SJIF Impact Factor (2026): 8.863| ISI I.F. Value: 1.241| Journal DOI: 10.36713/epra2016 ISSN: 2455-7838(Online)
EPRA International Journal of Research and Development (IJRD)
Volume: 11 | Issue: 2 | February 2026 - Peer Reviewed Journal

MICROBIAL GENOMICS AND FUNCTIONAL METAGENOMICS FOR OIL SPILL BIOREMEDIATION: A SYSTEMATIC REVIEW

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Article DOI: https://doi.org/10.36713/epra26198
DOI No: 10.36713/epra26198

ABSTRACT

Background: Oil spills are a longstanding risk to the marine and coastal ecosystem, thus requiring efficient bioremediation processes. Microbial genomics and functional metagenomics are robust tools for the study of hydrocarbon-degrading communities, their catabolic pathways and applications in bioremediation. This systematic review of evidence from multiple oil-impacted ecosystems describes microbial response, functions and degradation mechanisms.

Methods: A bibliographical search was conducted following the PRISMA recommendations in databases such as Cochrane, Web of Science, Scopus, ResearchGate and Google Scholar. Fourteen studies were included from screened records through duplicate removal, title/abstract screening and full text extraction and presented via thematic synthesis.

Findings: Oil exposure constantly caused marked microbial re-structuring, where Proteobacteria were the most abundant group, and Archaea, as well Eukaryota constituted minor fractions. An initial signature of rich oil exposure was the dominance by particular taxa, giving way to increased diversity during succession. Degradation of hydrocarbons proceeded along oxygen and substrate dependent aerobic and anaerobic pathways, with selective reduction of short and mid-chain alkanes while long chain alkanes and polycyclic aromatic hydrocarbons were persistent. Pathway abundance tripled for functional genes among hydrocarbon degradation, nitrogen metabolism, stress response and xenobiotic processing. Active expression and high degradation efficiency were verified through metatranscriptomic and laboratory analyses. Oil contamination also linked the processing of hydrocarbons to nitrogen turnover and impacted bioremediation efforts.

Conclusion: Oil spills mediate predictable taxonomic and functional changes, increase the metabolic potential of microbial communities, and demonstrate microbial communities evolved capacity for bioremediation in varied environments. Multi-omics approach coupled with field trials should be integrated in future studies to optimize interventions.

KEYWORDS: *Microbial communities, Oil Spill Bioremediation, Hydrocarbon degradation, Functional metagenomics*

1.0 INTRODUCTION

Oil spills continue to remain one of the most devastating anthropogenically induced disturbances in natural ecosystems. It releases complex mixtures of aliphatic hydrocarbons (AHs), polycyclic aromatic hydrocarbons (PAHs), resins, and asphaltenes into marine, coastal, and terrestrial environments (Barron et al., 2020; Hidalgo et al., 2020). Large-scale spills, such as the Deepwater Horizon disaster, have called attention to the persistent nature of petroleum contamination, spatial variability, and long-term ecological effects (McClain et al., 2019). In addition to acute toxicity, spills perturb biogeochemical cycles, food webs, and maintain chronic stressors on microbial communities that mediate ecosystem resilience and recovery (Philippot et al., 2021).

Microorganisms are the major contributors to the natural attenuation of petroleum hydrocarbons and serve as a basis for oil spill bioremediation. Many bacteria and archaea-heterotrophs commonly harbor metabolic pathways for the degradation, mineralization, and/or sequestration of hydrocarbons in both aerobic and anaerobic conditions (Dhar et al., 2025). Many hydrocarbon-degrading taxonomic groups, such as the Proteobacteria, Actinobacteria, and Firmicutes, have been identified in classical culture-dependent studies (Dhar et al., 2025). Nevertheless, culturing-based methods recover only a minor fraction of the total microbial diversity present within an environment and yield little information on community-level functional potential, metabolic plasticity or in situ activity (Kostka et al., 2014).

The investigation of oil-impacted environments has been radically revolutionized by microbial genomics and high-throughput sequencing (Mason et al., 2012). Metagenomics, metatranscriptomics, and genome-resolved approaches now offer the ability to fully characterize the composition of microbial communities, as well as their functional gene repertoires and active metabolic processes, in the absence of cultivation (Mason et al., 2012). These methods uncovered the high degree of functional redundancy, rapid microbial turnover, and metabolically convergent ecosystems spanning from spatially isolated oil-impacted locations (Hidalgo et al., 2020).

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Whole-genome analyses have also identified extensive reservoirs of previously undescribed hydrocarbon-degrading microorganisms (Somee et al., 2022), highlighting the deficiencies in reference-based annotations and the complexity of microbial responses to oil exposure.

Recent reports also suggest that hydrocarbon degradation is highly interactive with broader ecosystem functions such as nitrogen, sulfur and iron cycling, stress response mechanisms, viral interactions, and metabolite turnover (Pandolfo et al., 2023). Aerobic and anaerobic degradation pathways are influenced by oxygen concentration, hydrocarbon characteristics, nutrient availability, spill history, and age of the spill (Folayan et al., 2023). These factors interact to shape rates of degradation rate and remaining contamination. Concurrently, bioremediation techniques, including biostimulation and bioaugmentation, have the potential to modulate microbial community dynamics, but their long-term success and ecological implications remain debated (Maqsood et al., 2024).

Despite the rapid growth of genomics in oil spill studies, such research remains fragmented across environments, methodological approaches, and temporal scales (Harik et al., 2022). A systematic synthesis integrating microbial community restructuring, functional gene diversity, metabolic pathways, and empirical validation of biodegradation is needed to consolidate current knowledge and identify unifying patterns. This paper presents a systematic review and synthesis of studies characterizing genomic and functional metagenomic composition in oil-contaminated environments. The current review aims to elucidate how microbial communities respond to oil spills, the functional mechanisms underpinning hydrocarbon degradation, and the implications for bioremediation strategies across diverse ecosystems.

2.0 METHODS

2.1 Study Design and Reporting Framework

This systematic review explored microbial genomics and functional metagenomics in oil spill bioremediation. The review was performed and presented according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines.

2.2 Literature Search Strategy

A thorough search was conducted in Cochrane, Web of Science, Scopus, ResearchGate, and Google Scholar. Search terms were composed with the use of Boolean operators and consisted of oil spill, petroleum hydrocarbons, bioremediation, microbial genomics, metagenomics, and hydrocarbon degradation. The reference lists of the pertinent articles were also reviewed for additional studies.

2.3 Eligibility Criteria

Studies were included if they:

- Studied oil-impacted marine, shoreline, intertidal, deep-sea or terrestrial ecosystems
- Applied genomic, metagenomic, metatranscriptomic, or genome-resolved approaches
- Discussed the composition of microbial communities, gene contents, or processes for hydrocarbon degradation.

Publications dedicated to physicochemical remediation without any microbial or genomic findings were also excluded.

2.4 Study Selection and Data Extraction

After excluding duplicates, titles and abstracts of retrieved studies were screened for relevance. Full text was also reviewed. Details extracted from all relevant studies included sequencing strategy, taxonomic composition, repertoires of functional genes and pathways for the degradation of hydrocarbons, biogeochemical coupling, and experimental or field studies validating biodegradation.

2.5 Data Synthesis

The results were synthesized qualitatively through theme integration. Results were categorized into coherent subthemes on microbial community structure, succession patterns, functional potential, gene expression activities, metabolic pathways analyses, and bioremediation strategies. Fourteen studies satisfied the review eligibility criteria. The flow PRISMA below sums up the screening and selection process (Figure 1).

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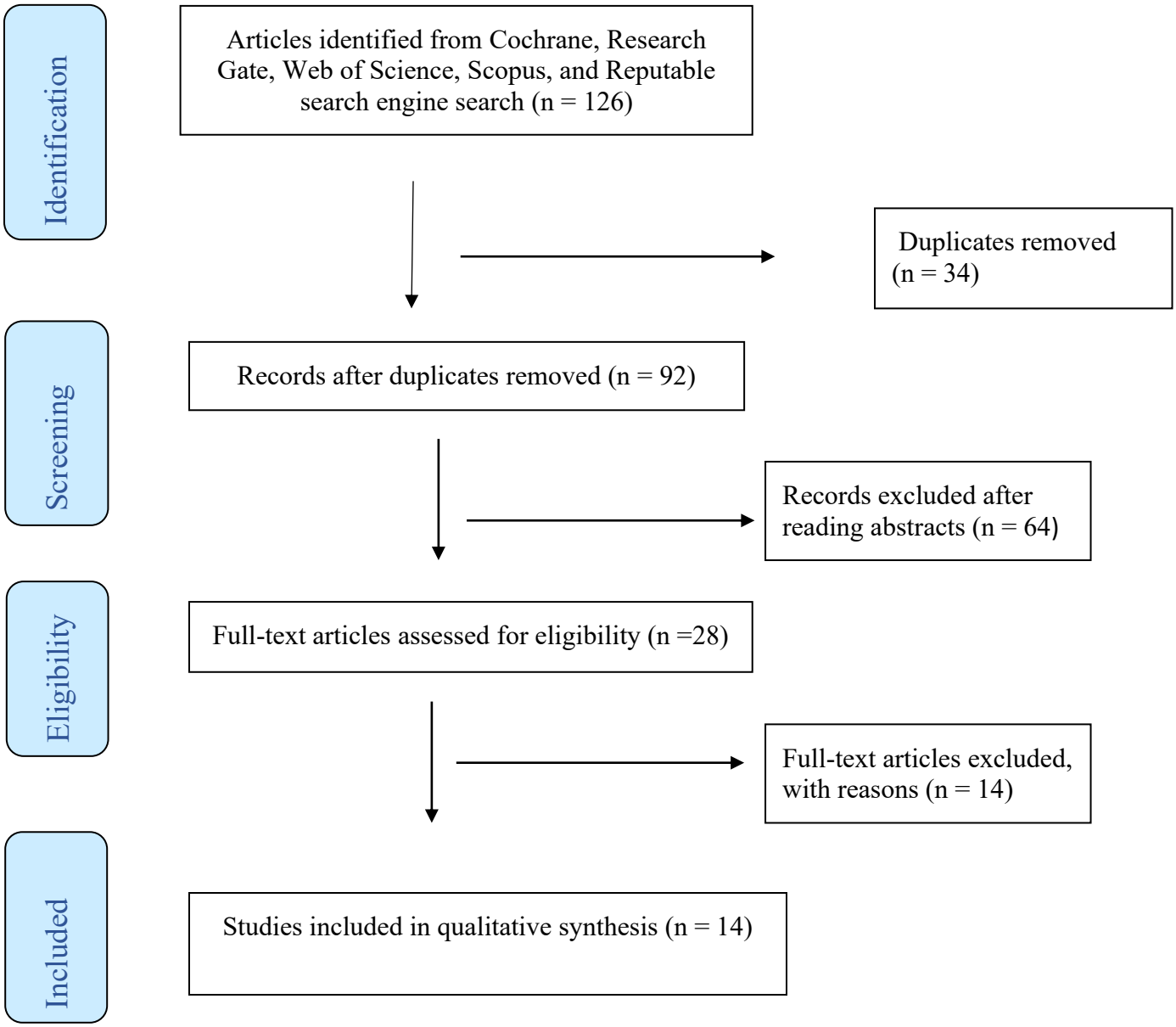


Figure 1: PRISMA Flow diagram showing the article selection process.

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3.0 RESULTS

3.1 Oil Spill-Driven Restructuring of Microbial Communities Across Environments

Oil contamination reshaped microbial communities in marine water columns, coastal sands, deep-sea sediments, intertidal zones, and terrestrial soils. Factors like hydrocarbon levels, oxygen supply, spill duration, and habitat type drove these changes (Banet et al., 2021; Karthikeyan, Kim, et al., 2020; Kimes et al., 2013; Kimes et al., 2014; Mason et al., 2012; Mason et al., 2014; Pacwa-Płociniczak et al., 2020; Redmond & Valentine, 2012; Song et al., 2021). Bacteria dominated assemblages in every setting, while Archaea and Eukaryota remained minor components (Kimes et al., 2013; Song et al., 2021).

Metagenomic sequencing from oil-affected marine waters produced over 10 Gbp of high-quality data. This effort identified 518,265 non-redundant genes, with about 58% assigned to Bacteria (Song et al., 2021). Deep-sea sediments showed bacterial sequences at 95 to 97% of total reads. Archaea made up 2.2 to 4.2%, mainly Euryarchaeota near the Deepwater Horizon wellhead (Kimes et al., 2013).

Multivariate analyses linked microbial beta diversity to total petroleum hydrocarbon concentrations, dissolved inorganic nitrogen gradients, and distance from spill sources (Kimes et al., 2013; Lamendella et al., 2014; Mason et al., 2014; Song et al., 2021). Sediments within 5 km of the DWH wellhead carried the highest TPH levels, above U.S. EPA standards. Their microbial groups differed sharply from those in less contaminated or clean sites (Mason et al., 2014). Deep-water plumes saw a sharp drop in diversity compared to background waters. Bacterial cell counts rose from roughly 5.5×10^3 cells ml^{-1} to over 10^5 cells ml^{-1} (Mason et al., 2012; Redmond & Valentine, 2012). Comparisons across distant sites like the Gulf of Mexico, Bohai Bay, and Norwegian waters showed similar functional and taxonomic patterns. These depended more on oil exposure than on location (Kimes et al., 2013; Song et al., 2021).

3.2 Taxonomic Composition, Dominance Patterns, and Successional Dynamics

Proteobacteria stood out at the phylum level in oil-affected sites. They accounted for 32 to 65% of annotated genes and reads in marine waters and sediments (Karthikeyan, Kim, et al., 2020; Kimes et al., 2013; Kimes et al., 2014; Mason et al., 2012; Mason et al., 2014; Redmond & Valentine, 2012; Song et al., 2021). Bacteroidetes comprised 9 to 10% in marine metagenomic data. Actinobacteria, Firmicutes, and Acidobacteria appeared at lower levels but contributed to overall diversity (Song et al., 2021). Archaea mainly consisted of Euryarchaeota, Thaumarchaeota, and Crenarchaeota. Sulfate-reducing and methanogenic groups increased near spill centers (Kimes et al., 2013).

Key genera in these environments included Pseudomonas, Marinobacter, Alcanivorax, Shewanella, Streptomyces, Bacillus, Flavobacterium, Mycobacterium, Paenibacillus, and Rheinheimera (Kimes et al., 2013; Kimes et al., 2014; Lamendella et al., 2014; Pacwa-Płociniczak et al., 2020; Song et al., 2021). Genus annotations ranged from 27 to 46%. This gap reflected limited reference genomes for oil degraders (Song et al., 2021). Deep-sea sediments near spills enriched sulfate-reducing Deltaproteobacteria such as Desulfatibacillum, Desulfobacterium, Desulfococcus, Desulfovibrio, and Geobacter (Kimes et al., 2013).

Strong dominance by a limited number of taxa was observed during early oil exposure, followed by increased diversity during later successional stages (Karthikeyan, Kim, et al., 2020; Kimes et al., 2014; Mason et al., 2012; Mason et al., 2014; Pacwa-Płociniczak et al., 2020; Redmond & Valentine, 2012). Deep-water plumes started with one Oceanospirillales unit taking 80 to 90% of 16S rRNA sequences and over 60% of metagenomic reads. Outside plumes, it stayed at 3 to 5% (Mason et al., 2012; Redmond & Valentine, 2012). Aging plumes shifted to Colwellia and Cycloclasticus. After well capping, diversity rose with methylotrophs like Methylococcaceae, Methylophaga, and Methylophilaceae, plus Flavobacteria and Rhodobacterales (Kimes et al., 2014; Redmond & Valentine, 2012).

Intertidal sediments favored Gammaproteobacteria initially. Alphaproteobacteria dominated in oxygen-rich phases. Long low-oxygen periods boosted sulfate-reducing Deltaproteobacteria (Karthikeyan, Kim, et al., 2020). Terrestrial soils followed spill age-dependent successions. A 1975 site enriched Firmicutes and Gammaproteobacteria, while A 2014 site kept Chloroflexi and Thermi but gained oil-degrading ability in four years despite hyper-arid conditions (Banet et al., 2021). Bioaugmented soils began with Rhodococcus or Mycobacterium dominance. These later gave way to Acetobacteraceae and Acidimicrobiales, matching natural communities (Pacwa-Płociniczak et al., 2020).

3.3 Hydrocarbon Composition and Temporal Depletion Patterns

Chemical tests on beaches and sediments hit by oil showed hydrocarbon makeup that lined up well with the original source oils. This included MC252 crude from the DWH spill (Lamendella et al., 2014). Total petroleum hydrocarbon levels were undetectable and increased up to 2072 mg/kg. The worst hotspots turned up in heavily oiled beach spots (Lamendella et al., 2014).

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Studies show clear patterns over time. Short and mid-length alkanes from C8 to C20 broke down first, while longer chains over C20 and branched alkanes persisted over time (Kimes et al., 2014; Lamendella et al., 2014; Parthipan et al., 2017). More than a third of tainted samples had polycyclic aromatic hydrocarbons. Three and four ring types like fluorene, phenanthrene, chrysene, and pyrene showed up at the highest levels. Two ring versions depleted from lighter hit areas (Lamendella et al., 2014).

Weathering processes wiped out BTEX compounds, naphthalene, and C9 to C16 n-alkanes. In return, oxyhydrocarbons built up to over half the leftover mass in sand patties (Kimes et al., 2014). Declines in TPH concentrations were positively correlated with sampling time across contaminated sites (Lamendella et al., 2014).

3.4 Expansion of Functional Gene Repertoires and Functional Redundancy

Metagenomic studies revealed a substantial expansion of functional gene diversity in environments affected by oil (Karthikeyan, Kim, et al., 2020; Karthikeyan, Rodriguez-R, et al., 2020; Mason et al., 2014; Pacwa-Płociniczak et al., 2020; Scott et al., 2014; Song et al., 2021). Contaminated sediments held more than three times as many unique functional annotations as uncontaminated ones, with 660 compared to 184. Enriched categories included genes for aromatic compound metabolism, sulfur metabolism, membrane transport, secondary metabolism, and xenobiotic degradation (Mason et al., 2014).

Marine water samples yielded specific counts through functional annotation. Researchers identified 4112 NAD(P)-dependent dehydrogenases, 2521 acyl-CoA dehydrogenases, 545 cytochrome P450 genes, and 85 alkB genes tied to alkane oxidation (Song et al., 2021). Intertidal sediments undergoing oxic–anoxic cycling exhibited increased abundance of genes associated with hydrocarbon degradation, nitrogen fixation, nutrient scavenging, stress response, and iron acquisition (Karthikeyan, Kim, et al., 2020). Oil seep sediments displayed the highest diversity of nitrogen metabolism genes (131 genes), many absent from both spill-impacted and uncontaminated sediments (Scott et al., 2014).

Work at a global level through the Genome Repository of Oil Systems gathered 2059 MAGs and SAGs. These formed 1536 species-level clusters across 63 bacterial and archaeal phyla (Karthikeyan, Rodriguez-R, et al., 2020). Only 4.25% of clusters came from cultured taxa. Nearly 45% of Deepwater Horizon genomes matched known species at less than 50% average amino acid identity. Although 82% of genomes proved restricted to specific habitats, core genes for hydrocarbon degradation appeared consistently across different systems. Such conservation pointed to widespread functional redundancy, even as the underlying taxonomy changed (Karthikeyan, Rodriguez-R, et al., 2020).

3.5 Aerobic and Anaerobic Hydrocarbon Degradation Pathways

Researchers found genes for both aerobic and anaerobic hydrocarbon breakdown in all samples studied. The mix of pathways depended mainly on oxygen levels and the types of hydrocarbons present (Banet et al., 2021; Karthikeyan, Kim, et al., 2020; Kimes et al., 2013; Kimes et al., 2014; Mason et al., 2012; Mason et al., 2014; Pacwa-Płociniczak et al., 2020; Parthipan et al., 2017). Aerobic pathways took the lead in oil plumes, surface waters, and oxygen-rich sediments. These pathways featured alkane monooxygenases, alcohol and aldehyde dehydrogenases, cyclohexane monooxygenases, and ring-hydroxylating dioxygenases (Kimes et al., 2014; Mason et al., 2012; Mason et al., 2014; Song et al., 2021).

Deep-water plume metagenomes showed full n-alkane degradation pathways. Aromatic and PAH genes appeared less often and showed weak expression (Mason et al., 2012). Sediment studies reconstructed complete cyclohexane breakdown paths similar to those in Brachymonas petroleovorans (Mason et al., 2014). Anaerobic genes like assA, bssA, and full benzoyl-CoA reductase sets stayed limited to sediments near the DWH wellhead. There, these genes made up as much as 15% of all functional annotations (Kimes et al., 2013).

Genome-resolved work pulled out 49 MAGs. Nearly half encoded full aerobic alkane oxidation paths. About 12% had anaerobic alkane degradation. A third carried aerobic aromatic paths, and another 12% showed anaerobic aromatic ones (Karthikeyan, Kim, et al., 2020).

3.6 Active Transcription of Degradation Pathways and Enzyme-Level Validation

Metatranscriptomic data proved that hydrocarbon degradation genes worked actively in the field (Karthikeyan, Kim, et al., 2020; Kimes et al., 2014; Lamendella et al., 2014; Mason et al., 2012; Song et al., 2021). Beach sand from contaminated sites produced about 17 million reads that matched hydrocarbon gene databases. This gave 3,553 unique matches for monooxygenases, dioxygenases, and PAH enzymes (Lamendella et al., 2014). Gentisate pathway genes stayed active, which pointed to ongoing aerobic aromatic breakdown (Lamendella et al., 2014).

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Marine water column samples expressed close to 5,000 KEGG orthologs. Energy metabolism, nitrogen handling, secretion systems, and biofilm genes saw big boosts. Photosynthesis genes dropped off (Song et al., 2021). In plumes, Oceanospirillales transcripts filled 46 to 69% of expressed genes. Alkane monooxygenases topped the list, but PAH genes barely registered (Mason et al., 2012).

Lab tests backed up these field findings. Pseudomonas stutzeri NA3 and Acinetobacter baumannii MN3 hit peak alkane hydroxylase activity on day 3, at 176 and 170 μmol min^{-1} mg^{-1} protein. Monocultures degraded 78 to 84% of crude oil. Mixed groups reached 86%, wiping out C8 to C15 hydrocarbons completely and partly breaking down C16 to C28 ones (Parthipan et al., 2017).

3.7 Coupling of Hydrocarbon Degradation with Nitrogen Cycling and Metabolite Turnover

Oil contamination disrupted nitrogen cycling processes in every environment studied. Studies identified strong upregulation of nitrogen metabolism genes in marine settings affected by oil, particularly those involved in nitrate and nitrite transport along with regulatory systems like NtrC and NtrX (Song et al., 2021). Researchers also found diazotrophic bacteria such as Candidatus Macondimonas diazotrophica linked directly to hydrocarbon breakdown pathways (Weiman et al., 2021).

Intertidal sediment samples from oiled areas showed nif gene expression more than five times higher than in controls. Over 65% of the genomes in these samples carried the nifH gene, especially under oxygen-rich conditions. Meanwhile, narG expression rose during periods of low oxygen (Karthikeyan, Kim, et al., 2020). When researchers compared nitrogen metabolism across oil seeps, spill sediments, and clean sites, they noted clear differences in profiles. Anammox genes appeared most frequently in seep areas (Scott et al., 2014). Models of metabolomic turnover further suggested that all sediments consumed net nitrogen, though seeps showed the highest rates, followed by spill-impacted zones and then uncontaminated ones (Scott et al., 2014).

3.8 Stress Response, Transport Systems, Viral Interactions, and Bioremediation Interventions

Oil-impacted metagenomes contained abundant genes for transport, efflux, and stress responses. These included ABC-type multidrug transporters, AcrB efflux pumps, SecA translocation systems, metal ion transporters, and recF pathway components for DNA repair (Song et al., 2021). CRISPR-Cas systems and phage-related genes occurred widely. Analysis detected 1,149 CRISPR loci together with Cas proteins, prophage regulators, recombinases, and lysozymes, all pointing to ongoing virus-host dynamics (Song et al., 2021).

Enrichment cultures produced 18 distinct bacterial isolates, mostly Gammaproteobacteria from genera like Pseudomonas, Marinobacter, Alcanivorax, Vibrio, and Rheinheimera. Many grew using crude oil alone as their carbon source and targeted straight-chain alkanes and PAHs (Lamendella et al., 2014). These strains produced biosurfactants that improved oil availability, achieving emulsification rates of 36 to 39% and yields as high as 4.68 g/L in lab tests (Parthipan et al., 2017).

Terrestrial soil experiments demonstrated that biostimulation with water and nutrients cut GRO plus DRO levels by up to 85% in older spills and about 50% in newer ones. Bioaugmentation offered only modest extra gains (Banet et al., 2021). Metagenomic data revealed sharp initial shifts in function after bioaugmentation, with boosts in xenobiotic degradation pathways that later stabilized to match untreated soils (Pacwa-Płociniczak et al., 2020).

4.0 DISCUSSION

The growing body of evidence from metagenomic, metatranscriptomic and multi-omics studies demonstrates that microbial communities in oil-impacted marine systems experience rapid, well-regulated and functionally relevant changes. In both deep-sea and surface systems, the early microbial responders are Gammaproteobacteria, Oceanospirillales, Alcanivorax, Marinobacter and Colwellia (Kimes et al., 2014; Lamendella et al., 2014; Mason et al., 2012; Redmond & Valentine, 2012; Weiman et al., 2021). This suggests that overall successional trends are conserved based on hydrocarbon availability. These taxa exhibit metabolic stratification where specific members are involved in different stages of hydrocarbon degradation, implying that hydrocarbon biodegradation is a distributed community function opposed to specific species' activities (Karthikeyan, Kim, et al., 2020; Weiman et al., 2021). The temporal change of degraders from alkane to aromatic hydrocarbon specialists reflects the dynamic adjustment of microbial communities responding to changes in substrate composition, oxygen availability and redox conditions (Karthikeyan, Kim, et al., 2020; Kimes et al., 2014; Redmond & Valentine, 2012).

Functional comparisons among studies suggest that the metabolic potential of microbial communities is plastic. Aerobic alkane monooxygenase, cyclohexane degradation and β-oxidation pathways are the among those consistently enriched in plume and sediment communities. On the other hand, anaerobic hydrocarbon degradation genes, such as bssA and assA are only expressed under oxygen limited or anoxic conditions in sediments and intertidal zones (Karthikeyan, Kim, et al., 2020; Kimes et al., 2013; Kimes et al., 2014; Mason et al., 2014). Crucially, co-enrichment of genes implicated in nitrogen, sulfur and phosphorus cycling indicates that the

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degradation of hydrocarbons is closely linked to broader biogeochemical processes and allows microbial populations to maintain activity in nutrient-limited environments (Karthikeyan, Kim, et al., 2020; Scott et al., 2014). The combination of metabolomics and metagenomics additionally supports these predictions, showing that genetic potential corresponds to active degradation and metabolite turnover in situ (Kimes et al., 2013; Scott et al., 2014).

Both community structure and functional outcome are influenced by environmental factors such as oxygen gradients, nutrient availability, temperature and natural gas composition. Oxic-anoxic cycling results in prolonged biodegradation and the sequential appearance of microbial groups, while psychrophilic alkane decomposers such as Colwellia flourish under low temperatures and methane oxidation frequently lags behind alkane metabolism (Karthikeyan, Kim, et al., 2020; Redmond & Valentine, 2012). These observations highlight that the microbial dynamics are site specific and bioremediation treatments ought to be designed in a context-specific manner. Additionally, the ubiquitous presence of CRISPR elements, prophage sequences and lateral gene transfer events suggests an involvement of viral interactions and horizontal gene transfer in modulating community robustness and evolution of hydrocarbon degraders (Song et al., 2021; Weiman et al., 2021). This functional connectivity could serve to promote resistance of biodegradation functions in oil-impacted ecosystems that are both spatially and temporally variable.

Overall, this review highlights the promise of omics-based approaches to inform mitigation responses for oil spills. By integrating microbial succession with functional gene expression and environmental parameters, predictive models can prioritize key taxa and metabolic pathways for targeted bioremediation, serve as a tool to guide the application of nutrient amendments, and monitor ecosystem recovery (Karthikeyan, Kim, et al., 2020; Kimes et al., 2014; Weiman et al., 2021). Importantly, even after apparent taxonomic recovery, functional profiles often remain altered, suggesting that functional metrics may provide a more sensitive indicator of ecosystem health than taxonomic composition alone.

5.0 CONCLUSION

This systematic literature review reveals that oil spills induce major and consistent shifts in the composition of microbial communities in marine, intertidal, deep-sea, and onshore habitats. Microbial communities are primarily influenced by the concentration of hydrocarbons, oxygen availability, spill age and habitat type with Bacteria dominating both taxonomic composition and functional profiles, whereas Archaea and Eukaryota occupy distinct ecological niches. Oil contamination causes initial blooms of a few, dominant oil-degrading taxa that give way to community expansion, with all taxa showing comparable successional patterns that appear coordinated across geography. Functional metagenomics and metatranscriptomics indicate a high degree of redundancy in hydrocarbon degradation pathways, including aerobic and anaerobic pathways. These are interconnected with nitrogen cycling, metabolite turnover, and stress responses which enable resilience and adaptability to impacted ecosystems. Experimental validation of the laboratory results indicates that closely related taxa degrade multiple classes of hydrocarbons effectively, offering applicational relevance for genomic inferences to bioremediation.

6.0 RECOMMENDATIONS

Considering the body of evidence presented here, future studies and approaches for remediation should seek to include genomic, metagenomic, and transcriptomic profiling to determine hydrocarbon-degrading taxa as well as functional genes from various habitats. For bioremediation, there should be a site-specific optimization of the pros and cons by using both natural microbial succession and adding tailored interventions such as nutrient biostimulation, bioaugmentation, biosurfactant application monitoring to maintain degradation potential over time. Long-term observations of the dynamics in microbial community composition and associated metabolic activity are required to gain insight into ecosystem recovery trajectories and adjust management strategies in an increasingly variable environment. Furthermore, the development of culture collections and improvements in genome-resolved analysis could bridge the gap between in situ functional potential and lab-based bioremediation approaches to scale-up and apply microbial methods to oil-impacted ecosystems in the US and around the world.

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