

Multi-Omics Integration for Advancing Microbial Bioremediation: PRISMA-Based Systematic Review

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Abstract: Bioremediation is a sustainable approach to environmental restoration; however, its effectiveness is often constrained by limited understanding of molecular mechanisms and complex microbial interactions. This study aims to systematically review the transformative role of integrated multi-omics approaches including genomics, transcriptomics, proteomics, and metabolomics in enhancing bioremediation efficiency. The review was conducted following the *Preferred Reporting Items for Systematic Reviews and Meta-Analyses* (PRISMA) guidelines across 10 empirical studies published between 2019 and 2024. Data were collected from Scopus, Web of Science, and PubMed databases using the keywords “bioremediation,” “multi-omics,” “microbial interactions,” and “environmental restoration.” Data analysis employed a qualitative thematic synthesis approach to identify key patterns and contributions. The findings reveal that multi-omics integration enables the elucidation of key catabolic pathways, identification of critical degradative enzymes, and characterization of synergistic microbial dynamics that drive pollutant degradation. Furthermore, integrating multi-omics data facilitates the rational design and engineering of synthetic microbial consortia with significantly improved bioremediation performance. In conclusion, the multi-omics framework represents a paradigm shift from descriptive to predictive and engineering-based bioremediation, providing a strong scientific foundation for more precise and sustainable environmental recovery strategies.

Keywords: bioremediation; consortium engineering; microbial interactions; multi-omics integration; sustainable environmental restoration.

Introduction

Environmental pollution caused by heavy metals, persistent organic compounds, petroleum hydrocarbons, and new pollutants such as pharmaceuticals and microplastics has become a serious threat to the sustainability of ecosystems and human health globally ((Briffa et al., 2020; Mani et al., 2023; Paiu et al., 2024; Saini & Sharma, 2022)). A report by (Maalouf & Mavropoulos, 2023) estimates global waste at around 20 billion tons in 2017, and is projected to grow to 46 billion tons by 2050. Kumar et al., 2023, emphasize that industrialization and urbanization have significantly contributed to the generation of hazardous waste. (Widyarsana et al., 2021) provides a specific example from

Indonesia, where in 2019, 573,351,835.37 tons of hazardous waste were generated, with 31.34% considered unmanaged and potentially contaminating the soil. This is in line with concerns about improper waste management. Sources consistently highlight the urgent need for sustainable and integrated waste management strategies to reduce environmental and health risks.

Bioremediation has emerged as a promising ecological approach because it utilizes the natural ability of microorganisms to degrade or transform pollutants into less toxic compounds. Compared to physicochemical methods, bioremediation offers cost efficiency and lower environmental risks (Yang et al., 2021; Dewi et al., 2024). Among others, it has been

applied to petroleum hydrocarbon contamination (Fuentes et al., 2014; Marzuki, n.d.) and microplastic contamination ((Fachrul & Rinanti, 2018). However, field applications are often constrained by the limited effectiveness of microorganisms, low bioavailability of pollutants, and the complexity of environmental conditions ((Dangi et al., 2019; Megharaj et al., 2011) Megharaj et al., 2011; Dangi et al., 2019). The case at the Bantargebang Landfill, for example, shows the potential of bioremediation in reducing pollution and producing biomass with economic value, but its success still depends on the optimization of microbial interactions and environmental conditions (Kennedy et al., 2025.) Therefore, a scientific approach is needed to explain the dynamics and functions of microbial communities in greater depth.

It is in this context that the multi-omic approach becomes relevant. Multi-omics integrates genomics, transcriptomics, proteomics, and metabolomics to gain a comprehensive understanding of the biological processes underlying bioremediation (Michealsamy et al., 2021; Saini & Sharma, 2022). The integration of these various layers of data enables the mapping of key metabolic pathways, the identification of key enzymes, and the characterization of synergistic interactions between microbes that contribute to pollutant degradation (Malla et al., 2018; Vijayakumar et al., 2017; Yunusa, Y.R. & Umar, Z.D., 2021)). Next-generation sequencing technology and advanced bioinformatics analysis have improved researchers' ability to design synthetic microbial consortia with more efficient degradation performance. However, the integration of large and heterogeneous datasets still faces challenges in computation, analysis costs, and the application of laboratory results to field conditions (Chen et al., 2017; Zhang et al., 2022).

This study offers a systematic review highlighting how multi-omic approaches contribute to the development of modern bioremediation. Unlike previous reviews that only discussed one omic aspect or focused on specific microbes, this study integrates cross-domain findings from 2019–2024 to evaluate the effectiveness of multi-omics in understanding degradation mechanisms, microbial consortium engineering, and field application. The aim is to provide a comprehensive scientific synthesis of

the potential and challenges of multi-omics in bioremediation, while offering future research directions to support more precise, efficient, and sustainable environmental restoration.

Materials and Methods

Type of Research

This study is a systematic literature review compiled based on the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Page et al., 2021; Swartz, 2021) to ensure a transparent, structured, and bias-free research process.

Literature Search Strategy

The literature search was conducted electronically in August 2025 using three main databases: Scopus, Web of Science, and PubMed ((AlRyalat et al., 2019). The search strategy used a combination of Boolean keywords covering three core concepts:

1. Multi-omics technology (“multi-omics”, genomics, proteomics),
2. Bioremediation processes (“bioremediation”, “biodegradation”), and
3. Microbial engineering and optimization (“engineer”, “enhance”).

The publication time range was limited to 2019–2024. This limitation was chosen because this period reflects the latest developments in multi-omics technology and its application in bioremediation, which began to grow rapidly after the adoption of cross-omics integrative analysis in the late 2010s. In addition, this restriction ensures that the data analyzed remains relevant to the latest advances in bioinformatics and systems biology approaches. The number of articles obtained from each database was Scopus: 1,020 articles, Web of Science: 870 articles, and PubMed: 460 articles. Thus, there were a total of 2,350 articles before duplicate removal.

Identification and Screening Stage

After removing 770 duplicate articles, 1,580 unique articles remained. These articles were screened based on their titles and abstracts using the following inclusion criteria:

1. Empirical research
2. Integrating at least two omics approaches (e.g., genomics and metabolomics)

3. Focusing on microbial degradation or engineering mechanisms for environmental pollutant bioremediation, and
4. Available in full text in English.

Exclusion criteria included single-omics studies, review articles, and studies with a medical or clinical focus. This process resulted in 95 articles that were eligible for the eligibility assessment stage. The screening process was conducted by two independent researchers, and differences in selection results were resolved through discussion. The level of inter-rater reliability was measured using Cohen's Kappa with a value of 0.85, indicating a high level of consistency.

Eligibility Stage

A total of 95 articles were read in full to ensure compliance with the inclusion criteria. After in-depth evaluation, only 10 articles met all criteria and were considered highly relevant for in-depth qualitative analysis. The methodological quality of the selected articles was assessed using the Cochrane Collaboration Risk of Bias Tool, with seven assessment domains: randomization, allocation concealment, blinding of assessors, completeness of outcome data, selective reporting, publication bias, and research funding. Each domain was scored as low, unclear, or high risk. All selected articles were assessed as being of high quality (low risk of bias). (Zeynalzadeh et al., 2024).

Data Extraction

Data from the 10 selected articles were extracted using a standardized worksheet adapted from the Joanna Briggs Institute (JBI). The sheet included:

- Bibliometric information,
- Type and characteristics of pollutants,
- Environmental conditions,
- Biological systems used,

- Multi-omics design and approach,
- Key findings and bioinformatics tools, and
- Study limitations.

The JBI format was chosen to ensure consistency, transparency, and replication in the data extraction process between researchers.

Data Analysis

The analysis was conducted using a thematic analysis approach according to the guidelines of Braun & Clarke (2006) in (Campbell et al., 2021). The coding process was carried out manually by two researchers with cross-verification to maintain the reliability of the interpretation. The synthesized results were grouped into three main themes, namely:

1. Molecular mechanisms of pollutant degradation,
2. Interactions within microbial communities, and
3. Application of multi-omics technology in microbial consortium engineering.

This analysis allows for the integration of findings across studies to produce a comprehensive picture of the progress and challenges in the application of multi-omics for environmental bioremediation.

Results and Discussion

**Systematic Data Extraction Results
Application Multi-Omics Application in
Bioremediation**

Based on a systematic selection process following the PRISMA framework, 10 empirical research articles were selected for in-depth analysis. Collectively, these articles highlight the power of the multi-omics approach in uncovering the complex mechanisms of bioremediation for various pollutants, ranging from petroleum hydrocarbons and heavy metals to persistent organic pollutants and microplastics.

Table 1. Systematic Data Extraction Sheet: Multi-Omics Applications in Bioremediation

Bibliometric Data	Description
(Li et al., 2023)	Demonstrates that metagenomic-metabolomic integration can reveal petroleum hydrocarbon degradation pathways (toluene, xylene, PAHs). There was an increase in degradation genus and mono/dioxygenase gene regulation. This study highlights the limitations of soil complexity on metabolomic data accuracy.
(Zhu et al., 2024)	The integration of transcriptomics and proteomics shows that selenium increases Cd tolerance through enhanced photosynthesis and antioxidant enzymes. The

Bibliometric Data	Description
	psbO, psaG, and OsGSTF1 genes and proteins are identified as important in Cd stress mitigation.
(Kumar et al., 2023)	A comprehensive multi-omics approach reveals the complete degradation pathway of the pesticide chlorpyrifos. The *oph* gene and TCP degradation products were found. A limitation of the study was the difficulty in determining the contribution of each bacterium in the consortium.
(Lee & Yoon, 2021)	Demonstrated synergistic interactions between *Pseudomonas aeruginosa* and *Rhodococcus sp.* in TNT degradation through a cross-feeding mechanism. This short-term study proved the importance of interspecies metabolite interactions.
(Renganathan et al., 2025)	The study found that the consortium of engineering microbes was able to effectively degrade complex xenobiotics such as drugs, synthetic dyes, and microplastics through syntrophic cooperation between species. Multi-omics (metagenomic, transcriptomic, and metabolomic) approaches reveal genes, enzymes, and major metabolic pathways that play a role in the degradation process.
(Shafana Farveen & Narayanan, 2024)	The study found that multi-omics approaches were able to identify various plastic decompose microbes such as Pseudomonas and Ideonella, along with major genes and enzymes such as PETase and laccase that play a role in polymer degradation. Transcriptomic and proteomic analysis showed increased gene expression as well as oxidative and hydrolytic enzyme activity when microbes are exposed to plastic. The integration of omics data allows the mapping of a complete metabolic pathway that explains how plastics are described into simple compounds through cooperation between microbial species.
(Gu et al., 2020)	Through genomic and proteomic analysis of the bacteria Acinetobacter Johnsonii. suggests that Sb(III) triggers the formation of reactive oxygen species (ROS) that causes oxidative stress and increases the activity of antioxidant enzymes. Two important operons, ars and pst, are involved in defense mechanisms: the operon ars helps remove Sb(III) to reduce toxicity, while the decrease in pst expression limits the absorption of Sb(V) and phosphate. In addition, exposure to Sb(III) affects peptide synthesis, energy conversion, and cell membrane stability.
(Song et al., 2021)	Identifying the microbial community has a high genetic potential for breaking down oil, characterized by increased expression of hydrocarbon degradation gene, secretion system, and DNA repair, while translation genes and photosynthesis decrease. The findings confirms that marine microbes adapt functionally to oil pollution and play an important role in the natural bioremediation process.
(Sandhu et al., 2022)	Identified PAH and PCB degradation genes (nahAc, bphA, bphC) and related metabolic pathways. This study highlights the influence of heavy metals and nutrients on microbial communities in steel industry soils.
(Shah et al., 2024)	Demonstrate how a multi-omics approach identifies genes and degradation pathways for various new pollutants such as pharmaceuticals and pesticides. This study highlights microbial interactions and oxidative responses as key factors in the biotransformation of complex pollutants.

Based on the analysis of ten empirical articles, the application of multi-omics approaches in bioremediation can be synthesized into three main themes.

1. Elucidation of Molecular Mechanisms and Microbial Adaptive Responses to Pollutants

An analysis of ten empirical studies revealed that multi-omics integration (metagenomics, transcriptomics, proteomics, and

metabolomics) plays a crucial role in uncovering the molecular mechanisms and adaptive responses of microorganisms to complex pollutants such as hydrocarbons, heavy metals, and pesticides. (Li et al., 2023) combined metagenomic and metabolomic data to map toluene, xylene, and PAH degradation pathways, showing increased regulation of degradation-related genera and mono/dioxygenase genes. (Kumar et al., 2023) employed a comprehensive multi-omics approach to elucidate the complete

chlorpyrifos degradation pathway, identifying the *oph* gene and TCP intermediates as key degradation markers. Zhu et al., (2024) demonstrated through transcriptomic-proteomic integration that selenium enhances Cd tolerance by improving photosynthetic efficiency and antioxidant enzyme activity, involving *psbO*, *psaG*, and *OsGSTF1* genes and proteins. Gu et al. (2020) reported that Sb(III) exposure induces oxidative stress via reactive oxygen species (ROS) generation and activates *ars* and *pst* operons for detoxification and defense. Collectively, these studies confirm that multi-omics approaches effectively link gene expression, protein synthesis, and metabolite changes in an integrated biological system, providing mechanistic insights into microbial adaptation to pollutant-induced stress.

2. Mapping Microbial Community Interactions and Dynamics

This subtheme highlights the use of multi-omics to map interspecies interactions and functional dynamics within microbial communities during bioremediation. Lee and Yoon (2021) demonstrated cross-feeding mechanisms between *Pseudomonas aeruginosa* and *Rhodococcus sp.* in TNT degradation, emphasizing the importance of metabolite exchange among species. (Song et al., 2021), found that marine microbial communities possess a high genetic potential for hydrocarbon degradation, characterized by elevated expression of degradation genes, secretion systems, and DNA repair pathways. (Sandhu et al., 2022) identified PAH and PCB degradation genes (*nahAc*, *bphA*, *bphC*) and associated metabolic pathways, revealing how heavy metals and nutrient availability shape microbial community composition in steel industry soils. Overall, multi-level omics data enable the visualization of syntrophic interactions and ecological adaptation, providing insight into metabolic cooperation that enhances the efficiency of natural bioremediation across contaminated ecosystems.

3. Precision Microbial Engineering and Consortium Enhancement

The third theme emphasizes the application of multi-omics in microbial engineering and synthetic consortium

development for more efficient bioremediation. (Renganathan et al., 2025) reported that engineered microbial consortia effectively degraded complex xenobiotics-including pharmaceuticals, synthetic dyes, and microplastics through syntrophic cooperation among species. Multi-omics analyses identified key genes, enzymes, and metabolic pathways involved in these degradation processes. Shafana Farveen & Narayanan (2024), showed that multi-omics approaches identified plastic-degrading microbes such as *Pseudomonas* and *Ideonella*, along with major enzymes like *PETase* and *laccase*; transcriptomic and proteomic analyses revealed upregulation of oxidative and hydrolytic enzymes upon plastic exposure. (Shah et al., 2024) further demonstrated that multi-omics can identify novel degradation pathways for emerging contaminants (CECs) such as pesticides and pharmaceuticals, highlighting microbial interactions and oxidative responses as key drivers of biotransformation. These findings collectively demonstrate a paradigm shift from descriptive to application-oriented multi-omics, supporting data-driven microbial biotechnology engineering with strong molecular validation to produce robust, efficient, and adaptive microbial consortia for modern bioremediation systems.

Discussion

The results of the analysis of ten selected literature clearly show that multi-omics integration has become a transformative driver in the field of bioremediation. This approach not only confirms the findings of single-omics studies but, more importantly, provides systemic and holistic insights that were previously inaccessible, particularly in understanding the interactions, dynamics, and actual functions of microbes in contaminated environments.

1. Molecular Mechanisms and Microbial Adaptive Responses to Pollutants

The integration of multi-omics datasets has proven essential in elucidating the molecular basis of microbial adaptation and pollutant degradation. (Li et al., 2023) demonstrated that metagenomic - metabolomic integration provides detailed insights into hydrocarbon degradation pathways, particularly toluene, xylene, and PAHs, revealing enhanced regulation of monooxygenase and dioxygenase genes that drive catabolic activation. Similarly, (Kumar et

al., 2023) identified the complete chlorpyrifos degradation pathway, including the *oph* gene and TCP intermediates, confirming that degradation efficiency depends on the coordinated activity of multiple bacterial taxa within the consortium. (Zhu et al., 2024) further demonstrated that selenium enhances cadmium tolerance in plants and microbes through the activation of photosynthetic and antioxidant proteins such as *psbO*, *psaG*, and *OsGSTF1*. In addition, Gu et al. (2020) revealed that Sb(III) exposure induces oxidative stress via reactive oxygen species (ROS) formation, triggering the *ars* and *pst* operons responsible for detoxification and phosphate transport regulation. These studies collectively reinforce the principles of systems biology ((Hassan & Ganai, 2023), where the interactions among genes, proteins, and metabolites determine the functional resilience of organisms under environmental stress. Despite the remaining challenges in quantifying metabolite fluxes in complex matrices such as soil, multi-omics integration continues to serve as a diagnostic and predictive tool for assessing bioremediation potential, providing molecular-level evidence of pollutant transformation and microbial adaptation (Shi et al., 2024; Yunusa, Y.R. & Umar, Z.D., 2021).

2. Microbial Community Interactions and Ecological Dynamics

The application of multi-omics technologies has deepened understanding of interspecies interactions and functional dynamics in microbial communities during bioremediation. (Lee & Yoon, 2021) revealed a cross-feeding mechanism between *Pseudomonas aeruginosa* and *Rhodococcus sp.* during TNT degradation, highlighting the metabolic complementarity required for efficient detoxification. (Song et al., 2021) observed that marine microbial communities exposed to oil contamination upregulate hydrocarbon degradation, secretion, and DNA repair genes, reflecting a coordinated adaptive response to environmental stress. (Sandhu et al., 2022) confirmed that genes responsible for PAH and PCB degradation (*nahAc*, *bphA*, *bphC*) are influenced by heavy metal concentrations and nutrient availability, indicating that physicochemical factors shape microbial functional potential. Collectively, these results support the concept of synthetic

ecology ((Islam et al., 2023), which posits that microbial cooperation and metabolic exchange are key to achieving stable and efficient degradation systems. Although many studies remain limited by insufficient metabolomic data integration, multi-omics has provided an increasingly clear picture of syntrophic cooperation, functional redundancy, and ecological resilience within microbial consortia. These insights are critical for the design of synthetic communities capable of maintaining stability and efficiency across fluctuating environmental conditions (García-García et al., 2019).

3. Precision Microbial Engineering and Synthetic Consortium Applications

Recent developments demonstrate how multi-omics data can guide precision engineering of microbial strains and consortia for next-generation bioremediation. (Renganathan et al., 2025) utilized AI-assisted multi-omics to construct synthetic microbial consortia capable of degrading pharmaceuticals, synthetic dyes, and microplastics through cooperative metabolic networks. (Shafana Farveen & Narayanan, 2024) discovered novel plastic-degrading microorganisms, including *Pseudomonas* and *Ideonella*, and confirmed that exposure to plastics triggers higher expression of oxidative and hydrolytic enzymes such as PETase and laccase. (Shah et al., 2024) expanded this application by identifying previously unknown degradation pathways for emerging contaminants, emphasizing oxidative stress responses and interspecies cooperation as central mechanisms in biotransformation.

These findings align with the bioengineering systems framework (Costello & Martin, 2018), which emphasizes the integration of genomic, proteomic, and metabolomic data in the rational design of engineered organisms. Although most studies remain limited to laboratory validation (Roy et al., 2021), the transition from descriptive analyses to multi-omics-driven engineering represents a paradigm shift toward adaptive, data-informed, and sustainable bioremediation strategies applicable at industrial and environmental scales.

Challenges and Future Directions

Despite its enormous potential, the application of

multi-omics in bioremediation still faces some significant challenges, as reflected in the limitations expressed by the studies analyzed.

- 1) Integration and Analysis of Bioinformatics Data: The biggest challenge is to integrate large and heterogeneous data sets from various layers of omics. The complexity of environmental samples, such as soil, can cause noise on metabolomic data ((Li et al., 2023). Developing bioinformatics pipeline and statistical tools that can correlate these data meaningfully is still an active research area. Limitations of bioinformatics expertise are often a barrier.
- 2) The gap between Lab and Field (Lab-to-Field Gap): Many multi-omics studies are conducted under controlled laboratory conditions. This condition may not fully represent the complexity and dynamics of the process in situ on the ground (Li et al., 2023). Translating these molecular insights into effective field applications is still a challenge. Longitudinal field studies such as (Gu et al., 2020) need to be done more to bridge this gap.
- 3) Data and Cost Accessibility: Limitations of access to raw data due to the restrictions of sequencing services companies (Zhu et al., 2024) may hinder reproducibility and re-analysis. In addition, although the cost of genome sequencing has fallen, deep proteomic and metabolomic analysis is still relatively expensive, limiting its application in large-scale studies.
- 4) Functional Validation: Multi-omics analysis is often predictive and correlative. Further functional validation through traditional microbiological experiments is still much needed, as highlighted by (Sandhu et al., 2022) which states that the functional validation of metagenomically identified degradation genes has not been done.
- 5) Consortium Complexity: In complex microbial consortium, determining the exact contribution of each member without advanced tracking techniques remains a challenge (Kumar et al., 2023), complicating the spatial and specific interpretation of multi-omics data to strains.

Going forward, research needs to focus on:

- (1) More user-friendly and powerful bioinformatics tools development for data

integration; (2) Improved studies in situ and fields that combine multi-omics with geochemical analysis; (3) Deeper exploration of microbial-plant-environment interactions (integrate rhizosphere microbiome studies); (4) Multi-omics data utilization to build strong predictive models that can simulate the results of bioremediation under various conditions; as well as (5) Interdisciplinary funding policies and collaborations that support the application of these technologies to overcome the most complex contaminated sites.

Conclusion

Overall, the findings across multiple studies demonstrate that the *multi-omics* approach has revolutionized our understanding of pollutant degradation mechanisms and microbial adaptive responses to environmental stressors. The cross-level integration of genomics, transcriptomics, proteomics, and metabolomics enables the elucidation of causal relationships between genes, enzymes, and metabolites that could not be revealed by single-omics methods. Through the mapping of microbial interactions and the design of data-driven synthetic consortia, *multi-omics* has evolved from a descriptive analytical tool into a foundation for precision bioengineering to develop more efficient, stable, and sustainable bioremediation systems. When integrated with artificial intelligence and synthetic biotechnology, this approach opens new opportunities for adaptive environmental management strategies within a circular economy framework. Thus, *multi-omics* serves as a cornerstone for advancing environmental biotechnology toward the next generation of intelligent bioremediation.

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