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Analysis of the diversity of microbial communities in typical domestic sewage

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Abstract: This review paper mainly introduces the relationship between domestic sewage treatment and microbial communities. First, the paper provides an overview of the source and composition of domestic sewage and the importance of microbial diversity in domestic sewage treatment. Then, the paper summarizes the current research status of microbial communities in typical domestic sewage. In the second part, the paper explores the factors affecting the microbial diversity in domestic sewage[i]. Then, in the third part, the paper describes the diversity of microbial communities in typical domestic sewage, respectively from the biological classification community composition and functional classification community composition. In the fourth part, the paper explores the ecological functions of microbial communities in domestic sewage. Finally, in the fifth part, the paper analyzes the influence of the traditional sewage treatment process and the new sewage treatment technology on the microbial community, and introduces the indicator role and assessment method of the microbial community. It provides an important reference for further research and optimization of domestic sewage treatment.

1. Introduction

Domestic sewage is an inevitable product in the process of urbanization, which contains a lot of harmful substances and microorganisms. Microorganisms are one of the most abundant and diverse groups in the biological world and play important functions in ecosystems. [1]However, the discharge and treatment of domestic sewage will cause serious effects on the microbial community, which may lead to the reduction of microbial diversity and the change of community structure, which will affect the normal performance of ecological function. Therefore, it is important to study and explore the effects of sewage treatment on microbial communities and the mechanism of ecological function recovery for the protection and improvement of environmental quality.

2. Literature review

2.1. Source and composition of domestic sewage

Domestic sewage refers to the wastewater produced in People's Daily life, the main sources include urban sewage, industrial wastewater and rural sewage. Domestic sewage of urban residents mainly comes from household water, bath, toilet washing, etc., containing detergent, oil, alkaline substances, organic matter, etc[2]. Industrial wastewater is the wastewater discharged in the industrial production process, which may contain heavy metals, organic matter, acid and alkaline substances, etc. Rural domestic sewage mainly comes from farmland irrigation, rural residents water, containing pesticides, fertilizers, organic matter, etc. The composition of domestic sewage is complex and diverse, including organic matter, nutrients, microorganisms, heavy metals, chemicals, etc., which has a certain impact on the environment and human health.[3]

2.2. Importance of microbial diversity

Microbial diversity refers to the number and degree of diversity of various kinds of microorganisms present in the microbial group. Microbial diversity is important for the stability and function of terrestrial ecosystems. First, microbial diversity is the most abundant and most extensive biodiversity in the Earth's biosphere. Microrobes include bacteria, fungi, viruses, protozoa, etc., which are widely found in soil, water, air and organisms, a large number and variety. Microbial diversity maintains ecosystem stability and health. Second, microorganisms play an important role in the earth's ecosystem[4]. They are involved in the material cycle of the earth, such as the decomposition of organic matter, nitrogen cycle, carbon cycle, etc., and play an important role in maintaining the balance and function of the ecosystem. Microorganisms are also able to form symbiotic relationships with plants, providing nutrients and other beneficial substances to promote plant growth and health. In addition, microorganisms also play an important role in the remediation of environmental pollution. Certain microorganisms can degrade toxic substances, such as petroleum pollutants and heavy metals, thus reducing the impact of environmental pollution on the ecosystem[5]. For example, Trichomold bacteria break down organic matter in nature, helping to decompose dead plants and animal tissues into organic matter, form soil and promote plant growth; they play a key role in the nitrogen cycle, converting nitrogen into ammonia or nitrate that plant can absorb, so that plants can grow; Trichomold bacteria are widely used in sewage treatment and waste treatment, helping to purify water and remove pollutants. Oxammonia ammonia bacteria are the key microorganisms for the transformation of ammonia nitrogen into nitrate, which promote the removal of ammonia nitrogen from the soil and prevent excessive accumulation of soil ammonia nitrogen, which is very important for plant growth environment. Ammonia-oxidized bacteria are used in biological treatment systems to degrade ammonia nitrogen in sewage, helping to purify water bodies and maintain water quality. Aminooxidized archaea usually exist in extreme environments, such as high temperature spring water, high salinity lakes, etc. Their existence indicates that life can survive in extreme conditions, which provides important information for scientists to study the limiting conditions of life. Aminooxidized archaea also participate in the nitrogen cycle in some extreme environments, converting ammonia nitrogen to nitrate and promoting the nitrogen cycle.[6]

2.3. Current status of microbial communities in typical domestic sewage

In the research field of microbial communities in typical domestic sewage, many scientists have made important contributions, including researchers from both domestic and foreign countries. For example, Professor Mark van Loosdrecht of the Dutch University of Technology developed the "anammox"[7] microbial process for the efficient removal of ammonia nitrogen wastewater. Professor Katherine D. McMahon of the University of Wisconsin used molecular biology techniques to study the composition and function of microbial communities in domestic sewage and explore its impact on sewage treatment performance. Professor Bruce E. Rittmann of Arizona State University has developed a microbial community-based technology for the treatment and removal of organic pollutants in domestic sewage[8]. The research results of these scientists represent the international in-depth exploration of microbial communities in typical domestic sewage, and many domestic researchers have made important contributions in this field and promoted the development of sewage treatment technology in China.

3. Factors influencing the microbial diversity in domestic sewage

3.1. Sewage treatment methods

3.1.1. Traditional sewage treatment process

Traditional sewage treatment processes usually include steps such as physical treatment, chemical treatment and biological treatment. In the physical treatment, sewage through the grid, sand tank and other equipment to remove solid substances, and then into the chemical treatment stage, through the addition of chemical agents to remove dissolved organic matter and nutrients[9]. Finally, the sewage enters the biological treatment stage, where pollutants such as organic matter and nitrogen and phosphorus are further removed by the microbial communities such as suspended biofilm or activated sludge[10]. However, the traditional sewage treatment process has a great impact on microbial diversity, and the chemical substances and mechanical operations in the treatment process can affect the selection of microbial communities, which may lead to the decrease of microbial communities and the loss of certain specific microbial groups.

3.1.2. New sewage treatment technology

The new wastewater treatment technology show unique advantages in microbial diversity. For example, biofilm-based technologies (such as MBR, MBBR, etc.) can provide a large number of attachment surfaces and provide an environment for microorganisms to grow and attach, thus promoting the diversity of microbial communities. Moreover, some novel bioreactors, such as anaerobic reactors and microbial fuel cells, are also able to create specific microbial habitats that encourage the growth of specific types of microorganisms, thereby increasing the diversity of microbial communities[11]. Furthermore, novel sewage treatment technologies include the use of biotechnology, nanotechnology, and bioelectrochemistry to promote the increase in microbial diversity by changing treatment conditions and providing a suitable environment. Overall, the new sewage treatment technologies have the potential to improve microbial diversity and can provide better support for the efficiency and stability of sewage treatment processes.

3.2. Pollution sources and environmental factors

3.2.1. Degree of urbanization

With the progress of urbanization, population density increases, urban infrastructure construction and industrial activity increases, leading to an increase in the concentration of pollutants in domestic sewage. These pollutants include organic matter, heavy metals and chemicals, which have a direct impact on the composition and diversity of microbial communities. Increased urbanization also leads to land-use changes, reducing the area of natural habitats and limiting microbial diversity.[12]

3.2.2. Pollutant concentration

High concentrations of contaminants adversely affect microbial survival and growth, potentially leading to degradation and loss of diversity in microbial communities[13]. Some toxic substances, such as heavy metals, organic pollutants and antibiotics, can selectively kill certain microorganisms, leading to structural and functional changes in microbial communities. Moreover, excessive pollutant concentrations may also lead to stress and adaptive changes in microbial communities, which in turn affect microbial diversity.[14]

3.2.3. Temperature and pH values

The sensitivity of microorganisms to temperature and pH is determined by their physiological properties, with their adaptability to these two factors. Changes in temperature and pH can alter the structure and function of microbial communities and thus influence microbial diversity. Higher or lower temperatures and pH may limit the survival and reproduction of some microorganisms, leading to changes in microbial communities and reduced diversity[15]. Therefore, proper control of temperature and pH is crucial to maintaining microbial diversity during domestic sewage treatment.

3.2.4 Other environmental factors

Other environmental factors also include oxygen concentration, dissolved oxygen concentration, nutrient availability, etc. Oxygen concentrations and dissolved oxygen concentrations directly influence microbial physiological activities and metabolic pathways, thus influencing the diversity of microbial communities. Nutrient availability influences microbial growth and reproduction rates, which in turn affects the species composition and diversity of microbial communities. Other environmental factors such as light intensity, water flow speed, and salinity may also have an impact on microbial diversity. In conclusion, pollution sources and environmental factors are important drivers of changes in microbial diversity in domestic sewage.[16]

4. The diversity of microbial communities in typical domestic sewage

4.1. Biological taxonomic community composition

4.1.1. Bacteria

Bacteria are a class of unicellular microorganisms with diverse morphological and metabolic pathways. In domestic sewage, the bacteria are very diverse, including a broad spectrum of bacterial strains and unknown microorganisms. For example, the bacteria have excellent decomposition ability, which can quickly decompose organic waste into basic inorganic substances, promote the degradation of organic substances in wastewater and convert them into absorbable nutrients, thus maintaining the ecological balance of water body. The presence of the genus of bacteria helps to prevent the excessive accumulation of organic matter in the wastewater, reduce water pollution, and protect the quality of the water environment. The bacteria have the ability to quickly oxidize ammonia nitrogen to nitrate, effectively reducing the ammonia nitrogen content in wastewater. Through the transformation of ammonia nitrogen, ammonia oxidized bacteria help maintain the balance of nitrogen in water and prevent the occurrence of nitrogen pollution in water. This microorganism plays a key role in the biological treatment system, ensuring the safe discharge of wastewater, and also plays a positive role in the protection of water environment and ecological balance.

4.1.2. Archaea

Archaea, a distinct class of prokaryotes, exhibit some similarities with bacteria but differ in terms of their biological characteristics and genome structure. In domestic sewage, archaea are relatively less diverse and present in lower quantities compared to other microorganisms. However, despite their limited abundance, archaea play crucial roles in the sewage treatment process.One significant function of archaea in domestic sewage treatment is their involvement in anaerobic granular sludge formation. Archaeal species such as Methanosarcina and Methanosaeta contribute to the production of methane gas through the anaerobic digestion of organic matter. This not only aids in the removal of organic pollutants but also helps generate renewable energy.Another important function of archaea in sewage treatment is ammonia oxidation. Certain archaeal groups, particularly within the Nitrososphaera and Nitrosopumilus genera, perform the crucial step of ammonia oxidation, converting ammonia into nitrite[17]. Ammonia-oxidizing archaea are an important microbial group. It have excellent ammonia nitrogen conversion capacity, which can quickly convert the ammonia nitrogen in wastewater into nitrate, playing a key role in purifying water bodies. Aminooxidized archaea play an important role in the treatment of domestic sewage, helping to maintain the balance of nitrogen in water, but also providing support for the stability and efficiency of wastewater treatment system. Their active participation ensures that domestic sewage can be effectively treated, thus protecting the environment and human health.

4.1.3. Fungi

Fungi are a class of eukaryotes that differ greatly from bacteria and archaea. In domestic sewage, the fungal diversity is relatively low and low in number. However, the degradation ability and ecological function of fungi in sewage cannot be ignored. Fungi can break down organic substances and participate in sewage treatment processes. In addition, fungi can coexist or compete with bacteria to have effects on the structure and function of microbial communities. Therefore, the study of fungi in domestic sewage treatment is also very important.[18]

4.1.4. Virus

Viruses are acellular microorganisms characterized by protein-coated shells that enclose nucleic acids. In domestic sewage, there is a rich diversity of viruses, including various types of RNA viruses and DNA viruses. These viruses have the ability to infect bacteria and other microorganisms, thereby influencing the composition and function of microbial communities. Moreover, viruses can also act as carriers of diseases in domestic sewage, posing potential risks to human health. Monitoring and controlling viruses in domestic sewage treatment are essential aspects of ensuring public health and environmental safety. Effective monitoring methods include the detection and quantification of viral particles or specific viral genetic material. By implementing appropriate disinfection measures, such as chlorination or ultraviolet irradiation, the spread of viruses can be minimized during the treatment process. Furthermore, it is crucial to consider the potential for virus dissemination through effluent discharge or the application of treated sewage sludge in agricultural or environmental settings. Proper treatment and management practices should be adopted to minimize the transmission of viruses to humans and the environment. Overall, monitoring and controlling viruses in domestic sewage treatment play a vital role in preventing the spread of diseases and protecting public health. By implementing rigorous monitoring protocols and employing effective treatment strategies, we can mitigate potential risks associated with viral contamination and ensure the safe and sustainable management of domestic sewage.

4.2. Functional classification of the community composition

4.2.1. Degradation capacity

Microbes, including bacteria, archaea, and fungi, play a vital role in the degradation, decomposition, and transformation of organic substances present in sewage, such as proteins, carbohydrates, and fats found in organic wastewater. These microorganisms utilize diverse metabolic pathways to break down complex organic compounds into smaller molecules and further transform them into inorganic substances[19]. Mucormold bacteria have excellent organic degradation ability, can decompose dead plant and animal tissues, transform them into organic matter, promote the formation of soil and plant growth. They can break down the organic wastes in the waste, such as wood, paper, etc., to accelerate the natural degradation process of these wastes and reduce the accumulation of solid waste[20]. Ammonia oxidized bacteria can quickly convert ammonia nitrogen in wastewater into nitrite and nitrate, thus reducing the concentration of ammonia nitrogen in water and maintaining the nitrogen balance in water. Aminoarchaea usually exist in extreme environments, they have the ability to survive under extreme conditions such as high temperature and high salinity, and may participate in the degradation process of organic matter in extreme environments.

4.2.2. Antibiotic resistance

Due to the continuous use and discharge of antibiotics, domestic sewage often harbors microbial communities with antibiotic resistance[21]. The presence of antibiotic resistance genes in these communities can facilitate the spread of resistance among different microorganisms, posing a significant threat to human health and environmental safety. Antibiotic-resistant bacteria and genes can persist in wastewater treatment plants and may be released into the environment through effluent discharge or sludge application[22]. The dissemination of antibiotic resistance genes increases the risk of treatment failure for infectious diseases and limits the effectiveness of antibiotics in clinical settings. Therefore, monitoring and controlling antibiotic-resistant microbial communities are crucial aspects of domestic sewage treatment. Implementing strategies such as antimicrobial stewardship, proper disposal of expired or unused antibiotics, and advanced treatment technologies can help mitigate the spread of antibiotic resistance in domestic sewage systems. Additionally, enhancing public awareness about the responsible use of antibiotics and promoting research on alternative treatment options are essential for addressing this growing concern. By effectively monitoring and controlling antibiotic resistance microbial communities, we can safeguard public health and preserve environmental integrity[23].

4.2.3. Ecosystem functions

Microbial communities play a crucial role in maintaining the stability and functioning of ecosystems during domestic sewage treatment, particularly in the nitrogen, phosphorus, and sulfur cycles. Bacteria, bacteria, and archaea play important roles in the ecosystem. Mucormycosis bacteria are a kind of anaerobic bacteria, which can decompose organic substances and release methane gas, which participates in the methane cycle process and has a certain impact on the production of greenhouse gases[24]. Ammonia oxidation bacteria participate in the process of ammonia oxidation, which oxidizes ammonia to nitrous acid, and then is converted to nitric acid. This process is a key step in the nitrogen cycle and plays an important role in maintaining the balance of nitrogen in water and soil. In addition, ammonia oxidation archaea are a class of archaea that survive in high temperature, high pressure and low oxygen environment, which can use the ammonia oxidation process to generate energy. This has important implications for the maintenance of some extreme environmental ecosystems.

5. Ecological functions of microbial communities in domestic sewage

5.1. Role of beneficial microorganisms

In domestic sewage, there exist microorganisms that provide benefits to both the environment and human beings. For instance, the genus bacteria are involved in the decomposition and fermentation of organic matter, converting organic matter into methane gas. This is very important for the treatment of domestic sewage and for the operation of the treatment plants, because the methane gas can be captured and used as renewable energy sources. Ammonia-oxidized bacteria participate in the ammonia oxidation process, which transforms the ammonia nitrogen in wastewater into nitrite and nitric acid, so as to remove harmful substances in wastewater. This is very critical for nitrogen pollution control in wastewater treatment[25]. Alternatively, amidoarchaea can use the ammonia oxidation process to generate energy. During wastewater treatment, the presence of oxidized amidoarchaea can provide an additional energy source, maintain the balance of microbial communities, and accelerate the decomposition of organic material in wastewater.

5.2. Possible pathogenic microorganisms

In addition to beneficial microorganisms, domestic sewage can harbor pathogenic microorganisms that pose potential risks to human and environmental health. Pathogenic bacteria, viruses, and other microorganisms may be present in domestic sewage, and their presence and spread can lead to water, soil, and air pollution, as well as the occurrence of infectious diseases. Therefore, it is crucial to monitor and control the presence of pathogenic microorganisms during the domestic sewage treatment process[26]. Vigilant monitoring and effective control measures are necessary to safeguard public health and maintain the integrity of the environment.

6. The relationship between the domestic sewage treatment and the microbial community

6.1. Effect of traditional sewage treatment process on microbial communities

Traditional sewage treatment processes have certain effects on the community of bacteria, ammonia bacteria, and ammonia archaea. In the traditional sewage treatment process, the activated sludge method or the aeration tank method is usually used for biological treatment. These treatment methods mainly focus on the removal of organic matter and pollutants such as nitrogen and phosphorus. However, these methods are highly selective for bacterial species and may have some inhibitory effects on some specific microbial communities[27]. Bacteria of the genus Mucorus are a class of anaerobic bacteria that may be limited by oxygen supply in traditional sewage treatment processes, thus affecting their activity and function during treatment. Ammonia-oxidized bacteria require appropriate nitrogen oxidation conditions, including ammonia nitrogen concentration and oxygen supply. Insufficient nitrogen oxidation or the presence of competitive microorganisms in traditional treatment processes may affect the growth and function of ammonia-oxidizing bacteria[28]. Similarly, the presence of ammonia-oxidized archaea in traditional processing processes may also be limited, and anaerobic conditions and appropriate ammonia oxidation conditions are critical for their growth and function.

6.2. Effect of the new sewage treatment technology on the microbial community

New sewage treatment technologies (such as membrane bioreactors, biological filters, microbial fuel cells, etc.) have higher treatment efficiency and resource utilization rate compared with traditional processes. These techniques have greater flexibility in the selection and control of microbial communities[29]. For example, membrane bioreactors can control the retention or retention of microorganisms by selective screening of membrane aperture and membrane materials, realizing the precise control of microorganisms in sewage. The introduction of new technologies can promote the diversity of microbial communities and improve the treatment effect and system stability.

7. Conclusion

Domestic sewage discharge and treatment have important effects on microbial communities, so enhanced research and improvement of wastewater treatment technology are needed to reduce the negative impact on microbial diversity[30]. At the same time, we also need to strengthen environmental education and publicity to raise public awareness of the importance of sewage treatment and the correct treatment methods, so as to promote environmental protection and sustainable development. Only through joint efforts can we protect the balance of the ecosystem, reduce the impact of domestic sewage on the environment, and lay a healthier and more livable environmental foundation for sustainable development in the future.

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