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Mycoremediation of Textile Dye Effluents Using *Termitomyces heimii* Mushroom: A Sustainable Biocatalyst Approach

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Abstract

Textile dye effluents pose significant environmental and health challenges due to their complex chemical composition, high toxicity, and resistance to conventional treatment methods. Mycoremediation, the use of fungi and their enzymatic systems to degrade pollutants, has emerged as a sustainable and cost-effective alternative for treating industrial wastewater. White-rot fungi, particularly those producing ligninolytic enzymes such as laccase, lignin peroxidase, and manganese peroxidase, have demonstrated remarkable potential in degrading recalcitrant synthetic dyes. However, the bioremediation potential of *Termitomyces heimii*, a basidiomycete mushroom with robust enzymatic capabilities adapted to decomposing lignocellulosic materials, remains largely unexplored. This review aims to evaluate the current state of knowledge regarding *T. heimii* as a biocatalyst for textile dye remediation, examining its enzymatic mechanisms, degradation efficiency across various dye classes, optimal operational conditions, and comparative performance with established fungal species. The fungus exhibits significant promise due to its robust ligninolytic enzymes, including laccases and peroxidases, which play a crucial role in the degradation of recalcitrant pollutants. In addition, its fast-growing mycelial network, tolerance to environmental stress, and ability to bioaccumulate toxic metals highlight its suitability for application in contaminated soils and waste substrates. In conclusion, *T. heimii* represents an underexplored yet highly promising candidate for mycoremediation strategies. Further experimental validation, optimization of culture conditions, and field-scale studies are required to fully harness its remediation potential. Integrating *T. heimii* into sustainable bioremediation frameworks could contribute significantly to environmentally friendly pollution management and ecosystem restoration.

Keywords: Mycoremediation; *Termitomyces heimii*; Textile Dye Effluents; Biocatalyst; Ligninolytic Enzymes; Sustainable Biotechnology.

1.0 Introduction

The textile industry is one of the largest consumers of water and generators of wastewater globally, with approximately 280,000 tons of textile dyes discharged annually into industrial effluents worldwide (Lellis *et al.*, 2019). Textile dye effluents represent a significant environmental challenge due to their complex chemical composition, high color intensity, variable pH, elevated biochemical oxygen demand (BOD), and the presence of toxic and recalcitrant synthetic dyes (Holkar *et al.*, 2016).

The discharge of textile dye effluents into aquatic ecosystems results in severe environmental degradation. The intense coloration of wastewater, even at concentrations as low as 1 mg/L, could block the light penetration through water bodies, disrupting the photosynthetic activity of aquatic plants and phytoplankton (Kant, 2012). This reduction in primary productivity cascades through the food web, affecting entire aquatic ecosystems. Moreover, many synthetic dyes, particularly azo dyes, which constitute approximately 60-70% of all textile dyes, are resistant to biodegradation and persist in the environment for extended periods (Saratale *et al.*, 2011). The accumulation of these dyes in sediments and their bioaccumulation in aquatic organisms pose long-term ecological risks (Carmen & Daniela, 2012).

The health implications of textile dye pollution are profound and multifaceted. Many synthetic dyes and their degradation products are known to be mutagenic, carcinogenic, and teratogenic (Sharma *et al.*, 2000). Azo dyes, upon reductive cleavage, release aromatic amines such as benzidine and other compounds classified as Group 1 carcinogens by the International Agency for Research on Cancer (IARC) (Chung, 2016). Human exposure to these compounds through contaminated drinking water or consumption of bioaccumulated toxins in fish has been linked to bladder cancer, liver damage, and other serious health conditions (Chequer *et al.*, 2013).

The degradation of synthetic dyes is of utmost importance for mitigating their toxicity and harmful effects on aquatic ecosystems to ensure safer wastewater management and environmental sustainability. Bioremediation is one of the most common and effective cleaning methods to remove industrial toxicants and pollutants from the environment. The process involves the utilization of microorganisms to degrade the synthetic dyes into non-coloured compounds, or it could also mineralize them completely under specific environmental conditions (Singh, 2017; Kumar *et al.*, 2011; Khan *et al.*, 2013). This biotechnological approach has gained substantial attention in recent decades as a sustainable and cost-effective alternative to conventional physicochemical remediation methods (Pointing, 2001; Singh, 2006).

Different microbes, such as bacteria, yeasts, and fungi, have been reported for the textile dyes degradation. The use of fungi (mushrooms) and their associated enzymatic systems, mycelia, and fruiting bodies to degrade, absorb, or detoxify pollutants from soil, water, or air can be referred to as mycoremediation (Stamets, 2005). As natural biocatalysts, mushrooms possess the unique ability to break down complex and toxic compounds into simpler, less harmful forms through the secretion of powerful extracellular enzymes (Rhodes, 2014). For example, several types of fungi, such as *Trametes versicolor, Phlebia radiata*, and *Pleurotus spp*. have been producing laccase enzyme, which is associated with lignin and dyes degradation (Hammel *et al.*, 1992; Heinfling *et al.*, 1997; Paszcynski & Crawford, 1991; Podgornik *et al.*, 1999; Singh *et al.*, 2006).

Termitomyces is a unique genus of basidiomycete fungi belonging to the family *Lyophyllaceae*, known for its obligate symbiotic relationship with termites (Makonde *et al.*, 2013). Among the approximately 40 species in this genus, *Termitomyces heimii* is widely distributed across tropical and subtropical regions of Asia and Africa (Nout & Aidoo, 2002). These mushrooms have traditionally been consumed as food and used in ethnomedicine, valued for their nutritional content and purported health benefits (Tibuhwa, 2014). *T. heimii* is one of the underexplored mushroom species for mycoremediation applications, as its cultivation is challenging despite its vast potential for enzymatic identification. Recent research has revealed various substrate compositions for the activity of lignocellulose-degrading enzymes from *T. heimii*, including lignin peroxidase, manganese peroxidase, β-glucosidase, a- L-arabinofuranosidase, and laccase (Yang *et al.*, 2020). However, further utilization and implementation are limited as it requires large-scale cultivation for the production of lignocellulose enzymes.

This review aims to comprehensively evaluate the existing knowledge base regarding *T. heimii* and related species, with particular emphasis on their potential application in the mycoremediation of textile dye effluents. The review will examine the enzymatic capabilities of *T. heimii*, compare its remediation potential with established fungal biocatalysts, assess the practical challenges of implementation, and evaluate the sustainability credentials of *T. heimii*-based remediation systems. Through this comprehensive analysis, we aim to establish whether *T. heimii* represents a viable and advantageous alternative or complement to existing mycoremediation approaches for addressing the pressing environmental challenge of textile dye pollution.

2.0 Textile Dye Effluent and Its Environmental Impact

2.1 Overview of Dye Classes (azo, anthraquinone, reactive, vat dyes)

Textile dye effluents comprise several synthetic dyes that vary in chemical composition, application techniques, and environmental interactions. Azo, anthraquinone, reactive, and vat dyes are the predominant types utilized in the textile industry, each contributing distinctly to environmental contamination.

2.1.1 Azo Dyes

Azo dyes constitute the predominant category of textile dyes, comprising around 60–70% of worldwide dye output. They possess one or more azo bonds (–N=N–), which confer vibrant and diverse hues (Benkhaya *et al.*, 2020). Azo dyes, while chemically diverse and economically viable, pose significant environmental risks due to their durability and resistance to natural degradation. In anaerobic settings, they may experience reductive cleavage to produce aromatic amines, substances recognized for their mutagenic and carcinogenic characteristics. Their permanence in wastewater results in enduring chromatic pollution, diminished light penetration in aquatic environments, and toxicity to microorganisms (Ramamurthy *et al.*, 2024).

2.1.2 Anthraquinone Dyes

Anthraquinone dyes possess polycyclic aromatic frameworks originating from anthracene. These dyes yield vibrant blue, violet, and green hues with exceptional photostability. Nonetheless, its inflexible ring configuration leads to reduced biodegradability, resulting in accumulation in sediments and longer persistence. Their breakdown frequently generates hazardous intermediates that might adversely affect aquatic organisms. Anthraquinone dyes are regarded as environmentally persistent pollutants, contributing to chemical oxygen demand (COD) and prolonged ecological stress (Jamal *et al.*, 2022).

2.1.3 Reactive Dyes

Reactive dyes are extensively utilized for coloring cellulose fibers, including cotton. They establish covalent connections with fiber molecules, guaranteeing superior colorfastness. Nevertheless, their elevated water solubility and generally low fixation rates (merely 60-70% adherence to fabric) result in substantial amounts being discharged into effluents (Adane *et* *al.*, 2021). Consequently, reactive dye effluents exhibit elevated salinity, high pH, and substantial COD and BOD concentrations. Their chromophores and reactive groups are resistant to biodegradation and may induce aquatic toxicity, change microbial populations, and disrupt enzymatic processes in receiving waters.

2.1.4. Vat Dyes

Vat dyes, such as indigo, are water-insoluble pigments that necessitate reduction (often using sodium dithionite) to transform them into a soluble leuco form for application (Maulik *et al.*, 2022). The dye is re-oxidized on the fiber to revert to its insoluble form. This method produces effluents abundant in alkaline compounds, reducing agents, sulfites, and various inorganic chemicals. Such residues can result in significant elevations in water alkalinity and sulfate concentrations, causing oxygen deprivation, harmful effects on fish, and disruption of aquatic ecosystems. Moreover, insoluble dye particles may last in sediments, exacerbating turbidity and inducing benthic stress.

2.2 Persistence and Toxicological Effects on Aquatic Ecosystems

Textile dye effluents constitute a significant environmental concern owing to the chemical stability, recalcitrance, and toxicity of numerous synthetic dyes employed in the textile sector. In the past five years, multiple studies have demonstrated that dyes such as azo, anthraquinone, and reactive dyes possess significant resistance to natural degradation due to their intricate aromatic structures and halogenated or sulfonated substituents (Sudarshan *et al.*, 2023).

The durability of dyes in aquatic systems significantly modifies essential physicochemical properties. One of the principal environmental impacts is color pollution, which diminishes water clarity and decreases light penetration. Decreased light availability hinders photosynthesis in phytoplankton and submerged macrophytes, hence diminishing primary productivity and modifying oxygen dynamics in aquatic ecosystems (Akter *et al.*, 2024). Prolonged exposure to these conditions disrupts ecological equilibrium, resulting in diminished algal biomass, alterations in species composition, and compromised food web interactions. Moreover, elevated dye concentrations are often correlated with heightened chemical oxygen demand (COD) and biological oxygen demand (BOD) owing to the presence of organic dye molecules and accompanying substances such as surfactants, salts, and mordants. Increased COD/BOD levels reduce dissolved oxygen, resulting in hypoxic or anoxic conditions harmful to fish and invertebrate populations (Sudarshan *et al.*, 2023).

Recent ecotoxicological research has demonstrated significant evidence that textile dyes and their breakdown products induce acute and chronic toxicity in aquatic organisms. Laboratory and field studies indicate that exposure to dye-contaminated water causes oxidative stress, marked by excessive production of reactive oxygen species (ROS), lipid peroxidation, and reduction of antioxidant enzymes in fish species such as *Oreochromis niloticus* and *Cyprinus carpio* (Ishaq *et al.*, 2020). Oxidative stress is often associated with hematological changes, compromised gill function, and diminished metabolic activity, ultimately impacting growth, behavior, and survival. Dyes have been demonstrated to damage membrane integrity, induce mitochondrial dysfunction, and reduce reproductive efficiency in invertebrates, particularly crabs and mollusks (Kitamura *et al.*, 2023). Reactive dyes, although very water-soluble, can cause neurotoxicity, enzyme inhibition, and compromised immunological responses even at sublethal concentrations, suggesting their potential to impact aquatic communities with prolonged exposure.

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A significant issue is the bioaccumulation and trophic transfer of dyes and their hazardous degradation products. Persistent dyes tend to adsorb onto sediments and organic particles, where they may persist for years due to low biodegradation rates. Benthic creatures consume these contaminated particles, allowing dye chemicals to enter the food chain (Saidon *et al.*, 2024). Research has shown that aromatic amines and persistent color molecules accumulate in fish tissues, such as the liver, gills, and muscle, raising concerns regarding biomagnification and potential hazards to human health. Moreover, microbial populations in aquatic ecosystems are profoundly influenced by prolonged exposure to dyes. Dye toxicity can modify microbial diversity, inhibit advantageous biodegrading populations, and enhance the persistence of resistant strains, ultimately compromising natural water purification processes (Alzain *et al.*, 2023).

The current study highlights that the durability and toxicity of textile dyes present enduring challenges to the structure, function, and resilience of aquatic ecosystems. Ongoing dye pollution lowers biodiversity, undermines ecological relationships, disrupts nutrient cycling, and reduces ecosystem services linked to pristine water and robust biota. Due to the widespread application of dyes globally and the insufficient treatment of dye effluents in numerous developing areas, comprehending the environmental dynamics and toxicological effects of dyes is crucial for implementing effective remediation strategies, ecological safeguards, and sustainable industrial practices.

2.3 Chemical Complexity and Challenges in Biodegradation

The biodegradation of textile dyes is chiefly impeded by their chemical complexity, characterized by structurally diversified chromophores, numerous aromatic rings, halogenated substituents, sulfonic acid groups, and metal-complex forms. These molecular characteristics are deliberately engineered to ensure superior colorfastness and resilience to environmental factors, yet they also render dyes resistant to microbial degradation. Azo dyes, the predominant category, confer exceptional stability and resistance to oxidative degradation because of their unique structure (azo bonds (–N=N–) connecting aromatic rings), which creates challenges for the mineralization of bacteria (Alzain *et al.*, 2023). Anthraquinone dyes similarly include polycyclic aromatic cores that are resistant to enzymatic oxidation; their electron-withdrawing substituents additionally hinder microbial metabolism by diminishing enzyme binding affinity (Saidon *et al.*, 2024). Reactive dyes, despite their high solubility, possess reactive vinyl sulfone or dichlorotriazine groups that facilitate covalent interaction with fibers, although they also contribute to persistence in wastewater due to increased hydrophilicity and limited biodegradability (Sudarshan *et al.*, 2023).

A significant issue in dye biodegradation stems from the presence of sulfonic groups, which enhance water solubility while diminishing dye adsorption to microbial cell surfaces, thus restricting the first interaction necessary for enzymatic destruction. Sulfonated dyes typically necessitate certain microbial strains with specialized transport systems or desulfonating enzymes, which are not commonly found in natural environments (Akter *et al.*, 2024). Metal-complex dyes complicate biodegradation due to the central metal ion (e.g., Cu, Co, Cr), which stabilizes the dye structure and inhibits microbial enzyme systems, especially oxidative enzymes like laccases and peroxidases. These metals can also induce toxicity in microbial consortia, hence diminishing total biodegradation rates. The existence of several chromophores or auxiliary substituents on a single molecule is typically observed in high-performance disperse and vat dyes, which introduces further steric hindrance, complicating enzymatic cleavage.

The microbial breakdown of textile dyes typically necessitates certain enzyme pathways, including azoreductases, laccases, manganese peroxidases, and lignin peroxidases. Nevertheless, numerous environmental bacteria do not possess the whole enzymatic arsenal necessary for the complete mineralization of dye molecules (Ishaq *et al.*, 2023). Partial degradation can yield intermediates, such as aromatic amines, phenols, or quinones, which may exhibit more toxicity, mutagenicity, or recalcitrance than the original dye, hence complicating treatment methods (Kitamura *et al.*, 2023). Environmental factors, including elevated salinity, extreme pH levels, and temperature variations in textile wastewater, impede microbial activity. Additionally, the presence of surfactants, detergents, and heavy metals further disrupts the microbial communities essential for effective biodegradation (Sudarshan *et al.*, 2023).

The intricate chemical structure of textile dyes, marked by stable aromatic frameworks, reactive substituents, metal complexes, and sulfonated groups, poses significant problems for microbial biodegradation. These structural obstacles impede breakdown, affect the generation of hazardous intermediates, restrict microbial diversity, and diminish therapeutic efficacy. Current research highlights the necessity for genetically modified microorganisms, enzyme-driven therapies, and customized microbial communities to address these chemical and biological challenges (Alzain *et al.*, 2023).

2.4 Urgent Need for Eco-Friendly, Low-Cost Treatment Systems

Textile dye pollution is a significant global issue, as substantial quantities of inadequately treated or untreated dye effluent are released from dyeing and finishing processes, particularly by small and medium enterprises (SMEs) in low- and middle-income nations that lack the financial resources for advanced wastewater treatment. This necessitates an immediate demand for sustainable, cost-effective treatment systems that are efficient, user-friendly, and durable in actual industrial environments. Recent evaluations and assessments indicate that expenses, energy requirements, chemical usage, operational intricacy, and the production of secondary waste (e.g., sludge, exhausted adsorbents) constitute the primary obstacles hindering the extensive implementation of conventional advanced treatments (e.g., AOPs, ozonation, high-grade membrane filtration) in numerous textile clusters; thus, research and pilot initiatives are shifting towards economical biological, passive, and nature-based solutions (Periyasamy, 2024).

2.4.1 Nature-Based Systems: Constructed Wetlands & Floating Treatment Wetlands

Constructed wetlands (CW), encompassing subsurface flow, surface flow, and floating treatment wetlands (FTWs), have consistently been identified as cost-effective and resilient solutions for the reduction of color and organic load in textile effluent, especially when integrated with suitable pre-treatment methods such as settling and neutralization. Constructed wetlands utilize plant absorption, microbial degradation in the rhizosphere, adsorption to substrates, and photodegradation to attain significant removal of chemical oxygen demand (COD) and dyes in pilot and field investigations; current trials indicate removal efficiencies above 80-90% for some dyes and COD fractions when systems are tuned. CWs are low-energy, necessitate minimal operating expertise, and can be scaled for decentralized treatment. Constraints encompass land area prerequisites, seasonal performance fluctuations, and reduced kinetics compared to designed reactors (Amasa *et al.*, 2025).

2.4.2 Biosorption Using Agricultural Wastes & Biochar

Adsorbents derived from locally sourced biomass (such as coconut shell, rice husk, and sawdust), modified biochar, clays, and spent agricultural residues exhibit very competitive adsorption capabilities for both cationic and anionic dyes, while also being cost-effective to manufacture. Biochar and magnetic biochar provide straightforward separation and potential regeneration; their valorization (transforming waste into adsorbent) enhances circular-economy value. The literature emphasizes the necessity of standardized production and regeneration techniques, along with lifecycle assessment, to prevent secondary pollution from exhausted media (Ghzal *et al.*, 2025).

2.4.3 Phytoremediation and Floating Wetlands for Decentralized Reuse

Indigenous aquatic flora (*Phragmites, Typha, Eichhornia*) and constructed floating islands can eliminate dyes, decrease COD, and facilitate reuse for non-potable applications. They are particularly appealing for decentralized treatment in rural or peri-urban dyeing facilities. Yield and absorption differ among species, dye chemistry, and contact duration; plants may collaborate with rhizospheric microorganisms to enhance removal efficiency (Ali *et al.* 2025).

2.4.4 Integrated/Hybrid Low-Cost Trains

Numerous evaluations highlight hybrid systems (e.g., coarse sedimentation → constructed wetland/bioreactor → biosorption polishing) as viable methodologies: the hybrid strategy leverages cost-effectiveness while achieving superior overall removal and targeting various pollutant fractions (suspended solids, soluble dyes, recalcitrant molecules). These trains can be modular to accommodate available land and budgetary constraints (Khan *et al.*, 2022).

2.4.5 Enzyme-Based Treatment and Immobilized Biocatalysts

The application of pure or crude enzyme preparations, such as laccases and peroxidases, frequently immobilized on economical carriers, facilitates the selective oxidation of chromophores under ambient conditions while minimizing sludge production. Enzymatic processes can be incorporated as refinement units subsequent to adsorption or biological treatments. The primary challenges are the cost of enzymes, which can be mitigated through crude-enzyme systems and on-site manufacturing, and the retention of activity (Chaurasia *et al.*, 2025).

2.4.6 Fungal and Microbial Bioremediation (white-rot fungi, adapted bacterial consortia)

White-rot fungus, along with other ligninolytic fungi, generates extracellular oxidative enzymes (laccases, lignin peroxidase, manganese peroxidase) that can decolorize a diverse array of dyes under mild circumstances. Co-cultures and tailored consortia can enhance the breadth and velocity of deterioration. The benefits include less energy expenditure, potential for mineralization instead of mere phase transfer. Constraints include sensitivity to wastewater toxicity, the necessity for nutrient equilibrium and residence duration, as well as obstacles associated with scaling up. Recent bench and pilot experiments demonstrate significant decolorization rates for several dyes, promoting the advancement of immobilized fungal beds or fungal biofilters (Herath *et al.*, 2024).

In response to the limitations and high costs of conventional treatment methods, mycoremediation has emerged as a promising sustainable biotechnology for textile effluent treatment (Anastasi *et al.*, 2013). The sustainability credentials of mycoremediation are multifaceted and compelling. White-rot fungi in particular have been widely studied for dye decolorization because of their ligninolytic enzymes; such fungal approaches have shown high decolorization under mild conditions and can be integrated into low-cost treatment programs (Torres-Farradá *et al.*, 2024; Pundir *et al.*, 2024). Furthermore, spent mushroom substrate (SMS) from cultivation can be used as a sorbent or biocatalyst carrier, improving economics and circularity (Llanaj *et al.*, 2023).

3.0 The Genus *Termitomyces*: Ecology and Biotechnological Value

3.1 Ecological Role of *Termitomyces* in Symbiosis with Termites

Associations between termites and fungi are considered in two categories: firstly, interactions that affect the discovery and consumption of food or its nutrient value, but which fall short of mutualism; secondly, the cultivation of fungus-combs (*Termitomyces* spp.) within the nesting system by Macrotermitinae, where there is an obligate reliance on the fungus and which in most cases appears to contribute to the degradation of plant structural compounds, especially xylans. In the first category, most information is available for pest termites and it is possible to show, in different species or circumstances, roles for fungal colonizers of decaying wood (or for their metabolic products) as attractants, repellents, conditioners, toxins, and nutritional supplements.

Termitomyces and fungus-growing termites (subfamily Macrotermitinae) have an obligatory mutualistic relationship in which the termites grow the fungus on decaying plant matter inside their nests. Complex lignocellulosic material, such as cellulose and lignin that termites cannot effectively digest on their own are broken down by *Termitomyces*. Tough plant polymers are broken down by fungi into simpler chemicals, which termites then eat and further break down with the help of gut microorganisms to create a two-step digestive system. Furthermore, *Termitomyces* uses oxidative enzymes and redox chemistry (such as Fenton reactions) to aid in the detoxification of secondary plant chemicals. Through effective plant biomass breakdown and termite colony nutrition and survival, this symbiosis improves nutrient recycling, soil health, and ecosystem productivity. An intricate natural bioconversion mechanism that is essential to tropical and subtropical environments is highlighted by this interaction (Poulsen *et al.*, 2014; Schalk *et al.*, 2021; Akinsemolu, 2023).

3.2 Abundance of Cellulases, Hemicellulases, and Lignin-Degrading Enzymes

The fact that *Termitomyces* encodes an average of 16 distinct laccases that are differently transcribed and may have diverse substrate spectra and reactivities is especially noteworthy. Laccases are thought to be not necessary for the breakdown of lignin (Wang *et al.*, 2018), but their presence probably helps with the partial oxidation of aromatic phenolic and nonphenolic moieties, which promotes additional fragmentation and depolymerization. It is also important to note that the β-ether units found in lignin substructures can be effectively oxidized and cleaved by the generated (aryl)-alcohol oxidases through single-electron transfer processes (Wang *et al.*, 2018). Additionally, our analysis offers unambiguous genetic and biochemical proof that *Termitomyces* secretes a class II peroxidase, a reactive MnP, a DyP, and a UPO—all of which are known to oxidize a wide range of substrates. Although none of these enzymes can break down lignin on its own, when combined, they should be able to partially depolymerize lignin, which is required for other enzymes of termite or microbial origin to get past the polymer's physical barriers and reach their target substrates inside the dense polymer.

3.3 Secondary Metabolites with Antimicrobial or Antioxidant Activity

It has been documented that the genus *Termitomyces* produces secondary metabolites with significant antioxidant and antibacterial properties. The effectiveness of various

Termitomyces species extracts, such as hot water, ethanol, and chloroform extracts, against a variety of bacterial and fungal pathogens, such as *Staphylococcus aureus, Klebsiella pneumoniae, Pseudomonas aeruginosa,* MRSA, and *Candida* species, has been examined in a number of studies. Strong antibacterial efficacy of *Termitomyces* hot water extracts, particularly against *S. aureus*, is indicated by the minimum inhibitory concentrations (MICs) of 0.67±0.29 mg/ml. *E. coli* has been observed as the most resistant towards the chloroform extracts of *Termitomyces* with an MIC of 1.67±0.58 mg/ml (Gebreselema *et al.*, 2019). The deviation of antimicrobial activities was influenced by various factors such as the polarity of the solvents, the extraction process and the concentration of the phytochemicals and bioactive compounds present in the extracts (Gebreselema *et al.*, 2019; Glamoclija & Sokovic, 2017; Das *et al.*, 2017).

In the same study, the ethanol extracts of *Termitomyces* have shown a considerable antioxidant effect with maximum scavenging activities of 63% and the inhibitory concentration (IC_{50}) value at 50 ug/ml (Gebreselema *et al.*, 2019). The bioactive secondary metabolites found in *Termitomyces* mushrooms, such as polyphenols, phenolic compounds (such as pyrogallol and cinnamic acid), and polysaccharides, contribute to their antioxidant activity and capacity to scavenge free radicals. These antioxidants hold promise as natural remedies for conditions linked to oxidative stress (Tharu *et al.*, 2022).

3.4 Potential for Biodegradation of Lignocellulosic and Xenobiotic Compounds

Through a variety of processes, the genus *Termitomyces* exhibits a high potential for biodegradation of lignocellulosic and xenobiotic substances. Numerous lignocellulolytic enzymes, such as cellulases, xylanases, manganese peroxidases, dye-decolorizing peroxidases, laccases, aryl-alcohol oxidases, and unspecific peroxygenases, are secreted by *Termitomyces* fungi. Together, these enzymes decompose the intricate components of plant biomass, including cellulose, hemicellulose, and lignin. The fungus depolymerizes lignin to make cellulose and hemicellulose more accessible by using both enzymatic routes and Fenton chemistry, a redox process that produces hydroxyl radicals. The termite-fungus symbiosis for nutrient intake and carbon cycling in ecosystems depends on the effective decomposition of lignocellulosic biomass, which is enhanced by this dual strategy (Schalk *et al.*, 2021; Yi *et al.*, 2025).

Additionally, research has demonstrated that *Termitomyces* mycelia may considerably lower the amount of cellulose, hemicellulose, and lignin in agricultural leftovers like maize straw. Substances like arginine can accelerate the rate of disintegration. Yi *et al.* (2025) suggest that *Termitomyces* actively converts plant waste into broken-down, more accessible chemicals by secreting lignocellulolytic enzymes and engaging in metabolic activity.

4.0 Comparative Analysis of *T. heimii* and Other Mushrooms as Mycoremediators

Table 4.1 revealed a comparison of fungal species investigated for the bioremediation of synthetic dyes and organic pollutants, emphasizing their enzymatic systems, degradation efficiencies, and analytical validation techniques. The comparative data strongly support the growing research that fungi with well-developed ligninolytic enzyme systems are among the most effective biological agents for the degradation of textile dyes and other chemical contaminants.

The performance of *Termitomyces* spp. against the azo dye Congo red highlights the significance of enzymatic diversity and synergy in effective mycoremediation. The production of fungal biomass from *Termitomyces* was optimized using different media such as Potato Dextrose Agar, Malt Extract agar, Modified Melin Nokrans and Pridham-Gottlieb Modified by Kueti (PGK). Malt extract media revealed the maximum fungal biomass growth

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over the other. The decolorization efficiency of up to 99.9% was recorded at lower dye concentrations (25 mg/l) by 0.5-3.5 g of fungal biomass and at the highest dye concentration (250 mg/ml), the decolorization was achieved at 55.2% by 3.5 g/within three days of incubation. The degraded products of dye were analysed by FTIR and it was depicted that the degraded products were adsorbed with fungal cell wall material and decolorized the aqueous dye solution (Jackson & Gomathi, 2021). These results showed the significant potential of *Termitomyces* spp. in wastewater treatment, especially for the azo dyes detoxification.

The detoxification and decolorization of textile dyes from wastewater have been demonstrated in various studies via adsorption and degradation by filamentous fungi (Jadhav *et al.*, 2010). Enzymes such as cellobiose dehydrogenase, xylanase and other lignocellulosic enzymes exudated by the fungus might be responsible for the activities. In addition, the optimization strategies of azo dye biodegradation and biosorption by *Termitomyces* sp., such as modifying the parameters (pH, temperature, quantity of biomass, organic adsorbents, etc.), would be significantly potent for different dye concentrations (Jackson & Gomathi, 2021).

A previous study had revealed a potential degradation (43-55%) of dichlorodiphenyl trichloroethane (DDT) by the fungal substrate of *Lentinus edodes* over 28 days of incubation (Prathima & Vidya, 2023). DDT and its metabolites have been identified as one of the major pollutants in agriculture (Foght *et al.*, 2001). Lignolytic enzyme (laccase, LiP and MnP) activities have been correlated for the degradation of DDT and soil pollutants. *T. heimii* emerges as a particularly promising yet underexplored species. Although quantitative degradation efficiency data for dichloro diphenyl trichloroethane (DDT) are currently unavailable (ND), the presence of important ligninolytic enzymes with considerable activities such as laccase (25.9-49.5%), lignin peroxidase (32.7-61.10%), and manganese peroxidase (35.8-65.4%), suggests strong inherent bioremediation potential for *T. heimii* (Prathima & Vidya, 2023).

The lack of reported efficiency values reflects a methodological gap rather than a biological limitation. Given that *T. heimii* is ecologically adapted to lignocellulose-rich termite mounds and exhibits rapid mycelial colonization, it is plausible that optimized culture conditions could significantly enhance its degradation efficiency.

The comparative performance of other fungi further contextualizes the potential of *T. heimii*. *Aspergillus niger* achieved rapid Congo red degradation (97%) within six days, verified by UV–Vis, FTIR, and LC-MS/MS analyses (Asses *et al.*, 2018), demonstrating strong metabolic versatility. *Pleurotus sajor-caju* showed high decolorization efficiency (84.4%) of Reactive Black 5 within 36 hours under optimized conditions using response surface methodology, underscoring the importance of process optimization in maximizing fungal remediation efficiency (Murugesan *et al.*, 2007). In contrast, *Ganoderma lucidum* exhibited moderate efficiency (60.53%) over a prolonged incubation period, suggesting slower degradation kinetics despite the presence of ligninolytic enzymes (Pratiwi *et al.*, 2017).

Notably, the mixed culture of *Pleurotus florida* and *Rhizoctonia solani* achieved near-complete degradation (98.54%) of Brilliant Green dye, highlighting the advantages of synergistic enzyme interactions in co-culture systems (Kumar & Naraian, 2016). However, while effective, mixed cultures introduce challenges related to process control, reproducibility, and large-scale application, reinforcing the appeal of single-species systems such as *T. heimii*.

Overall, the *Termitomyces heimii* represents a sustainable and biologically efficient candidate for future mycoremediation strategies. Future research should prioritize quantitative efficiency assessment, optimization of culture parameters, toxicity evaluation of degradation by-products, and scale-up feasibility studies. Addressing these aspects will be essential for translating the promising laboratory-scale potential of *T. heimii* into practical applications for textile wastewater treatment and environmental restoration.

Table 4.1
Bioremediation potential of different mushroom species

Mushroom Species	**Dye Type(s)**	**Enzymes**	**Bioremediation Efficiency (%)**	**Validation method**	**References**
Termitomyces spp.	Azo dye (Congo red)	Laccase, Lignin peroxidase, Manganese peroxidase, Xylanase, Cellobiose dehydrogenase	55.2 (high dye concentration) – 99.9 (low dye concentration	-FTIR confirmed azo bond breakdown after 3 days of incubation.	Jackson & Gomathi (2021)
Termitomyces heimii	Dichloro-diphenyl-trichloro-ethane (DDT)	Laccase, Lignin peroxidase, Manganese peroxidase	ND	ND	Prathima & Vidya (2023)
Lentinus edodes	Dichloro-diphenyl-trichloro-ethane (DDT)	Laccase, Lignin peroxidase, Manganese peroxidase	43-55	-GC confirmed the degradation of DDT after 28 days of incubation with *L. edodes* substrate.	Prathima & Vidya (2023)
Aspergillus niger	Congo red	Lignin peroxidase, Manganese peroxidase, deaminas	97	Uv-Vis, FTIR, and LC-MS/MS proved the degradation of congo red-dye after 6 days of incubation.	Asses *et al.*, (2018)

Pleurotus sajor-caju	Azo dye reactive black 5 (RB-5)	Laccase	84.4	Response Surface Methodology (RSM) showed the optimum decolorisation of RB-5 was achieved at 36 hours of incubation with 62.5 mg/l of dye.	Murugesan *et al.*, (2007)
Ganoderma lucidum	Naphtol Black dye (NB dye)	Lignin peroxidase, Manganese peroxidase	60.53	Maximum decolorisation was observed using a spectrophotometer after 30 days of incubation at varying concentrations (20-100 ppm) of NB dyes.	Pratiwi *et al.*, (2017)
Mixed culture of *Pleurotus florida* and *Rhizoctonia solani*	Brilliant green dye	Laccase, Manganese peroxidase	98.54	Submerged fermentation of *P. florida* and *R. solani* in combination for 12 days showed maximum dye degradation.	Kumar & Naraian (2016)

ND: not determined

Conclusion

The increasing discharge of textile dyes and toxic pollutants necessitates sustainable and eco-friendly remediation approaches. Mycoremediation offers an effective biological alternative to conventional treatment methods. This review highlights *T. heimii* as a promising yet underexplored fungal mycoremediator due to its robust ligninolytic enzyme system, rapid mycelial growth, and adaptability to polluted environments. Evidence suggests that pollutant removal by *T. heimii* occurs primarily through enzymatic biodegradation rather than simple adsorption, indicating genuine detoxification potential. Although current research is largely laboratory-based, further optimization, scale-up studies, and toxicity assessments could enable its integration into sustainable wastewater treatment and environmental restoration strategies.

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