NEW INSIGHTS INTO THE REMEDIATION OF POLLUTED SOILS USING ENDOPHYTIC FUNGI

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Abstract

Soil pollution is a growing global concern and one of the most challenging environmental issues today, involving the human sector as well. Innovative soil remediation strategies are needed to conserve the natural resources of the environment. Endophytes are present in all plants species, living symbiotically in a continuum dynamic mutualism. Among multiple changing roles, safeguarding the host in terms of increasing resistance to abiotic factors has been widely demonstrated. Following these physiological changes, host plants have beneficial potential in degrading pollutants from contaminated soils. Enzymes produced by host plants along with endophytes may also, degrade macromolecule compounds into small molecules or convert more toxic substances into less toxic substances to increase their adaptability. Phytoremediation technology with endophyte fungi is an ecological alternative strategy that has been documented as a promising technology for remedying contaminated soils. This review article aims to piece together the physiological, chemical and genetical mechanisms employed in phytoremediation techniques mediated by endophytic fungi and highlight the importance of the plant-microbiome ecology.

Key words: endophytic fungi, hydrocarbon degradation, soil, bioremediation.

INTRODUCTION

Global industrialization has led to pollution of the environment, freshwater, and topsoil. Heavy metals are naturally occurring pollutants found in the Earth's crust and difficult to decompose. The compounds exist as ores in rocks and are recovered as minerals. High-level exposure to heavy metals can result in their release into the environment where remain toxic for extended periods (Masindi et al., 2020; Bala et al., 2022). The use of endophytic fungi for bioremediation of polluted environments, particularly contaminated soils, is a promising approach. Studies have shown that endophytic fungi colonizing host roots can have a positive impact on soil productivity and characteristics. Endophytic fungi during growth not only promote the nutrients in the soil by decomposition, but also reduce the toxicity of the soil (Chen & Dai, 2013).

A literature survey was conducted to reveal the importance of endophytic fungi in the remediation of contaminated soils. The main databases used were CAB Direct and PubMed. This review presents new perspectives on the bioremediation of soils polluted with hydrocarbons by involving endophytic fungi and highlighting the relationships in host plants and their microbiome. A survey of the literature was performed to show the differences regarding the number of articles which focused on the significance of endophytic fungi in the remediation of contaminated soils. The abstract search was conducted using simple and combined keywords such as "endophytic fungi", "endophytic fungi in hydrocarbon degradation", "soil pollution", "fungi in polluted soil", "phytoremediation" and "phytoremediation with endophytic fungi". The number of indexed publications containing "endophytic fungi" was similar in both databases (CAB Direct – 10,923 and PubMed -11,227).

When we compared "phytoremediation" searchterm with "phytoremediation with endophytic fungi", the number of hits was highly different: CAB Direct and PubMed - 17,445 and 58,127 entries, respectively, for the simple keyword, and for the combined one, 79 hits and 365 hits, respectively. The low number of entries is due

to the novelty of the topic regarding the involvement of endophytic fungi in the bioremediation of polluted soils. Conversely, the number of entries for "soil pollution" was very high for both databases, 161,792 hits in CAB Direct and 700,713 results in PubMed. The number of entries of "fungi in polluted soil", revealed a high interest with 105,466 entries in PubMed and only 8176 entries in CAB Direct. This survey reveals a keen interest in researching environmentally friendly methods and techniques for contaminated soils.

BIOREMEDIATION WITH ENDOPHYTIC FUNGI

Bioremediation is a process that refers to the use of biological agents such as bacteria, fungi, algae and plants for the degradation and detoxification of hazardous substances and contaminants from soil, water, and other environments (Khatoon et al., 2021). It is considered a cost-effective and environmentally friendly technology under the green biotechnology area (Khalid et al., 2021). Bioremediation of polluted environments, especially contaminated soils, using endophytic fungi is a promising approach. Over the years, studies have shown that endophytic fungi that colonize the host roots can positively affect the productivity of the soil and its characteristics. In bioremediation, endophytes are able to stimulate host plant growth in polluted soils by increasing the production of endogenous auxins and can positively influence nitrogen fixation process (Rajkumar et al., 2009; Nandya et al., 2020). Endophytic fungi can accumulate soil pollutants through the root parts of plants. For instance, *Piriformospora indica* a filamentous fungus with an endophytic character in a wide range of plant roots and with abilities similar to a mycorrhiza can colonize *Zea mays* roots, promoting plant growth and root development. Therefore, since plant roots penetrate deep soil layers, *P. indica*-maize mutualistic combination enhanced petroleum breakdown by relying on host-derived shelters and nutrients for their endophytic partner. This is especially helpful for treating deep-reaching contamination (Zamani et al., 2016; He et al., 2020). The symbiotic interaction between plants of meadow fescue (*Festuca pratensis*) and two endophytic fungi of the *Neotyphodium* species can support the synthesis of dehydrogenase, which assists in the degradation of PAHs (Soleimani et al., 2010; Saravanan et al., 2020). Another study points out the benefits of an endophytic fungi consortium on *Lactuca sativa* plants cultivated in cadmiumcontaminated soil. The endophytic fungi-treated group had a greater foliar and root biomass compared to the control group (Bibi et al., 2018; Soldi et al., 2020). In a laboratory experiment, endophytic fungi were also inoculated on *Festuca arundinacea* samples to asses their positive effects on this host at increasing lead concentrations. The results showed a better performance of the plants treated with the endophyte consortium for each of the growth parameters recorded, thus reducing the harmful effects of the heavy metal (Soldi et al., 2020). *Aspergillus* strain *G16* associated with *Brassica juncea* and *Trichoderma* strain *H8* associated with *Acacia auriculiformis* improved plant growth (44% and 167% respectively) in cadmium and nickel contaminated soils. Together, these two strains induced a higher plant yield (178%) compared to control plants in contaminated soils (Jiang et al., 2008). Plants which can colonize heavy metal polluted soils and highly accumulate heavy metals in their above-ground tissues are called hyperaccumulator plants, a promising tool for phytoextraction of heavy metal-contaminated soils (Baker & Brooks, 1989; Baker, 2000; Sigel et al., 2013). A non pathogenic *F. oxysporum*, isolated from the Zn/Cd co-hyperaccumulator *Sedum alfredii* grown in a Pb or Zn mined area, was able to increase *S. alfredii* root systems and function, metal availability and accumulation, and plant biomass, and thus phytoextraction efficiency (Zhang et al., 2012; Zheng et al., 2016).

The endophytic fungi *Pestalotiopsis microspora* was uniquely able to grow on synthetic polymer polyester polyurethane as the sole carbon source under both aerobic and anaerobic conditions (Russell et al., 2011; Deng & Cao, 2016) suggesting its potential use for treatment of white plastic pollution. Toxic metals can be accumulated in large amounts within the mycelia of endophytic fungi. Yet, studies on the mechanisms behind metal transport and detoxification are scarce (Zahoor et al., 2017; Khalid et al., 2021).

FUNGAL BIO-MECHANISMS INVOLVED IN HYDROCARBONS DEGRADATION

Polycyclic aromatic hydrocarbons (PAHs) are a class of organic compounds that are dangerous environmental pollutants and can cause health problems. Of the more than one hundred known PAHs, 16 have been identified as priority pollutants. The use of very diverse biological machineries, including endophytic fungi, collected from contaminated sites, has emerged as a safe and sustainable ecological approach to the degradation of PAHs (polycyclic aromatic hydrocarbons) and PHs (petroleum hydrocarbons). Since the first isolation of hydrocarbon-degrading bacteria in 1913 by Söhngen (Söhngen, 1913), over 79 genera of bacteria were found to be able to use hydrocarbons as a sole source of energy and other were detected as able to degrade or transform hydrocarbons (Head et al., 2006; Prince et al., 2010). Fungi can remediate pollutants through several mechanisms and various mechanisms such as bioabsorption, precipitation, biotransformation and sequestration were proposed. Filamentous fungi have been reported as bioremediation agents due to their extensive mycelial networks and enzyme-secreting activities. These high redox potential enzymes, such as manganese peroxidase (MnP), laccases (Lac) and lignin peroxidases (LiP) for the oxidation of lignin are generally not substrate specific as they can oxidise a wide range of xenobiotics including pesticides, plastics and hydrocarbons (Asemoloye et al., 2020; Daccò et al., 2020). Mycoremediation significantly removes or degrades metals, persistent organic pollutants and other emerging contaminants (Kumar et al., 2021).

Endophytic fungi *Penicillium atrovenetum*, *Thermomyces lanuginosus, Penicillium canescens*, *Trichocladium opacum* and *Aspergillus niger* were assessed for the efficacy to utilize PHs as their source of carbon. All fungi were isolated from *Eichhornia crassipes* samples on minimal salt broth (MSB) containing petroleum hydrocarbons and were observed to have increased growth rates (Wahab et al., 2022). The plant-endophyte interaction system could remediate polycyclic aromatic

hydrocarbon contamination *in vivo* by promoting the expression of metabolism-related genes. The endophytic fungi *Phomopsis liquidambaris*, isolated from stem of *Bischofia polycarpa* demonstrated a good capacity in the remediation of phenanthrene in interaction with rice. The results showed that the removal rate of phenanthrene in the root was higher than that in the leaf and that in large part was due to the presence of the endophytic fungus (Hussain et al., 2018; Chen et al., 2019; Iqbal et al., 2019; Fu et al., 2022). Crude oil and diesel were efficiently degraded in liquid culture by two filamentous fungi, *Aspergillus ustus* and *Purpureocillium lilacinum*, isolated from an artificially contaminated soil. *P. lilacinum* was more potent in degrading hydrocarbons and exhibited the highest crude oil (44.55%) and diesel (27.66%) removal rates and the highest biodegradation constant (Benguenab & Chibani, 2021). Endophytic species of *Verticillium, Xylaria*, *Colletotrichum*, *Clonostachys Saccharicola*, *Phomopsis* and *Aspergillus* were isolated from plants collected in a natural habitat contaminated with crude oil and were reported as able to degrade petroleum hydrocarbon, quantified by infrared spectroscopy and gas chromatography (Marín et al., 2018). Also, assessment of seven endophytic fungi living in mangroves showed the ability of *Nigrospora* sp., *Aspergillus niger, Aspergillus* sp., *Curvularia* sp., *Pestalotiopsis aduinta*, *Fusarium* sp., and *Cladosporium* sp. to degrade hydrocarbons, using FT-IR spectroscopy analysis (Sawant & Rodrigues, 2020). Effective bioremediation strategies require consideration of physicochemical parameters and catabolic properties of degrading microbial communities. It is important to note that most microorganisms are not readily cultivable and cannot be easily characterized, which poses a significant challenge for microbiologists (Mishra et al., 2020). Yet, multiple fungal strains were reported to be able to remove or metabolize contaminants (Table 1).

Still, technological and economic constraints remain. Despite the existence of problems, the use of high-throughput genomic approaches in bioremediation is still in its early stages of development.

Table 1. Overview of the bioremediation potential of fungi - contaminants and bio-active fungal species

PLANT-MICROBIOME

Plant microbiome ecology is a multidisciplinary field that explores the complex relationships between plants and their associated microbial communities. It provides insights into the fundamental processes that shape plant-microbe interactions and the potential for using the plant microbiome for sustainable agriculture and environmental management.

The microbiome of plants comprises bacterial, fungal, and archaeal communities that are associated with their host plants in the rhizosphere, phyllosphere and endosphere (Tardif et al., 2016; Mitter et al., 2019). The microbiome has gained significant attention in both research and applied science. Some key areas where the plant-microbiome has proven to be an important and useful technique are agriculture and crop production, industrial processes and biotechnology, environmental monitoring and restoration, as well as lately bioremediation and waste management. The microbiome plays a vital role in bioremediation, which involves the use of microorganisms to degrade or transform pollutants into less harmful forms (Bala et al., 2022). The microbiome is used in bioremediation in hydrocarbon degradation, heavy metal remediation, chlorinated compound degradation, xenobiotic transformation, land and water remediation. Microbes can colonize the rhizosphere, phyllosphere, and live inside plant tissues as endophytes. Fungal microorganisms, which have an endophytic lifestyle, play an important role in all plant processes.

Plant-associated microbes have an essential mission in the growth and development of their hosts by producing various plant growth hormones, including auxins and gibberellins. These two hormones are known to promote stem elongation, seed germination, and flowering in
plants. By producing gibberellins, root-By producing gibberellins, rootassociated microbes contribute to the overall growth and development of plants. Auxin production is a common trait found in all plantassociated microbes (Yadav et al., 2017). Environmental factors, such as soil type, climatic conditions, land management practices, and plant genotype, shape the composition and functioning of the plant microbiome.

Plant microbiome ecology investigates how these factors influence microbial community structure, diversity, and activity, and how they, in turn, impact plant performance and ecosystem functioning (Fonseca et al., 2017; Dastogeer et al., 2020). Certain species of arbuscular mycorrhizal fungi (AMF) that promote plant growth have been found to hinder it in specific circumstances, such as low light, low temperature, or phosphorus (P) availability (Smith & Smith, 1996; Johnson et al., 1997; Sergaki et al., 2018). The activity of AMF can be inhibited by the soil microbiota, as demonstrated by Svenningsen et al. (2018). This emphasises the importance of conducting field
experiments to gain a comprehensive experiments to gain a comprehensive understanding of microbe behaviour. The study of microbiomes in polluted soils is a relatively recent field, and pinpointing the exact first study on this topic can be challenging. However, one of the pioneering studies that laid the foundation for understanding the microbiome of polluted soils was published in 2003 by Anne Spain and Elizabeth Alm (Spain & Alm, 2003). Genomic analysis is a culture-independent technique that enables the quick study of various samples, such as water and soil, through the development of sequencing technology. Recent advances in next-generation sequencing (NGS) have

allowed for comprehensive genomics, metagenomics, and bioinformatics analysis of microbial communities, providing unparalleled insight into key bioremediation mechanisms. Nucleotide databases and *in silico* tools are used to advance research on the role of microbes in pollutant degradation and the identification of
new genes responsible for microbial new genes responsible remediation (Sharma & Kumar, 2021). These recent advances in metagenomics and amplicon sequencing have provided new insights into plant symbioses, including the structure and assembly of symbiotic microbial communities (Vandenkoornhuyse et al., 2015).

MICROBIOME DIVISIONS INTO MICRO-ECOSYSTEMS - RHIZOSPHERE, ENDOSPHERE AND PHYLLOSPHERE

The rhizosphere zone is the 1-10 mm part of soil immediately surrounding the roots, which is influenced by the plant through its root exudates, mucilage and dead plant cells (Cai et al., 2017). The rhizosphere organisms that are most frequently studied for their benefits include mycorrhizae, rhizobium bacteria, plant growthpromoting rhizobacteria (PGPR), and biocontrol microbes (Hinsinger et al., 2009; Dastogeer et al., 2020). Symbiotic fungi colonize the rhizosphere region in soil or the internal tissues of plants. They usually obtain carbon from the host plant and return essential soil elements to the plant, while also improving water and nutrient uptake (Priyashantha et al., 2023). Studies confirmed the existence of a central microbiome by identifying members of *Xanthomonadales, Rhizobiales*, *Sphingomonadales, Burkholderiales* in the rhizosphere of six plant species: *Artemisia argyi*, *Ageratum conyzoides*, *Erigeron annuus*, *Bidens biternate*, *Euphorbia hirta* and *Viola japonica* (Lei et al., 2019; Santos et al., 2021). Experimental data have shown the importance of the rhizosphere microbiome in rhizoremediation and plant growth in contaminated sites. Thus, it is obvious that microbial assisted rhizoremediation has the potential to remove toxic compounds (Kotoky et al., 2018). Bacteria, and to some extent archaea, are important members of endosphere communities and as microbes that interact with their host plants, provide them with benefits.

Endophytic microorganisms colonize the endosphere and have been shown to metabolize pollutants and influence plant development ability (Taghavi et al., 2005; Tardif et al., 2016). The endophytic community in the roots can differ significantly from the adjacent soil community. Generally, the diversity of the endophytic community is lower than that of the microbial community outside the plant (Schlaeppi et al., 2014; Dastogeer et al., 2020). Scientists employ various methods, including DNA sequencing, metagenomics, microscopy, and culturing techniques, to study the endosphere microbiome.

The study of the endosphere microbiome has
practical applications in agriculture, applications horticulture, and environmental management. By improving the beneficial interactions between plants and endophytes, crop productivity can be improved, with the need for chemical inputs reduced, stress tolerance enhanced, and sustainable agriculture practices promoted. The phyllosphere refers to the aerial surface of a plant, including the stem, leaf, flower, and fruit. It is considered to be relatively nutrient-poor when compared to the rhizosphere and endosphere (Dastogeer et al., 2020). The phyllosphere microbiome has important implications for plant health and ecology. It is a dynamic and unique environment that provides microhabitats for microbial colonization. It offers nutrients, moisture, and physical structures that support the growth and survival of microorganisms. The composition and dynamics of the phyllosphere microbiome can vary depending on factors such as plant species, leaf age, environmental conditions and interactions with neighboring microorganisms. The phyllosphere actively acquires its microbiome through vertical transmission (from mother plants or seeds), horizontal transmission (from the environment), or mixed modes from neighbouring microbial reservoirs (Bright & Bulgheresi, 2010). Phyllosphere endophytes are primarily transmitted systemically through xylem but can also enter through leaf epidermal openings such as stomata, lenticels, and hydathodes (Compant et al., 2010).

The most common groups of bacteria (*Proteobacteria, Bacteroides, Firmicutes, and Actinobacteria*) are usually residing on the phyllosphere of different plant species including model plants *Arabidospis thaliana* and *Citrus* species (Reisberg et al., 2013; Kembel et al., 2014; Durand et al., 2018; Carvalho et al., 2020). In addition to bacteria, the phyllosphere also supports a significant diversity of yeasts and filamentous fungi.

MICROBIOME TOWARDS APPLIED SCIENCE - AT WHAT STAGE ARE WE?

Over the last decade, research on microbiomes has altered our understanding of the complexity and structure of microbial communities. The observations were complemented by progress that largely led to a significant reduction in highyielding screening costs (Cullen et al., 2020).

We can mention some examples of real-world bioremediation projects that have successfully utilized the microbiome with the project Deepwater Horizon Oil Spill: Following the Deepwater Horizon oil spill in the Gulf of
Mexico in 2010, where microbial Mexico in 2010, where microbial bioremediation played a significant role in oil degradation (Kimes et al., 2014). Microbial bioremediation techniques were employed to help mitigate the contamination with radionuclides of soil and water in the affected areas of Chernobyl Nuclear Disaster. *Penicillium* and *Cladosporium*, were found to effectively accumulate and immobilize radioactive isotopes, reducing their mobility in the environment (Zhdanova et al., 1991). Australia has a vast and diverse landscape, making it susceptible to various forms of soil contamination. The country has embraced bioremediation practices that leverage the microbiome to restore contaminated soils. Australian researchers and environmental practitioners have utilized microbial communities to remediate sites affected by mining activities, agricultural pollution, and other sources of soil contamination. Using structural equation modeling, a prediction model was developed to predict the impact of future climate change scenarios on soil microbial biodiversity in sub-Saharan Africa. The model predicts that increased temperatures and decreased precipitation will have a negative effect on soil microbial biodiversity in countries like Kenya, while the fungal biodiversity of Benin will benefit from the increase in annual precipitation. This study can provide important

information to support conservation efforts in countries heavily reliant on rain-fed agriculture and most vulnerable to the impacts of climate change. (Cowan et al., 2022).

CONCLUSIONS AND FUTURE PERSPECTIVES

Nowadays, the main biological means to clean soil are bioremediation and phytoremediation. These are two commonly processes used approaches for cleaning up contaminated soils. Either with microorganisms, such as bacteria and fungi, to degrade or transform contaminants in the soil into less harmful substances or using plants to remove, degrade, or stabilize contaminants in the soil.

Currently, specialized techniques for monitoring the genome, transcriptome, and proteome of microbial communities broad the path towards successful and efficient bioremediation techniques. The endophytes induce a quicker establishment of plants in these conditions, which accelerates the restoration of deteriorated areas.

Thus, reducing the presence of bioactive metals and improving the ecology, variety of soil microflora, and soil fertility, reestablishing healthy crop production. In conclusion, more research is required to study the mechanisms of degradation and in situ bioremediation of the fungal microorganisms.

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