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CHALLENGES OF MICROBIOLOGICAL SAFETY OF WATER SUPPLY, SANITATION AND HYGIENE. LITERATURE REVIEW.

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Abstract

Introduction. Microbiological safety of water supply, sanitation and hygiene (WASH) is one of the priority tasks in maintaining and strengthening the public health.

The **purpose** of this work was to review the results of foreign and domestic sanitary and microbiological studies on the microbiological safety of water supply, sanitation and hygiene (WASH).

Search Strategies. The authors of this article codeveloped a search strategy that was the same for each database. Traditional search of sources by keywords was carried out in the PubMed, Scopus, Web of Science and Google Scholar databases in English, Russian and Kazakh languages with inclusion and exclusion criteria. Fifty-three sources out of 116 were selected as analytical materials. The depth of the search was from 1977 to 2020. *The criteria for including publications in the review* were as follows: publications in Russian and English that are in open full-text access and contain statistically confirmed conclusions. Summary reports, newspaper articles and personal messages were excluded from the review.

Results. Ensuring the microbial safety of the drinking-water supply relies on the use of many barriers from the water collection to the consumer in order to prevent contamination from drinking water or reduce it to acceptable levels, not harmful to health. Safety is enhanced when multiple barriers against contamination are established, including protecting water resources, selecting and implementing a range of appropriate treatment measures, and regulating distribution systems (piped or non-piped) to maintain and protect the quality of treated water. The preferred strategy is a regulatory approach that focuses on preventing or reducing the entry of pathogens into water sources, and on reducing reliance on water treatment to remove pathogens.

Conclusion. Thus, ensuring the microbial safety of WASH requires the following: an assessment of the entire system to determine the potential harmful factors that may affect it; determination of control measures to reduce or eliminate these harmful factors as well as operational monitoring to ensure the effective functioning of barriers from infection within the system; and developing regulatory plans to describe actions to be taken both under normal conditions and in unforeseen circumstances.

Key words: antibiotic resistance; microbial contamination; quality control; water supply, sanitation and hygiene (WASH).

Резюме

ПРОБЛЕМЫ МИКРОБИОЛОГИЧЕСКОЙ БЕЗОПАСНОСТИ ВОДОСНАБЖЕНИЯ, САНИТАРИИ И ГИГИЕНЫ. ОБЗОР ЛИТЕРАТУРЫ.

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Введение. Обеспечение микробиологической безопасности водоснабжения, санитарии и гигиены (ВСГ) является одной из приоритетных задач в сохранении и укреплении здоровья населения.

Целью настоящей работы явился обзор результатов зарубежных и отечественных санитарно-микробиологических исследований по проблеме обеспечения микробиологической безопасности водоснабжения, санитарии и гигиены (ВСГ).

Стратегия поиска. Авторы этой статьи совместно разработали стратегию поиска, которая была одинаковой для каждой базы данных. Традиционный поиск источников по ключевым словам проводился в базах данных PubMed, Scopus, Web of Science и Google Scholar на английском, русском и казахском языках по критериям включения и исключения. В качестве аналитического материала были выбраны пятьдесят три источника из 116. Глубина поиска составляла с 1977 по 2020 год. *Критерии включения* публикаций в обзор были следующими: полнотекстовые публикации на русском и английском языках, находящиеся в открытом доступе и содержащие статистически подтвержденные выводы. Краткие отчеты, газетные статьи и личные сообщения были исключены из обзора.

Результаты. Обеспечение микробной безопасности питьевого водоснабжения основано на использовании множества преград на пути от водосбора до потребителя в целях предупреждения заражения питьевой воды или сокращения заражения до уровней, которые не вредны для здоровья. Безопасность возрастает, если установлено множество преград по предупреждению заражения, включая защиту водных ресурсов, надлежащий выбор и осуществление ряда мер по очистке, а также регулирование систем распределения (водопроводных или не водопроводных) для поддержания и защиты качества обработанной воды. Предпочтительной стратегией является подход регулирования, при котором основной акцент ставится на предупреждении или сокращении проникновения патогенных микроорганизмов в источники воды, а также на уменьшении зависимости от процессов очистки для удаления патогенов.

Заключение. Таким образом, обеспечение микробной безопасности ВСГ требует проведения оценки всей системы для определения потенциальных вредных факторов, которые могут воздействовать на эту систему; определения мер контроля, необходимых для сокращения или устранения вредных факторов, а также оперативного мониторинга для обеспечения эффективного функционирования преград от заражения в рамках системы; и разработки планов регулирования для описания действий, предпринимаемых как в нормальных условиях, так и в непредвиденных обстоятельствах.

Ключевые слова: *антибиотикорезистентность; водоснабжение, санитария и гигиена (ВСГ); контроль качества; микробное заражение.*

Түйіндеме

СУМЕН ЖАБДЫҚТАУ, САНИТАРИЯ ЖӘНЕ ГИГИЕНАНЫҢ МИКРОБИОЛОГИЯЛЫҚ ҚАУІПСІЗДІГІНІҢ МӘСЕЛелЕРІ. ӘДЕБИЕТ ШОЛУ.

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Кіріспе. Сумен жабдықтау, санитария және гигиенаның (ССГ) микробиологиялық қауіпсіздігін қамтамасыз ету халықтың денсаулығын сақтау мен нығайтудағы басым міндеттердің бірі болып табылады.

Бұл жұмыстың мақсаты сумен жабдықтау, санитария және гигиенаның (ССГ) микробиологиялық қауіпсіздігін қамтамасыз ету мәселесі бойынша шетелдік және отандық санитариялық-микробиологиялық зерттеулердің нәтижелеріне шолу жасау болды.

Іздену стратегиясы. Осы мақаланың авторлары әр дерекқорға бірдей болатын іздеу стратегиясын бірлесіп жасады. Түйінді сөздер бойынша дереккөздерді дәстүрлі іздеу PubMed, Scopus, Web of Science және Google Scholar дерекқорларында ағылшын, орыс және қазақ тілдерінде қосу және шығару критерийлеріне сәйкес жүргізілді. Аналитикалық материалдар ретінде 116-дан елу үш дереккөз таңдалды. Іздеу тереңдігі 1977 жылдан 2020 жылға дейін болды. Жарияланымдарды шолуға қосу критерийлері мыналар болды: ашық толық мәтінді қолжетімді және статистикалық расталған қорытындылары бар орыс және ағылшын тілдеріндегі жарияланымдар. Қысқаша есептер, газет мақалалары және жеке хабарламалар шолудан шығарылды.

Нәтижелері. Ауыз сумен жабдықтаудың микробтық қауіпсіздігін қамтамасыз ету ауыз су арқылы жұқпаларды жұқтырудың алдын алу немесе оны денсаулыққа зиянды емес деңгейге дейін азайту үшін су жинаудан тұтынушыға дейінгі көптеген кедергілерді қолдануға негізделген. Егер су ресурстарын қорғауды, тазарту жөніндегі бірқатар шараларды тиісті таңдауды және жүзеге асыруды, сондай-ақ өңделген судың сапасын сақтау және қорғау үшін тарату жүйелерін (су құбыры арқылы немесе су құбыры арқылы емес) реттеуді қоса алғанда, жұқпа жұқтырудың алдын алу бойынша көптеген кедергілер орнатылса қауіпсіздік артады. Артықшылықты стратегия-бұл реттеу тәсілі, онда қоздырғыштардың су көздеріне енуінің алдын алуға немесе азайтуға, сондай-ақ қоздырғыштарды жою үшін тазарту процестеріне тәуелділікті азайтуға баса назар аударылатын реттеу тәсілі қалаулы стратегия болып табылады.

Қорытынды. Осылайша, ССГ-ның микробтық қауіпсіздігін қамтамасыз ету осы жүйеге әсер етуі мүмкін ықтимал зиянды факторларды анықтау үшін бүкіл жүйені бағалауды; зиянды факторларды азайту немесе жою үшін қажетті бақылау шараларын анықтауды, сондай-ақ жүйе шеңберіндегі жұқпа жұқтырудан кедергілердің тиімді жұмыс істеуін қамтамасыз ету үшін жедел мониторингті; қалыпты жағдайда да, күтпеген жағдайда да қабылданатын әрекеттерді сипаттау үшін реттеу жоспарларын әзірлеуді талап етеді.

Түйінді сөздер: антибиотикке төзімділік; микробтық ластану; сумен жабдықтау, санитария және гигиена (ССГ); сапаны бақылау.

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Introduction

Microbiological safety of water supply, sanitation and hygiene (WASH) is one of the priority tasks in maintaining and strengthening public health. There is an obvious need for targeted action to reduce morbidity associated with the growing anthropogenic impact of biological pollution mediated through water systems [13-18].

WASH quality and safety issues are attracting more and more attention from public health authorities, microbiologists, engineers and epidemiologists. There are acute questions regarding disinfection-resistant microbial populations, antibiotic resistance, the transmission of virulence factors between microorganisms, and the need to minimize anthropogenic impact on water supplies. However, there are little research on the microbiology of WASH and its influence on public health. Microbiological safety of WASH should become one of the priority areas of scientific research, as there is an urgent need for information to support decision-making and response to emergencies [33,46,50].

The aim of this study was to review the results of foreign and domestic sanitary and microbiological studies on the microbiological safety of water supply, sanitation and hygiene (WASH).

Search Strategies

The authors of this article codeveloped a search strategy that was the same for each database. Traditional search of sources by keywords was carried out (Table 1) in the PubMed, Scopus, Web of Science and Google Scholar databases in English, Russian and Kazakh languages with inclusion and exclusion criteria noted below. Fifty-three sources out of 116 were selected as analytical materials. The depth of the search was from 1977 to 2020.

The criteria for including publications in the review were as follows: publications in Russian and English that are in open full-text access and contain statistically confirmed conclusions.

Summary reports, newspaper articles and personal messages were excluded from the review.

Table 1.

Keywords used during the search in the PubMed, Scopus, Web of Science and Google Scholar databases.

Search Number – Database	Keywords Combination
1 – PubMed	“antibiotic resistance”, “microbial contamination”, “quality control”, “water supply, sanitation and hygiene”, “WASH”
2 – Scopus	“antibiotic resistance” AND “microbial contamination” AND “quality control” AND “water supply, sanitation and hygiene” OR “WASH”
3 – Web of Science	“antibiotic resistance” AND “microbial contamination” AND “quality control” AND “water supply, sanitation and hygiene” OR “WASH”
4 – Google Scholar	“antibiotic resistance”, “microbial contamination”, “quality control”, “water supply, sanitation and hygiene”, “WASH”
Sum of databases searches	PubMed AND Scopus AND Web of Science AND Google Scholar

Results and Discussion

1. Microbiocenosis of water from water supply and sewerage systems

Water supply systems are designed and operated to deliver biologically safe and chemically pure water to the consumer. However, these systems represent an ecological niche in which microorganisms live and multiply. In this case, microbial ecology is regulated by the technical state and operating conditions of the water supply system, which can make microbial communities in the form of biofilms, which are found in dry sediment and running water. According to various sources, the total number of microorganisms in tap water ranges from 10^4 to 10^6 CFU per liter [42,48]. The microbial composition of water is influenced by many aspects: from the length and shape of the distribution network to the pipe material [27,29,33,36-37,47]. The main problem of determining the microbiome of drinking water is that it dynamically changes at all stages of water treatment.

The greatest risk of microbial pollution is associated with the consumption of water contaminated with human or animal (or birds) faeces. Faeces are able to be a source of various pathogenic microorganisms such as bacteria, viruses, protozoa and helminths. Faecal pathogens are a major problem in setting health-related microbial safety goals. Water quality in terms of microbial contamination often varies in a wide range. Short-term peak concentrations of pathogens can significantly increase the risk of disease and trigger outbreaks of WASH-related disease. Therefore, to ensure the microbial safety of drinking water, it is not an option to rely solely on checking the final state of the water, even if it is done frequently. Due attention should be paid to the basics of water safety and the implementation of comprehensive water safety plans (WSPs) to ensure the safety of drinking water at all times and thereby preserve the health of the population [20,42]. The main reasons for the spread of fecal water pollution are often as follows [25]:

- proximity of local sewerage systems;
- breakdowns in nearby sewers;
- proximity of municipal solid waste (MSW) landfills and livestock farms to the water source;
- breakdowns in the water treatment system and its misuse.

An important factor affecting water supply systems is the qualitative and quantitative composition of opportunistic pathogenic microflora (OPM). The gram-negative nonfermentable bacteria (GNNB) are more common than all other microorganisms, many of them are representatives of the hydrobiont microflora. Among the OPMs, the genera *Acinetobacter*, *Burkholderia*, *Brevundimonas*, *Chryseobacterium*, *Sphingomonas*, *Stenotrophomonas*, *Pseudomonas*, *Legionella*, *Mycobacterium*, *Ochrobactrum* and were found [28,45]. Special mention should go to *Acinetobacter*, *Pseudomonas* and *Stenotrophomonas*, which are carriers of natural genetic determinants of antibiotic resistance and have the ability to spread them. The presence of biofilm-forming microorganisms such as *Bradyrhizobium* in the water supply system not only leads to a change in water quality, but also forms biofilms on the water supply network. Such biofilms, when added with other microorganisms, including pathogens, become a constant source of deterioration in the quality of water supply and can be removed only through the replacement of the water supply network [28].

In many recent studies, the environment is considered as a recipient of both drug-resistant bacteria and a reservoir and source of resistance genes. Water supply and sewerage systems are recognized by World Health Organization (WHO) as one of the critical points in the spread of antibiotic resistance [51]. Water is one of the most important factors in the spread of genetic determinants of antibiotic resistance [49]. In addition, many of them have been obtained from aquatic microflora [34,52]. There are multiple data on the distribution of the determinants of antibiotic resistance NDM-1, which provides resistance to the entire range of beta-lactam antibiotics, and is often combined with Qnr-type resistance and various Aminoglycosides modifying enzymes. The spread of extended spectrum beta-lactamases (ESBLs) in wastewater has been repeatedly proven on a world-wide basis [24,30,50,53]. Therefore, drinking and waste water can be both a source of microorganisms producing determinants of antibiotic resistance, and antibiotic resistance genes themselves.

The spread of drug resistance has been observed among bacteria as indicators of faecal water contamination. Genes for resistance to antimicrobial agents have been identified among the representatives of the Enterobacteriaceae family (in particular, *Escherichia coli*, *Salmonella* spp., *Klebsiella* spp., *Yersinia pestis* and *Shigella* spp.) and *Staphylococcus aureus* (in particular, MRSA). Untreated wastewater contains concentrated levels of pathogenic and non-pathogenic microbes and antibiotics. Wastewater and untreated wastewater can enter surface one through combined sewers. During heavy rainfall, wastewater treatment plants with combined storm-water collectors may experience overflows exceeding their design capacity, and thus mixed water may be discharged without complete treatment. The annual concentrations of resistant

coliform microorganisms discharged from the combined sewers were about 5000 times higher than from wastewater treatment plants [32]. A global monitoring of urban wastewater has made it possible to assess systematic differences in the number and diversity of genes for antimicrobial resistance [26]. There were significant regional differences that correlated more with social and economic factors than with antibiotic use. Two clusters of antibiotic resistance gene abundance were identified: the first cluster consisted of high-income countries in Europe, North America and Oceania, and the second cluster included low- and middle-income countries in Africa, Asia and South America. The first cluster had a high abundance of a limited number of antibiotic resistance genes encoding macrolide resistance genes. In the second cluster, a large number of different resistance genes from different classes of drugs were found. The largest discrepancy in the distribution of resistance genes was found in India, Vietnam and Brazil, suggesting that these countries may be hot spots for the emergence of new antibiotic resistance mechanisms. This statement was proven in 2011 with the emergence of a new type of beta-lactamase NDM-1 [23,26,46].

Pathogenic bacteria found in hospitals and other health care facilities and resistant to all or almost all of the existing antibiotics are of increasing concern in the world. Antibiotics, pharmaceutical residues, bacteria and antimicrobial resistance genes were found in hospital wastewater after the following types of treatment [31]:

- urban wastewater treatment plants (i.e. the hospital was the source of indirect discharge);
- local sewerage systems;
- without any treatment before discharge into surface waters (i.e. direct discharge).

Antibiotics and antibiotic residues can enter urban wastewater as a result of the removal of pharmaceuticals, urine and feces of patients taking medications, as well as antimicrobials for washing surfaces, hands and clothing. Untreated wastewater can mix with pretreated and/or untreated medical waste, creating a hot spot for the proliferation of antibiotic resistance genes. Additionally, wastewater from health care facilities contains a higher concentration of pathogenic and opportunistic bacteria that can spread or acquire genes or be secreted (i.e. multiply faster than other bacteria in wastewater due to mutation) from wastewater [35].

In addition to faecal pathogens, other harmful microbial organisms (for example, *Dracunculus medinensis*, toxic cyanobacteria and *Legionella*) can pose a risk to public health under certain circumstances. In the infectious stages of many helminths, such as parasitic roundworms and flatworms, people can become infected through drinking water. Since a single mature larva or fertilized egg can cause infection, they must be absent from drinking water. However, the waterway is of relatively little importance for helminth infestation, with the exception of guinea worm [28].

Legionella bacteria are omnipresent in the environment and can penetrate at elevated temperatures, which are sometimes observed in drinking water distribution systems, and more often in hot and warm ones. Exposure to *Legionella* in drinking water is through inhalation and can be controlled by implementing basic water quality measures in buildings and by maintaining residual disinfection

throughout the water distribution system. *Legionella* does not cause disease in healthy people, but it can cause a sense of discomfort due to unpleasant taste and odor, or discoloration of drinking water. Growth that occurs after drinking water has been treated is often referred to as "regrowth". It is usually reflected in the measurement of the increasing number of microorganisms determined by the plate method (NMDPM) in water samples [51].

A public health concern with cyanobacteria is related to their ability to produce a range of toxins known as "cyanotoxins" [28]. Cyanobacteria, unlike pathogenic bacteria, do not spread in the human body after ingestion; they spread only in the aquatic environment. Although toxic peptides (e.g. microcystins) are usually found in cells and thus can be largely destroyed by filtration, toxic alkaloids such as cylindrospermopsin and neurotoxin also enter the water and can penetrate filtration systems.

Therefore, the safety of drinking water depends on some factors including the quality of the source water, the effectiveness of treatment, the reliability and integrity of the engineering infrastructure, and the possibility of re-growth of microorganisms in the pipes. Hazards can potentially compromise water quality at every step of production and delivery of drinking water. Distribution systems may be less prone to pollution than open surface water catchment areas. However, biofilms, deposits and corrosion products can contain pathogens from ineffective handling or disruption to the distribution system. Hidden in sediment or embedded in biofilm and bumps, pathogens can be released during repair or cleaning as a result of erosion caused by sudden changes in the flow structure or as a result of continuous natural separation of biofilm. The survival of pathogens depends on their nature, microbial activity in the biofilm and some environmental factors. Thus, there is a need to attract additional resources to control the water microbiocenosis from water supply and sewerage systems.

2. Methods of water quality control in terms of microbial contamination

When our country introduced the Sanitary Rules called "Sanitary and Epidemiological Requirements for Water Sources, Water Withdrawal Points for Household and Drinking Purposes, Household and Drinking Water Supply, Places of Cultural and Household Water Use and Safety of Water Bodies" [11] as well as "Hygienic Requirements for Surface Waters Protection" [12], a new regulatory framework has been created. It provides for the need for direct detection of viruses in drinking water, surface and waste waters. The classical and most reliable method of controlling viral water contamination is the direct isolation of viruses on cell cultures. However, it is known that many epidemiologically significant viruses (for example, hepatitis A, rotaviruses, noroviruses, etc.) are not cultivated on cells traditionally used in the practice of virus isolation or are cultivated in special cultures with great difficulty. At the same time, working with cell cultures requires special laboratory equipment, qualified personnel and significant material costs. It should also be noted that the obtained results are of a retrospective nature, which reduces both the significance of this method as a planned one in practice and water quality control in relation to viral contamination according to epidemiological indications [5].

Concerning the water quality in terms of microbial contamination, the checking necessarily includes microbiological testing. In most cases, it involves the analysis of indicator faecal microorganisms, but sometimes it may also include an assessment of the density of specific pathogens. These checking approaches involve testing water at source, water immediately after treatment, water in distribution systems, or household water reserves. The quality of drinking water is tested for microbial contamination includes *Escherichia coli* as an indicator of faecal contamination. *Escherichia coli* is strong evidence of recent contamination by faeces that must not be present in drinking water. The main requirements for indicator and sanitary-indicative microorganisms are as follows [19,41]:

1. A common source of entry into the environment with pathogenic microorganisms;
2. Equal resistance to environmental factors and disinfecting agents with pathogenic microorganisms;
3. The quantitative predominance of indicator microorganisms over pathogenic ones;
4. Indicator microorganisms must have a stable correlation with pathogenic ones in order to assume the quantitative content of the latter by the number of the former;
5. Indicator microorganisms must not multiply in the environment;
6. Simplicity and rapidity of methods for isolating indicator microorganisms;
7. Non-pathogenicity of indicator microorganisms.

However, in practice, testing for thermotolerant coliform bacteria may be an acceptable alternative in plenty of cases. While *Escherichia coli* is a useful indicator, it has some limitations. Enteroviruses and protozoa are much more stable to disinfection, that is why the absence of *Escherichia coli* does not necessarily indicate release from these microorganisms. Under certain conditions, it is desirable to include bacteriophages [6,19].

As the sanitary microbiology developed, there was a constant discussion regarding various microorganisms and indicators that could be used as criteria of viral water pollution: *Escherichia coli*, coliphages, clostridia, viral antigens of RNA and DNA of viruses, water turbidity, etc. Coliform bacteria and *Escherichia coli* cannot perform the function of indicator microorganisms in relation to viral contamination, since viruses are more resistant to the effects of chemical and physical environmental factors and disinfecting agents from water treatment than bacteria according to the data of domestic and foreign scientists [1,7-8].

The literature [2-4,9] describes outbreaks of viral hepatitis related to the use of drinking water with standard bacteriological parameters. The question of the possibility of introducing clostridia into routine sanitary and virological control as an indicator microorganism is debatable. Unlike coliform bacteria, clostridia are more resistant to various factors and water treatment agents than intestinal viruses. In this regard, water disinfection requires significantly higher doses of chlorine, ozone and other disinfectants, which can contribute to a sharp increase in the formation of trihalomethanes, haloform compounds, free radicals, aldehydes, etc., having an adverse effect on public health and causing long-term biological effects. In addition,

Clostridia do not meet the requirements for indicator microorganisms in many other parameters.

In his works, K.K. Toguzbaeva and her colleagues assume [21] that there is a trend for microbial pollution of drinking water, which directly affects public health and increases the number of acute enteric infections and viral hepatitis. Preliminary calculations based on the regression dependence revealed a direct and strong positive correlation between microbial pollution of drinking water and an increase in the number of these diseases among the studied group of people. However, in terms of microbiological indicators in the region, the percentage of non-standard water samples from centralized water supply systems decreased from 0.59% in 2009 to 0.4% in 2013, from decentralized water supply systems from 1.3% in 2009 and to 1.08% in 2013. K.K. Toguzbaeva et al. [21] came to the following conclusions:

1. The most adequate indicators of viral water pollution are coliphages and markers of DNA and RNA viruses, determined by PCR and RT-PCR, respectively;
2. Markers of DNA and RNA viruses in a water sample indicate the direct presence of viruses in water and their species, as well as their possible quantitative level, which requires epidemiological alertness.

Having studied the rural population of the Almaty region and their sanitary and hygienic living conditions [10,22], a group of researchers led by B.A. Ramazanova came to the conclusion that the analysis of the water quality of decentralized water supply sources by microbiological indicators gave grounds to state a tendency towards its improvement. During the study period in this region, 9.0% of working water pipelines did not meet sanitary and epidemiological requirements, including 52.8% due to the lack of sanitary protection zones, 28.5% due to the lack of the necessary treatment facilities and 44.3% did not have disinfection facilities. In a number of districts, the unsatisfactory condition of the existing water pipelines was simultaneously caused by several of the above reasons.

Ensuring the microbial safety of the drinking-water supply relies on the use of many barriers from the water collection to the consumer in order to prevent contamination from drinking water or reduce it to acceptable levels, not harmful to health [38-39,40,42-44]. Safety is enhanced when multiple barriers against contamination are established, including protecting water resources, selecting and implementing a range of appropriate treatment measures, and regulating distribution systems (piped or non-piped) to maintain and protect the quality of treated water. The preferred strategy is a regulatory approach that focuses on preventing or reducing the entry of pathogens into water sources, and on reducing reliance on water treatment to remove pathogens.

Thereby, outbreaks of waterborne diseases associated with microbial contamination are underinvestigated. Data on outbreaks caused by many etiological agents tend to rarely affect water supply networks, since backflow and growth events are likely not to be recognized and reported unless an entire building with a large number of people is affected. There is a need for epidemiological studies that aim at microbial contamination of water. Surveillance systems help to track trends in causes and risk factors for waterborne diseases, but they are not very susceptible and not able to

serve as a fast warning system for water-related health problems in a particular community due to reporting delays. Therefore, epidemiological studies of the risk of endemic diseases associated with microbial contamination of drinking-water should be carried out and developed with sufficient capacity and resources to address the shortcomings of previous studies.

Conclusion

Thus, ensuring the microbial safety of WASH requires the following: an assessment of the entire system to determine the potential harmful factors that may affect it; determination of control measures to reduce or eliminate these harmful factors as well as operational monitoring to ensure the effective functioning of barriers from infection within the system; and developing regulatory plans to describe operations to be taken both under normal conditions and in unforeseen circumstances. These measures are three components of the WSPs. Insufficiency to ensure the microbiological safety of WASH can lead to outbreaks and fatal epidemics.

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Contribution of the authors:

Alua O. Omarova: planned the study and wrote parts of the final paper;

Ilya A. Belyayev: performed the review and wrote the first version of the paper;

Saule B. Akhmetova: performed the review and wrote the first version of the paper;

Nurbek Zh Yerdosov: performed the review and wrote the first version of the paper;

Chingiz U. Ismailov: collected and processed the sources;

Azamat D. Kharin: collected and processed the sources.

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