Microbial Ecology of Wastewater Treatment Processes: Trends, Challenges, and Perspectives

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Abstract

Microbial remediation is the most promising, effective, cheapest, and environmentally friendly treatment method for biodegrading a broader range of toxic substrates and metabolites from wastewaters discharged from households, industry, and pharmaceuticals. Currently, micro-organisms must be used as decontamination tools, which in turn reduce the contaminants load of the sewage ecosystem and prevent future detrimental effects on the environment and aquatic ecosystem. Microbial consortia and sewage sludge are completely dependent on the level of water pollution. Many factors can modulate the microbial ecology from autotrophic to heterotrophic bacteria, such as titres of organic and inorganic wastes, hydrocarbons from disposal of solvents, micro-plastics, medicines, fibres, and heavy metal contaminants dissolved in sewage wastewater. The main microbial species found in 95% of polluted and sewage water are *Bacteroidetes*, *Acidobacteria*, *Escherichia coli*, coliforms, *Aeromonas hydrophila*, *Klebsiella pneumonia*, *Vibrio* sp., *Mycobacterium* sp., *Rhodobacter*, *Hyphomicrobium*, *Firmicutes*, *Nitrosomonas* sp., and *Pseudomonas* sp.. Proteobacteria (21–65%) is the dominant class of bacteria found in municipal sewage ecosystem. Beta-proteobacteria, the most abundant class of proteobacteria, also help to break down

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organic wastes and promote nutrient cycling in the ecosystem. When treating biological wastewater systems, the ecology of the microbial communities and their dynamics are always considered. Most genera of sewage decomposer belong to *Betaproteobacteria*, *Acidobacteria*, *Bacteroidetes*, and other genera of aerobic, anaerobic, and facultative microbes such as Flavobacteriaceae, Verrucomicrobiaceae, Pseudomonadaceae, and Comamonadaceae. These bacterial communities are often used in the sewage treatment plants of bioreactors or activated sludge. Molecular studies identified core microbial communities that help to design efficient activated sludge plants. Currently, advanced molecular techniques and/or approaches such as next-generation sequencing, metagenomics, and transcriptomics studies are helping us to determine the metabolic function of microbial consortia through gene sequencing to identify the abundant genera and process critical micro-organisms in activated sludge wastewater treatment systems.

13.1 Introduction

Due to a boost in the human population, urban expansion, and industrialization with rapidly advancing technology cause a serious threat to the environment and water ecosystem. Accumulation of different toxic contaminants in the ecosystem will in turn causes adverse effects to human health, ecology, and the environment. In developing countries, water wastes composed of 20–30% annual solid wastes. Wastewater is defined as suspended or dissolved organic and inorganic impurities over the layer of water bodies in the form of liquid or solid wastes. The incidence of water pollution is increasing throughout the past couple of decades through micro-pollutants from household products, and industrial by-products like drugs, pesticides, micro-plastics, and chemicals making nuisances within the water bodies and land ecosystems (Daughton and Ternes 1999; Grandclément et al. 2017). These wastes originated from the household and industrial by-products and accumulated in the nearby groundwater ecosystem. Therefore, a number of techniques have been proposed in the recent literature on wastewater treatment methods that can help in the management and control of water pollution through wastewater decontamination and the recycling process (Kumar et al. 2018, 2020; Agrawal et al. 2021).

Among the various wastewater treatment methods, techniques such as the physical, chemical, and microbial treatment of wastewater are continually improving over time. Some of the techniques include physical treatment of wastewater such as artificial aeration, sedimentation, water diversion, and mechanical algae removal (Zhang et al. 2010; Liu et al. 2014) and chemical treatment of wastewater through

chemical oxidation, precipitation, flocculation, adsorption, chelation, and algae removal with chemicals were used (Wu et al. 2018).

Microbial degradation of waste products is the most popular, natural, and standard technique used in the biological remediation process for both terrestrial and aquatic ecosystems. The use of living micro-organisms as a bioremediation technique to break down suspended solids from wastewater was first used by George M. Robinson (Vidali et al. 2002). The microbial degradation of various organic and inorganic wastes takes place with the help of the metabolic activities of various microbial genera (Kumar and Chandra 2018; Kumar and Shah 2021). Water pollution can be controlled through the use of microbial degradation techniques in combination with the degradation activities of various microbial consortia of Betaproteobacteria, Acidobacteria, Bacteroidetes, and other related genera with the help of various biological treatment plants for wastewater recycling. When treating biological wastewater, the ecology of the microbial communities and their dynamics are always taken into account in order to detect the titres of the environmental contaminants' load in particular groundwater and sewage ecosystems.

13.2 Composition of Contaminants in Sewage Wastewater

Municipal wastewater consists primarily of 99.9% water with 0.1% suspended contaminants. The current environmental threat to the freshwater and aquatic ecosystem is eutrophication. Most wastewater by-products come from various industrial sewage treatment plants and household products, which consist of organic substances such as proteins, complex carbohydrates, long unsaturated fatty acids, oils, nitrogen, phosphorus, heavy metals, pesticides, various pharmaceutical products, and micro-plastics (Chowdhury et al. 2016; Eerkes-Medrano et al. 2019). A heavy load of nitrogenous compounds, heavy metals, and organic compounds leads to the development of algal blooms above the surface of the water, and some of these inorganic contaminants are non-biodegradable and accumulate in tissues of various living beings (Grizzetti et al. 2012). Traditional water treatment plants are not well equipped to break down the new and emerging pollutants that result from complex wastewater production and hazardous by-products of industry (Norvill et al. 2016). There is, therefore, an urgent need to develop more environmentally friendly methods for water treatment. Some of the most commonly found organic and inorganic pollutants are discussed below.

13.2.1 Inorganic Contaminants

Most of the inorganic contaminants many times show high concentrations of toxic metals beyond the recommended limit for drinking water. These inorganic contaminants include dissolved chloride, sulfate, nitrate, nitrite, ammonia, cadmium, lead, mercury, arsenic, phosphate, carbonate, calcium, magnesium, potassium, and various types of nutrients and salts, which generally exist in the form of dissolved

cations and anions in wastewater composing total dissolved solids (TDS) (Ehrlich et al. 1997; Nickson et al. 2000)), including large-scale discharge of traces of antibiotics like ciprofloxacin, erythromycin, trimethoprim, sulfapyridine, and norfloxacin in all the food, faeces, pharmaceuticals flush, and wastewater supplies (Chen et al. 2018). Heavy metal impurities are not biodegradable and therefore increase their chances of accumulating in the living body. These are copper, nickel, zinc, cadmium, mercury, lead and arsenic, barium, beryllium, selenium as well as some of the aromatic compounds and hydrocarbons from the disposal of solvents, micro-plastics, medicines, fibres (cotton swabs, hair, hygiene articles, faeces), oil, soap, grease, and hazardous substances (Lim et al. 2010; Kumar et al. 2012). The accumulation of higher concentrations of these critical pollutants in domestic and sewer bodies causes environmental pollution and a public health crisis. Most of the water polluted with the traces elements like barium, beryllium, selenium, arsenic, and cyanide are responsible for different health crises related to cardiovascular, liver, lung, and bone diseases due to high metal load in drinking water (Wones et al. 1990; Cooper and Harrison 2009). These metal contaminants are also adversely affecting the recycling of bio-solids and chemical waste from contaminated sewage.

13.2.2 Organic Contaminants

Emerging organic contaminants that are produced by various industrial chemical reactions such as oxidation, reduction, hydrolysis and their by-products such as volatile organic chemicals (VOCs) include solvents and organic chemicals such as bisphenols, plasticizers/resins, methyl tertiary butyl ether, trichlorethylene (TCE), styrene, benzene, toluene, and vinyl chloride. Some of the organic industrial compounds such as petroleum hydrocarbons, gasoline additives, adhesives, degreasers, fragrances, and fuel additives are included (Pal et al. 2014). Many studies are based on the quality of shallow groundwater, which is heavily contaminated with perfluorooctanoic acid (PFOA), which makes up 80% of all PFAAs found in groundwater. Some of the contaminants of pharmaceutical origin, including carbamazepine, N,N-diethyl-meta-toluamide, sulfamethoxazole, phthalates, and so on, were widespread in untreated groundwater samples for irrigation (Lesser et al. 2018).

13.3   Microbial Diversity of Sewage Water

The microbial diversity in wastewater consists of different types of micro-organisms including algae, fungi, bacteria, protozoa, etc. (Cai and Zhang 2013). Bacterial genera make up 90–95% of total wastewater communities. Microbial genera such as Proteobacteria (25–45%) are the dominant strains present in the sewage water as in the order of alpha-proteobacteria, followed by beta-proteobacteria and gamma-proteobacteria (Tanaka et al. 2012; Zhang and Shao 2013). Besides, other dominant groups of sewage water ecosystems are Bacteroidetes (20–40%), Chloroflexi (3–17%), and Acidobacteria (2–15%), and major human bacterial pathogens like

enteric pathogens *Klebsiella* sp., *Vibrio* sp., *Shigella* sp., *Salmonella* sp., and *Escherichia coli* cause gastrointestinal infections, while other related species of bacteria like *Mycobacterium* sp. and *Pseudomonas* sp. are opportunistic bacteria which cause respiratory diseases and immune-suppressive diseases and are the most common inhabitants of wastewater (Cai and Zhang 2013; Anastasi et al. 2012; Levy et al. 2010). Some of the commonly reported bacterial strains in wastewater are listed in Table 13.1.

13.4   Wastewater Treatment Methods

There are many qualitative and quantitative methods of monitoring water quality from different supply sources through different biological treatment plants (Fig. 13.1). Test methods and parameters can be divided into three categories.

13.4.1 Physical Tests

These tests comprise the water properties judge on the basis of its colour, odour, taste, and turbidity. Change in colour of water is due to the presence of algae, vegetables, weeds, manganese and iron, and other mineral oils. Change in odour and taste of water is due to the presence of decaying organic matter including weeds, algae, and industrial wastes containing ammonia, heavy metals, phenol, long-chain fatty acids, and other hydrocarbons and foul odour is also due to the heavy growth of micro-organisms over the surface of the water. The presence of turbidity in sewage water is due to the presence of suspended solids, colloidal wastes, and soil erosion. High turbidity makes filtration expensive.

13.4.2 Chemical Tests

Chemical measurement of the water quality can be analysed through the detection of pH, biocides, toxic chemicals, and heavy metals, and total dissolved biochemical oxygen demand (BOD) and chemical oxygen demand (COD). Measurement of the pH of water for calculating relative acidity and alkalinity of water drinking water must have acidity and alkalinity range between 6.5 and 8.5. In the marine ecosystem, pH values below 4 do not support the growth of living organisms while low pH values help in effective chlorination. Treated wastewater through chlorination typically has higher concentrations of particles (1–10 NTU for secondary treated wastewater). High BOD means low oxygen concentration to support life and indicates high organic pollution.

Table 13.1 Microbial communities of sewage water

Microbial genera	Function	Pathogenicity	References
Proteobacteria, Alphaproteobacteria, Gammaproteobacteria	Dominant phylum of sewage water	Commensal of sewage water plants comprising subdominant abundant groups *Firmicutes, Bacteroidetes, Actinobacteria, and Chloroflexi*	Huang et al. (2018)
Bacteroides	Common inhabitant of sewage water. Ferment carbohydrates that result in the production of a pool of volatile fatty acids	The fimbriae and agglutinins of *B. fragilis* function as adhesins; the capsular polysaccharide, LPS, and numerous histolytic enzymes are the most important virulence determinants in the bacteria	Wexler (2007)
Enterococcus	Enterococcus species used as probiotics or in the food industry or as starter cultures enterococci have become nosocomial pathogens causing bacteraemia	Virulence factors include the extracellular protein Esp and aggregation substances (Agg), both of which help in the colonization of the host	Fisher and Phillips (2009)
Faecalibacterium	An anti-inflammatory commensal bacterium of sewage water	Non-pathogenic, in turn, have a potentially important role in promoting gut health used as a promising probiotic	Sokol et al. (2008)
Acetoanaerobium	Anaerobic bacteria that produce acetate from H_2 and CO_2	Their biodegradation efficiency in wastewater reported	Rainey (2015)
Aquabacterium	*Aquabacterium parvum* B6, nitrate-dependent Fe (II)-oxidizing bacteria; helps in the improvement of biological nitrogen removal in an up-flow bioreactor for wastewater treatment	*Aquabacterium commune* commonly found in drinking water biofilms	Zhang et al. (2016)
Candidatus Nitrotoga	Nitrite-oxidizing bacteria (NOB); metabolize nitrite to nitrate, which is removed via assimilation and denitrification processes	Play a key role in contaminants from freshwater	Boddicker and Mosier (2018)
Streptococcus	Faecal streptococcus is used as the best indicator organism in organic waste	Some species are potentially pathogenic, and in *streptococcus pseudopneumonia* the *ply* gene plays a role in pathogenicity	Jepsen et al. (1997)

(continued)

Table 13.1 (continued)

Microbial genera	Function	Pathogenicity	References
Subdoligranulum	Non-pathogenic sewage commensals	Used as probiotic and associated with improved metabolic health	Van hul et al. (2020)
Chryseobacterium	Phosphate solubilization, plant growth promotion	No pathogenicity but suppresses *Phytophthora* blight	Singh et al. (2013)
Comamonadaceae	Widely used in degradation and remediation of wastewater contaminants	Most genera are not regarded as pathogenic	Gumaelius et al. (2001)
Comamonas	*Comamonas* spp. are capable of assimilatory and dissimilatory nitrate reduction and are considered as denitrifying bacteria. The resultant nitrite can be further converted to ammonia by nitrite reductase (*Nir*) producing microbes	The virulence factors comprise several genes responsible for bacterial motility and adherence	Wu et al. (2018)
Dechloromonas	Denitrifying bacteria; help in enhanced nitric oxide production under salt or alkaline stress conditions, also able to reduce benzene, perchlorate, and oxidize chlorobenzoate, toluene, and xylene	Non-pathogenic and this organism is used for bioremediation	Salinero et al. (2009)
Geothrix	Sulphur and Fe-oxidizing autotrophic denitrifying bacteria	Non-pathogenic but used for remediation of nitrate polluted effluent	Zhang et al. (2019)
Nitrosomonas	Nitrifying bacteria; help in providing nitrogen to plants and limiting carbon dioxide fixation. It converts ammonium ions or ammonia into nitrites	Non-pathogenic	Arp et al. (2002)
Nitrospira	Nitrite-oxidizing bacteria; help in the conversion/ oxidation of nitrite to nitrate	Non-pathogenic	Daims and Wagner (2018)
OM27 clade	Non-culturable bacteria, high coral coverage on reefs due to abundances of the OM27 clade	Non-pathogenic	Apprill et al. (2021)

Table 13.1 (continued)

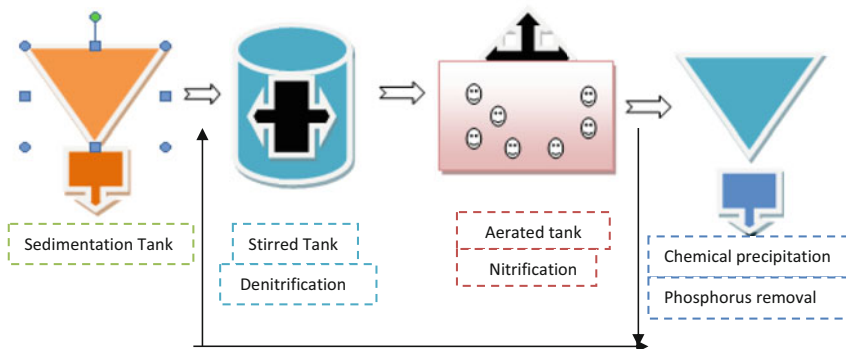| Microbial genera	Function	Pathogenicity	References
Proteocatella rhodoferax	Ruminal hydrolytic bacteria; help in the hydrolysis of microalgal biomass	–	Carrillo-Reyes and Buitr (2017)
Simplicispira	Gram-negative bacteria found in activated sludge that help in phosphorus removal	Non-pathogenic, novel denitrifying bacteria found in sludge	Lu et al. (2007)

Fig. 13.1 Tertiary treatment system of wastewater

13.4.3 Microbial Tests

Bacteriological analysis helps to study the faecal load and microbial load in a particular water sample using established culture methods. Although it is possible to detect most of the pathogenic microbial contaminants by counting the total bacteria, Coliforms, *E. coli, Salmonella* sp., *Pseudomonas* sp., etc. through different culture tests. Conversely, the lack of faecal commensals suggests that pathogens are also likely to be absent. Using normal intestinal bacteria such as *E. coli* have been used as a bioindicator of faecal burden, it is a well-established principle for monitoring and evaluating the microbial safety of water supplies. Some of the well-known culture methods used for the testing of water quality index are listed below.

13.4.3.1 Direct Plate Count
This method involves plating the drinking or wastewater directly into the nutrient agar or VRBA Agar plate to count different microbial colonies by diluting the original sample so that the colonies are between 30 and 300 per plate of inoculums volume. Typical media include MacConkey agar to count Gram-negative bacteria such as *E. coli* or plate count agar for a general count at 37 °C for 24 h (Gilchrist et al. 1977).

13.4.3.2 Multiple Tube or IMViC Method

It is a group of individual tests (indole, methyl red, Voges–Proskauer, and citrate) known as IMViC that are used to count total coliforms in wastewater or drinking water. The identification of 87 species representing 7 genera in the Enterobacteriaceae family was completed with a typical IMViC test within 48 h after incubation of the culture tubes (Barry et al. 1970).

13.4.3.3 ATP Testing

This test is also known as adenosine triphosphate test, used for the detection of active micro-organisms in water. ATP is released by living cells which can be measured directly by its reaction with the naturally occurring enzyme fireflyluciferase using a luminometer. The amount of light produced is directly proportional to the number of living micro-organisms present in the water samples (Birmele et al. 2010).

13.4.3.4 Membrane Filtration

This method is similar to the conventional plate count method, where membrane vacuum filters are used and these filters are placed on presterilized nutrient medium or Endo Agar within sealed plates. These filters have a millimetre grid printed on them and can be reliably used to count the number of colonies under a microscope (International Organization for Standardization 2000).

13.5   Types of Bioreactors Used for Wastewater Treatment

The treatment, purification, and decomposition of the sewage water are carried out with the help of various bioreactors and water treatment systems such as anaerobic sequencing batch bioreactors, fluidized bed bioreactors, bio-augmentation, membrane bioreactors, and activated sludge treatment systems. These biological sewage treatment systems are used for the decomposition of the various household and industrial by-products such as organic and inorganic waste, waste containing sulfur, phosphorus, and nitrogen, heavy metals and other toxic elements, heavy metal pollution of the sewage ecosystem. The type of sewage treatment plant used depends on the composition of the waste products present in the wastewater bodies. The biological removal of water waste (BOD) involves the use of anaerobic processes reactor (Anaerobic Expanded Bed Reactor; AEBR). The second type of anaerobic reactor system is a contact anaerobic process which includes an anaerobic fluidized bed reactor (ANFLOW), an anaerobic up-flow sludge blanket (UASB), an anaerobic sequencing batch reactor (ASBR), etc. However, for the removal of BOD along with the nitrification process biolac-aerated lagoon, optional aerated lagoon, sequencing batch reactor (SBR), cyclic activated sludge system (CASS), etc. are widely used bioreactors. These types of bioreactors are used for selectively performed nitrification, denitrification, ammonification, phosphorus and sulphur removal.

13.6   Structure and Function of Microbial Communities in Activated Sludge and Wastewater Treatment Plants

Characterization of microbial diversity and their community structure in the wastewater treatment plants was helpful in order to set up the microbial composition and operational activities of the different bioreactors. Microbial diversities in the treatment plants have been used to set the flocculation, sludge bulking, foaming process of activated sludge plants as bioreactor operational settings. The most commonly reported microbial phylum in the sewage water plants is Proteobacteria, Betaproteobacteria, Acidobacteria, and Bacteroidetes (Meerbergen et al. 2016). These bacterial genera show very high efficiency in the removal of COD (chemical oxygen demand) along with the decomposition of various organic contaminants. Microbial species contain various organic acids, enzymes, antioxidants, and metallic chelates (Freitag and Meihoefer 2000), and these secondary metabolites help in the oxidation of the sulphur, phosphorus, ammonia, nitrogenous wastes containing compounds (Liu et al. 2014). *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Bacillus subtilis* these bacterial strains are able to form biofilms and remove various toxic elements, oil and metal contaminants from waste water treatment plants (Rice et al. 2007; Branda et al. 2006; Zhao et al. 2006). Similarly, cyanobacteria, photosynthetic bacteria found in water bodies, act as an indicator of water pollution, and *Pseudomonas* sp. is able to degrade various polymeric substrates and micropolythenes. Acinetobacter and Arcobacter were dominant genera in sewage treatment plants (Marti et al. 2013). The structures of the algae and bacteria symbiosis are adapted for wastewater treatment.

Another dominant genus in the sewage treatment plants are the *Flavobacteriaceae*, *Verrucomicrobiaceae*, *Pseudomonadaceae*, and *Comamonadaceae*.

These types of bacteria are often used in the sewage treatment plants of bioreactors or activated sludge. The most numerous types of bacteria that are used to treat dissolved organic pollutants belong to genera *Tetrasphaera*, *Trichococcus*, *Candidatus*, *Microthrix*, *Rhodoferax*, *Rhodobacter*, and *Hyphomicrobium*, followed by the archaeobacteria with the Euryarcheota (McIllroy et al. 2015). The process of adsorption followed by degradation was the main functional unit of activated sludge carried out by the microbial species. The growth and activities of these dominant bacterial genera increased from day 1 to day 12, reached the maximum operational taxonomic unit (OTU) number, then decreased slightly, and finally stabilized (Shchegolkova et al. 2016). While some of the associated bacterial genera such as Pseudomonadaceae, Streptococcaceae, and Enterobacteriaceae show increased growth and turbidity from day 1 to day 9, it then gradually decreases and increases as on days 13 and 15 of the incubation time in the bioreactor and then stabilizes. Most sewage treatment plants avoid the use of filamentous bacteria because of their excessive growth behaviour, which leads to foaming and flocculation disorders in the operation of sewage reactors. Hence, the estimation of the microbial community structure in wastewater is by the next-generation sequencing will be the most important parameter of any of the bioremediation treatment facilities.

13.7 Molecular Techniques for Next-Generation Wastewater Management

The most intensely explored areas of current research in the field of wastewater treatment are the use of genetically modified micro-organisms and recombinant DNA technology to treat three main groups of wastewater pollutants, namely persistent organic pollutants (POPs), polycyclic aromatic hydrocarbons (PAHs), pentachlorobiphenyls (PCBs), and pesticides. Evaluation of the microbial community structure living in the wastewater ecosystem becomes easier with the help of cutting-edge technologies such as 16S rRNA sequencing, fluorescence in situ hybridization, and gene clone library which in turn assess the diversity of the microbial population due to high levels of contamination and toxicity of environmental pollutants. Therefore, different communities of the bacterial population in the sewage treatment plants can be analysed by 16s rRNA gene sequencing (Guo and Zhang 2012). In order to measure the microbial diversity in the serial passage electro-bioreactor, DNA amplicons were produced after the isolation of the entire genomic DNA from sewage treatment plants. The identification of microbial alpha (α) and beta (β) diversity analyses were performed using statistical tools called QIIMETM (version 1.9.1) (Kuczynski et al. 2011). Likewise, another advanced statistical tool for identifying microbial community structure and genome sequencing called PICRUSt (phylogenetic study of communities through reconstruction of unobserved states) was used together with KEGG (Kyoto Encyclopedia of Genes and Genomes) to identify bacterial communities in wastewater and determine their functionality through dominant OTU gene sequences and another microbial database called the Ribosomal Database Project (RDP) classifier that is used to identify the pathogenic genera that inhabit the sewage treatment plant as microbial communities.

13.8 Contribution of Nanotechnology in Wastewater Decomposition

Nanotechnology is the rapidly developing and environmentally friendly process that can be used instead of conventional technologies for water treatment. Manufacture of nanoparticles as a by-product of green chemistry, which leads to less dangerous chemical production when decontaminating water samples or wastewater. Nano-agglomerates from mixed oxides such as iron–titanium, iron–zirconium, iron–manganese, iron–cerium, and other amalgams have been synthesized and successfully used to remove and purify water contaminants. Just like the Nao particles, nanoceramic filters are used to remove viruses and bacteria and to chemically absorb the dissolved heavy metals from the wastewater. These nano-ceramic filters consist of nano-alumina fibres and micro-glass with a high positive charge (Shah and Ahmed 2011). Nowadays use of filtration membranes with hollow tubes along with carbon nanotubes will effectively remove heavy metals and bacteria such as *E. coli* and *Staphylococcus aureus* from contaminated water. Another bioremediation technology called permeable barrier reactor (PBR) helps in the remediation of

organic and inorganic contaminants from biological groundwater. Nanoscale zero-valent iron is a mixture of Fe(II) and Fe(III) oxide with a particle size of 10–100 nm. The nanoparticles help destroy polychlorinated hydrocarbons, arsenates, selenates, pesticides, and dyes (Yukti et al. 2020).

13.9 Challenges and Future Outlook

The bioremediation of wastewater through microbial degradation has been the most effective, inexpensive, and environmentally friendly method to date. The biological treatment of sewage treatment plants is a necessary prerequisite for the ecological biological rehabilitation of wastewater bodies. An increasing concentration of toxic metabolites in wastewater can further deteriorate the quality of the groundwater. Various microbial consortia of Betaproteobacteria, Bacteroidetes, Acidobacteria, Chloroflexi, *Tetrasphaera*, *Trichococcus*, etc. are used in wastewater treatment, which can help reduce the overall load of organic, inorganic, and heavy metals. The optimization of different microbial consortia and culture parameters leads to an increase in the efficiency of sewage treatment plants and a greater reduction in environmental pollutants from wastewater. Nowadays, various molecular and next-generation sequencing technologies are used to identify the microbial composition of sewage treatment plants, which can be helpful for the future design and modulation of the microbial composition of the different sewage treatment plants.

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