



The effects of per- and polyfluoroalkyl substances on environmental and human microorganisms and their potential for bioremediation

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Utilised in a variety of consumer products, per- and polyfluoroalkyl substances (PFAS) are major environmental contaminants that accumulate in living organisms due to their highly hydrophobic, lipophobic, heat-resistant, and non-biodegradable properties. This review summarizes their effects on microbial populations in soils, aquatic and biogeochemical systems, and the human microbiome. Specific microbes are insensitive to and even thrive with PFAS contamination, such as *Escherichia coli* and the *Proteobacteria* in soil and aquatic environments, while some bacterial species, such as *Actinobacteria* and *Chloroflexi*, are sensitive and drop in population. Some bacterial species, in turn, have shown success in PFAS bioremediation, such as *Acidimicrobium sp.* and *Pseudomonas parafulva*.

KEY WORDS: bioremediation; environment; microbiome; PFAS; toxicity

Per- and polyfluoroalkyl substances (PFAS) are a large group of over 9,000 fluorinated carbon compounds used in a wide range of industrial and consumer applications thanks to their heat resistance, non-degradability, and hydro- and oleo/lipophobicity. Industrial applications include aqueous film-forming foams, coatings, and surfactants, whereas consumer applications include non-stick cookware, shampoos, cleaners, paints, and food packaging materials (1–4) (Figure 1). Their continued consumer and industrial use have made PFAS a major environmental and human health concern, as they contaminate soils, groundwater, rivers, lakes, drinking water, and the atmosphere.

They affect microbial communities across these diverse environments by disrupting their biogeochemical activities in water and soil, with a ripple effect on the organisms in the higher trophic level of the food chain, including humans and their microbiome (5–10).

This, in particular, affects their beneficial symbiotic role in animal and human metabolism through digestion and absorption of nutrients in the gut, neutralising drugs, and synthesis of vitamins that aid immune response (7), which may ultimately advance to the development of metabolic diseases (8). This evidence in mice models (7, 8) is driving research for comparable results in humans, although the knowledge of PFAS-induced microbial dysbiosis and metabolic syndrome in humans is limited and very much understudied.

Over the years, different environmental remediation strategies have been designed to degrade PFAS contaminants in the environment (11). This includes nanofiltration designs, reverse osmosis in household drinking water (12), and biodegradation. However, heavily fluorinated domains in the molecular structure of PFAS make them resistant to degradation and present a major challenge to environmental scientists, regulators, and government agencies in the development of active remediation methods (11). One possible avenue is microbial degradation, which has proved effective and cheap in the elimination of chlorinated compounds, gasoline spills, and most common industrial wastes (13).

The aim of this review is to take a closer look at the published and unpublished data on the complex relationship between PFAS and healthy microbiome in humans, microbial populations in the environment, and the utilisation of microbial species in bioremediation of PFAS in the environment.

PFAS: PROPERTIES AND CLASSIFICATION

Perfluoroalkyl and polyfluoroalkyl substances (PFAS) are synthetic compounds with at least one carbon-fluorine bond (CF). Some of the most common PFAS include perfluoroalkyl acids



Figure 1 Most common sources of PFAS in the environment

(PFAAs), perfluoro octane sulphonate (PFOS), perfluorooctanoic acid (PFOA), and other fluoroalkyl substances (14, 15) (Figure 2).

Over the last 30 years, efforts have been made to characterise PFAS by their functional groups, from Banks et al. (14) in 1994 to the Organization for Economic Co-operation and Development/United Nations Environment Program (OECD/UNEP) in 2019–2021, which commissioned a report identifying 4730 substances

(15, 16). Thanks to the further efforts of OECD, the European Chemical Agency (ECHA), and the US National Institutes of Health (NIH), by 2022 this number has grown to over 9,000 (17, 18).

PFASs are broadly classified as polymeric and non-polymeric, based on their chemical composition and the length of side chains (Table 1). The higher the number of carbon chains, the higher their hydrophobicity and bioaccumulation (19). Recent classification

Table 1 Polymeric and non-polymeric PFAS classification and examples (7, 11)

	Perfluoroalkyl Substances (PerFASs)	Acronym	Formula	Examples	
Non-polymeric PFAS	Perfluoroalkyl acids	PFAAs	$C_nF_{2n}+1R$	PFHxS, PFOA	
	Perfluoroalkane sulphonates	PFSAs	$C_nF_{2n}+1SO_3^-$	PFOS	
	Perfluorocarboxylic acids	PFCAs	$C_nF_{2n}+1COO^-$	C8-PFPA	
	Perfluoroalkyl phosphonic acids	PFPAs	$C_nF_{2n}+1(O)P(OH)O^-$	C8-PFPiA	
	Perfluoroalkane sulphonamides	FASA	$C_nF_{2n}+1SO_2NH_2$	FOSA	
	Perfluoroalkyl ether acids	PFEAs	$C_nF_{2n}+1O-C_mF_{2m+1}$	GenX	
	Perfluoroalkyl sulphonamideotic acids	FASAAs	$C_nF_{2n}+1SO_2NHCH_2COOH$	FOSE, MeFOSA	
	Polyfluoroalkyl Substances (PolyFASs)				
	Fluorotelomer alcohols	FT	$C_nF_{2n}+1CH_2CH_2OH$	FTO	
	Polyfluoroalkyl phosphoric acid esters	PAPs	$(O)P(OH)_3-X(OCH_2CH_2C_nF_{2n+1})_x$	diPAP	
Fluorotelomer saturated aldehydes	FTALs	$C_nF_{2n}+1CH_2CHO$	8:2 FTAL		
Fluorotelomer unsaturated aldehydes	FTUALs	$C_nF_{2n}+1CF=CHCHO$	4,8-Dioxa-3H-perfluorononate		
Polymeric PFAAs	Fluoropolymers	FPS		PFTE	
	Perfluoropolyethers	PFPEs	$HOCH_2O-(C_mF_{2m}O)_n-CH_2OH$	PFPE-BP	
	Side-chain fluorinated aromatics	sc-F	C_nF_{2n+1} -aromatic rings	Fluoriated methacrylate	

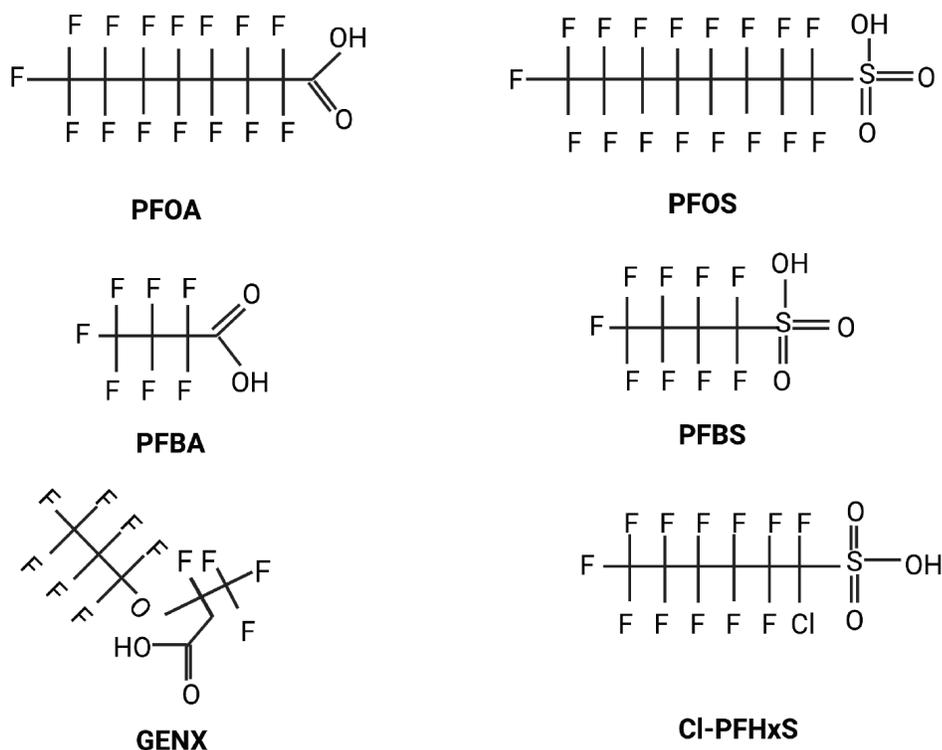


Figure 2 Chemical structure of some common long- and short-chain PFAS. PFOA – perfluorooctanoic acid (long-chain); PFOS – perfluorooctane sulphonate (long-chain); PFBS – perfluorobutane sulphonate (short-chain); PFBA – perfluorobutanoic acid (short-chain); GenX – hexafluoropropylene oxide dimer acid; PFHxS – 1-chloro perfluorohexane sulphonate

groups them in three classes: perfluoroalkyl substances (PerFAS), polyfluoroalkyl substances (PolyFAS), and fluorinated polymers. PerFAS are straight-chain, fluorinated aliphatic compounds with a fully fluorinated methyl or methylene carbon atom. PolyFAS are branched-chain fluorinated alkyl compounds. They may have a non-fluorinated aromatic ring with a fluorinated methyl or methylene carbon group and an aliphatic side chain or a fluorinated aromatic ring with a fluorinated methyl or methylene carbon group with an aliphatic side chain (19). Fluorinated polymers are further divided into three subclasses: fluoropolymers, perfluoropolyether, and side-chain fluorinated polymers.

The structure and chain lengths of PFAS confer different physiochemical and functional properties in regard to their transport, accumulation, and degradation in the environment. PFAS with an aliphatic fluorinated long carbon chain which ranges from C4–17 bioaccumulate more easily and resist biodegradation due to the strong C-F bonds (19).

Substantial efforts have been made to restrict the production and ban the use of long-chain PFAS in commercial and consumer products, PFOS and PFOA in particular (20). However, precursors of PFOS and PFOA, perfluoroalkyl carboxylic acids (PFCAs), perfluoroalkyl sulphonic acids (PFSAs), fluorotelomer alcohols (FTOHs), and shorter-chain PFAS such as GenX are still being produced and, therefore, still present pollution risk (Figure 3).

PFAS AND THE HUMAN MICROBIOME

The human microbiome comprises 10–100 trillion microbes (9) which inhabit the entire human body, such as the gut, skin, and mouth. Its importance is obvious in different functions of the skin, intestinal homeostasis, nutrient absorption, and overall host health.

The major source of PFAS pollution in humans are industrial and municipal waste-water treatment plants (WWTPs). WWTPs also contribute directly to the release of PFAS into the atmosphere, freshwater, and soil through recycled wastewater and the release of contaminated sewage sludge as biosolid for fertilisation (21, 22). Over 300 chemicals from the environment have already been characterised in different human clinical samples (20), which has shifted focus of many microbiome projects on the diet and disruption of endogenous microbial populations and their diversity in humans (23). A nine-year study across the US (24) detected PFOS, PFOA, perfluorohexane sulphonate (PFHxS), and perfluorooctanoate (PFNA) in over 95 % of 7,876 participants. Another, more recent study (25) reported high levels of PFOA in overweight and obese 12–18 year-old children (25).

Another important source of air pollution are PFAS-containing materials such as upholstery, stain-resistant carpets, textiles, paints, and food packaging materials disposed of in landfills. There in the landfills, PFAS precursors degrade into more lightweight and volatile PFAS such as fluorotelomer alcohols (FTOHs) and end up in the atmosphere through aerobic and anaerobic processes causing air

pollution (26, 27). However, no research data have specifically identified microbial species in the human oral/respiratory microbiome affected by airborne PFAS.

Long-chain perfluoroalkyl carboxylates (such as PFOA) and sulphonates (such as PFHxS) accumulate highly in plants and animals (30), whereas humans mostly accumulate PFAS through contaminated drinking water, non-stick cookware, food packaging, and food (31, 32). Food accounts for the bulk of exposure, which ranges about 16–99 % for PFOA, 81–199 % for PFOS, and 38–96 % for PFCAs and PFSA (33). In addition, animals raised and plants grown in PFAS-contaminated areas have shown high concentrations of PFAS (34). This level of contamination is evident in the end products such as eggs, grain, milk and meat, and fruit and vegetables (34–37).

PFOA, PFOS, and GenX are reported to be highly toxic to the intestinal microbiome by murine model and *ex vivo* human studies of intestinal bacteria. The microbial abundance of *Collinsella aerofaciens*, a major bacterial species active in the metabolism of carbohydrates in the human gut is altered at varying concentrations of PFOA, PFOS, and GenX. However, *Escherichia coli* is insensitive to these chemicals even at concentrations higher than the reported tolerance of *Collinsella sp.* PFOA (39). A study of PFAS effects on Zebra fish (38) showed changes in the gut microbiome, inflammation, oxidative stress, impaired lipid metabolism, decreased levels of triglycerides and fatty acids, and compromised intestinal epithelial layer barrier. Our preliminary data show differences in the sensitivities of human microbiome bacteria to PFOA, PFOS, and GenX to (39), suggesting that the ingestion of these toxic chemicals from food and water can alter the gut microbiome and ultimately impair human metabolism. However, much more research is needed to evaluate the impact of PFAS on human microbiome and metabolic activity. In addition, identifying the genetic markers in

the affected microbial species might help to elucidate biological functions and pathways affected by PFAS in humans.

PFAS and microbes in the environment

PFAS are present in all ecosystems (40–42) and can easily affect microbes native to these systems/habitats, whose major function is to maintain biotic processes such as nutrient cycling, decomposition of organic matter, and biodegradation of pollutants. Considering that microbes have a brief lifecycle and replicate rapidly due to simple genome, they quickly respond to environmental stress through genetic mutations and may be a good model to study PFAS toxicity. (43). Here we detail the effects of PFAS contamination on microbes in different environmental systems.

Aquatic ecosystems

PFAS have been found in a variety of aquatic systems, from rivers, lakes, and streams to groundwater, municipal sewage, treated drinking water, rainfall, and snow (44, 45). Volatile PFAS and their precursors, such as fluorotelomer carboxylic acids (FTCA), fluorotelomer unsaturated carboxylic acids (FTUCA), fluorotelomer sulphonate (FTSA), and perfluoroalkane sulphonamido acetic acid (FASAA) undergo a metabolic transformation in the atmosphere to produce short-chain PFSA and PFCA that end up in the aquatic environment. These short-chain PFAS are highly reactive with water (48), easily bioaccumulate in the aquatic food chain, and are toxic to many aquatic organisms (such as invertebrates and green algae) (49).

Due to high hydrophobicity, long-chain PFAS often have an even greater potential for bioaccumulation in aqueous environments and organisms (50). They are often released directly into surface waters from fluorine chemical plants or WWTPs (51). In Fuxin,

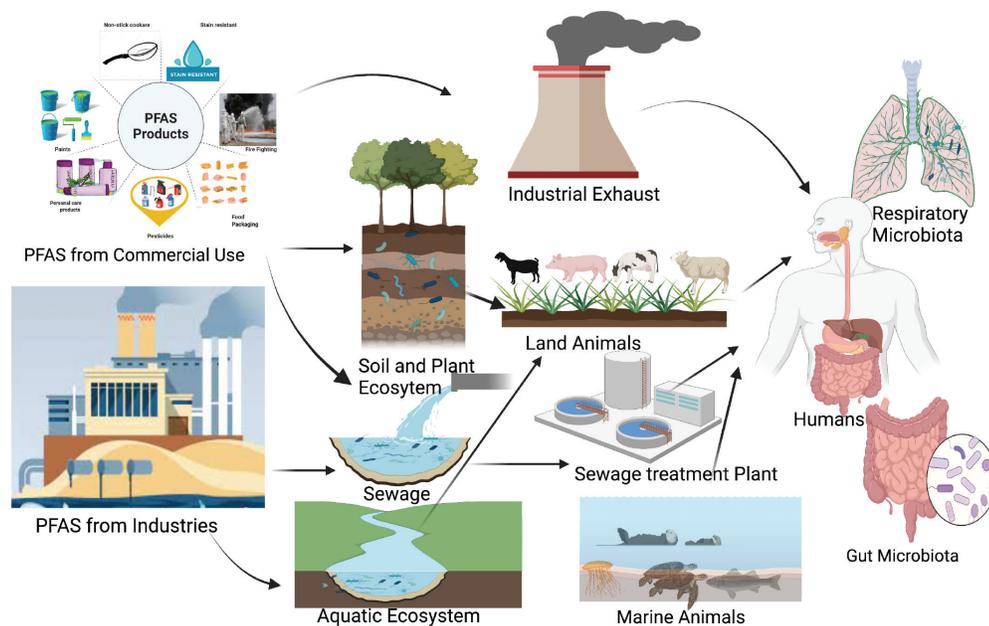


Figure 3 PFAS transport across different ecosystems

China, the levels of PFOA have been reported to reach up to 524 ng/L in the groundwater and 668 ng/L in the river (52), which is way above the recommended regulatory standards.

Carbon build-ups in aquatic ecosystems contribute substantially to the control of metabolic activities of environmental microbiomes (53) and to the growth of planktonic bacteria and protozoa. However, PFAS reduce the amount of biogenic and total dissolved carbon in water, which adversely affects many microbial communities and nutrient cycling and composition in aquatic habitats (54, 55). PFOS and PFNA have also been reported to biomagnify in the food web of aquatic animals (56).

Exposure to PFAS significantly affects the balance of bacterial population. There are reports of reduced bacterial diversity and drops in the populations of *Actinobacteria* and *Bacteroidetes* (57) in favour of *Verrucomicrobia*, *Proteobacteria* (58, 59), and *Photobacterium phosphoreum* in surface water (60, 61). These studies also report that perfluoro butanoic acid (PFBA) interferes with the transfer of nutrients in bacteria (60), while perfluorotetradecanoic acid (PFTeDA) moves up the food chain from heterotrophic bacteria to amoebae (protozoa) (59). Some genera, such as *Bacteroidetes*, *Proteobacteria*, and especially *Acidobacteria*, have been reported resistant to PFAS concentrations of up to 20 mg/L (62) (Table 2).

The molecular mechanism of PFAS toxicity to microbes involves oxidative stress, which damages the cell membrane and DNA, rendering some bacteria inactive (63, 64).

Sediments provide a habitat for a wide variety of benthic organisms, and much of their biomass includes microorganisms important for ecological processes such as biodegradation, biogeochemical cycling, and bioremediation (66–70).

Pollutants such as PFAS seem to have a major role in structuring microbial communities and their function in aquatic sediments (71, 72). Long-chained PFAS tend to build up over time (65, 73), which, once a threshold is crossed, may have irreversible negative effects on microbial populations and the structure of the benthic zone (74–77). In such conditions, tolerant and sulphate-reducing strains like the *Desulfococcus* genus and GOUTA19, become dominant microbial communities, and diversity drops (77–79).

PFAS in drinking water and health effects

Reports about the occurrence and toxicity of PFAS in drinking water come from all over the world (28, 48, 80). Average concentrations range between <10 ng/L and 1200 ng/L (81–85).

Table 2 Impact of PFAS and its compounds on aquatic and soil microbes

Microbes/Genus	Response to PFAS exposure	PFAS compound	References
<i>Sediminibacterium</i> , <i>Opatutus</i> , <i>Lateolibacter</i> , <i>Microcystis</i>	Increase	PFAS	48
<i>Photobacterium phosphoreum</i>	Increase	PFCA, PFOS, PFOA	58, 61
<i>Actinobacteria</i> and <i>Bacteroidetes</i>	Decrease	PFAS	106
<i>Verrucomicrobia</i> and <i>Proteobacteria</i>	Increase	PFAS	106
<i>Proteobacteria</i> and <i>Chloroflexi</i>	Decrease	PFOS	62
<i>Desulfococcus</i> and <i>GOUTA19</i>	Abundant/ Increase	PFAS, PFOS, PFOA	77, 79

PFAS occurrence in drinking water has been linked to several sources such as nearby fluorochemical production plants, PFAS-based firefighting foam (86), WWTPs, and surface runoff (87). Even at low concentrations (ng/L) PFAS in drinking water may have deleterious effects on human health as PFAS tend to build up in the liver and affect liver function (88). PFAS contamination of drinking water at levels above the United States Environmental Protection Agency (US EPA) health-based reference level of 70 ng/L (89) have also been associated with pregnancy-induced high blood pressure, hypertension, and preeclampsia as well as testicular and kidney cancers. Continued testing of drinking water and implementation of regulatory measures is therefore essential for keeping PFAS concentrations below this limit.

Soil ecosystems

Soil takes the lead as a sink for persistent chemical pollutants released into the environment from sources such as fluoride plants, aqueous film-forming foam from fire training sites, and sludge and biosolids from WWTPs, landfills, and incineration plants (6, 90–92). PFAS accumulate in soil over time and persist there for a long time, affecting micro and macro-organisms, which are abundant and serve to decompose organic matter, recycle biogeochemicals and nutrients, and remediate soil of contaminants (5, 43).

Soils are mostly contaminated by PFOS, because of their widespread and long-time application (94), but all PFAS change the structure of soil and, consequently, the distribution and function of microbial communities (5, 75, 93, 94). A recent study relying on a next generation sequencing technology (95) showed that PFOA in low concentrations affect bacterial diversity in soil less than PFOS. As for PFAS toxicity in soil microbial species, the mechanisms include membrane disruption, oxidative stress, and DNA damage-induced inactivation and/or death in *Escherichia coli* (96). In *Pseudomonas putida* PFOA is more toxic when combined with either chromium or tetra butyl ammonium (97).

PFAS contamination usually affects the diversity and composition of soil microbial communities. Long-chained PFAS and PFAS with the sulphonic group are more toxic to soil microbial flora than short-chained PFAS with carboxylic groups (97). There are reports, sometimes apparently controversial, that some important bacterial groups are eliminated, such as *Cyanobacteria* (75, 78), or depleted, such as *Chloroflexi*, *Haliangium*, *Latescibacteria*, and some

species of the genus *Acidobacteria* (6, 35, 75). Higher PFC concentrations are also known to impede the growth and metabolism of the *Bacillus* spp. (95) and *Sphingomonas paucimobilis* (104, 105).

Other groups seem to thrive, such as *Firmicutes*, some *Acidobacteria*, and *Actinobacteria* (75). Comparative studies of bacterial communities affected by PFAS contamination point to potential changes in soil nutrients (5, 97, 98), total carbon, and pH (99). Elevated PFOA concentrations in sediments seem to boost some populations of *Proteobacteria* (100–102), such as *Pseudomonas* spp., which may be owed to their ability to defluorinate fluorotelomer alcohols by removing multiple CF₂ groups to form shorter-chain PFCAs (102), which are less toxic (95, 103) and quicker to degrade (95). Besides *Proteobacteria*, *Verrucomicrobia* also seem to withstand PFAS contamination (106) (Table 2).

Greater abundance of some bacteria in contaminated soils provides an insight into which bacterial groups could be used to enhance PFAS biodegradation and bioremediation.

The effects of PFAS on soil organic content

As PFAS contamination affects the composition and diversity of microorganisms in soil, so does it affect its organic matter content (107, 108). Soil microorganisms are active in biogeochemical cycling and play an important role in pollutant degradation (109). The effect of PFAS on soil microbial populations may therefore affect the microbial diversity and ability to carry out geochemical processes in the soil (109, 110).

PFAS-induced changes in the abundance of fungi and bacteria may reflect on the organic content in soil and eventually carbon content available for cycling. However, possible connections with biogeochemical cycles have not been elucidated yet.

Zhalnina et al. (111) studied the effect of PFAS on the nitrogen cycle (nitrification and denitrification) and related cycle genes in 61 ammonia-oxidising microorganisms and reported that PFAS did not affect the ammonia monooxygenase gene abundance in bacteria but reduced it significantly in archaea. In fact, PFAS treatment seems to have favoured the growth of *Acidovorax temperans* in the soil. *A. temperans* is notorious for reducing the nitrate content in soil, and its proliferation implies nitrate depletion in PFAS-contaminated soils (Table 3). In contrast, nitrate- and sulphate-reducing bacterial genera, such as *Acidobacteria*, and *Gammaproteobacteria*, are inhibited by PFAS (35), leading to an increase in the level of nitrates and sulphates in the soil (35). Nitrates and sulphate concentrations and pH levels of contaminated soils influence nutrient availability, which, in turn, influences which plants will grow there.

As for the carbon cycle, PFAS are reported to inhibit glycoside hydrolases and interrupt carbohydrate metabolism and membrane transport in soil microbes (99). In addition to glycoside hydrolase inhibition, long-chain PFAS inhibit the activity of sucrase and urease (75).

Impact of PFAS contamination on vegetation

Several studies have shown that PFAS accumulate in spring wheat, oats, potatoes, maize, perennial ryegrass, winter wheat, winter

Table 3 Impact of PFAS on soil microbial communities and associated biogeochemical cycles

PFAS	Impact on population	Bacteria groups impacted	Potential nutrient cycle associated	References
PFOS	Increase	<i>Bacterioidetes</i>	Nitrogen cycle	34, 94, 127
PFOS/PFOA	Increase	<i>Alphaproteobacteria</i>	Nitrogen cycle, Sulphur cycle, carbon cycle	5, 75,
PFOA, PFOS	Increase	<i>Gammaproteobacteria</i>	Nitrogen cycle	5, 75, 126
PFOA, PFOS	Increase	<i>Acidobacteria</i>	Carbon cycle, nitrogen cycle	5, 34, 75, 127, 128
PFOS	Increase	<i>Firmicutes</i>	Nitrogen cycle	75, 129, 130
PFOA, PFOS	Increase/Decrease	<i>Chloroflexi</i>	Sulphur cycle	5, 34, 75, 127, 131
PFOS, PFOA	Increase/Decrease	<i>Actinobacteria</i>	Nitrogen cycle	5, 75
PFAS	Decrease	<i>Thermoleophilia</i>	Sulphur cycle	5
PFOS, PFAS	Decrease	<i>Deltaproteobacteria</i>	Sulphur cycle	5, 75

Table 4 Microbial species and mechanisms by which they biodegrade PFAS

Bacterial species	Biodegradation mechanism	PFAS	References
<i>Acidimicrobium</i> sp. S. A6	Defluorination	PFOA, PFOS	124
<i>Synechocystis</i> sp. PCC 6803	Decarboxylation, 2x reductive & oxidative defluorination, trifluoromethyl loss	PFOA, PFOS	132
<i>Pseudomonas parafulva</i> S. YAB1	Decarboxylation	PFOA	133
<i>Pseudomonas aeruginosa</i> S.HJ4	C-C bond cleavage	PFOS	10
<i>Pseudomonas plecoglossicida</i> 2.4-D	Decarboxylation, desulphonation	PFOS	134
<i>Gordonia</i> sp. S. NB4-1Y	Desulphonation	FTSA, FTAB	135
<i>Mycobacterium vaccae</i>	Dechlorination	FTOH	136

rye, canola, winter barley, carrots, and cucumber through soil (112–115). The last two studies (114, 115) point to the use of sewage effluent as fertiliser that contaminates the soil and then crops. Lechner and Knapp (114) further discourage the idea of air-to-plant transfer, as plants growing on soil not fertilised by sludge showed no increase in PFAS concentrations.

MICROBIAL BIOREMEDIATION OF PFAS

As we indicated earlier, strong covalent bonds between PFAS atoms make them resist biodegradation by microbial metabolism. Biodegradation has proven successful with oil and gas spills, chemical and industrial wastes, and other environmental pollutants. Although our current knowledge of microbial metabolism of fluorinated compounds is modest, enormous progress has been made towards microbial biodegradation of highly fluorinated alkyl compounds. Recent concepts involve direct targeting of specific PFAS molecules and regions that have fewer fluorine atoms, such as fluorobenzene, fluoroacetate, perfluorohexylethanol, and perfluorohexylsulphonate (61, 116–118). They also rely on combined knowledge of microbiology, enzyme biochemistry, and chemistry.

Bioremediation has a number of advantages over the classical physical and chemical remediation methods, including incineration, whose major drawback is the release of hazardous hydrogen fluoride and other toxic gases in the air. Other methods of PFAS elimination from water involve reverse osmosis, nanofiltration, and activated carbon filtration, yet these methods have not proven effective, safe, and reliable (120–122).

In contrast, biodegradation of PFOA and PFOS using activated sludge under low oxygen conditions has been reported successful (123). Success in defluorination has also been reported with fluoroacetate dehalogenase in the biodegradation of difluoroacetate, 2,3,3,3-tetrafluoropropionic acid, and trifluoroacetate (124). Microbial degradation of chlorides involves different mechanisms based on four types of reactions: oxidation/reduction, hydrolysis, substitution, and elimination. Bacterial species with reported success in PFAS bioremediation include *Acidimicrobium sp.* and *Pseudomonas parafulva* (Table 4).

CONCLUSION

Physical, chemical, and biological methods are being explored to immobilise, eliminate, or degrade PFAS in the environment, and microbial remediation shows promise. It would be interesting to know how soil microbial bacteria adapted to PFAS can help in soil remediation, and especially how much PFAS they can take up and metabolise.

Another venue of action should involve more stringent regulations to minimise the use of PFAS and with it the threat it poses to the living organisms and humans.

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Conflicts of interest

None to declare.

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Djelovanje per- i polifluoroalkilnih tvari na okolišne i ljudske mikroorganizme i njihov potencijal za bioremedijaciju

Budući da se koriste u izradi raznih potrošačkih proizvoda, per- i polifluoroalkilne tvari (engl. *per- and polyfluoroalkyl substances*, krat. PFAS) veliki su zagađivači okoliša koji se nakupljaju u živim organizmima zbog svoje izrazite hidrofobnosti, lipofobnosti, otpornosti na toplinu i biološke nerazgradljivosti. Ovaj članak donosi sažeti pregled njihova djelovanja na populacije mikroba u tlu, vodnim i biogeokemijskim sustavima te na humanom mikrobiomu. Pojedini su mikrobi neosjetljivi na zagađenje PFAS-om, čak i napreduju, poput bakterije *Escherichia coli* i proteobakterija u tlu i vodi, a osjetljive su pojedine bakterijske vrste, poput rodova *Actinobacteria* i *Chloroflexi*, pa im se smanjuje populacija u takvom okruženju. Neke su se, pak, bakterije pokazale uspješnima u bioremedijaciji, poput vrsta *Acidimicrobium* sp. i *Pseudomonas parafuiva*.

KLJUČNE RIJEČI: bioremedijacija; mikrobiom; okoliš; PFAS; toksičnost