by disinfection) and *Rotavirus* (82 % removed by disinfection); lower levels are reported for *Adenovirus* (73 %) [6]. Considering the structure of infectious agents identified in tap water in 2020–2023 even after mandatory disinfection, as shown in Figure 2, we should assume *Rotavirus* to be the most resistant to disinfectants used in water treatment in the RF; *Adenovirus*, *Norovirus* and *Enterovirus* were a bit less resistant. Studies reported that some of these viruses were resistant to water disinfection and ecological stressors, especially to inactivation by ultraviolet light [15, 23]. Given that, researchers emphasize the necessity to use the combined water disinfection method [5] to prevent risks of infections.

Bearing in mind that viruses causing Hepatitis A, COVID-19 and Astrovirus infection were either not detected or had very small proportions, we can assume that disinfection activities accomplished within water treatment in 2020–2023 in the RF were effective as regards elimination of these viruses.

Conclusion. Therefore, we analyzed the results obtained by testing tap water samples taken both prior to supply and directly from distribution networks. The analysis revealed that despite the descending trend identified over the period 2014–2023 in the proportion of samples not meeting sanitary-epidemiological requirements, such samples were still detected (on average, 0.57 % contained viruses and 0.21 % coliphages). This means risks of infectious diseases caused by intake of drinking water contaminated with enteric viruses.

Over 2014–2023, the proportion of tap water samples that did not meet safe standards per sanitary-microbiological indicators equaled the following: for *Rotavirus,* 1.41 % of samples (95 % CI: 1.33–1.49) (according to serological tests, 0.08 % of samples (0.06–0.10)); *Enterovirus,* 0.71 % of samples (95 % CI: 0.57–0.86) (according to PCR tests, 0.37 % of samples (95 % CI: 0.33–0.42)); *Adenovirus,* 0.52 % of samples (95 % CI: 0.38–0.70); *Norovirus,* 0.20 % samples (95 % CI: 0.16–0.24); *Astrovirus,* 0.14 % of samples (95 % CI: 0.11–0.18); *SARs-CoV-2,* 0.09 % (95 % CI: 0.03–0.20); *HAV,* 0.02 % of samples (95 % CI: 0.01–0.04) (according to serological tests, a bit higher, 0.09 % of samples (0.07–0.11)). The structure of virus contamination in tap water in 2020–2023 contained *Rotavirus* (52.6 ± 0.3 %), *Adenovirus* (18.8 ± 0.5 %), *Enterovirus* (13.9 ± 0.2 %), *Norovirus* (7.5 ± 0.1 %), *Astrovirus* (3.8 ± 0.1 %), and *SARs-CoV-2* (3.4 ± 0.2 %). This indicates the necessity to further investigate risk factors of some specific enteric virus infections associated with drinking water intake to predict incidence rates and take relevant preventive measures.

We found a strong direct correlation between the proportions of tap water samples deviating from safe standards per contents of coliphages and virus infectious agents ($r > 0.8$); however, use of molecular-genetic methods to identify nucleic acids in water established higher virus prevalence in comparison with conventional coliphage testing. This probably requires special attention when water safety is assessed using ‘coliphages contents’ as the basic regulated indicator. Absence of virus contamination in treated water confirmed by cultural methods and high levels of contaminations with antigens when PCR-tests are negative indicate it is necessary to develop additional reliable tests, which can confirm virus infectivity and presence of amplification reaction inhibitors.

Identification of viruses from various genera in drinking water indicates that drinking water intake can be a risk factor of enteric infections in Russia and that it is necessary to monitor virus resistance to disinfectants, to use combined disinfection techniques in water treatment, and to investigate a role that belongs to drinking water in occurrence of virus infections. The obtained data can be used for predicting incidence of some specific enteric infections and economic losses as well as for planning relevant preventive activities.

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References

1. Popova A.Yu., Kuzmin S.V., Mehantyev I.I. Assessment of Implementation Efficiency of the System Approach to Ensuring Safety of Public Drinking and Recreational Water Use on the Example of the Voronezh Region. *ZNiSO*, 2021, vol. 29, no. 8, pp. 7–14. DOI: 10.35627/2219-5238/2021-29-8-7-14 (in Russian).

2. Lavrik E.P., Trukhina G.M., Kravchenko A.G., Vysotin S.A., Vysotina A.T., Dmitrieva N.A. Sanitary and epidemiological features of recreational water use of the Tuapse district of the Krasnodar region. *Gigiena i sanitariya*, 2021, vol. 100, no. 9, pp. 910–916. DOI: 10.47470/0016-9900-2021-100-9-910-916 (in Russian).

3. Baydakova E.V., Unguryanu T.N., Mikhaylova R.I. On quantitative assessment of microbe risk caused by exposure to enteric viruses in drinking water. *Health Risk Analysis*, 2019, no. 2, pp. 108–114. DOI: 10.21668/health.risk/2019.2.12.eng

4. Erkhov A.A. SARS-CoV-2: Sewerage as a transmission route. *Stroitel'stvo i tekhnogennaya bezopasnost'*, 2023, no. 30 (82), pp. 105–112 (in Russian).

5. Rakhmanin Yu.A., Onishchenko G.G. Hygienic assessment of drinking water supply of the population of the Russian Federation: problems and the way their rational decision. *Gigiena i sanitariya*, 2022, vol. 101, no. 10, pp. 1158–1166. DOI: 10.47470/0016-9900-2022-101-10-1158-1166 (in Russian).

6. Ye X.Y., Ming X., Zhang Y.L., Xiao W.Q., Huang X.N., Cao Y.G., Gu K.D. Real-time PCR detection of enteric viruses in source water and treated drinking water in Wuhan, China. *Curr. Microbiol.*, 2012, vol. 65, no. 3, pp. 244–253. DOI: 10.1007/s00284-012-0152-1

7. Kluge M., Fleck J.D., Soliman M.C., Luz R.B., Fabres R.B., Comerlato J., Silva J.V.S., Staggemeier R. [et al.]. Human adenovirus (HAdV), human enterovirus (hEV), and genogroup A

rotavirus (GARV) in tap water in southern Brazil. *J. Water Health*, 2014, vol. 12, no. 3, pp. 526–532. DOI: 10.2166/wh.2014.202

8. Rashid M., Khan M.N., Jalbani N. Detection of Human Adenovirus, Rotavirus, and Enterovirus in Tap Water and Their Association with the Overall Quality of Water in Karachi, Pakistan. *Food Environ. Virol.*, 2021, vol. 13, no. 1, pp. 44–52. DOI: 10.1007/s12560-020-09448-8

9. Mejías-Molina C., Estarlich-Landajo I., Martínez-Puchol S., Bofill-Mas S., Rusiñol M. Exploring waterborne viruses in groundwater: Quantification and Virome characterization via passive sampling and targeted enrichment sequencing. *Water Res.*, 2024, vol. 266, pp. 122305. DOI: 10.1016/j.watres.2024.122305

10. Jacqueline C., Del Valle Arrojo M., Bellver Moreira P., Rodríguez Feijóo M.A., Cabrerizo M., Fernandez-Garcia M.D. Norovirus GII.3[P12] Outbreak Associated with the Drinking Water Supply in a Rural Area in Galicia, Spain, 2021. *Microbiol. Spectr.*, 2022, vol. 10, no. 4, pp. e0104822. DOI: 10.1128/spectrum.01048-22

11. Nedachin A.E., Dmitrieva R.A., Doskina T.V., Dolgin V.A. Comparative stability of poliovirus, hepatitis a virus and their RNA to the impact of ultraviolet radiation. *Gigiena i sanitariya*, 2019, vol. 98, no. 11, pp. 1240–1244. DOI: 10.47470/0016-9900-2019-98-11-1240-1244 (in Russian).

12. Bobun I.I., Buzinov R.V., Shishko L.A., Boltenkov V.P., Gudkov A.B. Features of Viral Contamination of Drinking Water in Arkhangelsk Region. *Ekologiya cheloveka*, 2016, no. 2, pp. 3–7 (in Russian).

13. Paklonskaya N.V., Amvrosieva T.V., Kaltunova Yu.B., Shilova Yu.A., Belskaya I.V. Wastewater based epidemiology as an effective tool for infection surveillance and biological hazards prevention. *Novosti mediko-biologicheskikh nauk*, 2022, vol. 22, no. 2, pp. 104–111 (in Russian).

14. Liang L., Goh S.G., Vergara G.G.R.V., Fang H.M., Rezaeinejad S., Chang S.Y., Bayen S., Lee W.A. [et al.]. Alternative fecal indicators and their empirical relationships with enteric viruses, *Salmonella enterica*, and *Pseudomonas aeruginosa* in surface waters of a tropical urban catchment. *Appl. Environ. Microbiol.*, 2015, vol. 81, no. 3, pp. 850–860. DOI: 10.1128/AEM.02670-14

15. Fongaro G., Nascimento M.A., Rigotto C., Ritterbusch G., da Silva A.D., Esteves P.A., Barardi C.R. Evaluation and molecular characterization of human adenovirus in drinking water supplies: viral integrity and viability assays. *Virol. J.*, 2013, vol. 10, pp. 166. DOI: 10.1186/1743-422X-10-166

16. Kumthip K., Khamrin P., Ushijima H., Maneekarn N. Detection of Six Different Human Enteric Viruses Contaminating Environmental Water in Chiang Mai, Thailand. *Microbiol. Spectr.*, 2023, vol. 11, no. 1, pp. e0351222. DOI: 10.1128/spectrum.03512-22

17. Chemeris A.V., Chemeris D.A., Magdanov E.G., Garafutdinov R.R., Nagaev N.R., Vakhitov V.A. Causes of false-negative PCR and how to avoid some of them. *Biomics*, 2012, vol. 4, no. 1, pp. 31–47 (in Russian).

18. Larin V.F., Zhukova L.I., Lebedev V.V., Rafeyenko G.K. Interference interaction of viruses in the regulation of an epidemic process. *Epidemiologiya i infektsionnye bolezni*, 2012, no. 1, pp. 25–29 (in Russian).

19. Sano D., Watanabe R., Oishi W., Amarasiri M., Kitajima M., Okabe S. Viral Interference as a Factor of False-Negative in the Infectious Adenovirus Detection Using Integrated Cell Culture-PCR with a BGM Cell Line. *Food Environ. Virol.*, 2021, vol. 13, no. 1, pp. 84–92. DOI: 10.1007/s12560-020-09453-x

20. Savostikova O.N., Mamonov R.A., Turina I.A., Alekseeva A.V., Nikolaeva N.I. Xenobiotics and products of their transformation in wastewater (literature review). *Gigiena i sanitariya*, 2021, vol. 100, no. 11, pp. 1218–1223. DOI: 10.47470/0016-9900-2021-100-11-1218-1223 (in Russian).

21. Takuissu G.R., Kenmoe S., Ndip L., Ebogo-Belobo J.T., Kengne-Ndé C., Mbaga D.S., Bowo-Ngandji A., Oyono M.G. [et al.]. Hepatitis E Virus in Water Environments: A Systematic Review and Meta-analysis. *Food Environ. Virol.*, 2022, vol. 14, no. 3, pp. 223–235. DOI: 10.1007/s12560-022-09530-3

22. Mendenhall I.H., Smith G.J.D., Vijaykrishna D. Ecological Drivers of Virus Evolution: Astrovirus as a Case Study. *J. Virol.*, 2015, vol. 89, no. 14, pp. 6978–6981. DOI: 10.1128/JVI.02971-14

23. Zaitseva N.V., Kleyn S.V., May I.V., Savochkina A.A., Kiryanov D.A., Kamaltdinov M.R., Vekovshinina S.A. Methodical grounds and experience gained in implementing complex assessment of activities aimed at risk to public health and effectiveness of measures to improve the quality of drinking water in centralized water supply systems. *Gigiena i sanitariya*, 2022, vol. 101, no. 11, pp. 1403–1411. DOI: 10.47470/0016-9900-2022-101-11-1403-1411 (in Russian).

Trukhina G.M., Badamshina G.G., Poptsova E.A., Yaroslavtseva M.A., Volostnova E.S., Guzairova E.R. Virus contamination of centralized water supply systems as a health risk factor: features of long-term dynamics in the Russian Federation. Health Risk Analysis, 2025, no. 2, pp. 87–97. DOI: 10.21668/health.risk/2025.2.07.eng

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