

Capability of *Phanerochaete chrysosporium* Fungi and *Pseudomonas putida* Bacteria for Removing Hydrocarbons: A Literature Review

Diah Ayu Prawitasari^{1*}, Naila Syafa'atul Udzma¹, Dwina Putri Faizani¹, Fanny Salma Raafi'atul Putri¹, Rifqi Ilham¹, Syafa'atush Shidqina Muttaqin¹

¹Environmental Engineering Study Program, Faculty of Civil Engineering and Planning, Universitas Islam Indonesia, Special Region of Yogyakarta, Sleman 55584, Indonesia

*Corresponding author's email: diahayuprawitasari@uii.ac.id

Received: 20 October 2025

Accepted: 26 November 2025

Abstract: Soil contamination by hydrocarbons and hazardous chemical compounds is a serious issue for environmental sustainability. Bioremediation is an environmentally friendly approach that utilizes microorganisms to degrade pollutants. This article is a literature review focusing on two key microorganisms: the fungus *Phanerochaete chrysosporium* and the bacterium *Pseudomonas putida*. Both are known to have synergistic abilities to break down complex hydrocarbons through ligninolytic enzymes and aromatic metabolic pathways. Literature data demonstrates the successful application of both in the remediation of oil-contaminated soil, textile wastewater, and chemical industry applications. The results of this study confirm that the effectiveness of bioremediation is strongly influenced by environmental conditions, such as pH, temperature, oxygen, and nutrient ratios. This study is expected to provide a comprehensive overview of the potential, mechanisms, applications, and factors influencing the effectiveness of *P. chrysosporium* and *P. putida*.

Keywords: bioremediation, hydrocarbon, *Phanerochaete chrysosporium*, *Pseudomonas putida*

1. INTRODUCTION

Soil is a fundamental element that supports life on Earth. Optimal soil quality is essential for plant development, environmental equilibrium, and human well-being. Human activities, particularly mining, produce hydrocarbon contamination in the soil, thereby decreasing its fertility and ecological functionality. Hydrocarbons are challenging to degrade, resulting in their persistence in the environment, particularly in soil, for extended durations, which adversely affects ecosystems. Globally, there have been multiple reports of hydrocarbon pollution incidents, including crude oil spills in marine environments that contaminate coasts and fuel leaks that contaminate terrestrial surfaces. These instances inflict harm on ecosystems, diminish land productivity, and result in considerable economic losses.

Polycyclic aromatic hydrocarbons (PAHs) generated from petroleum and combustion activities can remain in the soil for extended periods. This chemical may induce cancer and disturb the microbial equilibrium in the soil, thereby affecting plant growth (Zhang et al., 2023). Prolonged exposure to PAHs may elevate cancer risk and impair respiratory and reproductive functions in humans.

Various technologies have been developed to mitigate hydrocarbon contamination. Physical techniques such as adsorption and filtration can rapidly reduce pollutant concentrations, although frequently merely relocate toxins to an alternative medium. Chemical techniques, such as chemical oxidation and synthetic surfactants, can partially decompose hazardous substances; nevertheless, they may generate toxic byproducts and are frequently costly. Consequently, biological therapy or bioremediation is regarded as more ecologically sustainable as it utilizes the inherent capacity of microorganisms to decompose contaminants into harmless, simple chemicals. Bioremediation is the technology utilized for restoring biologically polluted soil conditions. Bioremediation depends on a microbial consortium rather than a singular microbe. This method is seen more efficient as many metabolic pathways might cooperate, therefore accelerating the breakdown process (Chen et al., 2020). Two significant microorganisms in previous bioremediation studies include the bacterium *Pseudomonas putida* and the fungus *Phanerochaete chrysosporium*. The bacterium *P. putida* is recognized for its ability to degrade aromatic hydrocarbons, including toluene, benzene, and xylene, whereas the fungus *P. chrysosporium* can produce lignolytic enzymes that efficiently decompose complex aromatic molecules. Both have been extensively utilized in the bioremediation of oil-contaminated soil, the treatment of industrial liquid waste, and the degradation of textile dyes.

This article aims to analyse the potential, degradation mechanisms, applications, case studies, and factors influencing the efficiency of utilizing microorganisms in bioremediation.

2. MATERIALS AND METHODS

This research uses a literature review methodology, including the collection, examination, and analysis of scholarly papers from both national and international sources published between 2016 and 2024. Several databases are used for searching papers, including ScienceDirect, SpringerLink, Google Scholar, and PubMed. The utilized keywords are in English, including ‘bioremediation’, ‘*Phanerochaete chrysosporium*’, ‘*Pseudomonas putida*’, and ‘hydrocarbons’, as well as in Indonesian: ‘bioremediasi’, ‘jamur *Phanerochaete chrysosporium*’, ‘bakteri *Pseudomonas putida*’, and ‘hidrokarbon’. The article selection process adheres to specific criteria: (1) research that explicitly involves one or both of these microorganisms; (2) an emphasis on the degradation of hydrocarbons or organic waste; and (3) the incorporation of research findings presented as measurable quantitative or qualitative data. Articles that failed to match the criteria or lacked relevance were excluded from this study.

3. RESULTS AND DISCUSSION

3.1. *Phanerochaete chrysosporium* fungi

Phanerochaete chrysosporium is a white-rot fungus recognized for its capacity to breakdown diverse persistent organic pollutants, including hydrocarbons, via its non-specific ligninolytic enzyme system (Kalia et al., 2022). This capability enables the fungus to decompose intricate hydrocarbon structures into more straightforward and less hazardous molecules (Daâssi & Almaghrabi, 2023). *Phanerochaete chrysosporium* has been recognized as a model fungus within the white-rot fungi category, proficient in the degradation of lignin and intricate aromatic compounds. Konan et al. (2024) assert that this fungus has a comprehensive lignolytic enzyme system, comprising manganese peroxidase (MnP), lignin peroxidase (LiP), and laccase, capable

of degrading lignin and mineralizing several detrimental xenobiotic chemicals concurrently. These enzymes collaborate to dismantle the robust bonds inside the polycyclic hydrocarbon structure (Pozdnyakova, 2012; Kurniawan et al., 2018). Hydrocarbons will undergo decomposition into smaller molecules by a sequence of oxidation and reduction events, converting them into less harmful or even innocuous compounds (Thirumalaivasan et al., 2024; Deshmukh et al., 2016; Zhu et al., 2025).

3.2. *Pseudomonas putida* bacteria

Pseudomonas putida is a prevalent saprophytic bacteria capable of utilizing several carbon and energy sources. These soil microorganisms have been extensively utilized as an experimental model to investigate the biodegradation of aromatic chemicals or hydrocarbons. The capacity to breakdown these molecules arises from the existence of many metabolic pathways, specifically through the expression of genes associated with the catabolism of hydrocarbons and aromatic compounds. This bacterium possesses significant potential for the bioremediation of PAH-contaminated settings, particularly owing to its capacity to decompose complex chemicals into simpler metabolites (Erwin et al., 2019). *P. putida* exhibits a resilient and adaptable metabolism, along with significant tolerance to many hazardous substances, rendering it a viable candidate for lignin breakdown and valorization (Zhou et al., 2025).

Recent research by Royet et al. (2025) using a transposon sequencing (Tn-seq) methodology to discover critical genes exhibiting tolerance to metals like cadmium, cobalt, copper, and zinc. The findings indicated that, alongside established genes such as *czcA-1*, *cadA-3*, *cadR*, and *pcoA2*, novel genes previously unlinked to metal tolerance were identified, specifically PP_5337 as a copper transcription regulator, *RoxSR* (PP_0887/0888) for cadmium tolerance, PP_1663 for cadmium, and PP_5002 for cobalt. This result enhances our comprehension of the adaptation mechanisms of *P. putida* under heavy metal stress, encompassing both active resistance via efflux pumps and passive tolerance mechanisms. This discovery further substantiates the viability of *P. putida* as a robust candidate for bioremediation in metal-contaminated settings. The adaptive capacity of *P. putida* renders it an appropriate candidate for bioremediation in intricately contaminated settings, encompassing locations with a combination of hydrocarbons and heavy metals. This bacterium possesses the capability to endure harsh environmental conditions, such as osmotic pressure and reactive oxygen species, commonly found at contaminated locations (Svenningsen et al., 2015; Craig et al., 2021).

3.3. Mechanism of hydrocarbon biodegradation

The main mechanisms in bioremediation involve biotransformation and biodegradation processes, where toxic compounds are converted into simpler and less harmful substances. For example, *Pseudomonas putida* breaks down aromatic compounds through the ortho pathway into catechol, which is then cleaved by the enzyme catechol 1,2-dioxygenase. The final product is pyruvate, which can directly enter the Krebs cycle (Harwood & Parales, 1996). On the other hand, fungi such as *Phanerochaete chrysosporium* produce lignin peroxidase and manganese peroxidase, which can break down the aromatic ring structures in PAHs into more easily degradable phenolic compounds (Cajthaml, 2015). In a consortium, the subsequent reaction of one microbe becomes the substrate for another, creating a highly efficient chain of metabolic pathways. This synergy allows for faster and more complete pollutant degradation compared to when microbes work individually, especially for hydrocarbon compounds that are resistant to degradation (Arisah et al., 2021) (Appanna et al., 1996). Comparative studies show that microbial consortia often achieve significantly higher levels of biodegradation compared to single cultures, especially in the context

of degrading xenobiotic compounds with complex molecular structures (Verma & Kuila, 2019). The synergy between microorganisms in this consortium can enhance the efficiency of the bioremediation process, enabling broader and faster pollutant degradation (Sayqal & Ahmed, 2021).

3.4. Study cases

There were eight previous study found related to the optimalization of polycyclic aromatic hydrocarbon (PAH) biodegradation. Those studies were collected from recent paper within last five years, from 2020 to 2025. The studies includes the use of *Pseudomonas putida* or *Phanerochaete chrysosporium* to degrade PAH such as crude oil (Annie et al., 2020), petroleum refinery sludge (Choudhury et al., 2022), and petroleum sludge-polluted soil (Ma et al., 2022), and sewage-sludge-amended soil (Chane et al., 2024).

Table 1. Study Cases from Previous Result for Optimalization of Biodegradation PAH

Author	Title	Result	Journal
Zhang et al. (2022)	Self-assembled fungus-biochar composite pellets (FBPs) for enhanced co-sorption-biodegradation towards phenanthrene.	The efficiency of fungus-biochar for phenanthrene biodegradation reaches >90%.	Chemosphere volume 286 Pt 3
Ma et al. (2022)	Enhancing bioremediation of petroleum sludge-polluted soil: The impact of fungal-bacterial consortium's application strategy.	The hydrocarbon removal efficiency reached 91.2% with the sequential inoculation strategy.	Applied Soil Ecology
Chane et al. (2024)	Persistent polycyclic aromatic hydrocarbons removal from sewage sludge-amended soil through phytoremediation combined with solid-state ligninolytic fungal cultures.	<i>Phanerochaete chrysosporium</i> , PAH reduction up to 52% (fungus only) and up to 60% (plant-fungus combination).	Fungal Biology volume 128(2)
Cui et al. (2021)	Stability and nutrients removal performance of a <i>Phanerochaete chrysosporium</i> -based aerobic granular sludge process by step-feeding and multi A/O conditions.	<i>Phanerochaete chrysosporium</i> , Enhancing the stability and efficiency of nitrogen and phosphorus removal in wastewater).	Bioresource Technology volume 341
Martínez-Toledo et al. (2022)	Evaluation of in-situ biosurfactant production by inoculum of <i>P. putida</i> and nutrient addition for the removal of PAH from aged oil-polluted soil.	In-situ biosurfactants enhance PAH degradation, with high efficiency within 10 days.	Biodegradation volume 33
Choudhury et al. (2022)	Enhanced methane production and hydrocarbon removal from petroleum refinery sludge after <i>Pseudomonas putida</i> pretreatment and process scale-up.	<i>Pseudomonas putida</i> can remove hydrocarbons by up to 57% and significantly increase methane production.	Bioresource Technology
Shandookh et al. (2024)	Bioremediation of hydrocarbon pollutants by <i>Pseudomonas putida</i> under optimal conditions.	<i>Pseudomonas putida</i> can degrade crude oil by up to 88.3% at pH 7 and a temperature of 35°C.	Advancements in Life Sciences
Annie et al. (2020)	Fate of Crude Oil in Soil Treated with <i>Pseudomonas putida</i> Immobilized on Coconut Coirpith a Lowcost Biocarrier	Immobilization in coconut fiber increases hydrocarbon degradation by up to 45%.	Soil and Sediment Contamination volume 29

4. CONCLUSION

Based on the discussion from various studies, it can be concluded that soil bioremediation using a consortium of bacteria and fungi offers a highly promising solution for environmental pollution management. Microbial consortia exhibit synergistic capabilities in breaking down complex harmful compounds such as pesticides, hydrocarbons, and heavy metals. The use of microorganisms from the species *Pseudomonas putida* and *Phanerochaete chrysosporium* has been proven effective in accelerating the degradation process through complementary metabolic pathways. The success of bioremediation is highly influenced by environmental conditions, the type of pollutant substrate, and the combination of microbes used. Therefore, further research to develop a consortium formulation that is more adaptable to various soil conditions is crucial for this technology to be widely applied in the field. Reducing the Total Petroleum Hydrocarbon (TPH) level from 5.8% to 0.98% in 35 days using the landfarming method and the addition of compost fertilizer.

REFERENCES

- Akhtar, S., Mohsin, A., Riaz, A. and Mohsin, F. (2023) 'Worldwide efficiency of bioremediation techniques for organic pollutants in soil: a brief review', *Geosfera Indonesia*, 8(1), p. 102. doi: 10.19184/geosi.v8i1.30875.
- Appanna, V. D., Gzásó, L. G. and Pierre, M. S. (1996) 'Multiple-metal tolerance in *Pseudomonas fluorescens* and its biotechnological significance', *Journal of Biotechnology*, 52(2), p. 75. doi: 10.1016/s0168-1656(96)01623-9.
- Arisah, F. M., Amir, A. F., Ramli, N., Ariffin, H., Maeda, T., Hassan, M. A. and Yusoff, M. Z. M. (2021) 'Bacterial resistance against heavy metals in *Pseudomonas aeruginosa* RW9 involving hexavalent chromium removal', *Sustainability*, 13(17), p. 9797. doi: 10.3390/su13179797.
- Craig, K., Johnson, B. R. and Grunden, A. M. (2021) 'Leveraging *Pseudomonas* stress response mechanisms for industrial applications', *Frontiers in Microbiology*, 12. doi: 10.3389/fmicb.2021.660134.
- Daâssi, D. and Almaghrabi, F. (2023) 'Petroleum-degrading fungal isolates for the treatment of soil microcosms', *Microorganisms*, 11(5), p. 1351. doi: 10.3390/microorganisms11051351.
- Deshmukh, R., Khardenavis, A. A. and Purohit, H. J. (2016) 'Diverse metabolic capacities of fungi for bioremediation', *Indian Journal of Microbiology*, 56(3), p. 247. doi: 10.1007/s12088-016-0584-6.
- Erwin, K., Johnson, W., Meichan, A. J. and Whitman, C. P. (2019) 'Preparation of dihydroxy polycyclic aromatic hydrocarbons and activities of two dioxygenases in the phenanthrene degradative pathway', *Archives of Biochemistry and Biophysics*, 673, 108081. doi: 10.1016/j.abb.2019.108081.
- Garrido-Sanz, D., Redondo-Nieto, M., Guirado, M., Jiménez, Ó. P., Millán, R., Martín, M. and Rivilla, R. (2019) 'Metagenomic insights into the bacterial functions of a diesel-degrading consortium for the rhizoremediation of diesel-polluted soil', *Genes*, 10(6), p. 456. doi: 10.3390/genes10060456.
- Gopinath, V., Giribabu, N., Mohan, P. S., Barathan, M., Govindarajan, V. K., Mani, A., Rahman, P. S. A. and Karsani, S. A. (2024) 'Environmental impact and human health effects of

- polycyclic aromatic hydrocarbons and remedial strategies: a detailed review', *Chemosphere*, 351, 141227. doi: 10.1016/j.chemosphere.2024.141227.
- Hendarko, S., Rukmi, M. G. I. and Indrawati, A. (1999) 'Isolasi dan karakterisasi *Pseudomonas* Sp dari limbah fenol serta kemampuan biodegradasinya', *Jurnal Kimia Sains Dan Aplikasi*, 2(4), p. 133. doi: 10.14710/jksa.2.4.133-137.
- Kalia, A., Sharma, S., Semor, N., Babele, P. K., Sagar, S., Bhatia, R. K. and Walia, A. (2022) 'Recent advancements in hydrocarbon bioremediation and future challenges: a review', 3 *Biotech*, 12(6). doi: 10.1007/s13205-022-03199-y.
- Kurniawan, A., Wirasembada, Y. C., Razaad, I. M. N., Novriansyah, A., Rafi, M. and Effendi, A. J. (2018) 'Hidrokarbon aromatik polisiklik pada lahan tercemar limbah minyak bumi: tinjauan pertumbuhan mikro-organisme, proses metabolisme dan biodegradasi', *Jurnal Ilmu Lingkungan*, 16(1), p. 9. doi: 10.14710/jil.16.1.9-24.
- Léon, M. T., Gómez, M. A. C., Román, J. C. and Sánchez, A. (2022) 'Soil quality evaluation of hydrocarbon polluted parcels', *Journal of Geoscience and Environment Protection*, 10(9), p. 27. doi: 10.4236/gep.2022.109002.
- Mahajan, M. and Prakash, A. (2025) 'Bacterial consortia as potential bioremediation agents for wastewater treatment: a comprehensive review', *International Journal of Advancement in Life Sciences Research*, 8(1), p. 16. doi: 10.31632/ijalsr.2025.v08i01.002.
- Majeed, B. K., Shwan, D. M. S. and Rashid, K. A. (2025) 'A review on environmental contamination of petroleum hydrocarbons; its effects and remediation approaches', *Environmental Science Processes & Impacts*. doi: 10.1039/d4em00548a.
- Manikandan, S. K., Hasnain, M., Ali, F., Jaiswal, K. K., Sheteiwiy, M. S., Klironomos, J. N. and El-Keblawy, A. (2025) *Advances in bioremediation of soil co-contaminated with hydrocarbon and heavy metals: mechanisms, challenges, and future directions*. doi: 10.2139/ssrn.5128340.
- Mohammed, S. A., Omar, T. J. and Hasan, A. H. (2023) 'Degradation of crude oil and pure hydrocarbon fractions by some wild bacterial and fungal species', *arXiv*. Available at: <https://doi.org/10.48550/arxiv.2301.08715>.
- Patowary, K., Patowary, R., Kalita, M. C. and Deka, S. (2017) 'Characterization of biosurfactant produced during degradation of hydrocarbons using crude oil as sole source of carbon', *Frontiers in Microbiology*, 8. doi: 10.3389/fmicb.2017.00279.
- Pozdnyakova, N. N. (2012) 'Involvement of the ligninolytic system of white-rot and litter-decomposing fungi in the degradation of polycyclic aromatic hydrocarbons', *Biotechnology Research International*, 2012, p. 1. doi: 10.1155/2012/243217.
- Prawitasari, D. A. (2019) *Peningkatan perolehan hidrolisat protein dari ampas hasil samping ekstraksi lutein dan zeaxanthin daun ubi jalar (*Ipomoea batatas* L.) varietas cilembu melalui pre-treatment ampas dengan jamur *Aspergillus niger**. [Unpublished thesis].
- Radhakrishnan, A., Pandiyan, B., Vasudevan, M., Natarajan, N., Chauhan, A., Arora, J., Ranjan, A., Rajput, V. D., Sushkova, S., Minkina, T., Basniwal, R. K., Kapardar, R. and Srivastav, R. (2023) 'Bioremediation of hydrocarbon pollutants: recent promising sustainable approaches, scope, and challenges', *Sustainability*, 15(7), p. 5847. doi: 10.3390/su15075847.
- Roszak, M., Jabłońska, J., Stachurska, X., Dubrowska, K., Kajdanowicz, J., Gołębiowska, M., Kiepas-Kokot, A., Osińska, B., Augustyniak, A. and Karakulska, J. (2021) 'Development of an autochthonous microbial consortium for enhanced bioremediation of PAH-

- contaminated soil', *International Journal of Molecular Sciences*, 22(24), p. 13469. doi: 10.3390/ijms222413469.
- Sayqal, A. and Ahmed, O. B. (2021) 'Advances in heavy metal bioremediation: an overview', *Applied Bionics and Biomechanics*, 2021, p. 1. doi: 10.1155/2021/1609149.
- Shandookh, F. K., Mohammed, M. K. and Jabbar, A. D. (2024) 'Bioremediation of hydrocarbon pollutants by *Pseudomonas putida* under optimal conditions', *Advancements in Life Sciences*, 11(4), p. 761. doi: 10.62940/als.v11i4.1963.
- Svenningsen, N. B., Pérez-Pantoja, D., Nikel, P. I., Nicolaisen, M. H., Lorenzo, V. de and Nybroe, O. (2015) 'Pseudomonas putida mt-2 tolerates reactive oxygen species generated during matrix stress by inducing a major oxidative defense response', *BMC Microbiology*, 15(1). doi: 10.1186/s12866-015-0542-1.
- Thirumalaivasan, N., Gnanasekaran, L., Kumar, S., Rajesh, D., Thanigaivel, S., Rajendran, S., Nangan, S. and Kanagaraj, K. (2024) 'Utilization of fungal and bacterial bioremediation techniques for the treatment of toxic waste and biowaste', *Frontiers in Materials*, 11. doi: 10.3389/fmats.2024.1416445.
- Verma, S. and Kuila, A. (2019) 'Bioremediation of heavy metals by microbial process', *Environmental Technology & Innovation*, 14, 100369. doi: 10.1016/j.eti.2019.100369.
- Zheng, X., Oba, B. T., Shen, C., Rong, L., Zhang, B., Huang, L., Feng, L., Liu, J., Du, T. and Deng, Y. (2023) 'Effect of the bacterial community assembly process on the microbial remediation of petroleum hydrocarbon-contaminated soil', *Frontiers in Microbiology*, 14. doi: 10.3389/fmicb.2023.1196610.
- Zhou, Q., Fransen, A. and Winde, J. H. de (2025) 'Lignin-degrading enzymes and the potential of *Pseudomonas putida* as a cell factory for lignin degradation and valorization', *Microorganisms*, 13(4), p. 935. doi: 10.3390/microorganisms13040935.
- Zhu, X., Cheng, S. P., Fang, Z., Zhen, G., Lu, X., Liu, H., Qi, J., Zhou, Z., Zhang, X. and Wu, Z. (2025) 'Studies on the treatment of anaerobically digested sludge by white-rot fungi: evaluation of the effect of *Phanerochaete chrysosporium* and *Trametes versicolor*', *Microbial Cell Factories*, 24(1). doi: 10.1186/s12934-024-02611-x.