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Review Article

Microbiome Engineering for Detoxification of Polycyclic Aromatic Hydrocarbons (PAHs), Polychlorinated Biphenyls (PCBs), Pesticides, Dyes, Dioxins, Arsenic (As), Mercury(Hg), Lead (Pb), Cadmium(Cd), Chromium(Cr)(VI), Pharmaceuticals and Microplastics: Challenges and Future Directions

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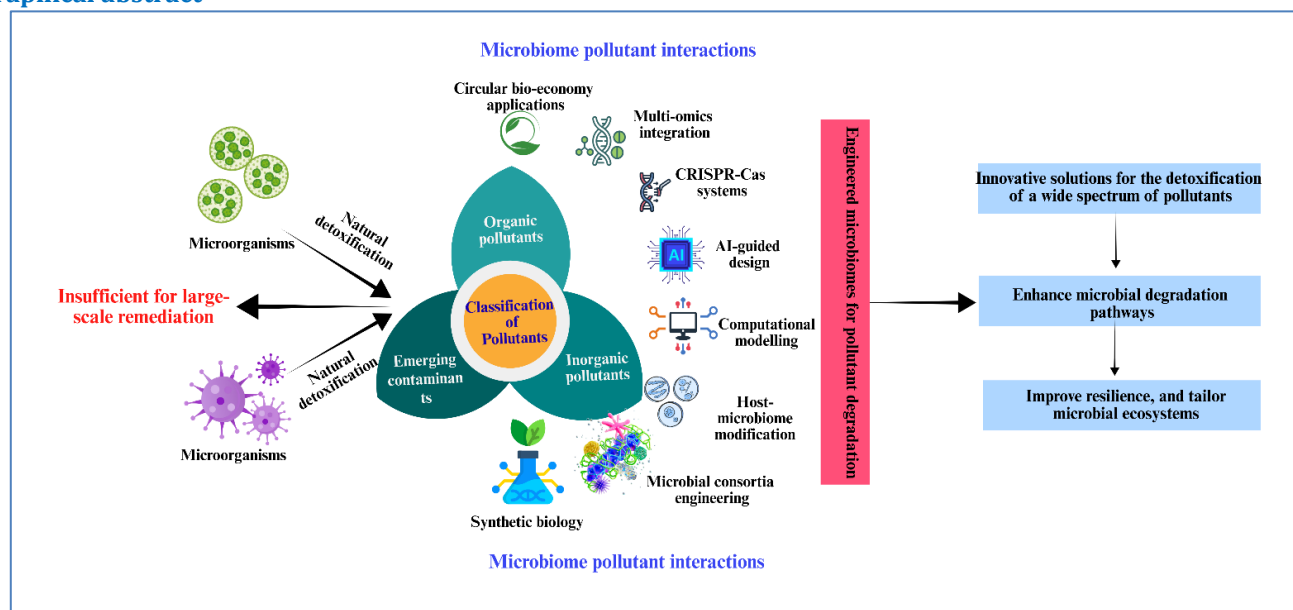
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Environmental pollution from hydrocarbons, heavy metals, plastics, pesticides, pharmaceuticals, and emerging contaminants poses severe ecological and public health risks. Microorganisms offer natural detoxification potential, yet their native capabilities are often insufficient for large-scale remediation. Advances in synthetic biology, microbial consortia engineering, host-microbiome modification, and computational modelling now allow the rational design of engineered microbiomes for pollutant degradation. This review synthesizes current knowledge on microbiome pollutant interactions, engineering strategies, case studies, and the associated ecological, regulatory, and technological challenges. Future directions, including AI-guided design, multi-omics integration, circular bio-economy applications, and human microbiome-based detoxification, are highlighted to provide a roadmap toward sustainable and safe environmental bioremediation

Keywords: Microbiome engineering, environmental pollutants, hydrocarbons, heavy metals, pesticides, pharmaceuticals

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Graphical abstract



Highlights:

- ✓ Microbiome engineering leverages natural microbial diversity to enhance detoxification of hydrocarbons, heavy metals, plastics, pesticides, pharmaceuticals, and emerging pollutants.
- ✓ Synthetic biology enables the design of microbes with novel catabolic pathways, optimized enzymes, and inducible degradation circuits.
- ✓ Engineered microbial consortia exploit division of labor and cross-feeding to achieve complete pollutant degradation.
- ✓ Host-associated microbiomes (plants, animals, humans) can be modified to detoxify environmental pollutants, expanding remediation beyond conventional ecosystems.
- ✓ Computational tools, multi-omics, and AI facilitate enzyme discovery, pathway optimization, and predictive modelling of microbial community behavior.
- ✓ Case studies demonstrate successful lab and pilot-scale applications, including hydrocarbon mineralization, plastic degradation, pesticide breakdown, and heavy metal sequestration.
- ✓ Key challenges include ecological risks, horizontal gene transfer, bio-containment, scalability, and regulatory and ethical considerations.
- ✓ Future directions focus on circular bio-economy integration, resilient synthetic ecosystems, AI-guided design, multi-omics integration, and microbiome-based human health interventions.

1. Introduction

Environmental pollution remains one of the most pressing global challenges of the 21st century, threatening ecosystem stability, biodiversity, and human health. Rapid industrialization, urbanization, and extensive use of chemicals in agriculture and manufacturing have led to the accumulation of a wide variety of pollutants, including heavy metals, pesticides, hydrocarbons, plastics, pharmaceuticals, and emerging contaminants such as per- and polyfluoroalkyl substances (PFAS). These compounds are often recalcitrant, persistent, and capable of bioaccumulation, resulting in long-term ecological damage and chronic human health risks ¹⁻³. Conventional physical and chemical methods for pollutant removal such as incineration, chemical neutralization, or adsorption are costly, energy-intensive, and frequently generate

harmful byproducts, highlighting the urgent need for more sustainable solutions ⁴. Microorganisms represent nature's most versatile detoxifiers, with metabolic pathways capable of transforming or mineralizing a wide range of xenobiotics and inorganic contaminants. Soil, aquatic, plant-associated, and host-associated microbiomes harbor enormous genetic and metabolic diversity that can be harnessed for pollutant detoxification. Natural biodegradation processes have been documented for hydrocarbons, pesticides, and heavy metals, yet the efficiency of native microbial communities is often insufficient for large-scale remediation ⁵⁻⁷. In this context, microbiome engineering, the deliberate modification of microbial communities or individual strains using synthetic biology, metabolic engineering, and systems biology approaches emerges as a powerful strategy to enhance the detoxification capacity of microbes and consortia ⁸⁻⁹. Recent advances in genome editing (e.g., CRISPR-Cas systems), high-throughput multi-omics, machine learning, and synthetic ecology provide unprecedented opportunities to design tailored microbial systems for pollutant remediation. Engineered strains can be equipped with novel catabolic pathways, designer enzymes, or biosorption mechanisms, while synthetic microbial consortia can exploit division of labor to achieve complex degradation processes. Furthermore, host-associated microbiome engineering (e.g., plants with engineered endophytes, or human gut microbiota designed to detoxify xenobiotics) extends the scope of environmental detoxification into both ecological and biomedical domains ¹⁰⁻¹². This review synthesizes current knowledge on microbiome engineering for detoxification of environmental pollutants. We begin by outlining the interactions between pollutants and microbial communities, then explore engineering approaches ranging from synthetic biology to computational design. Selected case studies illustrate successful applications, followed by discussion of ecological, regulatory, and bio-safety challenges. Finally, we highlight future directions at the interface of microbiome research, synthetic biology, and environmental biotechnology, envisioning a roadmap toward sustainable and safe pollutant detoxification strategies.

2. Environmental Pollutants and Microbial Interactions**2.1 Classification of Pollutants**

Environmental pollutants are chemically diverse, with varying persistence, bioavailability, and toxicity profiles. They can be broadly categorized into three main groups:

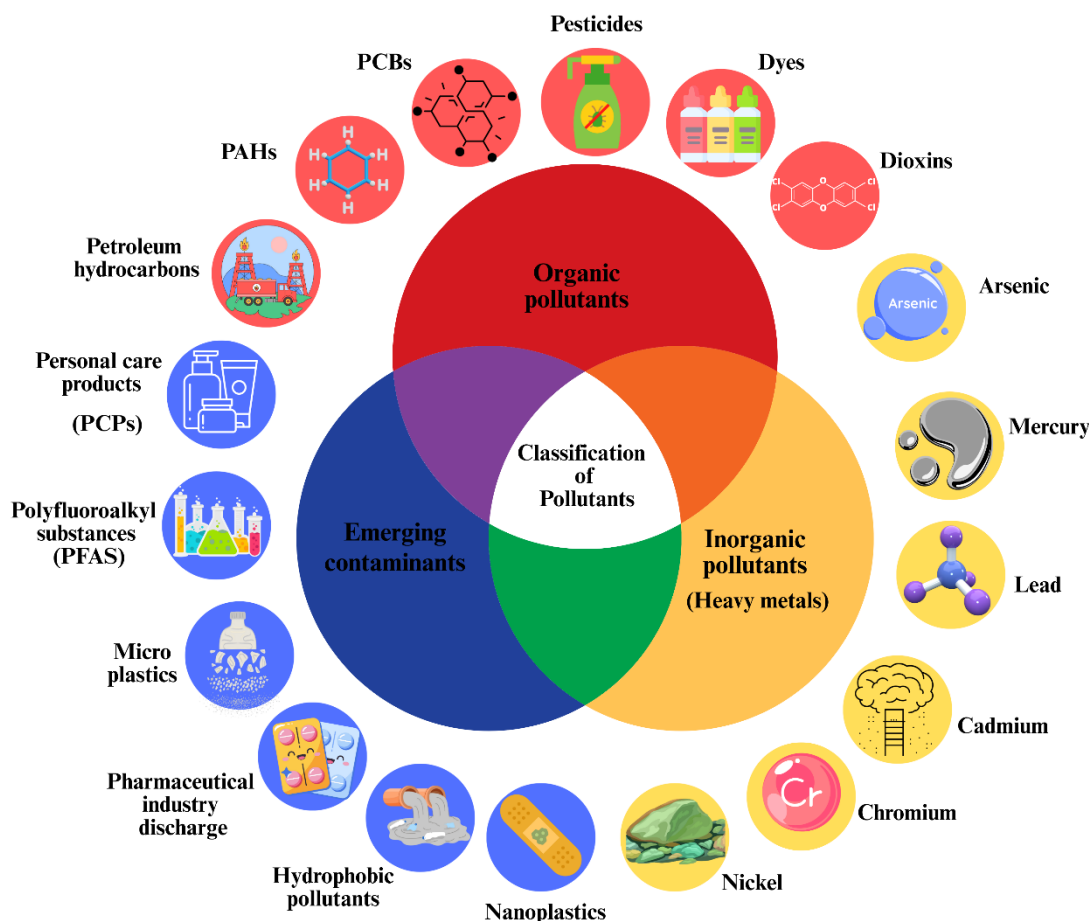


Figure 1: Classification of Pollutants

2.1.1. Organic pollutants- These pollutants include petroleum hydrocarbons, polycyclic aromatic hydrocarbons (PAHs), polychlorinated biphenyls (PCBs), pesticides, dyes, and dioxins, all of which pose significant environmental and health challenges due to their chemical persistence and resistance to natural degradation processes. Their high hydrophobicity promotes adsorption onto sediments and accumulation within aquatic and terrestrial biota, facilitating bio-magnification through food webs. Many of these compounds exhibit toxicological effects, including carcinogenicity, mutagenicity, and endocrine disruption, which can adversely affect both wildlife and human populations¹³. Additionally, their complex molecular structures, such as multiple fused aromatic rings in PAHs or halogen substitutions in PCBs, further impede microbial breakdown, necessitating specialized bioremediation strategies that exploit the metabolic versatility of environmental microorganisms to mitigate ecological and public health risk¹⁴.

2.1.2. Inorganic pollutants- Heavy metals, including arsenic (As), mercury (Hg), lead (Pb), cadmium (Cd), and chromium (Cr), represent a major class of persistent environmental contaminants due to their toxicity, non-degradability, and ability to bioaccumulate in living organisms. Unlike organic pollutants, metals cannot be mineralized or broken down into harmless constituents; instead, their environmental impact is

largely mitigated through microbial transformation processes that alter metal speciation, mobility, and bioavailability¹⁵. Microorganisms employ several mechanisms to detoxify metals, including enzymatic reduction (e.g., Cr (VI) to Cr(III)), methylation (e.g., conversion of inorganic Hg to methyl mercury or less toxic forms), intracellular sequestration via metallothioneins and metal-binding proteins, and biosorption onto extracellular polymeric substances. These microbial processes not only reduce metal toxicity but also influence their distribution in soils, sediments, and aquatic systems, thereby limiting ecological exposure. Harnessing these natural microbial capabilities through targeted microbiome engineering provides a promising approach for remediation of heavy metal-contaminated environments¹⁶.

2.1.3. Emerging contaminants- Emerging contaminants such as pharmaceuticals, personal care products (PCPs), per- and polyfluoroalkyl substances (PFAS), and micro plastics have become a growing concern due to their widespread presence, chemical persistence, and potential ecotoxicological effects¹⁷. These compounds are often structurally complex, containing multiple functional groups, halogen substitutions, or synthetic polymer backbones, which makes them highly resistant to conventional physical, chemical, and biological remediation methods. Pharmaceuticals and PCPs, including antibiotics,

analgesics, and synthetic hormones, can interfere with endocrine systems and promote the development of antimicrobial resistance. PFAS are highly stable fluorinated compounds known for bioaccumulation and long-range environmental transport, while microplastics can adsorb hydrophobic pollutants and act as vectors within aquatic and terrestrial ecosystems. Microbial degradation of these emerging contaminants is only beginning to be elucidated, with recent studies identifying enzymes capable of hydrolysis, oxidation, or depolymerization, highlighting the potential of harnessing specialized microbial communities for sustainable bioremediation strategies¹⁸.

2.2 Microbial Detoxification Mechanisms

Microorganisms interact with pollutants through several biochemical and physiological processes, many of which have been co-opted into engineered biodegradation strategies:

Biotransformation- Microorganisms detoxify hazardous environmental compounds by transforming them into less toxic or more bioavailable intermediates through a variety of enzymatic reactions, including oxidation, reduction, hydrolysis, and conjugation. Oxidative processes, often mediated by mono- and dioxygenases, introduce functional groups that increase substrate reactivity and solubility, facilitating further breakdown. Reductases participate in the transformation of halogenated or metal-containing compounds, lowering toxicity, while hydrolases catalyze the cleavage of ester, amide, or glycosidic bonds, enabling polymer or pesticide degradation. Conjugation reactions, such as glucuronidation or sulfation, further enhance excretion or sequestration. Collectively, these enzymes expand the metabolic repertoire of microbes, allowing them to degrade a wide range of xenobiotics and environmental pollutants¹⁹.

Mineralization- Certain microorganisms possess the metabolic capacity to fully mineralize environmental pollutants, converting them into innocuous end products such as carbon dioxide (CO₂), methane (CH₄), water (H₂O), and microbial biomass. This complete degradation, or mineralization, is particularly significant for hydrocarbons, polycyclic aromatic hydrocarbons (PAHs), and select pesticide compounds, where partial breakdown could otherwise generate toxic intermediates. Mineralization typically involves a coordinated sequence of enzymatic reactions, including oxidation, hydrolysis, and ring-cleavage pathways, often mediated by specialized oxygenases and hydrolases. By fully assimilating these compounds into central metabolic processes, microbes not only detoxify the environment but also contribute to nutrient cycling and the restoration of ecological balance.²⁰

Biosorption and bioaccumulation-Microorganisms employ biosorption and bioaccumulation mechanisms to immobilize, concentrate, or detoxify inorganic pollutants such as heavy metals and synthetic dyes. Cell wall components, including peptidoglycan, teichoic acids, and surface proteins, provide functional groups (e.g., carboxyl, phosphate, hydroxyl) that bind metal

ions through electrostatic interactions, chelation, or complexation. Extracellular polymeric substances (EPS) produced by biofilms further enhance pollutant sequestration by forming a hydrated matrix that traps contaminants and reduces their bioavailability. Additionally, intracellular sequestration systems, including metallothioneins, phytochelatins, and vacuolar compartments, actively store or detoxify metals, preventing cytotoxic effects. Collectively, these mechanisms allow microbes to mitigate inorganic pollution and maintain cellular homeostasis.²¹

Efflux and resistance systems- Native microbial communities frequently possess intrinsic resistance mechanisms, including efflux pumps, metal resistance genes, and detoxification operons, which enable them to survive and function in environments contaminated with otherwise toxic concentrations of pollutants. Efflux pumps actively expel toxic compounds from the cytoplasm, reducing intracellular accumulation, while metal resistance genes encode proteins that sequester, transform, or export heavy metals. Detoxification operons coordinate the expression of enzymes that metabolize or chemically modify xenobiotics. Through synthetic biology and metabolic engineering, these natural resistance systems can be optimized or introduced into other strains to enhance pollutant tolerance, degradation efficiency, and overall bioremediation potential in contaminated ecosystems²².

2.3 Microbiome-Pollutant Interactions in Different Ecosystems

Pollutant-microbiome interactions vary depending on the environmental niche, reflecting both selective pressures and available metabolic pathways:

2.3.1. Soil microbiomes-Soil hosts diverse microbial communities, including *Pseudomonas*, *Rhodococcus*, and *Mycobacterium*, which degrade hydrocarbons, pesticides, and polyaromatic compounds. Rhizosphere microbiomes also play a role in pollutant detoxification by synergizing with plant metabolism²³.

2.3.2. Aquatic microbiomes-Freshwater and marine microbes such as *Alcanivorax*, *Cycloclasticus*, and *cyanobacteria* contribute to degradation of oil spills, plastics, and pharmaceutical residues. Biofilm formation on surfaces such as microplastics further shapes pollutant-microbiome interactions²⁴.

2.3.3. Plant-associated microbiomes-Endophytic and rhizospheric microbes metabolize pesticides and heavy metals, sometimes transferring detoxified compounds into plants or protecting plant hosts from toxicity. Engineered endophytes hold promise for phytoremediation²⁵.

2.3.4. Host-associated microbiomes-Human and animal microbiotas are increasingly recognized as mediators of xenobiotic metabolism. Gut microbes can metabolize pharmaceuticals, endocrine disruptors, and dietary toxins, influencing host exposure and toxicity²⁶. This raises prospects for engineering probiotics as living therapeutics for pollutant exposure mitigation.

3. Microbiome Engineering Approaches

Engineering microbiomes for environmental detoxification integrates tools from synthetic biology, metabolic engineering, microbial ecology, and computational biology. The goal is to enhance or introduce metabolic pathways, optimize community dynamics, and ensure stable, safe deployment in diverse ecosystems.

3.1 Synthetic Biology and Metabolic Pathway Engineering

Synthetic biology allows precise introduction and optimization of catabolic pathways that microbes lack in their native genomes.

3.1.1. Gene editing tools- CRISPR-Cas systems, recombineering, and transposon mutagenesis enable rapid and precise integration of xenobiotic-degrading genes into microbial hosts. Engineered *E. coli* and *Pseudomonas* strains expressing enzymes such as organophosphate hydrolases, haloalkane dehalogenases, and oxygenases exemplify the power of targeted pathway insertion, facilitating efficient pollutant breakdown and advancing bioremediation strategies for diverse environmental contaminants.²⁷

3.1.2. Pathway assembly and optimization- Modular pathway construction using standardized biological parts, including promoters, ribosome binding sites, and regulatory circuits, enables precise fine-tuning of pollutant degradation kinetics in engineered microbes. Dynamic metabolic control strategies, such as inducible promoters that activate only in response to pollutant presence, help minimize unnecessary protein expression, thereby reducing metabolic burden and enhancing cell viability while maintaining efficient and targeted biodegradation performance in contaminated environments.²⁸

3.1.3. Designer enzymes- Directed evolution and computational protein design enable expansion of substrate specificity and catalytic efficiency in enzymes such as PETases for plastic degradation, peroxidases for dye detoxification, and reductases for metal reduction. These optimized enzymes can be expressed either in native degraders or heterologous microbial hosts, significantly enhancing degradation capacity and broadening the range of environmental pollutants that can be efficiently targeted for bioremediation.²⁹

3.2 Microbial Consortia Engineering

No single organism can efficiently degrade all pollutants; instead, synthetic consortia leverage metabolic complementarity:

3.2.1. Division of labor- Different microbes often specialize in sequential steps of pollutant degradation, working together in synergistic consortia. For instance, one bacterial strain may oxidize a hydrocarbon into a less complex intermediate, which another strain further metabolizes and ultimately mineralizes into CO₂ and water. Such division of labor enhances degradation efficiency, supports metabolic diversity, and allows microbial communities to tackle complex or recalcitrant

environmental contaminants more effectively than single strains alone.³⁰

3.2.2. Cross-feeding and syntrophy- Exchange of metabolites between microbial species promotes the completion of complex degradation pathways, where intermediates produced by one organism become substrates for another. To enhance stability and coordination, engineered communication modules such as quorum sensing circuits can be introduced, allowing microbes to synchronize metabolic activities. This cooperative interaction improves pathway efficiency, reduces competition, and ensures robust performance of synthetic consortia in environmental bioremediation applications.³¹

3.2.3. Resilience and adaptability- Synthetic microbial communities can be rationally designed to withstand environmental fluctuations such as changes in temperature, pH, or nutrient availability, thereby enhancing stability and reliability during field applications. Using modular design principles, consortia can be tailored to degrade specific pollutants or adapt to mixed contaminant sites, ensuring flexible and robust biodegradation strategies that are more effective than single-species systems in real-world environmental remediation scenarios.³²

3.3 Engineered Mobile Genetic Elements

Horizontal gene transfer (HGT) is a key mechanism driving microbial adaptation to environmental pollutants, and engineering mobile genetic elements can be used to accelerate the dissemination of degradation capabilities. Plasmids and phagemids carrying pollutant-degrading operons, such as those for hydrocarbons or pesticides, can be introduced into native microbial communities, while conjugative transfer systems facilitate in situ spread of catabolic functions, thereby enhancing the pollutant resilience of indigenous microbiota³³. Additionally, engineered phages capable of delivering degradation genes or regulatory circuits represent an emerging strategy that combines targeted genetic delivery with built-in ecological safety controls³⁴.

3.4 Host-Microbiome Engineering

Pollutant detoxification can be enhanced by engineering microbiomes associated with plants, animals, or humans:

3.4.1. Plant-microbe systems- Engineered rhizobacteria or endophytes play a crucial role in enhancing phytoremediation by expressing pollutant-degrading genes such as atrazine hydrolase, arsenate reductase, and other catabolic enzymes. These microbes colonize plant roots or internal tissues, directly breaking down toxic compounds while also promoting plant growth and stress tolerance. By improving pollutant bioavailability, detoxification, and uptake, such microbial partnerships significantly increase the efficiency, sustainability, and scope of phytoremediation strategies for contaminated environments.³⁵

3.4.2. Animal microbiomes- Gut microbes engineered for metal sequestration or pesticide degradation offer a

promising strategy to reduce pollutant toxicity in livestock exposed through contaminated feed. By incorporating genes that enable binding, transformation, or breakdown of harmful compounds, these microbes can neutralize toxicants directly within the gastrointestinal tract. This not only safeguards animal health and productivity but also minimizes the risk of pollutant residues entering the food chain, thereby enhancing food safety and environmental sustainability.³⁶

3.4.3. Human probiotics- Synthetic probiotics with specialized detoxification functions are emerging as innovative tools to combat pollutant-induced diseases. Engineered to bind heavy metals, degrade pesticides, or metabolize xenobiotics, these probiotics can actively reduce toxic burdens within the host. By restoring gut microbiome balance and neutralizing harmful compounds, they offer dual benefits of health protection and pollutant detoxification. Such interventions hold great potential for preventive medicine, food safety, and mitigating environmental toxin exposure in both humans and animals.³⁷

3.5 Computational Tools for Microbiome Design

Advances in computational biology accelerate rational design of engineered microbiomes:

3.5.1. Genome-scale metabolic models (GEMs)- Predicting pollutant degradation pathways and flux distributions in engineered microbes and microbial communities involves using metabolic modelling, genome-scale reconstructions, and systems biology tools. These approaches identify optimal enzyme networks, assess metabolic trade-offs, and guide genetic modifications, enabling efficient pollutant breakdown and resource utilization for enhanced bioremediation strategies.³⁸

3.5.2. Multi-omics integration- Metagenomics, transcriptomics, and metabolomics provide comprehensive insights into how microbes interact with pollutants at genetic, functional, and metabolic levels. These approaches uncover active microbial taxa, stress responses, and metabolic shifts, while also identifying novel pollutant-degrading enzymes. Such data guide enzyme engineering and synthetic biology strategies for targeted bioremediation.³⁹

3.5.3. Machine learning and AI- Predicting enzyme-substrate interactions, optimizing synthetic pathways, and modeling microbial consortia dynamics are essential for advancing pollutant biodegradation. Computational approaches, particularly deep learning, enable accurate predictions of enzyme specificity, activity, and stability. By analyzing large-scale metagenomics datasets, these tools accelerate the discovery of novel bio-degradative enzymes and guide rational engineering. Combined with pathway optimization, they facilitate the design of efficient microbial systems and consortia tailored for enhanced bioremediation of diverse environmental contaminants.

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3.5.4. Microbiome-pollutant interaction networks- Systems biology frameworks integrate multi-omics data to map functional interactions among microbial species, metabolic pathways, and environmental factors. By revealing synergistic relationships and complementary metabolic capabilities, these frameworks guide the rational selection of microbial partners for synthetic consortia design. This approach ensures optimized pollutant degradation, stability, and resilience of the community. Ultimately, systems biology enables the construction of tailored microbial consortia with enhanced efficiency for bioremediation and sustainable environmental management.⁴¹

4. Case Studies in Microbiome Engineering for Detoxification

Case studies illustrate how engineered microbes and synthetic consortia can transform pollutant detoxification from concept to proof-of-principle applications. These examples demonstrate both the opportunities and technical challenges of microbiome engineering.

4.1 Hydrocarbon Degradation

Petroleum hydrocarbons, including alkanes, aromatics, and PAHs, are major environmental pollutants from oil spills and industrial waste.

4.1.1. Engineered *Pseudomonas* strains- *Pseudomonas putida* has been genetically engineered to enhance the degradation of polycyclic aromatic hydrocarbons (PAHs) by incorporating extended alkane monooxygenase and dioxygenase pathways, enabling more efficient breakdown of complex hydrocarbon pollutants. Additionally, synthetic regulatory circuits have been designed to couple catabolic gene expression directly to pollutant detection, ensuring that degradation pathways are activated only in the presence of contaminants. This strategy improves overall bioremediation efficiency while reducing unnecessary metabolic burden on the host cells.⁴²

4.1.2. Marine consortia enhancement- Hydrocarbon-degrading bacteria, including *Alcanivorax* and *Cycloclasticus*, naturally dominate oil-contaminated seawater, playing a key role in breaking down petroleum compounds. Engineering microbial consortia by incorporating bio-surfactant-producing strains further enhances this process by increasing the solubility and bioavailability of hydrophobic hydrocarbons. These tailored communities facilitate faster uptake and metabolism of pollutants, significantly accelerating overall biodegradation rates and improving the efficiency and effectiveness of bioremediation strategies in marine oil spill environments.⁴³

4.2 Heavy Metal Detoxification

Heavy metals are non-degradable but can be transformed into less toxic or less bio-available forms.

4.2.1. Mercury detoxification- Engineered *E. coli* expressing the *merA* gene, which encodes mercuric reductase, efficiently converts toxic ionic mercury (Hg^{2+}) into volatile elemental mercury (Hg^0), a less

bioavailable and less harmful form. By coupling merA expression with metallothioneins, the cells first sequester mercury intracellularly, concentrating the metal for more effective reduction. This dual strategy enhances mercury detoxification, minimizes environmental bioavailability, and offers a promising approach for bioremediation of mercury-contaminated sites.⁴⁴

4.2.2. Arsenic and cadmium biosorption- Cyanobacteria engineered to overproduce extracellular polymeric substances (EPS) demonstrate a significantly enhanced ability to immobilize toxic metals such as arsenic and cadmium. The abundant EPS matrix provides numerous functional groups, including carboxyl, hydroxyl, and phosphate moieties, which act as binding sites for metal ions. By facilitating biosorption at the cell surface, this strategy reduces metal bioavailability, mitigates environmental toxicity, and offers a sustainable, biologically driven approach for heavy metal remediation in contaminated aquatic and soil ecosystems.⁴⁵

4.2.3. Chromium reduction- *Shewanella oneidensis* engineered with optimized and enhanced electron transport chains exhibits significantly improved reduction of toxic hexa-valent chromium (Cr^{6+}) to the less harmful trivalent form (Cr^{3+}). By boosting electron transfer efficiency, these engineered strains accelerate chromium detoxification and increase overall bioremediation capacity. This approach demonstrates substantial potential for practical applications in wastewater treatment, offering an effective, biologically driven method to mitigate heavy metal pollution and protect both environmental and human health.⁴⁶

4.3 Plastic and Micro-plastic Degradation

Plastic pollution is one of the most persistent global challenges.

4.3.1. PET degradation- The discovery of *Ideonellasakaiensis* PETase sparked extensive research into enzyme-based plastic degradation. Through directed evolution, researchers developed “fast PETases” with enhanced thermo stability and catalytic efficiency, capable of more rapid polyethylene terephthalate (PET) hydrolysis. Co-expression of PETase and MHETase in microbial hosts such as *Pseudomonas* and *Bacillus subtilis* enabled complete breakdown of PET into its monomers, terephthalic acid and ethylene glycol. This approach not only improves enzymatic plastic recycling but also offers a sustainable, biologically driven solution for mitigating plastic pollution.⁴⁷

4.3.2. Polyolefin degradation- Synthetic consortia combining oxidative bacteria (producing hydroxyl radicals to initiate breakdown) with hydrocarbon degraders showed enhanced polyethylene degradation. Such division-of-labor strategies mimic natural plastic-degrading microbiomes but with engineered efficiency.⁴⁸

4.3.3. Microplastic colonization- Engineered bio-film-forming bacteria expressing plastic-binding proteins

have shown enhanced ability to colonize micro plastic surfaces, creating stable microbial communities directly at the pollutant interface. This close physical association accelerates enzyme-substrate interactions, thereby improving degradation rates. By promoting localized activity and sustained bio-film growth, such strategies offer promising avenues for addressing the persistence of micro plastics in aquatic and terrestrial environments through more efficient and targeted biodegradation.⁴⁹

4.4 Pesticide and Herbicide Detoxification

Agricultural runoff contributes large amounts of toxic and persistent pesticides.

4.4.1. Organophosphate hydrolases- *E. coli* and *Pseudomonas* strains engineered with organophosphate hydrolase (OPH) demonstrated efficient degradation of toxic organophosphate pesticides such as parathion and chlorpyrifos. Further advancements involved fusing OPH with surface display proteins, enabling the creation of robust whole-cell biocatalysts. These engineered microbes provide practical solutions for field applications, offering scalable, reusable, and environmentally friendly approaches to detoxify contaminated soils and water systems.⁵⁰

4.4.2. Atrazine degradation- Synthetic operons carrying the *atzA*, *atzB*, and *atzC* genes have been constructed in engineered bacteria, enabling complete mineralization of the herbicide atrazine. While natural microbial strains often stall at partial degradation intermediates, these engineered operons overcome such bottlenecks by ensuring a seamless enzymatic pathway. This approach provides an efficient and reliable strategy for eliminating persistent herbicide residues from agricultural soils and water systems, supporting sustainable bioremediation efforts.⁵¹

4.4.3. Glyphosate biotransformation- Engineered microbes expressing glyphosate oxidoreductase (GOX) and C-P lyase enzymes have been developed to tackle the challenges of widespread glyphosate contamination. GOX initiates the breakdown of glyphosate into aminomethylphosphonic acid (AMPA), while C-P lyase further cleaves the stable carbon-phosphorus bond, converting it into less toxic, environmentally benign products. This dual-enzyme strategy enhances degradation efficiency and offers a promising bioremediation approach for agricultural soils and water systems heavily impacted by herbicide use.⁵²

4.5 Emerging Pollutants

Recent focus has shifted toward pollutants previously considered recalcitrant or unmanageable.

4.5.1. PFAS degradation- Engineered oxidative enzymes, including peroxidases and laccases, when combined with electroactive microbes, have demonstrated partial defluorination of per- and polyfluoroalkyl substances (PFAS), which are among the most chemically stable and persistent environmental pollutants. This synergistic approach leverages enzymatic oxidation alongside microbial electron transfer to break strong carbon-fluorine bonds, offering a promising strategy for mitigating PFAS contamination

in water and soil, and advancing the development of sustainable remediation technologies for these challenging pollutants.⁵³

4.5.2. Pharmaceutical residues: Synthetic microbial consortia engineered for hospital wastewater treatment have effectively degraded persistent pharmaceutical pollutants, including antibiotics like ciprofloxacin and carbamazepine. Incorporation of engineered quorum sensing modules allowed the consortia to maintain coordinated activity and structural stability, even under fluctuating pollutant loads and environmental conditions. This design enhances degradation efficiency, ensures robust performance, and offers a scalable, targeted approach for mitigating the impact of pharmaceutical contaminants in complex wastewater systems.⁵⁴

4.5.3. Endocrine disruptors: *Saccharomyces cerevisiae* engineered to express mammalian cytochrome P450 enzymes successfully bio-transformed endocrine-disrupting chemicals such as bisphenol A (BPA) and nonylphenol. This cross-kingdom metabolic engineering approach illustrates the potential of yeast as a versatile platform for xenobiotic degradation, enabling the integration of complex mammalian metabolic pathways into microbial hosts. Such strategies expand the toolkit for bioremediation of persistent organic pollutants in diverse environmental settings.⁵⁵

5. Challenges and Limitations

Despite significant progress, the deployment of engineered microbiomes for pollutant detoxification faces substantial scientific, ecological, and regulatory hurdles. These challenges must be addressed before large-scale or in situ applications can become feasible.

5.1 Ecological Risks

The introduction of engineered microbes into natural ecosystems carries potential ecological consequences:

5.1.1. Horizontal gene transfer (HGT): The release of engineered microbes carrying catabolic genes carries the risk of horizontal gene transfer to unintended microbial species. Such gene dissemination could disrupt native microbial communities, altering ecological balance and nutrient cycles, or create unforeseen interactions that may affect ecosystem stability. Careful risk assessment, containment strategies, and genetic safeguards are therefore essential to minimize ecological impact while harnessing the benefits of engineered biodegradation pathways in environmental applications.⁵⁶

5.1.2. Competition with native microbiota: Introduced engineered microbial strains may outcompete native microbial populations, potentially destabilizing established community structures and reducing overall ecosystem resilience. This competitive dominance can lead to decreased biodiversity, loss of functional redundancy, and impaired ecosystem services such as nutrient cycling and pollutant degradation. Careful evaluation of ecological compatibility, along with strategies to limit proliferation or contain engineered strains, is crucial to ensure that

bioremediation efforts do not inadvertently harm environmental stability⁵⁷.

5.1.3. Trophic cascades and ecosystem impact: Manipulating pollutant concentrations through microbial or chemical remediation can have cascading effects across ecosystems, indirectly impacting higher trophic levels. Changes in pollutant availability may alter food web dynamics, affect the health and reproductive success of plants and animals, and influence human exposure to residual or transformed contaminants. Careful ecological assessment is therefore essential to anticipate and mitigate potential unintended consequences while implementing bioremediation or pollutant management strategies⁵⁸.

5.2 Bio-containment Strategies

To mitigate ecological risks, robust containment systems are required:

5.2.1. Kill-switches: Synthetic genetic circuits designed to induce cell death under defined conditions, such as the absence of a supplied synthetic nutrient, provide an effective bio containment strategy for engineered microbes. These “kill-switch” systems prevent uncontrolled proliferation in natural environments, minimizing ecological risks. By ensuring that engineered strains survive only under controlled conditions, such circuits enhance the safety and regulatory compliance of bioremediation and other environmental applications involving genetically modified microorganisms.⁵⁹

5.2.2. Synthetic auxotrophy: Engineering microbes to require non-natural amino acids or synthetic nutrients for growth creates a built-in dependency that confines their survival to controlled environments. This metabolic restriction acts as a safety mechanism, preventing engineered strains from persisting or spreading in natural ecosystems. By linking viability to externally supplied compounds, such strategies enhance biocontainment, reduce ecological risks, and allow safer deployment of genetically modified microbes in bioremediation, industrial biotechnology, and other environmental applications.⁶⁰

5.2.3. Genetic firewalls: Recoding entire microbial genomes to incorporate non-standard codons or synthetic genetic elements can drastically reduce the potential for horizontal gene transfer (HGT) and limit compatibility with natural organisms. This genome-scale engineering enhances biocontainment by preventing unintended gene flow, reducing ecological risks, and increasing bio-safety. Such strategies provide robust safeguards for deploying engineered microbes in environmental or industrial applications, ensuring that synthetic strains remain confined and controllable within designated operational settings.⁶¹

Although promising, these strategies often face stability issues in fluctuating environments, underscoring the need for further refinement.

5.3. Scale-Up and Field Deployment

Moving from laboratory studies to real-world applications introduces new challenges:

5.3.1. Environmental variability: Environmental fluctuations in temperature, pH, oxygen availability, and pollutant concentrations can significantly impair the performance of engineered microbial functions. Such stresses may reduce enzyme activity, disrupt metabolic pathways, or compromise cell viability, leading to decreased degradation efficiency and inconsistent bioremediation outcomes. Designing robust strains with stress-tolerant traits or incorporating dynamic regulatory systems is therefore essential to maintain reliable function and resilience in variable and often unpredictable environmental conditions.⁶²

5.3.2. Delivery and survival: Maintaining long-term persistence and functional activity of engineered microbes in soil, water, or host-associated environments continues to be a significant challenge. Environmental stresses, nutrient limitations, competition with native microbiota, and predation can all reduce microbial survival and metabolic performance over time. Developing strategies such as protective bio-films, stress-resistant strains, or adaptive regulatory circuits is essential to sustain degradation activity and ensure the effectiveness of engineered microbes in real-world bioremediation and ecological applications.⁶³

5.3.3. Bioreactor vs. in situ approaches: Closed bioreactors provide a controlled environment for precise pollutant treatment, allowing regulation of factors such as temperature, pH, and microbial activity to maximize degradation efficiency. In contrast, in situ field applications enable treatment across larger and more dispersed contaminated sites, offering broader environmental reach. However, these open systems are subject to unpredictable conditions, fluctuating pollutant loads, and microbial competition, which can reduce stability and overall effectiveness compared with controlled bioreactor settings.⁶⁴

5.4 Regulatory and Ethical Considerations

The release of engineered microbiomes into open environments raises complex legal and societal challenges. Most countries currently lack specific regulatory frameworks for microbiome engineering, relying instead on general genetically modified organism (GMO) guidelines to ensure bio-safety⁶⁵. In addition, bio-security risks associated with the potential misuse of engineered microbes for harmful purposes necessitate robust oversight and monitoring⁶⁶. Public acceptance also remains a critical factor, as environmental release of engineered organisms may encounter resistance due to perceived ecological risks and ethical concerns, highlighting the need for transparent communication and active stakeholder engagement⁶⁷.

6. Future Directions

Microbiome engineering for pollutant detoxification is still in its early stages, but emerging technologies and conceptual frameworks are enabling scalable, safe, and multifunctional applications by integrating synthetic biology, computational modelling, and ecological principles. Coupling detoxification with resource

recovery aligns with circular bio-economy principles, as engineered microbes can up-cycle pollutants by transforming plastics into monomers, hydrocarbons into bio-fuels, or industrial waste into platform chemicals⁶⁸, produce value-added bio-products such as biodegradable polymers or specialty chemicals, and utilize waste streams from agriculture or petrochemical industries as feed stocks to close material loops⁶⁹⁻⁷⁰. A comprehensive understanding of microbiome-pollutant interactions requires multi-omics approaches, including metagenomics to uncover novel degradation genes and uncultured microbes, metatranscriptomics and proteomics to monitor real-time microbial responses under pollutant stress, metabolomics to map transformation products and evaluate pathway completeness, and systems biology frameworks to model degradation across microbial communities, bridging lab-scale findings to environmental contexts⁷¹. Artificial intelligence (AI) and machine learning accelerate biodegradation system design by predicting enzyme-substrate interactions for enzyme discovery, optimizing metabolic pathways to balance fluxes and reduce by products, and modelling interspecies interactions to design stable synthetic consortia⁷². Engineering synthetic ecosystems enhances resilience through self-regulating consortia that adjust catabolic activity via quorum sensing, ecological scaffolds such as bio-films or encapsulated matrices to improve survival and containment, and adaptive evolution strategies combined with computational design to maintain stability under fluctuating pollutant loads⁷³. Beyond environmental applications, microbiome engineering addresses public health challenges by designing gut microbiomes and engineered probiotics capable of binding heavy metals, degrading dietary toxins, or metabolizing xenobiotics to reduce systemic toxicity, developing preventive bio-therapeutics to protect vulnerable populations from long-term pollutant exposure, and employing multi-omics-guided personalized interventions for individualized detoxification strategies⁷⁴.

7. Conclusion

Microbiome engineering represents a transformative frontier in environmental biotechnology, offering innovative solutions for the detoxification of a wide spectrum of pollutants, from hydrocarbons and heavy metals to plastics and emerging contaminants. Natural microbial communities provide an invaluable foundation, but their intrinsic capacities are often insufficient for large-scale remediation. By leveraging synthetic biology, consortia design, computational modelling, and host-associated microbiome engineering, it is now possible to enhance microbial degradation pathways, improve resilience, and tailor microbial ecosystems for specific pollutants. The case studies reviewed herein illustrate both the promise and current limitations of engineered microbiomes. Laboratory and pilot-scale applications demonstrate substantial gains in pollutant degradation efficiency; however, challenges such as ecological risks, bio-containment, scalability, and regulatory uncertainties remain critical barriers to real-world implementation. Addressing these challenges

requires a combination of robust bio-safety frameworks, adaptive engineering strategies, and interdisciplinary collaboration across microbiology, systems biology, synthetic biology, environmental science, and policy. Looking forward, the integration of multi-omics, artificial intelligence, and circular bio-economy principles will enable microbiome engineering to move beyond pollutant removal toward sustainable and value-added solutions. Host-associated microbiomes, including human and plant systems, provide new frontiers for protective and preventive applications. With careful design, rigorous testing, and responsible governance, microbiome engineering holds the potential to mitigate environmental pollution at scale while contributing to human health, ecosystem resilience, and sustainable development.

List of abbreviations:

AI: Artificial intelligence

AMPA: Aminomethylphosphonic acid

As: Arsenic

BPA: Bisphenol A

Cd: Cadmium

Cr: Chromium

CRISPR-Cas: Clustered Regularly Interspaced Short Palindromic Repeats- Cas enzymes

EPS: Extracellular polymeric substances

GEMs: Genome-scale metabolic models

GOX: Glyphosate oxidoreductase

Hg: Mercury

HGT : Horizontal gene transfer

HGT: Horizontal gene transfer

OPH: Organophosphate hydrolase

PAHs: Polycyclic aromatic hydrocarbons

Pb: Lead

PCBs: Polychlorinated biphenyls

PCPs: Personal care products

PET: Polyethylene terephthalate

PFAS: Polyfluoroalkyl substances

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References:

1. Kolawole AS, Iyiola AO. Environmental pollution: threats, impact on biodiversity, and protection strategies. In Sustainable utilization and conservation of Africa's biological resources and environment 2023 Apr 18 (pp. 377-409). Singapore: Springer Nature Singapore. https://doi.org/10.1007/978-981-19-6974-4_14
2. Saxena V. Water quality, air pollution, and climate change: investigating the environmental impacts of industrialization and urbanization. Water, Air, & Soil Pollution. 2025 Feb; 236(2):73. <https://doi.org/10.1007/s11270-024-07702-4>
3. Padhiary M, Kumar R. Assessing the environmental impacts of agriculture, industrial operations, and mining on agro-ecosystems. In Smart internet of things for environment and healthcare 2024 Oct 22 (pp. 107-126). Cham: Springer Nature Switzerland. https://doi.org/10.1007/978-3-031-70102-3_8
4. Shafi'i AM, Raghav S, Shuaibu AM, Abdurrahman I, Raghav J, Sharma N. Toxicity Reduction in Waste: Chemical Methods and Strategies. In Waste Management for Smart Cities 2024 Dec 19 (pp. 185-201). Singapore: Springer Nature Singapore. https://doi.org/10.1007/978-981-97-8253-6_10
5. Rosenberg E. Holistic fitness: microbiomes are part of the holobiont's fitness. In Microbiomes: current knowledge and unanswered questions 2021 Mar 3 (pp. 101-160). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-030-65317-0_4
6. Saleem M. Global microbiome for agroecology, industry, and human well-being: opportunities and challenges in climate change. Microbiome Community Ecology: Fundamentals and Applications. 2015 Jan 21:125-52. https://doi.org/10.1007/978-3-319-11665-5_6
7. Chen M, Xu P, Zeng G, Yang C, Huang D, Zhang J. Bioremediation of soils contaminated with polycyclic aromatic hydrocarbons, petroleum, pesticides, chlorophenols and heavy metals by composting: applications, microbes and future research needs. Biotechnology advances. 2015 Nov 1; 33(6):745-55. <https://doi.org/10.1016/j.biotechadv.2015.05.003>
8. Leggieri PA, Liu Y, Hayes M, Connors B, Seppälä S, O'Malley MA, Venturelli OS. Integrating systems and synthetic biology to understand and engineer microbiomes. Annual Review of Biomedical Engineering. 2021 Jul 13; 23(1):169-201. <https://doi.org/10.1146/annurev-bioeng-082120-022836>

9. Bober JR, Beisel CL, Nair NU. Synthetic biology approaches to engineer probiotics and members of the human microbiota for biomedical applications. *Annual review of biomedical engineering*. 2018 Jun 4; 20(1):277-300. <https://doi.org/10.1146/annurev-bioeng-062117-121019>
10. Gallo G, Puopolo R, Carbonaro M, Maresca E, Fiorentino G. Extremophiles, a nifty tool to face environmental pollution: from exploitation of metabolism to genome engineering. *International journal of environmental research and public health*. 2021 May 14; 18(10):5228. <https://doi.org/10.3390/ijerph18105228>
11. Roell GW, Zha J, Carr RR, Koffas MA, Fong SS, Tang YJ. Engineering microbial consortia by division of labor. *Microbial cell factories*. 2019 Feb 8; 18(1):35. <https://doi.org/10.1186/s12934-019-1083-3>
12. Bai X, Huang Z, Duraj-Thatte AM, Ebert MP, Zhang F, Burgermeister E, Liu X, Scott BM, Li G, Zuo T. Engineering the gut microbiome. *Nature Reviews Bioengineering*. 2023 Sep; 1(9):665-79. <https://doi.org/10.1038/s44222-023-00072-2>
13. Song YF, Wilke BM, Song XY, Gong P, Zhou QX, Yang GF. Polycyclic aromatic hydrocarbons (PAHs), polychlorinated biphenyls (PCBs) and heavy metals (HMs) as well as their genotoxicity in soil after long-term wastewater irrigation. *Chemosphere*. 2006 Dec 1; 65(10):1859-68. <https://doi.org/10.1016/j.chemosphere.2006.03.076>
14. Siddiqui JA, Khan MM, Bamisile BS, Hafeez M, Qasim M, Rasheed MT, Rasheed MA, Ahmad S, Shahid MI, Xu Y. Role of insect gut microbiota in pesticide degradation: a review. *Frontiers in microbiology*. 2022 May 3; 13:870462. <https://doi.org/10.3389/fmicb.2022.870462>
15. Rahman Z, Singh VP. The relative impact of toxic heavy metals (THMs)(arsenic (As), cadmium (Cd), chromium (Cr)(VI), mercury (Hg), and lead (Pb)) on the total environment: an overview. *Environmental monitoring and assessment*. 2019 Jul; 191(7):419. <https://doi.org/10.1007/s10661-019-7528-7>
16. Olaniran AO, Balgobind A, Pillay B. Bioavailability of heavy metals in soil: impact on microbial biodegradation of organic compounds and possible improvement strategies. *International journal of molecular sciences*. 2013 May 15;14(5):10197-228. <https://doi.org/10.3390/ijms140510197>
17. Kumar A, Kumar A, Seema K, Kumari K. Detection and Remediation Techniques for Emerging Contaminants. In *Emerging Contaminants in Water and Wastewater: Sources and Substances* 2025 Feb 10 (pp. 223-253). Cham: Springer Nature Switzerland. https://doi.org/10.1007/978-3-031-82579-8_10
18. Kumar M, Mazumder P, Silori R, Manna S, Panday DP, Das N, Sethy SK, Kuroda K, Mahapatra DM, Mahlknecht J, Tyagi VK. Prevalence of pharmaceuticals and personal care products, microplastics and co-infecting microbes in the post-COVID-19 era and its implications on antimicrobial resistance and potential endocrine disruptive effects. *Science of The Total Environment*. 2023 Dec 15;904:166419. <https://doi.org/10.1016/j.scitotenv.2023.166419>
19. Pazmino DT, Winkler M, Glieder A, Fraaije MW. Monooxygenases as biocatalysts: classification, mechanistic aspects and biotechnological applications. *Journal of biotechnology*. 2010 Mar 1; 146(1-2):9-24. <https://doi.org/10.1016/j.jbiotec.2010.01.021>
20. Gupta A, Gupta R, Singh RL. Microbes and environment. In *Principles and applications of environmental biotechnology for a sustainable future* 2016 Oct 15 (pp. 43-84). https://doi.org/10.1007/978-981-10-1866-4_3
21. Atmakuri A, Yadav B, Tiwari B, Drogui P, Tyagi RD, Wong JW. Nature's architects: a comprehensive review of extracellular polymeric substances and their diverse applications. *Waste Disposal & Sustainable Energy*. 2024 Dec; 6(4):529-51. <https://doi.org/10.1007/s42768-024-00205-2>
22. Nguyen TH, Nguyen HD, Le MH, Nguyen TT, Nguyen TD, Nguyen DL, Nguyen QH, Nguyen TK, Michalet S, Dijoux-Franca MG, Pham HN. Efflux pump inhibitors in controlling antibiotic resistance: outlook under a heavy metal contamination context. *Molecules*. 2023 Mar 24; 28(7):2912. <https://doi.org/10.3390/molecules28072912>
23. Shelke DB, Chambhare MR, Sonawane HB, Islam NF, Patowary R, Das MR, Mohanta YK, Patowary K, Joshi SJ, Narayan M, Panda BP. Synergistic approaches in halophyte-microbe interactions: mitigating soil salinity and industrial contaminants for sustainable agriculture. *Discover Life*. 2025 Apr 14; 55(1):11. <https://doi.org/10.1007/s11084-025-09688-3>
24. Cao Y, Zhang B, Cai Q, Zhu Z, Liu B, Dong G, Greer CW, Lee K, Chen B. Responses of *Alcanivorax* species to marine alkanes and polyhydroxybutyrate plastic pollution: Importance of the ocean hydrocarbon cycles. *Environmental Pollution*. 2022 Nov 15; 313:120177. <https://doi.org/10.1016/j.envpol.2022.120177>
25. Agarwal P, Giri BS, Rani R. Unravelling the role of rhizospheric plant-microbe synergy in phytoremediation: a genomic perspective. *Current Genomics*. 2020 Aug 1; 21(5):334-42. <https://doi.org/10.2174/1389202921999200623133240>
26. Claus SP, Guillou H, Ellero-Simatos S. The gut microbiota: a major player in the toxicity of environmental pollutants? *Npj biofilms and microbiomes*. 2016 May 4; 2(1):1-1. [doi:10.1038/npjbiofilms.2016.3](https://doi.org/10.1038/npjbiofilms.2016.3)
27. Das N, Das A, Das S, Bhatawadekar V, Pandey P, Choure K, Damare S, Pandey P. Petroleum hydrocarbon catabolic pathways as targets for metabolic engineering strategies for enhanced bioremediation of crude-oil-contaminated environments. *Fermentation*. 2023 Feb 20; 9(2):196. <https://doi.org/10.3390/fermentation9020196>
28. Liu H, Yan S, Cheng X, Qiu X, Cheng Z, Tang H. Biosensors and biodegradation for emerging contaminants based on synthetic biology. In *Water Security: Big Data-Driven Risk Identification, Assessment and Control of Emerging Contaminants* 2024 Jan 1 (pp. 153-168). Elsevier. <https://doi.org/10.1016/B978-0-443-14170-6.00038-X>
29. Boro M, Chettri D, Bhadra S, Verma AK. An insight into pollutants and their degradation by microbial enzymes. *Biocatalysis and Biotransformation*. 2025 May 12:1-25. <https://doi.org/10.1080/10242422.2025.2499004>
30. Leahy JG, Colwell RR. Microbial degradation of hydrocarbons in the environment. *Microbiological reviews*. 1990 Sep; 54(3):305-15.
31. Pelz O, Tesar M, Wittich RM, Moore ER, Timmis KN, Abraham WR. Towards elucidation of microbial community metabolic pathways: unravelling the network of carbon sharing in a pollutant-degrading bacterial consortium by immunocapture and isotopic ratio mass spectrometry. *Environmental Microbiology*. 1999 Apr; 1(2):167-74. <https://doi.org/10.1046/j.1462-2920.1999.00023.x>
32. Ben Said S, Or D. Synthetic microbial ecology: engineering habitats for modular consortia. *Frontiers in microbiology*. 2017 Jun 16; 8:1125. <https://doi.org/10.3389/fmicb.2017.01125>
33. Liu P, Wen S, Zhu S, Hu X, Wang Y. Microbial Degradation of Soil Organic Pollutants: Mechanisms, Challenges, and Advances in Forest Ecosystem Management. *Processes*. 2025 Mar 20; 13(3):916. <https://doi.org/10.3390/pr13030916>
34. Wang H, Yang Y, Xu Y, Chen Y, Zhang W, Liu T, Chen G, Wang K. Phage-based delivery systems: Engineering, applications, and challenges in nanomedicines. *Journal of Nanobiotechnology*. 2024 Jun 25; 22(1):365. <https://doi.org/10.1186/s12951-024-02576-4>
35. Doty SL. Enhancing phytoremediation through the use of transgenics and endophytes. *New Phytologist*. 2008 Jul; 179(2):318-33. <https://doi.org/10.1111/j.1469-8137.2008.02446.x>
36. Feng P, Ye Z, Kakade A, Virk AK, Li X, Liu P. A review on gut remediation of selected environmental contaminants: possible roles of probiotics and gut microbiota. *Nutrients*. 2018 Dec 21; 11(1):22. <https://doi.org/10.3390/nu11010022>
37. Kurhaluk N, Kamiński P, Tkaczhenko H. Role of Gut Microbiota in Modulating Oxidative Stress Induced by Environmental Factors. *Cellular physiology and biochemistry: international journal of experimental cellular physiology, biochemistry, and*

- pharmacology. 2025 Aug 6; 59(S2):2-52. DOI:10.33594/000000799
38. Esvap E, Ulgen KO. Advances in genome-scale metabolic modeling toward microbial community analysis of the human microbiome. *ACS Synthetic Biology*. 2021 Aug 17; 10(9):2121-37. <https://doi.org/10.1021/acssynbio.1c00140>
 39. Srivastava U, Kanchan S, Kesheri M, Gupta MK, Singh S. Types of omics data: genomics, metagenomics, epigenomics, transcriptomics, proteomics, metabolomics, and phenomics. *Integrative Omics* 2024 Jan 1 (pp. 13-34). Academic Press. <https://doi.org/10.1016/B978-0-443-16092-9.00002-3>
 40. Chen X, Zhou X, Geng P, Zeng Y, Hu F, Sun P, Zhuang G, Ma A. Advancing biodegradation of petroleum contaminants by indigenous microbial consortia through assembly strategy innovations. *Chemical Engineering Journal*. 2023 Nov 1; 475:146142. <https://doi.org/10.1016/j.cej.2023.146142>
 41. Saraiva JP, Worrich A, Karakoç C, Kallies R, Chatzinotas A, Centler F, Nunes da Rocha U. Mining synergistic microbial interactions: a roadmap on how to integrate multi-omics data. *Microorganisms*. 2021 Apr 14; 9(4):840. <https://doi.org/10.3390/microorganisms9040840>
 42. Van Brummelen TC, Verweij RA, Wedzinga SA, Van Gestel CA. Enrichment of polycyclic aromatic hydrocarbons in forest soils near a blast furnace plant. *Chemosphere*. 1996 Jan 1; 32(2):293-314. [https://doi.org/10.1016/0045-6535\(95\)00339-8](https://doi.org/10.1016/0045-6535(95)00339-8)
 43. Harayama S, Kasai Y, Hara A. Microbial communities in oil-contaminated seawater. *Current opinion in biotechnology*. 2004 Jun 1; 15(3):205-14. <https://doi.org/10.1016/j.copbio.2004.04.002>
 44. Dash HR, Sahu M, Mallick B, Das S. Functional efficiency of Mera protein among diverse mercury resistant bacteria for efficient use in bioremediation of inorganic mercury. *Biochimie*. 2017 Nov 1; 142:207-15. <https://doi.org/10.1016/j.biochi.2017.09.016>
 45. Yadav AP, Dwivedi V, Kumar S, Kushwaha A, Goswami L, Reddy BS. Cyanobacterial extracellular polymeric substances for heavy metal removal: a mini review. *Journal of Composites Science*. 2020 Dec 23; 5(1):1. <https://doi.org/10.3390/jcs5010001>
 46. Ertani A, Mietto A, Borin M, Nardi S. Chromium in agricultural soils and crops: a review. *Water, Air, & Soil Pollution*. 2017 May; 228(5):190. <https://doi.org/10.1007/s11270-017-3356-y>
 47. García-Meseguer R, Ortí E, Tunon I, Ruiz-Pernía JJ, Arago J. Insights into the enhancement of the poly (ethylene terephthalate) degradation by FAST-PETase from computational modelling. *Journal of the American Chemical Society*. 2023 Aug 16; 145(35):19243-55. <https://doi.org/10.1021/jacs.3c04427>
 48. Mohammadi S, Moussavi G, Rezaei M. Enhanced peroxidase-mediated biodegradation of polyethylene using the bacterial consortia under H2O2-biostimulation. *Polymer*. 2022 Feb 1; 240:124508. <https://doi.org/10.1016/j.polymer.2021.124508>
 49. Munzone A, Pujol M, Badjoudj M, Haon M, Grisel S, Magueresse A, Durand S, Beaugrand J, Berrin JG, Bissaro B. Design of Plastic Binding Lytic Polysaccharide Monooxygenases via Modular Engineering. *Chem & Bio Engineering*. 2024 Sep 27; 1(10):863-75. <https://doi.org/10.1021/cbe.4c00125>
 50. Jain M, Yadav P, Joshi B, Joshi A, Kodgire P. Recombinant organophosphorus hydrolase (OPH) expression in *E. coli* for the effective detection of organophosphate pesticides. *Protein Expression and Purification*. 2021 Oct 1; 186:105929. <https://doi.org/10.1016/j.pep.2021.105929>
 51. Sajjaphan K, Shapir N, Wackett LP, Palmer M, Blackmon B, Tomkins J, Sadowsky MJ. *Arthrobacter aurescens* TC1 atrazine catabolism genes *trzN*, *atzB*, and *atzC* are linked on a 160-kilobase region and are functional in *Escherichia coli*. *Applied and environmental microbiology*. 2004 Jul; 70(7):4402-7. <https://doi.org/10.1128/AEM.70.7.4402-4407.2004>
 52. Giannakara M, Koumandou VL. New Insights on the Glyphosate-Degrading Enzymes CP Lyase and Glyphosate Oxidoreductase Based on Bioinformatics. *Bacteria*. 2024 Oct 2; 3(4):314-29. <https://doi.org/10.3390/bacteria3040021>
 53. Zhang L, Cui H, Zou Z, Garakani TM, Novoa-Henriquez C, Jooyeh B, Schwaneberg U. Directed evolution of a bacterial laccase (CueO) for enzymatic biofuel cells. *Angewandte Chemie International Edition*. 2019 Mar 26; 58(14):4562-5. <https://doi.org/10.1002/anie.201814069>
 54. Murshid S, Dhakshinamoorthy GP. Application of an immobilized microbial consortium for the treatment of pharmaceutical wastewater: Batch-wise and continuous studies. *Chinese Journal of Chemical Engineering*. 2021 Jan 1; 29:391-400. <https://doi.org/10.1016/j.cjche.2020.04.008>
 55. Sakaki T, Inouye K. Practical application of mammalian cytochrome P450. *Journal of bioscience and bioengineering*. 2000 Jan 1; 90(6):583-90. [https://doi.org/10.1016/S1389-1723\(00\)90001-X](https://doi.org/10.1016/S1389-1723(00)90001-X)
 56. Rossi F, Rizzotti L, Felis GE, Torriani S. Horizontal gene transfer among microorganisms in food: current knowledge and future perspectives. *Food microbiology*. 2014 Sep 1; 42:232-43. <https://doi.org/10.1016/j.fm.2014.04.004>
 57. Briones A, Raskin L. Diversity and dynamics of microbial communities in engineered environments and their implications for process stability. *Current opinion in biotechnology*. 2003 Jun 1; 14(3):270-6. [https://doi.org/10.1016/S0958-1669\(03\)00065-X](https://doi.org/10.1016/S0958-1669(03)00065-X)
 58. Samuel PO, Edo GI, Oloni GO, Ugbune U, Ezekiel GO, Essagah AE, Agbo JJ. Effects of chemical contaminants on the ecology and evolution of organisms a review. *Chemistry and Ecology*. 2023 Nov 26; 39(10):1071-107. <https://doi.org/10.1080/02757540.2023.2284158>
 59. Ma Y, Manna A, Moon TS. Advances in engineering genetic circuits for microbial biocontainment. *Current Opinion in Systems Biology*. 2023 Dec 1; 36:100483. <https://doi.org/10.1016/j.coisb.2023.100483>
 60. Calero P, Nikel PI. Chasing bacterial chassis for metabolic engineering: a perspective review from classical to non-traditional microorganisms. *Microbial Biotechnology*. 2019 Jan; 12(1):98-124. <https://doi.org/10.1111/1751-7915.13292>
 61. Ostrov N, Nyerges A, Chiappino-Pepe A, Rudolph A, Baas-Thomas M, Church GM. Synthetic genomes with altered genetic codes. *Current Opinion in Systems Biology*. 2020 Dec 1; 24:32-40. <https://doi.org/10.1016/j.coisb.2020.09.007>
 62. Satapathy T, Dhiwar P, Sahu P, Patel N, Tiwari K, Sahu L. Impact of conventional and advanced therapies in functional hair follicular regeneration in pesticide-induced hair loss: a Pharmacological perspective of review. *Journal of Drug Delivery & Therapeutics*. 2025 Jul 1; 15(7). doi.10.22270/jddt.v15i7.7293
 63. Afridi MS, Ali S, Salam A, César Terra W, Hafeez A, Sumaira, Ali B, S. AlTami M, Ameen F, Ercisli S, Marc RA. Plant microbiome engineering: hopes or hypes. *Biology*. 2022 Dec 7; 11(12):1782. <https://doi.org/10.3390/biology11121782>
 64. Chandran P, Suresh S, Balasubramain B, Gangwar J, Raj AS, Aarathy UL, Meyyazhagan A, Pappuswamy M, Sebastian JK. Biological treatment solutions using bioreactors for environmental contaminants from industrial waste water. *Journal of Umm Al-Qura University for Applied Sciences*. 2025 Jun; 11(2):185-207. <https://doi.org/10.1007/s43994-023-00071-4>
 65. Hardwick A, Cummings C, Graves Jr J, Kuzma J. Can societal and ethical implications of precision microbiome engineering be applied to the built environment? A systematic review of the literature. *Environment Systems and Decisions*. 2024 Jun; 44(2):215-38. <https://doi.org/10.1007/s10669-024-09965-y>
 66. Sasani MS. The importance of biosecurity in emerging biotechnologies and synthetic biology. *Avicenna Journal of Medical Biotechnology*. 2024 Oct; 16(4):223. doi:10.18502/ajmb.v16i4.16738
 67. Brossard D, Belluck P, Gould F, Wirz CD. Promises and perils of gene drives: Navigating the communication of complex, post-

- normal science. *Proceedings of the National Academy of Sciences*. 2019 Apr 16; 116(16):7692-7. <https://doi.org/10.1073/pnas.1805874115>
68. Contreras-Salgado EA, Sánchez-Morán AG, Rodríguez-Preciado SY, Sifuentes-Franco S, Rodríguez-Rodríguez R, Macías-Barragán J, Díaz-Zaragoza M. Multifaceted applications of synthetic microbial communities: advances in biomedicine, bioremediation, and industry. *Microbiology Research*. 2024 Aug 29; 15(3):1709-27. <https://doi.org/10.3390/microbiolres15030113>
69. Ventura M, Marinas A, Domine ME. Catalytic processes for biomass-derived platform molecules valorisation. *Topics in Catalysis*. 2020 Sep; 63(9):846-65. <https://doi.org/10.1007/s11244-020-01309-9>
70. Begum YA, Kumari S, Jain SK, Garg MC. A review on waste biomass-to-energy: integrated thermochemical and biochemical conversion for resource recovery. *Environmental Science: Advances*. 2024; 3(9):1197-216. DOI: 10.1039/D4VA00109E
71. Huertas JR, García MD, García CM. Granada, Spain. *Journal of Physiology and Biochemistry*. 2024; 80(1):S1-95. <https://doi.org/10.1007/s13105-024-01031-0>
72. Bhattacharjee A, Kumar A, Ojha PK, Kar S. Artificial intelligence to predict inhibitors of drug-metabolizing enzymes and transporters for safer drug design. *Expert Opinion on Drug Discovery*. 2025 May 4; 20(5):621-41. <https://doi.org/10.1080/17460441.2025.2491669>
73. Tariq A, Guo S, Farhat F, Shen X. Engineering synthetic microbial communities: diversity and applications in soil for plant resilience. *Agronomy*. 2025 Feb 20; 15(3):513. <https://doi.org/10.3390/agronomy15030513>
74. Bist P, Choudhary S. Impact of heavy metal toxicity on the gut microbiota and its relationship with metabolites and future probiotics strategy: a review. *Biological Trace Element Research*. 2022 Dec; 200(12):5328-50. <https://doi.org/10.1007/s12011-021-03092-4>