Sustainable strategies for combating hydrocarbon pollution: Special emphasis on mobil oil bioremediation

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Abstract

The global rise in industrialization and vehicularization has led to the increasing trend in the use of different crude oil types. Among these mobil oil has major application in automobiles and different machines. The combustion of mobil oil renders a non-usable form that ultimately enters the environment thereby causing problems to environmental health. The aliphatic and aromatic hydrocarbon fraction of mobil oil has serious human and environmental health hazards. These components upon interaction with soil affect its fertility and microbial diversity. The recent advancement in the omics approach *viz.* metagenomics, metatranscriptomics and metaproteomics has led to increased efficiency for the use of microbial based remediation strategy. Additionally, the use of biosurfactants further aids in increasing the bioavailability and thus biodegradation of crude oil constituents. The combination of more than one approach could serve as an effective tool for efficient reduction of oil contamination from diverse ecosystems. To the best of our knowledge only a few publications on mobil oil have been published in the last decade. This systematic review could be extremely useful in designing a micro-bioremediation strategy for aquatic and terrestrial ecosystems contaminated with mobil oil or petroleum hydrocarbons that is both efficient and feasible. The state-of-art information and future research directions have been discussed to address the issue efficiently.

Keywords: Mobil oil; Hydrocarbons; Biosurfactants; Biodegradation; Omics approaches

1. Introduction

Globally, machine/ mobil oil is recognized as a class of aliphatic and aromatic petroleum hydrocarbon compounds that are commonly used as a lubricating agent, metallic rust blockers, and emulsifying agents in a variety of large and small scale sectors (Sherry et al., 2017; Wang et al., 2019). The most ubiquitous environmental pollutants are petroleum hydrocarbons, such as cycloalkanes, n-alkanes, and polycyclic aromatic hydrocarbons (PAHs), which all pose significant environmental and public health problems (Gaur et al., 2021). Mobil/machine oil is unavoidably contaminating the environment and ecosystems such as water and soil sources, as their numerous uses and extensive usage grow each year (Mahla and Dhir, 2019). If not properly managed during shipping, storage, and post-use cleaning it gives birth to numerous environmental challenges and human health issues. Its remediation necessitates the use of multiple metabolic pathways found in various microorganisms (Laczi et al., 2020; Tetteh et al., 2021). According to the US Energy Information Administration, worldwide everyday petroleum consumption in 2021 is expected to be 100.90 million barrels (Gaur et al., 2021). The occurrence of oil spills has been studied globally, it was determined that 1,000 tonnes of oil were leaked in 2020, which was the least in the previous decade (ITOPF 2020). Nowadays, a major portion of petroleum components were recognized as environmental contaminants by the US Environmental Protection Agency (USEPA) due to the massive inadvertent entry of petroleum oil into the environment, and exposure to these contaminants leads to potential carcinogenic and mutagenic consequences (Khalid et al., 2021; Yap et al., 2021). As a result, it is of utmost importance to establish sustainable and environmental friendly solutions for the bioremediation of petroleum hydrocarbon contamination.

Recently bioremediation has been shown to have the potential of degrading or reducing machine oil in polluted soil when compared to chemical treatment (Wang et al., 2019). The degrader microorganisms can either be isolated from the native site or from a distinct polluted site. Moreover, numerous species of microbes such as bacteria (*Brachybacterium, Alcanivorax, Pseudomonas, Thallassolituus, Halomonas, Cycloclasticus*, *Marinobacter hydrocarbonoclasticus* SdK644) (Ivshina et al., 2017; Kumari et al., 2018; Pal et al., 2021; Yakimov et al., 2007); fungi (*Aspergillus, Drechslera, Curvularia, Fusarium, Mucor, Lasiodiplodia, Rhizopus, Penicillium, Trichoderma*) (Al-Hawash et al., 2019; Delsarte et al., 2018; Lladó et al., 2013) and green algae (*Scenedemus, Selenastrum, or Chlorella*) (García de Llasera et al., 2016; Greco et al., 2019; Takáčová et al., 2014) have been reported to be prospective in the degradation of hydrocarbons (aliphatic and aromatic), viz., n-alkanes, phenanthrene, naphthalene, pyrene and so on. Notwithstanding these advancements, many other molecular facts about the metabolic and ecological capabilities of bacteria remain unsolved. Assessment of metabolic pathways from a specific environment was only achievable once the genes were cloned from the entire DNA of that area. The transcription factors are being expressed heterologously to elucidate their link with a specific metabolic activity. This necessitated the development of gene expression systems based on different bacteria to test the functional relevance of genes in the microbiome (Escobar-Zepeda et al., 2015; Pal et al., 2018).

Increasingly, the study of microbial populations has revealed the genesis of sequencing technology, which has shown to be uniquely strong in unraveling the microbial world due to its potential to parallelly sequence a plethora of organisms. The development of omics techniques has increased our capacity to identify bacteria capable of digesting pollutants or lowering their harmful effects (Bhatt et al., 2021; Gaur et al., 2022a). High-throughput analytic technologies are highly beneficial in revealing insight on microbial population diversity. A recent study examined the microbial diversity of soil contaminated with machine oil using high-throughput sequencing techniques (Wang et al., 2019). The phyla Proteobacteria and Bacteroidetes, had the highest counts among the 45 phyla found in the polluted soil. The Proteobacteria and Bacteroidetes accounts for 52.73 % and 16.77 % of the overall microbial population in the soil sample, respectively. It corresponded to the findings of a recent study that discovered that 42-89% of microorganisms in soil belong to the genus Proteobacteria and play a key role in the breakdown of petroleum molecules (Abed et al., 2015). The high throughput of sequencing based technologies offers speed and reliability.

As a result, investigations based on metabolomics, meta-proteomics, meta-transcriptomics, and metagenomics approaches are uncovering important data regarding microbial metabolism and linkages (Bashiardes et al., 2016). Therefore, in this review, we focus on the use of microbial and omics techniques to gain insight into diversity and function microbial community dynamics in hydrocarbon contaminated environments. The sources and toxicity of mobil oil have been discussed along with cost-effective solutions for its remediation. A schematic for different approaches studied in this review is shown in Fig. 1. Furthermore, by combining genetic/genomic/metabolic engineering, the stability, catalytic potential, and enzyme production yield of bioremediation techniques can be improved. Also to the best of our knowledge there are less than 30 publication on mobil oil during last decade (Source: Pubmed, Keyword: mobil oil). Therefore, we undertook this study and the strategies discussed in this systematic review could be very valuable in developing an efficient and feasible micro-bioremediation strategy for aquatic and terrestrial ecosystems contaminated with mobil oil or petroleum hydrocarbons.

2. Sources and toxicity of mobil oil

Petroleum hydrocarbons are complex substances with an elemental composition of hydrogen, carbon, sulfur, nitrogen and oxygen molecules, and heavy metals. They primarily contain aliphatic (alkanes) and aromatic hydrocarbons (PAHs). Petroleum hydrocarbons are derived from diverse sources that includes gasoline, coal, crude oil, and mobil oil that occur naturally into the environment. Mobil oil is the synthetic motor oil that has been refined from crude oil. The used motor oil is rich in PAHs and heavy metals such as zinc, lead, calcium, magnesium, and barium that are harmful to humans as well as environment (Wasiu et al., 2015). The mobil oil contains mixtures of branched-chain aliphatic–aliphatic and alicyclic–alicyclic hydrocarbons (Nowak et al., 2019).

The toxic property of petroleum hydrocarbons is consistent and based on the bioavailability and solubility of the hydrocarbons. Depending on the source, the composition of the petroleum hydrocarbons differs (Arjoon and Speight, 2020). Overages, the environmental problems caused by petroleum hydrocarbons have attracted researchers' attention globally. Natural and anthropogenic activities are the major factors contributing to the spillage of hydrocarbons. Petroleum hydrocarbon spills are the natural harmful contamination source whereas overflow from land based sources, spilling pipelines, and accidental spills are the major anthropogenic sources leading to potential risks to living organisms and the environment (Vyas et al., 2022). Amongst the different components of hydrocarbons, PAHs are most persistent in the environment resulting in alteration in metabolism, cell structure, function, and cause mutation (Alzahrani and Rajendran, 2019). The natural sources of PAHs include forest fire, moorland fire, and volcanic eruptionswhereas anthropogenic sources include mobile, agricultural, domestic, and industrial emission sources (Gaur et al., 2020a; Patel et al., 2020; Sharma et al., 2022). The industrial sources of hydrocarbon include petrochemical industries, coke, and primary aluminium, cement and rubber manufacturing, power and commercial heat generation, and incinerators, etc. Furthermore, mobile sources (exhaust from various modes of transportation), residential sources (home activities such as burning wood, waste burning, and heating on an oil/gas burner), and agricultural emission sources are all included in the emissions of hydrocarbons (Patel et al., 2020). During thermal decomposition of motor oil, gasoline combustion products are formed, increasing the PAHs level contributing to cancer causing and mutagenic potential of the oils. Therefore, incomplete combustion of wood, oil, coal, and other organic substances, automobile emission, oil spills all are considered as the major source of PAHs. Inhalation, ingestion, and dermal contact are the three different routes for PAHs exposure such as inhaling vehicle exhaust and road dust and ingesting polluted water, smoked and grilled foods, and smoking, etc. De et al. (2009) have studied the emission and toxicity of PAHs from mobile emission sources; ethanol fuel vehicles and gasohol vehicles and reported that the emission of PAHs from ethanol-based vehicles (11.7 to 27.4 µg/km) was comparatively less than the gasohol ones (41.9 to 612 µg/km). Researchers suggested that benzo(b)fluoranthene, benz(a)anthracene, indeno(1,2,3-cd) pyrene, dibenz(ah)anthracene, benzo(a)pyrene, chrysene, and benzo(k)fluoranthene are the most studied PAHs responsible for causing cancer in humans (Abdel-Shafy and Mansour, 2016).

Crude oil pollution in soil produces hydrophobic conditions and affects the fertility of the soil. Oil pollution resulted in severe damage to soils, as soil provides surroundings for microbial diversity and other living organisms. Contamination of soil with petroleum-based lubricants causes harmful and unfavorable effects on biological life thus disrupting the functioning of an ecosystem (Nowak et al., 2019). The skin, lungs, liver, and kidney are the main affected organ in the living organisms by the toxic effects of crude oil in the environment (IGWE et al., 2016). Irwin and colleagues, investigated the impact of crude oil on wild duck and reported that the ingestion of 5% crude oil has delayed laying and significantly reduces oviposition and thickness of shell (Irwin et al., 1997). As a result, inhalation, absorption, and ingestion of crude oil indicate various ways for crude oil toxicants to enter the system, either directly or indirectly.Almeda et al., (2013) investigated adverse effects (lethal and sublethal) of crude oil exposure on adult and larval stages of zooplanktons such as necrosis, alteration in feeding, development, and reproduction and suggested that the larval stages of zooplanktons are highly sensitive to crude oil than the adult ones. It was reported that crude oil levels (concentration: 20 and 40 µL/L) cause 100% fatality after 16 h of exposure to scyphozoan *Pelagianoctiluca*. Furthermore, it was reported that median lethal concentration (LC_{50}) for cydippidand ephyralarvae ranged from 14.52 to 8.94 and 14.41 µL/L to 0.15 µL/L after 3, 6 d and 1, 3 d, respectively (Almeda et al., 2013).

3. Strategies for combating hydrocarbon pollution

3.1. *Microbial response towards hydrocarbon pollution*

3.1.1. *Microbial response towards Aliphatic hydrocarbons pollution*

Hydrocarbons are ubiquitous environmental pollutants resulting from industrial activity, transport, accidental leakage, and other anthropogenic activities. The soil contaminated with hydrocarbon had adverse effects on the plants tissue and animals causing mutation and death (Das and Chandran, 2011; Varjani et al., 2020c). Hydrocarbon has aliphatic fractions ranging from C1 to C40 that lacks functional groups and thus exhibit low chemical reactivity. Aliphatic hydrocarbons include 3 different groups; alkanes, alkenes, and alkynes. Microorganisms were considered an efficient tool for degradation and transformation of hydrocarbons into simple metabolites (Militon et al., 2010; Varjani et al., 2021a; Varjani and Upasani, 2021). But the biodegradation of various hydrocarbons present in contaminated sites is restricted due to the limited availability of these hydrocarbons to the microorganisms (Al-Hawash et al., 2018; Varjani et al., 2020b, 2020a). Aliphatic hydrocarbons are biodegraded in two ways: first, the monooxygenase enzyme acts on n-alkanes'terminal methyl group, producing primary alcohol, followed by its oxidation into aldehyde and fatty acids; second, the dioxygenase enzyme acting on the n-alkanes' terminal methyl group, producing peroxide, which is then converted into fatty acids (Chikere et al., 2011).

The indigenous microbes were reported to degrade the petroleum hydrocarbons as they exhibit the potential to utilize these as a carbon source for their growth and survival. High-throughput sequencing technology and microbial biotechnology have been developed to identify and screen a plethora of hydrocarbon utilizing/degrading bacteria from oil contaminated environments (Mishra et al., 2020) (detailed in section 3.2). It was reported that more than 79 bacterial genera including *Acinetobacter, Achromobacter, Burkholderia, Marinobacter, Arthrobacter, Alteromonas, Mycobacterium, Enterobacter, Streptobacillus, Pseudomonas, Staphylococcus,* and *Streptococcus* were found to degrade and influence the fate of petroleum hydrocarbons in the environment (Xu et al., 2018). The consortium of halotolerant bacteria namely *Stenotrophomonas maltophilia, Ochrobactrum sp.,* and *Pseudomonas aeruginosa* isolated from crude oil contaminated site of Gujrat was studied for the degradation of hydrocarbons. It was analyzed via gravimetric and gas chromatographic analysis that the consortium degrades 83.70% and 83.49% crude oil respectively (Varjani et al., 2015). It has been reported that *Acinetobacter sp.* can use n-alkanes with chain lengths ranging from C10 to C40 as their sole carbon source.

Diverse microorganisms such as bacteria, yeast, and fungi were primarily reported to degrade the hydrocarbons in marine and soil environments with an efficiency rate of 6% to 82%, 0.003% to 100%, and 0.13% to 50% for soil fungi, marine bacteria, and soil bacteria respectively (Das and Chandran, 2011). Other than this, several bacterial, fungal, and yeast genera isolated from petroleum contaminated sites namely *Gordonia, Brevibacterium, Aeromicrobium, Dietzia, Burkholderia, Mycobacterium and Graphium*, *Talaromyces, Amorphoteca, Candida, Yarrowia, Neosartorya, and Pichia* were found to be an effective organism for the hydrocarbon degradation (Das and Chandran, 2011). The ability to utilize aliphatic hydrocarbons and n-alkanes as a carbon source by yeast species, were attributed to the presence of microsomal cytochrome P450. Because the enzyme cytochrome P450 was identified from a yeast species such as *Candida tropicalis, Candida apicola,* and *Candida maltosa* were found to be involved in hydrocarbons degradation (Das and Chandran, 2011). Szulc et al., (2014) demonstrated an experiment to study the biodegradation efficiency of diesel oil-contaminated soil by bioaugmenting with a microbial consortium containing *Alcaligenes xylosoxidans, Aeromonas hydrophila, Pseudomonas putida, Pseudomonas fluorescens, S. maltophilia, Rhodococcus equi, Xanthomonas* sp., and *Gordonia sp.,* After 365 d of treatment, a high percentage of approx 89% biodegradation efficiency was observed. As a consequence, the use of bacterial consortia to improve biodegradation potential is an effective technique for the breakdown of petroleum hydrocarbons from contaminated areas (Szulc et al., 2014). The *Thermophilic geobacilli* was studied for their ability to degrade n-hexane in soil. It was recorded that 65% of n-hexane was degraded during a period of 40 d (Nzila, 2018).

3.1.2. The microbial response towards aromatic hydrocarbon pollution

Petroleum hydrocarbons consist of aliphatic and aromatic compounds which together make up 80% of crude oil (Brzeszcz and Kaszycki, 2018). Aromatic compounds have a wide range of natural and synthetic compounds containing aromatic rings. Aromatics compounds such as ethylbenzene, benzene, toluene, xylene (BETX), heterocyclic aromatics, chlorinated aromatics, and PAHs are toxic and pose harmful effects on the environment (Rathankumar et al., 2022). Amongst these, the PAHs contain low molecular weight hydrocarbons with 2 to 3 fused rings (phenanthrene, naphthalene, and anthracene) and other high molecular weight hydrocarbons with 4-5 fused rings (pyrene, chrysene, fluoranthene). Being highly hydrophobic in nature and complex structure they are persistent towards degradation and settled down to the sediment in an aquatic environment leading to direct risks to sedimentary organisms and indirect risks to other forms of life. Thus, aromatic hydrocarbon persistence in the ecosystem is a major concern (Brzeszcz and Kaszycki, 2018; Xu et al., 2015). Therefore, microbial degradation offers an approach towards the remediation of these hydrocarbons from the environment (Fig. 2). Microorganisms such as yeast, fungi, and bacteria utilize hydrocarbons as a sole source of carbon and energy for their growth and survival and effectively participate in the biodegradation of hydrocarbons. Bacterial genera such as *Pseudomonas, Mycobacterium, Sphingomonas, Alcaligenes,* and *Bacillus* has been extensively studied for the degradation of PAHs (Table 1). PAH degradation mechanisms differ between strains and are affected by a number of factors such as PAHs structural configuration, isomeric structures, Parent PAHs distinct substituted forms, nutritional and interaction competition between different microbial populations (Ahmad et al., 2020). Several degradation pathways were studied for the PAHs degradation such as meta-cleavage pathway for naphthalene degradation in *Pseudomonas putida*, and *Pseudoxanthomonas sp.* metabolic process for chrysene degradation. The former resulted in the degradation rate of

79.12 mg/L/d, and latter resulted in 60% degradation of chrysene in 12 d i.e., chrysene concentration reduced from 400 mg/L to 140 mg/L (Ahmad et al., 2020). Bisht and coworkers studied biodegradation of anthracene, chrysene, xylene, naphthalene, benzene, and toluene from bacterial isolates namely *Micrococcus varians, Kurthia sp., Bacillus circulans* and *Deinococcus radiodurans* isolated from rhizobacteria of *Populus deltoids*, *Kurthia sp*. and *B. circulans* yielded a favorable result among these isolates after 6 d of incubation and resulted in the degrading of 87.5% and 86.6% anthracene and 95.8% and 85.3%, naphthalene respectively (Bisht et al., 2010). Bacterial strains are widely studied for hydrocarbons degradation due to their rapid adaptability. The aerobic bacterial breakdown of different PAHs via oxygenase-mediated metabolism and the cytochrome P450-mediated pathway, resulted in the generation of cis-trans forms of dihydrodiols (Ghosal et al., 2016). It was reported that a large fraction of PAHs degrading isolates belong to the *Pseudomonas* and *Sphingomonads* which degraded aromatic hydrocarbons effectively. Additionally, Ghosal and coworkers studied the response of halotolerant bacteria towards hydrocarbon degradation and reported that Alphaproteobacteria (*Maricaulis* and *Roseovarius*) was associated with the degradation of low molecular weight PAHs, whereas Gammaproteobacteria (*Methylophaga* and *Marinobacter*) degrades high molecular weight PAHs. In the last several years the degradation of PAHs by fungal species has also been widely studied. Though various fungal species do not utilize PAHs as a sole source of carbon and energy but could co-metabolize them into oxidized products and carbon dioxide. Various ligninolytic fungi *(Phanerochaete chrysosporium* and *Pleurotusos treatus*) and non-ligninolytic fungi (*Cunning hamellaelegans*) were widely studied for the degradation of PAHs (Ghosal et al., 2016). It was suggested that nitrogen is an essential component that plays a key role in promoting the biodegradation of aromatic hydrocarbons from contaminated sites. Nitrate reducing bacteria such as *Magnetospirillum magneticum,* and *Azoarcus* species have been studied to accelerate the bioremediation of aromatic hydrocarbons pollutants (Xu et al., 2015).

3.2. Role of omics approaches in hydrocarbon remediation

Hydrocarbon-degrading microorganisms are abundant in the environment, but their identification is challenging due to the fact that their capacity to consume hydrocarbons is highly dependent on the substrate. Owing to the development of molecular biological technologies, the presence, and diversity of microorganisms in natural habitats can now be examined in much more detail (Patel et al., 2020). Therefore, the removal of these complex contaminants requires the cooperation of several microbial populations (Gaur et al., 2018). Sequencing technology advancements have enabled genomic analysis in a culture-independent manner that may be used to quickly examine any material, such as water or soil (Bharagava et al., 2018).

The omics approaches may have an impact on the degradation/detoxification pathways of pollutants, as well as in providing a better knowledge of the mechanisms underpinning bioremediation and bacterial metabolic activities (Fig. 3) (Dell' Anno et al., 2021). Furthermore, with the progress of Next-generation sequencing (NGS), new pathways in bioremediation have been uncovered. It is now feasible to get insight into significant biodegradative processes of bacteria that are found in the environment. In short, these omics approaches have improved our understanding of how microorganisms are structured, their way of interaction with other communities, and their participation in a complicated network of interactions between plants, microorganisms, and the environment (Malik et al., 2021). This section detailed the application of different omics approaches in the bioremediation of hydrocarbons.

3.2.1. Metagenomics

Recent technical advances for ensuring sustainable development include microbe-mediated environmental pollution remediation (Malla et al., 2018; Rane et al., 2022). Metagenomics is a tool for analyzing directly derived genetic material from environmental materials. Current research using metagenomics gives important visual and methodological approaches for analyzing the relationship between soil microbiota and environmental activities, as well as unique insights into the intricacies of the contaminated environment. Generally, nucleotide databases and in-silico tools are used, which is incredibly useful for understanding the role of microorganisms in contaminant degradation and revealing novel genes responsible for bioremediation (Mishra et al., 2021). Using sequence and function-based research methodologies, metagenomic reveals information about non-cultivable species' microbial populations in a niche habitat. To summarize, the main critical step involves extracting complete genomic DNA (metagenome) from the environment (soil, water, and sediments) (Sharma et al., 2021). The challenging aspects that act as barriers in successful whole genome extraction include a high concentration of different contaminants such as metals, aromatic hydrocarbons, and a low cell density. The analysis section of genomic DNA consists of four major methods: sequencing of metagenomes (using "direct" and "shotgun" sequencing approaches), screening of cloned DNA (metagenomics library), profiling at the transcript and proteomic levels, and identifying metabolic network (metabolomics) targeting various aspects of a particular microbial population related with a defined environment (Kumar et al., 2020). Together, these methodologies have enhanced our knowledge of the unculturable microscopic organisms and, as a result, have revealed rarely unknown insights into the prokaryotic world (Kumar et al., 2020; Malla et al., 2018). The presence of petroleum hydrocarbons into a virgin ecosystem alters its nature immediately. Many microbial species are killed or inhibited by the added hydrocarbons, altering the functioning of the microbial population and hence the ecosystem (Siddiqui et al., 2021). Physical (diffusion), physiochemical (condensation, disintegration, and absorption), biological (plant microbial and catabolism), and chemical processes (photo-oxidation, auto-oxidation), play a part in the environmental weathering of petroleum hydrocarbons (Truskewycz et al., 2019a). It is commonly acknowledged that microorganisms with various strategies for adaptation to and catabolizing hydrocarbons play an essential role in stabilizing an ecologically suitable ecosystem. Single microorganisms have been reported for enzyme-based hydrocarbon degradation, as well as consortia of microbes in symbiotic interaction, which aid in the process by providing real carbon sources (glucose) to enhance the rate of growth of hydrocarbon utilizing microorganisms or the accessibility of oil to microbes through biosurfactant secretion (Truskewycz et al., 2019a; Varjani and Upasani, 2017a).

Using NGS technology, many studies have been performed to analyze the microbial population in petroleum hydrocarbon-associated environments (Gupta et al., 2021; Pal et al., 2021; Zakaria et al., 2021). Actinobacteria, Firmicutes, Proteobacteria, Euryarchaeota, and others have been identified in diverse ecosystems contaminated by petroleum compounds (Pal et al., 2018). Archaea have also been mentioned as a possible resource for the bioremediation of hydrocarbons from adverse environments. *Natrialba* sp. C21 from saline water contaminated with oil has been reported in Ain Salah (Algeria) and was capable of surviving in salty conditions. This strain demonstrated good potential for degrading % (v/v) naphthalene and pyrene after 7 d of exposure in high saline conditions at 40 °C, pH 7.0 (Khemili-Talbi et al., 2015). Metagenomic investigations have been done using high-throughput microarrays, aside from a sequence-based screening of ambient metagenomic libraries. These have been used to study microbial populations and monitor biogeochemical cycles in the environment. For example, GeoChip microarrays with 83, 992 50-mer sequences expressing enzymes for biogeochemical (C, N, P, S) cycling, energy metabolism, heavy metal resistance, antimicrobial resistance, and biodegradation are now being employed (Bharagava et al., 2018).

During the past decade, particularly following the 2010 Gulf of Mexico oil disaster, significant information about the biodiversity of marine hydrocarbon-oxidizing bacteria (HOB) has been disseminated, and there have also been discoveries of seawater biodegrading bacteria. They include members belonging to the genus *Cycloclasticus* and *Alcanivorax*, which thrive in temperate marine ecosystems, *Thalassolituus diatoms*, which thrive in C12-C32 n-alkane-rich microcosms, alkane-degrading obligate psychrophiles *Oleispira* spp., and other genera members such as *Marinobacter*, *Acinetobacter*, *Roseobacter, Pseudomonas,* and *Rhodococcus* (Ivshina et al., 2017). Similarly, a metagenomic investigation of diesel degrading microbiota was performed using specific critical coding DNA sequences (CDSs). The active populations that were able to degrade both aromatic and aliphatic polycyclic hydrocarbons have been identified. The diesel-degrading consortium includes 76 amplicon sequence variations (ASVs) based on 16S rRNA gene sequencing, including *Pseudomonas, Aquabacterium, Chryseobacterium, and Sphingomonadaceae* (Garrido-Sanz et al., 2019). Shotgun metagenome sequencing of the consortia growing on diesel revealed redundant genes encoding enzymes involved with alkane oxidation at the beginning (AlkB, LadA, CYP450). Finally, the microcosms demonstrated the tested consortium's capability for rhizoremediation in actual diesel-polluted soil.

Furthermore, "omics" serve as a foundation for developing strains with enhanced capacities such as stress tolerance, expression based targeted pathways, elevated oxidizing activity, high competitiveness, and so on. To mineralize substituted polychlorinated compounds, three genetic components were inserted into a bacterium hybrid predicated on the hydrocarbon-oxidizing species *Cupriavidusnecator* H850 (Ramos et al., 2011). Meanwhile, amplicon-based metagenomics assists in the construction of a long-term framework for targeted bioremediation in soil or sediment by identifying the correct microbial species as targets. Microorganisms' phylogenetic analysis with contaminant degradation and survival capability in polluted environments can be exploited as biostimulants, whereas microorganisms with properties like position at site, massive growth, simple propagation, non-pathogenicity, and the ability to sustain and detoxify significant emissions of contaminants, on the other hand, can be employed for bioaugmentation (Redfern et al., 2019). Using the Spearman rank correlation statistics and a metagenomic approach, *Geobacter spp*. has recently been found as biostimulation targets (carrying PAHs relevant degradative genes), whereas *Sphingomonads spp*. and *Mycobacterium spp*. are bioaugmentation targets for creosote-contaminated soil (Redfern et al., 2019). Numerous microbial strain has been identified and reported in a study of effluent from a petroleum refinery belonging to the genera *Diaphorobacter*, *Comamonas*, *Thauera*, and *Pseudomonas* that possess genes that breakdown benzoate, biphenyl compounds, naphthalene, phenol, and toluene, among others (Silva et al., 2012; Variani, 2017). This means that a wide range of unique genes may be present, some of which may be capable of degrading other hydrocarbons as well as organic chemicals and assisting in bioremediation.

Overall, the case studies indicate that the framework can aid in the identification of bacterial targets for targeted environmental remediation. However, because the power of metagenomic-based techniques is restricted to microorganisms in our databases, we must continue to grow our databases.

3.2.2. Meta-proteomics/ Meta-transcriptomics

Moreover, metagenomics has the flaw of not being able to tell whether or not the identified genes are expressed. As a result, in order to better understand the expression pattern of genes that are upregulated or downregulated in response to changes in the microenvironment, metagenomic analysis is usually paired with meta-transcriptomics, or the sequencing of the mRNA of the microbial population (Malik et al., 2021). Because mRNAs are exceedingly unstable, meta-transcriptomic is not extensively utilized, while meta-proteomics does. The three basic procedures in meta-transcriptomics are direct RNA extraction from ambient samples and mRNA enrichment, mRNA to cDNA, and sequencing via next-gene sequencing (Gaur et al., 2022a). The meta-transcriptomics analysis may assist in identifying the gene expression pattern of the microbes in polluted environments, as well as the alteration in microbial expression that may have been caused due to contamination exposure. As a result, meta-transcriptomics has been investigated for assessing gene profiles by selectively mRNA enrichment by rRNA subtractive hybridization method has shown the presence of several genes involved in PAH degradation and metabolism (Kotoky et al., 2018). In the deep-sea hydrocarbon plume caused by the Deepwater Horizon (DH) oil disaster in the Gulf of Mexico, meta-transcriptome analysis has led to the identification of expression and enrichment of genes linked to aliphatic hydrocarbon degradation, chemotaxis, and motility (Mason et al., 2014). However, RNA analysis indicated that only the breakdown routes targeting simpler, aliphatic hydrocarbons were significantly transcribed, whereas pathways targeting more complicated, aromatic chemicals (such as benzene) were mainly inactive. This shows that coupled meta-omics sequencing might be useful in developing bioremediation techniques since it would be required to ensure that breakdown pathways are actively present in a microbial population (Franzosa et al., 2015).

Many hydrocarbon biodegradation genes were found to be more abundantly expressed in polluted soils with plantations, suggesting that interspecies interactions were more important in the remediation of pollutants. The researcher meta-transcriptomes the rhizospheres of four willow species, as well as the plant roots of two willow species, in petroleum originated hydrocarbon polluted and non-contaminated soil at a petroleum refinery site (Yergeau et al., 2018). The root meta-transcriptomes of two willow cultivars were studied, revealing that willow species impacted plant transcripts the most, whereas microbial transcripts were predominantly influenced by the level of contamination. For decades, microbes have been discovered in oil reservoirs, pipelines, and crude oil refineries. Recently, integrated metagenomics and meta-transcriptomics technique were used to determine the metabolic capacity and in-situ potential of microbial populations derived from the Jiangsu Oil Reservoir, China (Liu et al., 2018). Transcriptomic data reveal which members of the population are active, and it was reported that *Acinetobacter sp*. oxidizes alkanes to CO_2 in anaerobic conditions, whereas *Archaeoglobus* sp., predominantly converts alkanes to yield acetate, that may be ingested by *Methanosaeta* species. However, the expression of genes related to hydrocarbon degradation has been reported in oil spill-contaminated soils and seawaters (de Menezes et al., 2012; Lu et al., 2012; Mason et al., 2014, 2012; Rivers et al., 2013). Therefore, the implementation of these transcriptome techniques to polluted microbial mats would also provide additional or unique insight into microbial mat adaptation to hydrocarbon contamination (Aubé et al., 2020).

Since mRNA is unstable, meta-transcriptomics is not widely used, hence meta-proteomics is another viable alternative for elucidating the process at the protein level. The analysis of proteins expressed by microbes found in environmental (soil and water) samples is known as metaproteomics. It investigates and offers information on the microbial functional genes (Malik et al., 2021). Meta-proteomics assists in the identification of all expressed polypeptides in a sample at a certain period and under specific conditions. In microbial populations, meta-proteomics data acts as a connection between functional and genetic information (Gaur and Manickam, 2021a), and researchers can use this method to discover new functional genes and metabolic pathways, as well as determine which proteins are expressed in accordance with the changes in the substrate or environmental factors. Metaproteomics, like metagenomics and meta-transcriptomics, has limitations, but it delivers more information (Malik et al., 2021). Although the omics strategy is advantageous, there are still other obstacles to be solved. Furthermore, to gain more insights into microbial degradation genetics, a combination of two or more techniques, can offer a better alternative (Gaur et al., 2022a). In brief, the metaproteomic analysis is based on very efficient separation technologies, such as two-dimensional gel electrophoresis, as well as current bioinformatics and mass spectroscopy. With advances in bioinformatics software that permits broad protein profiling with flexibility, a label-free quantitative proteomic technique is now viable (Chandran et al., 2020).

Metaproteomics has also been used to investigate the differences in the expression of a protein involved in microorganisms' physiological responses to pollutants, as well as to identify the individual proteins implicated when exposed to a particular organic pollutant in a polluted environment (Kotoky et al., 2018). In addition, naphthalene-inducible dioxygenases, aldehyde dehydrogenase, putative monooxygenases, and catalase-peroxidase were shown to be triggered in *M.vanbaalenii* PYR-1 in the occurrence of high molecular weight PAHs during aromatic hydrocarbon catabolic pathways analysis (Kim et al., 2011). Similarly, *Burkholderiales* were identified as the active microbial species, as evidenced by the presence of a dioxygenase enzyme for the degradation of PAHs, in a metaproteomics study (Rabus, 2013). The discovery of 847 proteins from active fluorene and naphthalene degraders has been reported using a functional metaproteomics method, with *Burkholderiales, Actinomycetales,* and*Rhizobiales* accounting for 70% of the protein structures. The proteins discovered in the naphthalene degradation pathway, on the other hand, let researchers find that naphthalene degrading bacteria acquired 80% of carbon from PAH degradation. Meanwhile gentisate 1,2-dioxygenase, salicylate-5-hydroxylase, fumaryl pyruvate hydrolase, catechol 2,3-dioxygenase, and GST-like protein (NagJ) were found in the plume fringe BACTRAP (Herbst et al., 2013). Furthermore, meta-proteomics by itself can explain the complexities of microbial environmental remediation; consequently, interactomics and metabolomics or metabolic engineering are also used to better reveal the processes and pathways. As a result, functional characterization of genes utilizing an integrated approach of multi-meta-omics and Gene Ontology (GO) tools is the preferred method for developing a deeper insight into the molecular processes underlying multipartite interactions influencing rhizosphere bioremediation (Malik et al., 2021). Therefore, the analysis of the protein simultaneously expressed by all microbes present in an environment is not only important, but it may also give insights into microbial activity.

Overall, the success of metaproteomics is inextricably tied to the metagenomics approach, and following the continuous increase in access to metagenome sequencing, this field of study is beginning to generate an excessive volume of information that requires thorough and systematic analysis. Meanwhile, future studies should concentrate on combining metagenomics with metaproteomics inside the terrestrial ecosystem, which is dominated by uncultured microbes. Furthermore, when studying pollutants degradation, it is necessary to ensure that contaminant thresholds are observed throughout the study in order to determine whether the nonidentification of associated proteins with pollutant degradation is due to the absence of degradation activity or is obscured by the more widely available mechanisms.

3.3. Addition of biosurfactants

Biosurfactants were reported to exhibit multifarious applications and have been extensively employed for their antibacterial and bioremediation potential (Gaur et al., 2020b, 2019a, 2019b; Tripathi et al., 2020; Varjani et al., 2021b). Hydrocarbon pollutants released during petroleum exploitation, exploration, transportation, consumption, oil spills, and improper discharge of oil products cause environmental pollution and serious ecological problems. The soil pollution by mobil oil results in altered physical and chemical properties thereby exhibiting negative effects on plant growth parameters. Thus, soil and water contamination by petroleum-based hydrocarbons such as mobil oil is one of the most severe environmental problems displaying negative impacts on human health, microorganisms, and other living organisms in the ecosystem (Aparna et al., 2011). To reduce such hydrocarbon pollution by using conventional tools such as chemical and mechanical methods are expensive, time consuming, non-ecofriendly and release harmful and toxic products. Therefore, the use of microorganisms and their metabolites (biosurfactants) for the removal or degradation of hydrocarbon pollutants contaminated with petroleum hydrocarbons such as diesel oil, crude oil, gasoline, and mobil oil offers an efficient, economic, low cost and versatile alternative to the traditional treatment methods (Aparna et al., 2011; Varjani and Upasani, 2019, 2017b). The process of bioremediation of hydrocarbons may be enhanced with biosurfactants through one of the processes namely emulsification, solubilization, and mobilization (Gaur et al., 2022; Markande et al., 2021). At concentrations lower than the biosurfactant critical micelle concentration, the mobilization mechanism takes place. Biosurfactants reduce the interfacial tension between two different mediums such as water/air and water/oil at such concentrations, increasing the contact angle and lowering the capillary force. In turn, the solubilization process occurs above the CMC of biosurfactant, where biosurfactant molecules associate to form micelles by increasing the solubility of oil (Gaur and Manickam, 2021b; Markande et al., 2021). *Pseudomonas aeruginosa* was found to produce biosurfactants and serve as a hydrocarbon degrading bacterium in a hydrocarbon contaminated site. *P. aeruginosa* showed 52% and 87% reduction of crude oil on 7th and 21st d respectively (Aparna et al., 2011). Similarly, *Bacillus methylotrophicus* and *B. licheniformis* isolated from petroleum reservoir grown on hydrocarbon in an aqueous medium resulted in 90% removal of crude oil and recovered 37% heavy crude oil (Nikolova and Gutierrez, 2021). Kumar and colleagues studied the mobil oil biodegradation by biosurfactant producing bacterial consortium in mustard and wheat rhizosphere namely C1, C2, and C3. It was reported that in 150-180 d, bacterial consortium C1 and C3 were able to degrade 2% mobil oil with a 75.80% efficiency in the mustard rhizosphere and 73.66% in wheat rhizosphere respectively. During degradation of mobil oil hydrocarbon by the microbial consortium, phthalate esters were formed as an end product which was less toxic to humans and can be utilized for the softening the polyvinyl chloride (PVC) and as plasticizers. As a result, it was suggested that this bacterial consortium may be exploited not only for bioremediation of mobil oil from polluted sites but also for the manufacture of phthalates ester for a variety of industrial purposes (Kumar et al., 2013). *Chelidoniummajus L.* endophytic bacteria were isolated from a synanthropic plant was studied for their ability to produce biosurfactant and degrade hydrocarbon (Marchut-Mikolajczyk et al., 2018). Their degradation potential was reported in the range from 24 to 75.9% and 9 to 92.81% for waste engine oil and diesel oil, respectively. Parthipan and coworkers focused on a wide range of bacterial strains such as *Acinetobacter baumannii* MN3 and *Pseudomonas stutzeri* NA3 for the optimization of biosurfactant production and alkane hydroxylase, laccase, and alcohol dehydrogenase are examples of degradative enzymes that can be produced. These enzymes are thought to play an essential role in hydrocarbon degradation. It was reported that *P. stutzeri* showed 84% hydrocarbon degradation. Thus, effective biosurfactant-producing bacteria and their degradative enzyme producing capability suggested that these bacterial isolates can be used for biodegradation of hydrocarbon and bioremediation of other toxic pollutants (Parthipan et al., 2017). Santos et al., (2021) studied the effectiveness of biosurfactants for bioremediation of hydrocarbons on motor oil-contaminated soil. The addition of biosurfactant at 2xCMC concentration showed the highest removal of 95% oil after 90 d. In another study, the addition of biosurfactant from a *C. sphaerica* at CMC concentrations of 0.1%, 0.08%, and 0.05% showed the oil removal efficiency of 65%, 55%, and 30%, respectively (Santos et al., 2021). The biosurfactant enhances the rate of microbial degradation of hydrocarbons by implementing two mechanisms i.e., firstly by increasing the substrate bioavailability through emulsification and secondly by facilitating the involvement of bacterial cells with hydrophobic substrates during which there is a decrease in the cell surface hydrophobicity of bacterial cell (Patowary et al., 2017). A study reported that *Pseudomonas aeruginosa* strain PG1 exhibited excellent degradation of various hydrocarbon components using biosurfactant as an energy source in the route of degradation (Patowary et al., 2017).

4. Future Perspective

The discovery of new oil resources has met the global need for energy. These research initiatives increase the probability of exposure of the marine world to hydrocarbons (Beyer et al., 2016).

The ubiquitous presence of petroleum hydrocarbons poses a serious threat to the environment, economy, and human health. Critical analysis of meta-omics data helps understand the environmental variables that influence the growth and activity of hydrocarbon degrading communities (Mapelli et al., 2017). The existing technologies for reclamation of petroleum hydrocarbon-contaminated settings are costly and are typically performed off-site, necessitating the removal of contaminated soil physically. Meanwhile, all in-situ techniques have drawbacks, such as high costs (soil flushing), appropriateness/suitability for an explicit type of soil (soil vapor extraction), incapable to effectively addressing all polluted areas, the reclaimed area may not be satisfactory for development (solidification/stabilization), libration of unsuitable by-products (electrokinetic remediation), the possibilities for procedure's negative effects (chemical ozone) and insufficient decaying time (bioremediation) (Truskewycz et al., 2019b). Natural attenuation processes are insufficient to treat highly polluted areas rich in petrochemicals, at a significant rate. Therefore, emerging techniques such as bioremediation have been developed, as an ecologically sound and cost-effective substitute of traditional treatment methods.

Multi-omics studies are still insufficient and might be expanded to overcome gaps in addressing metabolism, expression of the gene, and the biology (cellular and molecular) of the bacteria engaged in the bioremediation. Numerous bacteria have crucial metabolic genes that could be passed on to other organisms. Genetically engineered microorganisms (GMOs) with enhanced ability to degrade contaminants will undoubtedly have a significant future in this sector (Kour et al., 2021). Extending our understanding of microbial genetics to enhance the effectiveness of microbes to break down contaminants and undertaking field research would undoubtedly serve as a stepping stone for advancements in this domain (Kour et al., 2021; Malla et al., 2018). It would also be exciting if large-scale bioremediation products could be produced.

Numerous putative microbial species have been associated with PAHs-remediation via unknown pathways, necessitating the use of an omics approach to investigate the complex behavior of novel species and their degradation processes. Omics technologies hold a big future for better understanding the bacteria' crucial role in PAHs degradation. Metagenomics identifies a population of microbes associated with a specific purpose; meta-trans/proteomics, provide knowledge of transcription and proteins of microorganism. However, for a comprehensive knowledge of rhizosphere-mediated PAH remediation, a variety of approaches should be used (Zhang et al., 2021). Consequently, the emphasis of debate must be expanded to include the involvement of the rhizosphere microbiome as a proper functioning for environmental remediation or rhizodegradation of PAH (Kotoky et al., 2018; Singha and Pandey, 2020). The greater number of microflora occurring in the environment with huge bioremediation potential is yet unknown due to restricted culture techniques. Without the requirement for laboratory cultivation, omic techniques can disclose the identity and characteristics of these unique bacteria and their endogenous enzymes (Bodor et al., 2020; Kaur, 2019). Furthermore, these technologies are significant in the contemporary context as effective strategies for better biodegradation potential (Sharma et al., 2018).

Aside from that, cost-effective biosurfactant synthesis is necessary for its wider implementation in the field of bioremediation by increasing the PAHs bioavailability (Kumar et al., 2021; Moutinho et al., 2021; Zang et al., 2021). Furthermore, many distinct enzymes involved in PAHs breakdown have also been discovered and characterized (Sakshi and Haritash, 2020). Therefore, experts are optimistic about the safe and ethical use of Genetically modified organisms (GMOs) as a low-cost option for PAHs biodegradation. with nontechnical considerations like environmental regulations and requirements. As a result of this review, it is reasonable to conclude that using coupled green degradation technologies like microbial consortia, rhizoremediation, organic addition, and biosurfactants secreting microorganisms, to control the remediation of PAH-contaminated areas may be adequate.

5. Conclusions

There have been numerous studies focusing on the bioremediation of crude oil as compared to mobil oil. Although the components of crude oil and mobil oil are quite similar (aliphatic and aromatic hydrocarbons), the biodegradation efficacy of bioremediation techniques may differ with the oil types. Researchers preferably isolate and use polluted site-specific (native) microorganisms, which can help with higher remediation effectiveness and can be employed alone or in consortia. Furthermore, there have only been a few studies on the remediation of mobil oil, that generate a demand to thoroughly investigate the remediation potential of microorganisms using omics approaches such as meta-genomics, meta-transcriptomics, and meta-proteomics. It was also shown that biosurfactants (of various chemical natures) produced by microorganisms offer environment friendly, microbial mediated techniques which increases the bioavailability and solubility of hydrocarbons. As a result, it may be concluded that meta-omics approaches might aid human and animal populations in resiliency following a mobil oil spill or contaminated zone.

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Conflict of interest statement

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Figure Captions:

Figure 1: Schematic representation of different approaches for combating crude oil contamination

Figure 2: Microbial aided biodegradation and use of biosurfactants

Figure 3: Omics approaches for bioremediation of mobil oil contamination

Table Legends:

Table 1: Microorganisms and their efficiency for degradation of different crude oil components

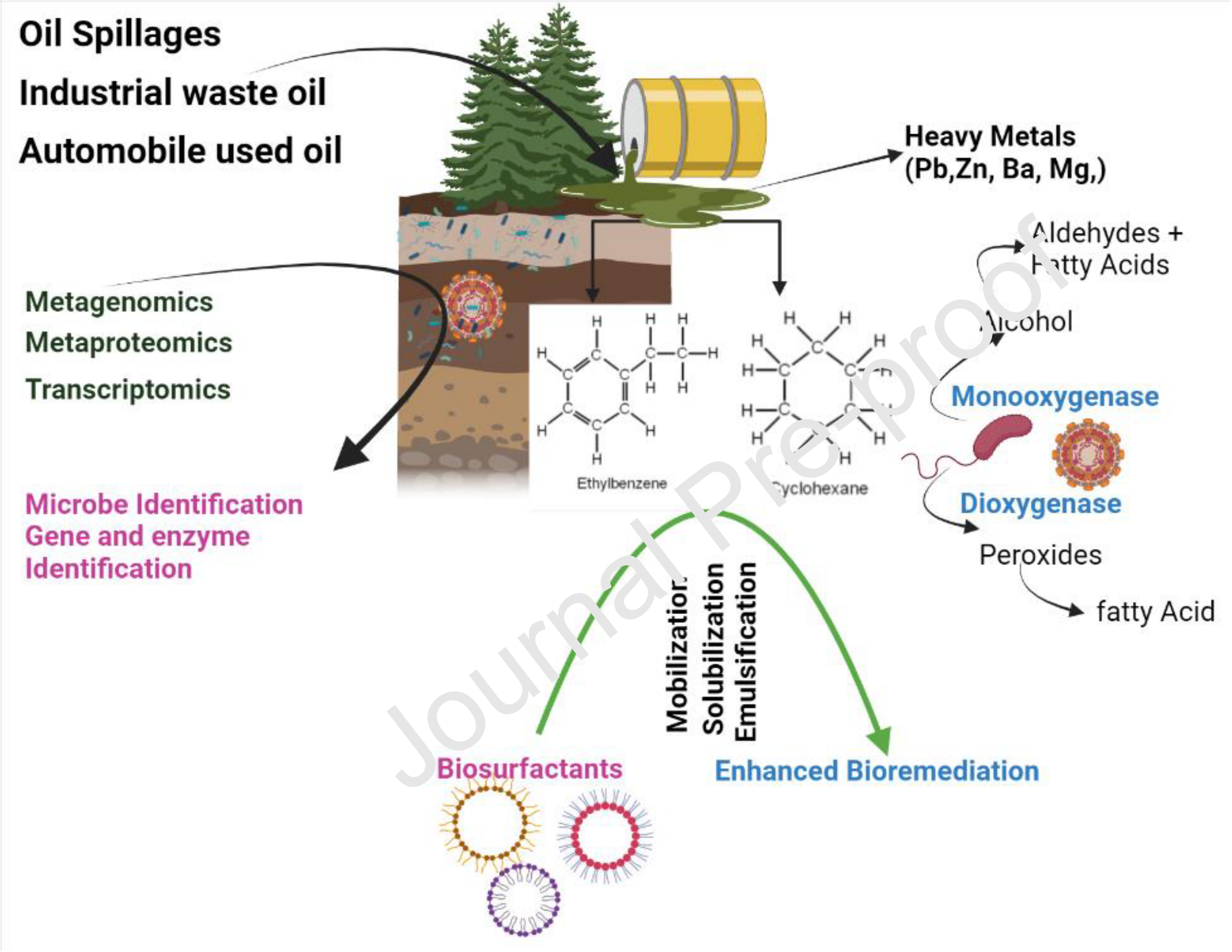

Figure 1: Schematic representation of different approaches for combating crude oil contamination

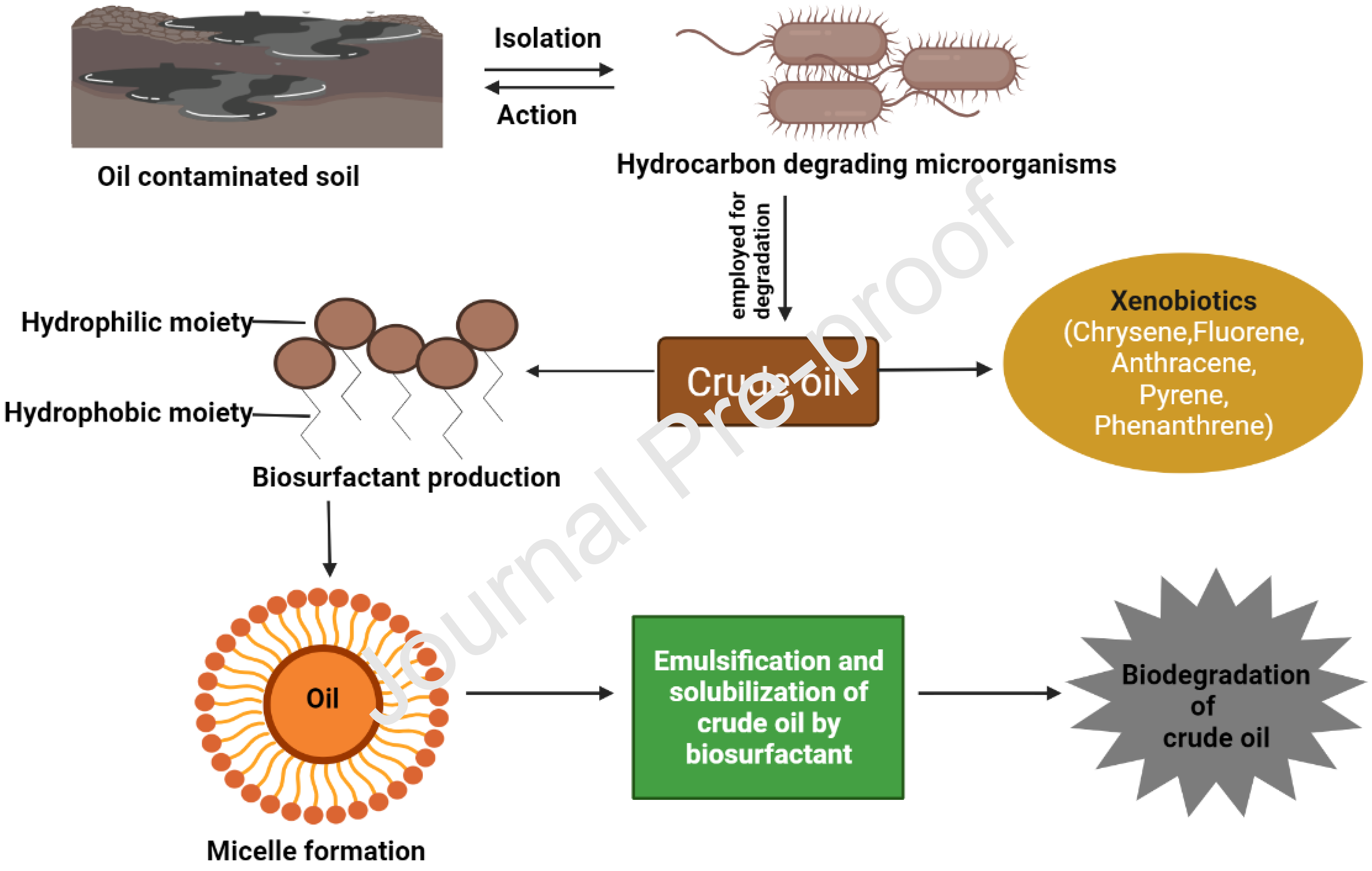

Figure 2: Microbial aided biodegradation and use of biosurfactants

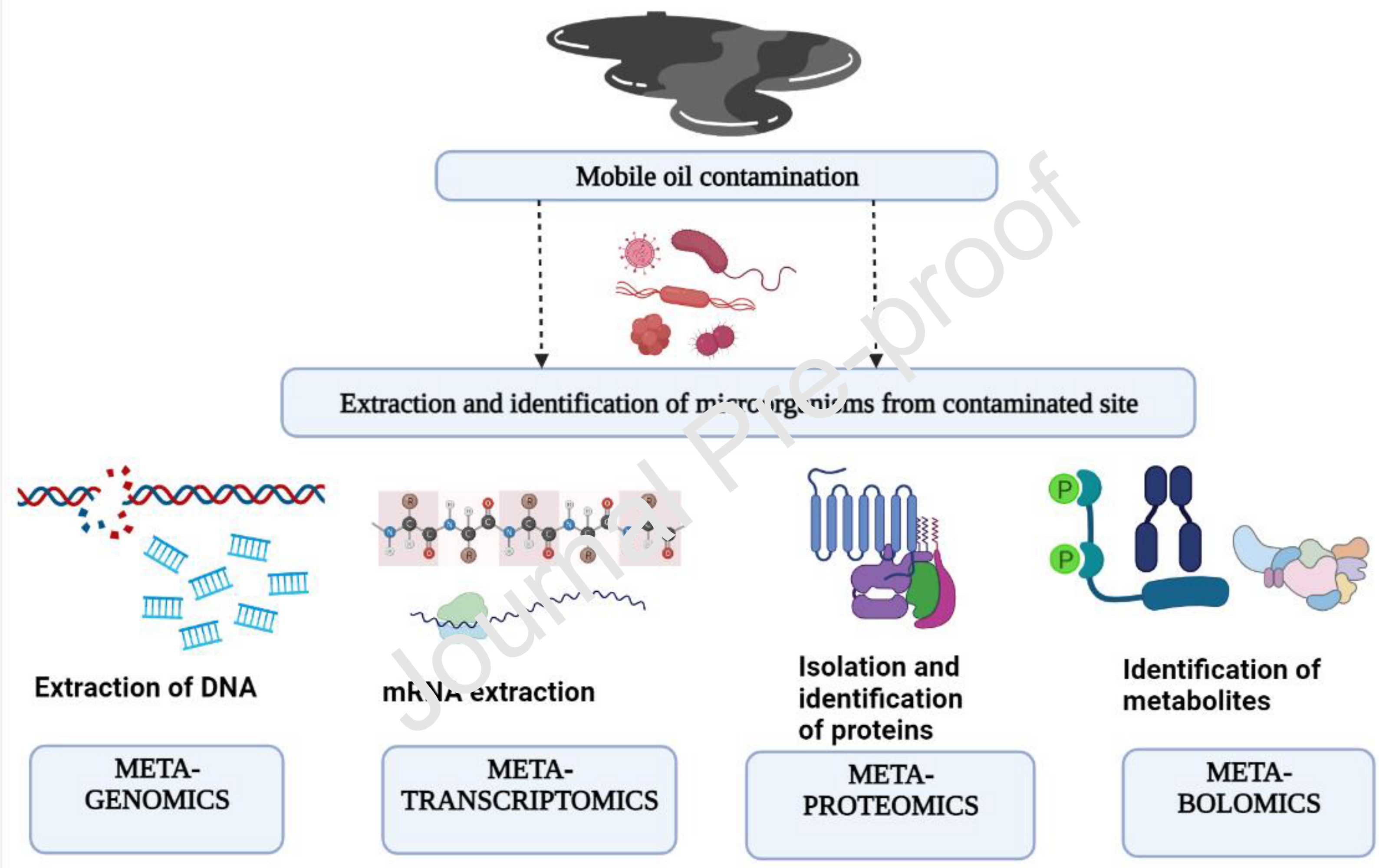

Figure 3: Omics approaches for bioremediation of mobil oil contamination

Table 1: Microorganisms and their efficiency for degradation of different crude oil components

Name	**Isolation source**	**Origin of oil type for microbial isolates**	**Component oil degraded**	**Time period**	**Degradation percentage**	**References**
Aliphatic hydrocarbons						
TPH	Industrial contaminated site	*Gammaproteobacteria*, *Deltaproteobacteria* and *Actinobacteria*	fraction of hydrocarbons	24 months	43%	(Militon et al., 2010)
Hydrocarbon	Organic contaminated land	Thermophilic bacteria	hexadecane	40 d	70%	(Stroud et al., 2007)
Crude oil	Crude oil-contaminated samples from Kuwait	*B. stearothermophilus* KTCC-B/S and KTCC-B2M	C15–C18 n-alkanes	5 d	88.5% and 79.4%	(Sorkhoh et al., 1993)
Alkanes	Deep petroleum reservoirs in Japan	*Bacillus thermoleovorans* strain	>C12 alkanes	12 d	60%	(Nzila, 2018)

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Alkanes	Deep petroleum reservoirs in the Minamiaga (Niigata) oil field	*Bacillus thermoleovorans* strain H41	>C15 alkanes	20 d	75%	(Kato et al., 2001)
Alkanes	deep subterranean oil-reservoir in northern China	*Geobacillus thermodenitrificans*	C25 to C35 n-alkanes	21 d	90.01 and 93.80%	(Wang et al., 2006)
Aromatic hydrocarbon						
PAHs	Coal-powered Raichur Thermal Power Station, India	*Pseudoxanthomonas* sp. PNK-04	Chrysene	12 d	60%	(Ahmad et al., 2020; Nayak et al., 2011)
PAHs	The rhizosphere of Populusdeltoides growing in Garhwal region, India	*Kurthiasp* and *B. circulans*	Anthracene	6 d	87.5% and 86.6%	(Ahmad et al., 2020; Bisht et al., 2010)

PAHs	rhizosphere of Populusdeltoides growing in Garhwal region, India	*Kurthiasp* and *B. circulans*	Naphthalene	6 d	95.8 % and 85.3 %,	(Ahmad et al., 2020; Bisht et al., 2010)
PAHs	PAH-contaminated soil	*Scopulariopsis brevicaulis*	Phenanthrene and benzo(a)pyrene	28 d	80% and 75%	(Ahmad et al., 2020)
PAHs	Culture in laboratory	*S. capricornutum, C. vulgaris, S. platydiscus and S. quadricauda*	fluoranthene and pyrene	7 d	77.5%, 47.8%, 50.4% and 50.5%	(Lei et al., 2007)(Ghosal et al., 2016)
Crude oil sludge	IOCL, Faridabad, India, and Ratnagiri, India	*Pseudomonas aeruginosa* and *Rhodococcus erythropolis*	n-hexadecane	6 week	90	(Cameotra and Singh, 2008)
Crude oil	ONGC fields of	*Ochrobactrum sp., Stenot*	C8–C35 and	75 d	83.70% and	(Varjani et al.,

	Gujarat, India	*rophomonas maltophilia,* and *P. aeruginosa*	C20–C40		83.49%	2015)
Crude petroleum oil	Oil and Natural Gas Corporation (ONGC) oil fields, Gujarat,	*Pseudomonas aeruginosa* NCIM 5514	paraffin(s) C8–C36+ hydrocarbons	60 d	61.03% and 60.63%	(Varjani and Upasani, 2016)
Crude oil	Gasoline and diesel spilled gas stations in Coimbatore city (India)	*Bacillus* sp. IOS1-7, *Corynebacterium sp.* BPS2-6, *Pseudomonas* sp. HPS2-5, and *Pseudomonas* sp. BPS1-8	gases, light naphtha and heavy naphtha, kerosene, light gas oil, and heavy gas oil	25 d	64%, 41%, 45% and 69%	(Sathishkumar et al., 2008)
Petroleum hydrocarbon	The immediate area surrounding an oil well in Zichang county, Yan'an city,	*Acinetobacter* SZ-1 strain KF453955	TPH	7 week	34%	(Wu et al., 2016)

	Shaanxi province, China					
Petroleum contaminated soil	Shaanxi province, China	*Pseudomonas stutzeri* GQ-4 strain KF453954, *Pseudomonas* SZ-2 strain KF453956, and *Bacillus* SQe2 strain KF453961	total petroleum hydrocarbons (TPH), alkanes, and polycyclic aromatic hydrocarbons (PAH)	8 week	58%	(Wu et al., 2017)
Crude oil, diesel, and kerosene	Polluted stream in Lagos, Nigeria	*Corynebacterium sp*., *Acinetobacter lwoff,* and *Psetrdornoncrs aeruginosa*	cycloalkane and aromatic HCs	14 d	88, 85, and 78%, respectively	(Adebusoye et al., 2007)
Petroleum componen	Petroleum-contaminated	Bacterium, *Citrobacter* and *Bacillus*	anthracene, phenanthrene,	10 d	62%, 75%, 85%,	(Wu et al., 2013)

ts	locations Wooster, OH, USA		and pyrene		respectively	
Fuel oil	Beach contaminated by the Prestige oil spill	*Alphaproteobacteria* and *Gammaproteobacteria*	linear and branched alkanes, PAHs [anthracene, fluoranthene, pyrene, benzo(a)anthracene, chrysene, and benzo(a)pyrene] and alkyl derivatives	60 d	75%, 73% and 30%, respectively	(Vila et al., 2010)
Petroleum hydrocarb	Contaminated soil samples from an oil	Bacteria (*Bacillus cereus, Pseudomonas sp*,	aromatic component	140 d	64% and 68%	(Grace Liu et al., 2011)

on oil	storage site	*Sphingomonas yanoikuyae*, etc.) and Fungi (*Candida guilliermondi, Aspergillus versicolor, Fusariumoxysporum*, etc)				

Sustainable strategies for combating hydrocarbon pollution: Special emphasis on mobil oil bioremediation

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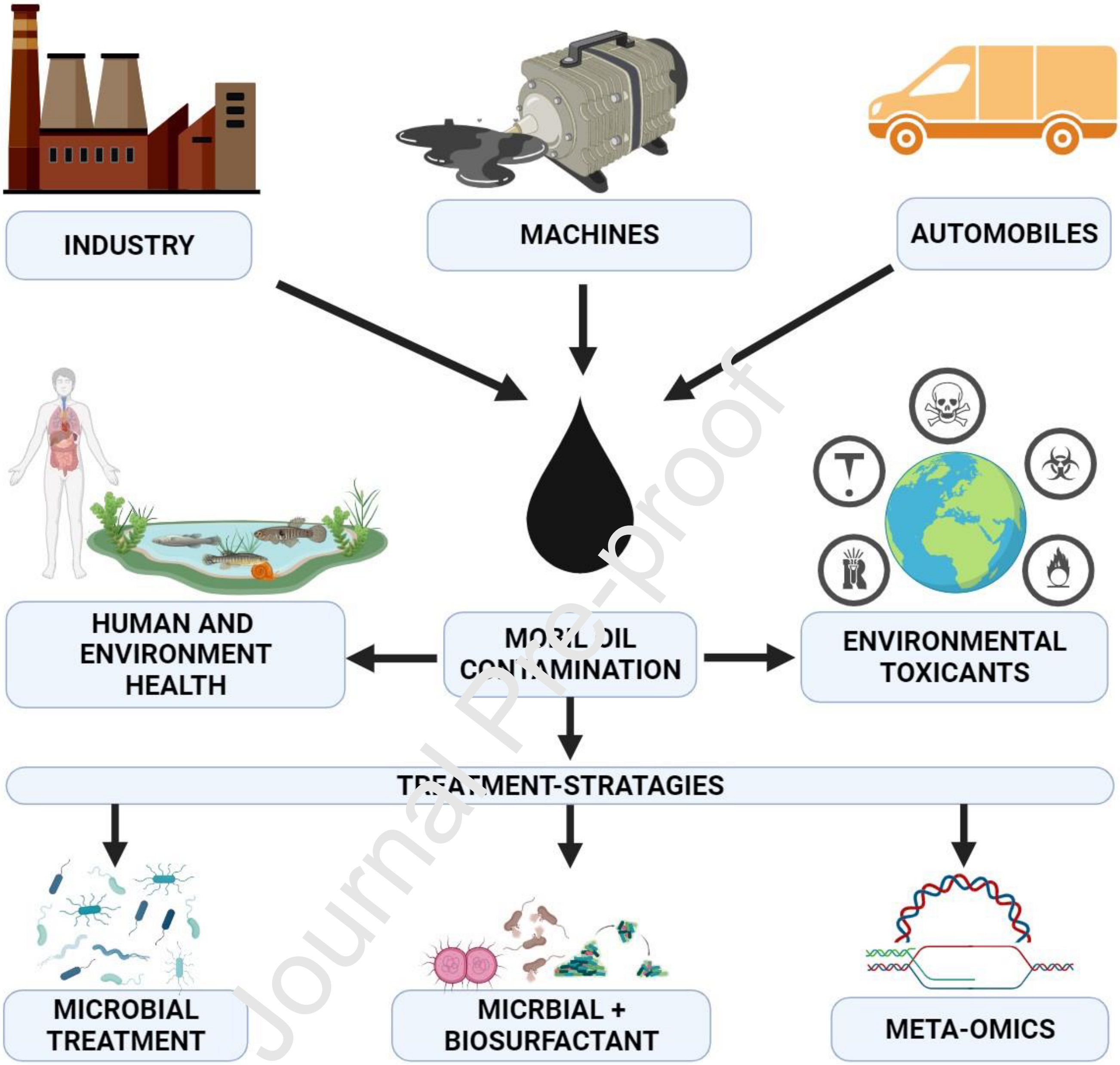

Graphical abstract

Highlights:

- Mobil oil waste contains aliphatic and aromatic hydrocarbons.
- Microbial aided degradation is effective for combating hydrocarbon pollution.
- Meta-omics approach aids in the identification of robust microbial strains.
- Biosurfactants addition increases the biodegradation of mobil oil.