

From candidate genes to field deployment: Engineering microbial consortia for degradation of persistent industrial chemicals

Oluwakorede Timothy Oki *

Georgia State University, Atlanta, GA, USA.

Magna Scientia Advanced Research and Reviews, 2026, 16(02), 190-196

Publication history: Received on 07 March 2026; revised on 15 April 2026; accepted on 17 April 2026

Article DOI: <https://doi.org/10.30574/msarr.2026.16.2.0054>

Abstract

Persistent industrial chemicals such as per- and polyfluoroalkyl substances (PFAS), chlorinated solvents, polycyclic aromatic hydrocarbons (PAHs), synthetic dyes, and plasticizers pose a risk to ecosystems and human health. The chemical degradation resistance, high mobility, and global dispersal, combined with the drawbacks of conventional single-strain bioremediation approaches, have resulted in limited and inconsistent efficacy in field applications. This narrative review evaluates recent advances in microbial consortia engineering aimed at improving the biodegradation of persistent pollutants, tracing progress from candidate gene and pathway discovery to real-world scalability and deployment. This review examines conceptual trends, technological innovations, and unresolved issues across multiple pollution categories. Selected case studies aided in extracting general design principles for functional microbial consortia. Important advances include the utilization of genome-resolved metagenomics and multi-omics for revealing previously unrecognized degradation pathways, the use of synthetic ecology techniques to accelerate metabolic handoffs and reduce competitive exclusion, and the progress in systems-level modeling for predicting community function and performance. Despite the advancements made, there are challenges in achieving reliable predictability, ecological robustness, and regulatory approvals. Laboratory successes often fail to translate linearly when applied in the field due to context-dependent microbial interactions and environmental heterogeneity. However, the field is gradually moving from reductionist biodegradation paradigms to ecology-informed, deployable microbial systems with future progress relying on the integration of evolutionary stability, site-specific environmental complexity, and policy-aware engineering frameworks.

Keywords: Microbial Consortia; Bioremediation; Persistent Organic Contaminants; Synthetic Ecology; Systems Microbiology; Environmental Biotechnology

1. Introduction

The build-up of non-degradable industrial chemicals is one of the most lasting legacies of twentieth-century industrialization (Rauseo et al., 2025). Per- and polyfluoroalkyl substances (PFAS), chlorinated solvents (trichloroethylene), polycyclic aromatic hydrocarbons (PAHs), azo dyes, plasticizers, and pharmaceutical residues are examples of compounds that persist in the environment for a long time (Moorchilot et al., 2024). Their chemical stability is exceptional due to strong carbon-halogen bonds, aromatic resonance, steric hindrance, and molecular structures specifically engineered to resist degradation (Vainauskas et al., 2023). These physicochemical features are a reason for their persistence in the environment. Consequently, such compounds are now frequently found in underground water, soil, sediment, surface water, and in living organisms, including areas geographically far from their places of production and use. The extensive presence of these compounds has raised profound concerns about chronic toxicity, bioaccumulation, endocrine disruption, and long-term ecosystem damage, while also revealing the limitations of conventional remediation methods (Youssef et al., 2025). Physicochemical methods such as excavation, incineration,

* Corresponding author: Oluwakorede Timothy Oki

adsorption, and advanced oxidation have been used to remove persistent industrial chemicals (Wang and Cui, 2025). These methods are effective in short-term risk reduction, but they tend to be very expensive and difficult to scale sustainably when applied to diffuse or low-concentration contamination. Moreover, numerous methods only move the contaminants from one environmental compartment to another without destroying them. Against this, biodegradation has been highlighted as a sustainable alternative, as it benefits from in situ treatment, low energy requirements, and potential for complete mineralization (Raheja et al., 2025; Nasrollahpour et al., 2025).

Early bioremediation methods were predominantly based on a reductionist paradigm focused on the isolation and the use of individual “super-degrader” strains that could transform specific target compounds. These efforts provided vital mechanistic insight and, in some cases, showed outstanding laboratory successes. However, the application of such methods to complex environmental settings has frequently failed to meet expectations under field conditions (Qattan, 2025). Introduced strains sometimes fail to last or show target functions in situ; therefore, they are affected by competition with local microorganisms, sensitivity to changing environmental conditions (Montaño López et al., 2022; O’Callaghan et al., 2022). All these failures have pointed out a fundamental discrepancy between simplified laboratory systems and the ecological complexity of real-world contaminated environments. Recognition of these limitations has triggered a change towards microbial consortia as the functional units of biodegradation (Cao et al., 2022). Instead of depending on single organisms to perform complete degradation routes, consortia distribute metabolic tasks across multiple interacting taxa. Such division of metabolic tasks can reduce metabolic load on individual organisms, enabling different enzymatic activities and improving resilience to environmental stress. It is important that consortia are not just assemblages of degraders but dynamic ecological systems shaped by cooperation, competition, cross-feeding, and evolutionary adaptation. This ecological viewpoint has transformed biodegradation to an emergent community-level process rather than a property of individual strains.

In recent years, improvements in metagenomics, systems biology, synthetic biology, and microbial ecology collectively changed microbial consortia identification, design, and evaluation (Kumar et al., 2025b). Genome-resolved metagenomics has made it possible to reconstruct microbial genomes from direct polluted areas, unveiling large reservoirs of previously uncharacterized catalytic potential (Hauptfeld et al., 2022). The methods have shown that for various classes of persistent industrial chemicals, the degradation pathways are dispersed among multiple organisms, with no single taxon encoding all required enzymatic steps. Complementary techniques such as stable isotope probing and metatranscriptomics have strengthened the link between genetic potential and in situ function (Overy et al., 2021). The developments in metabolic modeling and system-level analyses have shown emergent properties of microbial communities that are invisible at the single-organism scale (Kulyashov et al., 2023). Such properties include metabolic handoffs, syntrophic interactions, and context-dependent shifts in pathway utilization in response to environmental constraints. Synthetic biology has expanded the design space by allowing rational construction of defined consortia, adjusting interspecies interactions, and introducing regulatory circuits aimed at stabilizing community function (Wang et al., 2025). The combination of these developments has broadened the conceptual landscape from the question of “which microbe degrades which compound” to the more integrative challenge of “how communities collectively transform complex and heterogeneous chemical mixtures under real environmental conditions.”

Despite the rapid development of microbial consortia engineering for pollutant degradation, the field remains fragmented and disunited (Cao et al., 2022). A lot of research continues to focus on very specific pollutant classes, organisms, and highly regulated lab environments, limiting the transferable insights across different situations (Dhar et al., 2025). This has resulted in a poor understanding of the effectiveness of general design principles and resilient consortia. In addition, there are inconsistencies between the laboratory demonstration process and field deployment. Ecological instability, unpredictability of evolutionary changes, regulations concerning the use of genetically modified organisms, and the absence of standardized performance metrics are all factors contributing to the persistent gap between the proof-of-concept studies and large-scale remediation solutions (Eckerstorfer et al., 2025).

This narrative review synthesizes recent literature (2020–2025) across diverse types of persistent industrial chemicals to point out shared principles, new trends, and persistent challenges in microbial consortia engineering for biodegradation. This review also present comprehensive list of organisms and pathways, adopting a cross-cutting, concept-driven method that combines views from environmental microbiology, systems biology, and ecological engineering. By connecting candidate gene discovery to community assembly strategies and real-world deployment considerations, the review aims to offer a unifying framework that can shape future research and speed up the translation of microbial consortia from the laboratory to the field.

2. Emerging Trends and Thematic Analysis

2.1. From Candidate Genes to Distributed Metabolic Pathways

Identifying and studying individual catabolic genes, such as monooxygenases, dioxygenases, or dehalogenases, was a primary concern of early biodegradation research, which operated under the assumption that equipping a single organism with the appropriate enzyme machinery would enable effective pollutant removal (Xu et al., 2021; Esmaeel and Alfatlawi, 2022). Although these genes are considered the basis of the degradation process, recent studies emphasize that the complete mineralization of persistent industrial contaminants often relies on the partitioning of metabolic pathways among several organisms in a community (Xu et al., 2021). Genome-resolved metagenomic studies on PFAS-impacted areas have shown that partial defluorination steps are shared among different taxa, with no single microorganism encoding the full degradation sequence needed for complete breakdown (Shahsavari et al., 2021). In PAH-polluted sediments, similar patterns have been reported, where processes are performed by different community members (Idris and Erasmus, 2025). This emerging viewpoint changes candidate genes, not as isolated solutions but as functional modules incorporated within larger ecological networks. In such networks, functional redundancy, horizontal gene transfer, and tightly coupled metabolic handoffs can improve system robustness and resilience to perturbations (Yang et al., 2024; Jiang et al., 2025). Figure 1 shows the distributed degradation pathways across microbial consortia.

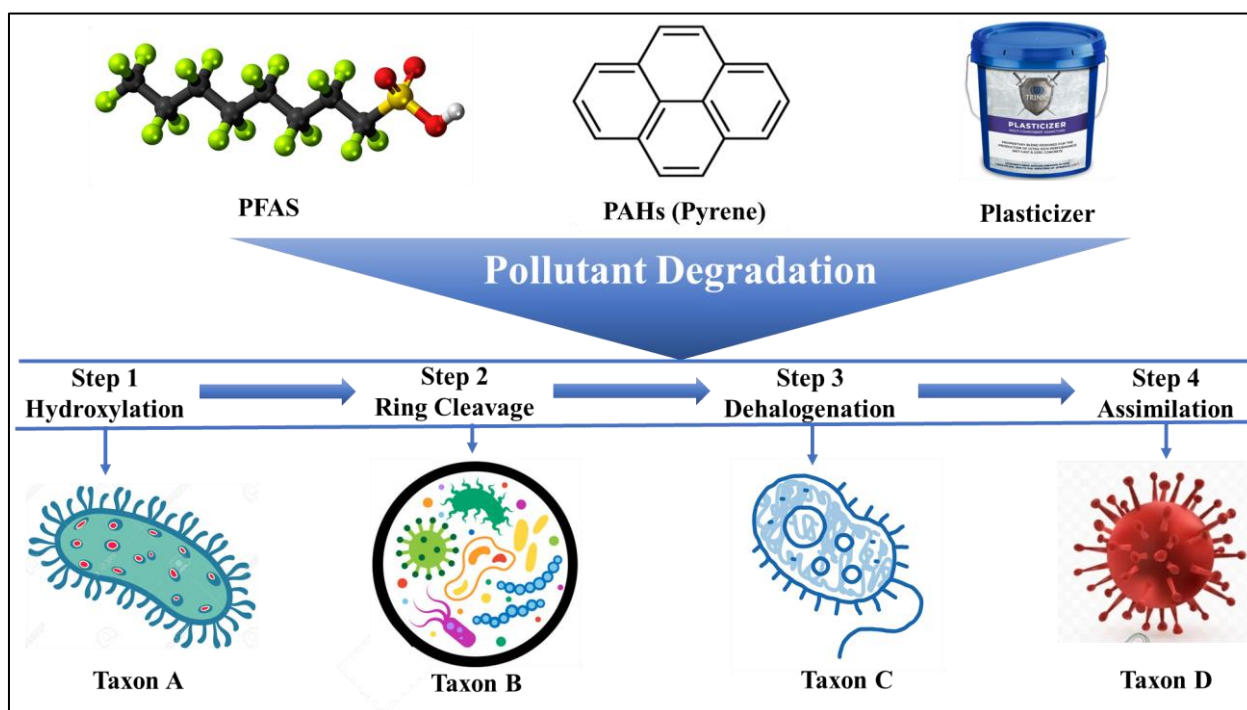


Figure 1 Distributed Degradation Pathways across Microbial Consortia

2.2. Engineering Synthetic Consortia versus Harnessing Native Communities

One of the major and continuous controversies in the field of bioremediation with microbial consortia is whether to resort to the use of rationally engineered synthetic consortia or to the stimulation and management of local microbial communities (Renganathan et al., 2025). The use of synthetic consortia allows for a very high level of control and understanding of the mechanics involved, which is clearly seen in the case of rationally put-together systems designed for synthetic dye degradation or reductive dechlorination of solvents, where the roles of metabolism and interspecies interactions are intentionally defined (Dhar et al., 2025). However, while they perform effectively in the laboratory, these consortia are often ecologically fragile, with limited duration and stability once released into the complex, competitive field environment (Kumar et al., 2025b). Conversely, biostimulation and bioaugmentation techniques aim to harness existing microbial communities adapted to the specific geological and ecological conditions of the site. Metatranscriptomic studies have shown that by adjusting nutrients or electron donors, pollutants can be transformed by native soil microorganisms without adding new strains (Nag et al., 2024). This approach is more environmentally friendly but comes with decreased predictability, reproducibility, and standardization across different sites. Emerging hybrid methods seek to address these issues by introducing engineered strains as primary functional agents, rather

than relying on native degraders (Renganathan et al., 2025). This ecology-informed strategy, consistent with modern ecological theory, has shown promising results in removing chlorinated solvent plumes, where engineered functions integrate with and enhance native community processes (Li et al., 2024). Table 1 shows the comparative advantages, limitations, and applications of synthetic hybrid and native microbial consortia strategies in bioremediation

Table 1 Comparative advantages, limitations, and applications of synthetic hybrid and native microbial consortia strategies in bioremediation.

Strategy	Key Advantages	Primary Limitations	Typical Applications
Synthetic consortia	High controllability and clarity of mechanism	Ecological fragility and limited persistence.	Laboratory
Hybrid approaches	Balance of control and resilience	Complicated design and unclear regulations	Field-scale remediation
Native communities	Site adaptation and ecological support	Low predictability and limited standardization	In situ biostimulation

2.3. Ecological Stability, Evolution, and Failure Modes

Recent studies have consistently shown that the ecological context is an integral part of the degradative function in microbial consortia (Davis et al., 2025). Failures do not come from the loss of specific catabolic genes but rather from disruptions in community organization, including the collapse of populations, invasion by non-contributing organisms, and imbalances in metabolic activities that interfere with cross-feeding interactions (Herren, 2020; Clegg and Gross, 2025). Long-term experimental studies have indicated that microbial communities undergo quick evolutionary changes that alter their structure and functional capabilities, speeding up the degradation of the pollutants through adaptive optimization; however, undermining engineered designs by changing their interaction networks and resource allocation (Estrela et al., 2021). These dynamics question simple engineering models, which consider stable genotypes and their interactions over time, emphasizing the necessity to embed evolution-aware and ecology-informed design principles into consortia advancement (Wang et al., 2025). Several innovative strategies, such as spatial structuring to reduce the impact of exploitative interactions, employing feedback control in gene expression to achieve a stable metabolic flux, and using ecological scaffold inert carriers and engineered biofilms, have been suggested to improve and maintain beneficial associations (Henderson et al., 2025). While these methods have shown potential under controlled laboratory conditions, their reliable application in complex and diverse field environments presents an unresolved challenge, highlighting the gap between conceptual progress and deployable remediation systems (Qattan, 2025).

2.4. Toward Field Deployment and Systems-Level Performance Metrics

Field deployment is the ultimate test for microbial consortia engineering. The designs, which are already optimized by the laboratory, operate in changing and possibly adverse geochemical, hydrological, and ecological conditions. In this context, successful case studies are gradually moving emphasis away from organism-centric metrics, such as the quantity of specific introduced strains, towards process-level outcomes, which directly reflect the effectiveness of remediation (Sharma et al., 2025). Data from pilot-scale and field deployments supervised through the application of integrated multi-omics approaches suggest that functional resilience is a stronger predictor of long-term performance than taxonomic stability alone (Smith et al., 2025). The underlying idea is that microbial communities can reorganize internally while retaining degradation function, provided that necessary metabolic capabilities are preserved. This has led to an increasing demand for the implementation of internationally accepted, system-wide performance criteria for bioremediation based on consortia, similar to those long used in wastewater and process engineering, which prioritize robust, reliable, and outcome-based evaluation (Glukhonina and Ibrahim, 2025). Such a shift in evaluation criteria is an important step in bridging the gap between innovation of experiments and regulatory acceptance of microbial consortia technologies in real-world remediation situations (Eckerstorfer et al., 2025).

3. Future Directions and Research Gaps

Despite rapid progress in microbial consortia engineering for bioremediation, several important research gaps continue to limit the transfer from concept to practice (Cao et al., 2022). The lack of development of reliable predictive models linking community composition, interaction structure, and metabolic potential to degradation kinetics rates under variable environmental conditions is a major challenge (Diener and Gibbons, 2023). At the same time, the ethical, social,

and regulatory frameworks governing the use of engineered consortia remain unclear, inconsistent, and highly variable across jurisdictions, thereby hindering both field testing and commercialization (Li et al., 2021; Kumar et al., 2025a). From a technological standpoint, the integration of machine learning techniques with mechanistic, process-based models entails excellent prospects for navigating the high-dimensional design space of microbial communities and extracting reliable design rules from complex datasets (Trivedi et al., 2025). From an ecological perspective, there is an increasing consensus that attempting to eliminate natural variability and evolution may be detrimental; rather, accepting and managing variability could lead to more adaptable and resilient systems for environmental remediation (Manzanera, 2025). Ultimately, the field's development will rely on closer and constant collaboration among laboratory scientists, field engineers, regulatory agencies, and affected communities, ensuring that technical innovations align with environmental realities, governance structures, and societal needs (Sharma and Bora, 2025).

4. Conclusion

Microbial consortia engineering is revolutionizing and reshaping the scope and potential of biodegradation methods for persistent industrial chemicals, shifting the focus away from the persistent pursuit of a single organism toward distributed metabolism, ecological resilience, and evolutionary dynamics. Studies show that effective and lasting pollutant removal occurs through coordinated interactions among diverse community members, each contributing partial metabolic functions that enable transformation pathways unaccomplished by individual strains. Thus, the success of consortia-based bioremediation depends on integrating promising candidate genes and pathways into functional, adaptable microbial communities rather than merely identifying these genes and pathways. With the progress of the field, the main challenge is connecting the knowledge of mechanisms with real practice. Genomics, multi-omics integration, systems modeling, and synthetic ecology have contributed to the development of rational consortium design; however, transforming these innovations into dependable, large-scale remediation technologies will require the explicit consideration of environmental variability, evolutionary processes, and regulations. Eco-variability and evolutionary development should be embraced instead of eliminated, as they may bring about more resilient and effective remediation systems. Consistent collaboration across different disciplines involving laboratory researchers, field engineers, policymakers, and stakeholders will be necessary to ensure that microbial consortia technologies grow in line with environmental and societal needs, thereby allowing their impactful and responsible use in solving persistent chemical pollution.

References

- [1] Cao, Z., Yan, W., Ding, M. & Yuan, Y. (2022). Construction of microbial consortia for microbial degradation of complex compounds. *Frontiers in Bioengineering and Biotechnology*, 10, 1051233.
- [2] Clegg, T. & Gross, T. (2025). Cross-feeding creates tipping points in microbiome diversity. *Proceedings of the National Academy of Sciences*, 122, e2425603122.
- [3] Davis, R. A., Mafune, K. K. & Winkler, M. K. (2025). Biodegradable hydrogels and microbial consortia as a treatment for soil dysbiosis. *Frontiers in microbiology*, 16, 1565940.
- [4] Dhar, S., Rout, S. S., Panda, A., Rout, A. K., Mistri, A., Kumar, M. & Behera, B. K. 2025. Bioremediation techniques: Principles, advantages, limitations, and prospects. *Advances in omics technologies: Exploring genomics, proteomics, and metabolomics*. Springer.
- [5] Diener, C. & Gibbons, S. M. (2023). More is different: Metabolic modeling of diverse microbial communities. *Msystems*, 8, e01270-01222.
- [6] Eckerstorfer, M. F., Dolezel, M., Miklau, M., Greiter, A., Heissenberger, A., Kastenhofer, K., Schulz, F., Hagen, K., Otto, M. & Engelhard, M. (2025). Environmental applications of gm microorganisms: Tiny critters posing huge challenges for risk assessment and governance. *International journal of molecular sciences*, 26, 3174.
- [7] Esmaeel, J. R. & Alfatlawi, M. (2022). Monooxygenase and dioxygenases by bacterial specific enzymes network. *International Journal of Health Sciences*, 10215-10222.
- [8] Estrela, S., Sánchez, Á. & Rebolledo-Gómez, M. (2021). Multi-replicated enrichment communities as a model system in microbial ecology. *Frontiers in microbiology*, 12, 657467.
- [9] Glukhonina, A. & Ibrahim, T. 2025. Advancing waste management in the oil and gas industry: Analyzing country-specific approaches in Iraq, Russia and Norway.

- [10] Hauptfeld, E., Pelkmans, J., Huisman, T. T., Anocic, A., Snoek, B. L., von Meijenfildt, F. B., Gerritse, J., van Leeuwen, J., Leurink, G. & van Lit, A. (2022). A metagenomic portrait of the microbial community responsible for two decades of bioremediation of poly-contaminated groundwater. *Water Research*, 221, 118767.
- [11] Henderson, A., Del Panta, A., Schubert, O. T., Mitri, S. & van Vliet, S. (2025). Disentangling the feedback loops driving spatial patterning in microbial communities. *npj Biofilms and Microbiomes*, 11, 32.
- [12] Herren, C. M. (2020). Disruption of cross-feeding interactions by invading taxa can cause invasional meltdown in microbial communities. *Proceedings of the Royal Society B*, 287, 20192945.
- [13] Idris, O. A. & Erasmus, M. (2025). Metagenomic approaches for optimising hydrocarbon pollution rhizoremediation. *International Journal of Environmental Research*, 19, 46.
- [14] Jiang, Y., Wang, Y., Che, L., Yang, S., Zhang, X., Lin, Y., Shi, Y., Zou, N., Wang, S. & Zhang, Y. (2025). Gutmetanet: An integrated database for exploring horizontal gene transfer and functional redundancy in the human gut microbiome. *Nucleic acids research*, 53, D772-D782.
- [15] Kulyashov, M. A., Kolmykov, S. K., Khlebodarova, T. M. & Akberdin, I. R. (2023). State-of-the-art constraint-based modeling of microbial metabolism: From basics to context-specific models with a focus on methanotrophs. *Microorganisms*, 11, 2987.
- [16] Kumar, D., Kumar, R., Sakshi & Kumar, A. (2025a). Ethical implications and regulatory frameworks for microbial products and processes: Microbial contributions to a circular economy. *Microbial Metabolomics: Recent Developments, Challenges and Future Opportunities*, 401-418.
- [17] Kumar, P., Chitara, D., Sengupta, S., Banerjee, P. & Rai, S. N. (2025b). Microbial consortia in biotechnology: Applications and challenges in industrial processes. *3 Biotech*, 15, 386.
- [18] Li, W., Zhang, W., Dong, J., Liang, X. & Sun, C. (2024). Groundwater chlorinated solvent plumes remediation from the past to the future: A scientometric and visualization analysis. *Environmental Science and Pollution Research*, 31, 17033-17051.
- [19] Li, X., Wu, S., Dong, Y., Fan, H., Bai, Z. & Zhuang, X. (2021). Engineering microbial consortia towards bioremediation. *Water*, 13, 2928.
- [20] Manzanera, M. (2025). From microbial consortia to ecosystem resilience: The integrative roles of holobionts in stress biology. *Biology*, 14, 1203.
- [21] Montañó López, J., Duran, L. & Avalos, J. L. (2022). Physiological limitations and opportunities in microbial metabolic engineering. *Nature Reviews Microbiology*, 20, 35-48.
- [22] Moorchilot, V. S., Aravind, U. K. & Aravindakumar, C. T. (2024). Occurrence of azo-dyes, plasticizers, and pah-bound microplastics: An emerging source and sink for hazardous compounds in indoor environments? *Air Quality, Atmosphere & Health*, 17, 425-438.
- [23] Nag, M., Lahiri, D., Ghosh, S., Sarkar, T., Pati, S., Das, A. P., Ram, D. K., Bhattacharya, D. & Ray, R. R. (2024). Application of microorganisms in biotransformation and bioremediation of environmental contaminant: A review. *Geomicrobiology Journal*, 41, 374-391.
- [24] Nasrollahpour, S., Purewal, S., Brar, S. K. & Das, R. K. (2025). Biodegradation of per-and polyfluoroalkyl substances: Mechanisms, challenges, and emerging strategies for sustainable remediation. *Environmental Science: Water Research & Technology*.
- [25] O'Callaghan, M., Ballard, R. A. & Wright, D. (2022). Soil microbial inoculants for sustainable agriculture: Limitations and opportunities. *Soil Use and Management*, 38, 1340-1369.
- [26] Overy, D. P., Bell, M. A., Habtewold, J., Helgason, B. L. & Gregorich, E. G. (2021). "Omics" technologies for the study of soil carbon stabilization: A review. *Frontiers in Environmental Science*, 9, 617952.
- [27] Qattan, S. Y. (2025). Harnessing bacterial consortia for effective bioremediation: Targeted removal of heavy metals, hydrocarbons, and persistent pollutants. *Environmental Sciences Europe*, 37, 85.
- [28] Raheja, Y., Sharma, P., Gaur, P., Gaur, V. K. & Srivastava, J. K. (2025). Advancing bioremediation: Biosurfactants as catalysts for sustainable remediation. *Biodegradation*, 36, 1-19.
- [29] Rauseo, J., Spataro, F. & Patrolecco, L. 2025. Persistent and emerging organic contaminants in natural environments. MDPI.

- [30] Renganathan, P., Gaysina, L. A., García Gutiérrez, C., Rueda Puente, E. O. & Sainz-Hernández, J. C. (2025). Harnessing engineered microbial consortia for xenobiotic bioremediation: Integrating multi-omics and ai for next-generation wastewater treatment. *Journal of Xenobiotics*, 15, 133.
- [31] Shahsavari, E., Rouch, D., Khudur, L. S., Thomas, D., Aburto-Medina, A. & Ball, A. S. (2021). Challenges and current status of the biological treatment of pfas-contaminated soils. *Frontiers in Bioengineering and Biotechnology*, 8, 602040.
- [32] Sharma, A. & Bora, P. (2025). Engineering synthetic microbial communities to restructure the phytobiome for plant health and productivity. *World Journal of Microbiology and Biotechnology*, 41, 228.
- [33] Sharma, K., Verma, A. & Dubey, R. 2025. Case studies of successful algal-microbial waste remediation. *Algal bioengineering and microbial synergy to green remediation*. Springer.
- [34] Smith, D. D., Subasinghe, R. M., Kehoe, C. & Grégoire, D. S. (2025). Multi-omics highlights challenges in assessing the composition and performance of microbial consortia for commercial applications. *bioRxiv*, 2025.2002.2026.640401.
- [35] Trivedi, P., Kumar, A., Gupta, N. & Patel, C. N. 2025. Artificial intelligence and machine learning in microbial degradation of pollutants and toxins. *Microbial metabolomics: Recent developments, challenges and future opportunities*. Springer.
- [36] Vainauskas, J., Borchers, T. H., Arhangelskis, M., McPherson, L. J. M., Spilfogel, T. S., Hamzehpoor, E., Topić, F., Coles, S. J., Perepichka, D. F. & Barrett, C. J. (2023). Halogen bonding with carbon: Directional assembly of non-derivatised aromatic carbon systems into robust supramolecular ladder architectures. *Chemical Science*, 14, 13031-13041.
- [37] Wang, J. & Cui, X. 2025. Remediation strategies for soil and water. MDPI.
- [38] Wang, Z., Wang, S., He, Q., Yang, X., Zhao, B., Zhang, H. & Deng, Y. (2025). Ecological design of high-performance synthetic microbial communities: From theoretical foundations to functional optimization. *ISME communications*, 5, ycaf133.
- [39] Xu, A., Zhang, X., Wu, S., Xu, N., Huang, Y., Yan, X., Zhou, J., Cui, Z. & Dong, W. (2021). Pollutant degrading enzyme: Catalytic mechanisms and their expanded applications. *Molecules*, 26, 4751.
- [40] Yang, J.-X., Peng, Y., Yu, Q.-Y., Yang, J.-J., Zhang, Y.-H., Zhang, H.-Y., Adams, C. A., Willing, C. E., Wang, C. & Li, Q.-S. (2024). Gene horizontal transfers and functional diversity negatively correlated with bacterial taxonomic diversity along a nitrogen gradient. *npj Biofilms and Microbiomes*, 10, 128.
- [41] Youssef, M. M., Helal, A. M. & Khedr, Y. I. (2025). Endocrine disrupting chemicals and human health: A review of toxicological mechanisms and regulatory challenges. *Journal of Biomedicine and Biochemistry*, 4, 14-26.