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Abstract

By producing lignocellulose-degrading enzymes, saprotrophic litter-decomposing Basidiomycetes can significantly contribute to the turnover of soil organic matter. The production of lignin- and polysaccharide-degrading enzymes helps in converting the waste litter into value-added compost. White-rot fungi (WRF) have tremendous potential for biodegradation of a variety of industrial pollutants. The capability of WRF for biodegradation of xenobiotics and recalcitrant pollutants has generated a considerable research interest in this area of environmental biotechnology. The broad spectrum for biodegradation of pollutants is due to the extracellular and nonspecific nature of the enzyme system of fungi, comprising mainly of lignin peroxidase (LiP), manganese peroxidase (MnP), versatile peroxidase, and laccase along with other ancillary enzymes. Differential biodegradation capabilities of WRF are mainly due to physiological differences among them, difference in their genetic makeup, and variable pattern and expression of complex lignin-modifying enzymes (LMEs). The activities of the LMEs can be increased by the addition of different low-molecular-mass mediators, mostly secreted by white-rot fungi themselves.

Keywords

Lignin • Laccase • White-rot fungi • Lignin-modifying enzymes
• Biodegradation • Bioremediation

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Introduction

Fungi are an important and diverse component of soil microbial communities. They provide essential ecosystem functions, such as decomposing organic matter, nutrient cycling, and in the case of mycorrhizal species, also nutrient transfer to plants. In forest ecosystems they are largely

responsible for breakdown of the abundant large biopolymers cellulose, hemicellulose, lignin, and chitin (Dighton et al. 2005; Kellner and Vandenbol 2010). Recent report suggests the importance of both ascomycetes, as well as Basidiomycetes, in key biogeochemical cycles (Kellner and Vandenbol 2010).

In terrestrial environments, Basidiomycetes are one of the most ecologically significant groups of fungi involved in the breakdown of litter components. They constitute a major fraction of the living biomass responsible for efficient degradation of many recalcitrant organic compounds in soil litter and the humic layer (Dix and Webster 1995; Steffen et al. (2007a, b). An efficient group of litter-degrading organisms are litter-decomposing Basidiomycetes, which produce a wide variety of oxidoreductases and hydrolytic enzymes and are also able to degrade lignin, the most recalcitrant litter component (Steffen et al. 2000). In contrast, Benner et al. (1986), in a study of lignocellulose degradation by microbial samples from two freshwater and two marine habitats, stated that bacteria rather than fungi were the predominant degraders of lignocellulose in aquatic habitat.

Basidiomycetes also have tremendous potential for biodegradation of a variety of industrial pollutants. The broad spectrum for biodegradation of pollutants is due to the extracellular and nonspecific nature of the enzyme system of white-rot fungi (WRF), comprising mainly of lignin peroxidase (LiP), manganese peroxidase (MnP), versatile peroxidase (VP), and laccase along with other accessory enzymes (Table 12.1). The biodegradation capabilities of WRF for different pollutants are variable, mainly due to physiological differences among them and variable pattern and expression of complex lignin-modifying enzymes (LMEs) in the presence of chemically different compounds (Asgher et al. 2008).

Extracellular hydrolases and oxidoreductases are involved in the breakdown of lignocellulose and are produced by many known bacteria, actinomycetes, and ligninolytic fungi. Lignocellulytic enzymes and their biotechnological application have already been discussed in earlier papers, but there is still an ongoing interest, especially in

their occurrence and environmental significance. Cellulases, in particular the complex consisting of endoglucanase, cellobiohydrolase, and beta-glucosidase, hydrolyze the long chains of cellulose, resulting in the liberation of cellobiose and finally glucose. Hemicelluloses, such as endo-1,4- β -xylanase or mannanase, are involved in the breakdown of different heterogeneous polysaccharide chains such as xylans and mannans.

Lignin, polysaccharides, and nitrogenous compounds contribute in the formation of humus (Varadachari and Ghosh 1984; Fustec et al. 1989; Inbar et al. 1989). The chemical pathway from organic matter to humus involves complex degradative and condensation reactions. According to Varadachari and Ghosh (1984), lignin is first degraded by extracellular enzymes to smaller units, which are then absorbed into microbial cells where they are partly converted to phenols and quinones. Thereafter, the substances are discharged together with oxidizing enzymes into the environment, where they get polymerized by a free-radical mechanism. Composting is a dynamic process carried out by a rapid succession of mixed microbial consortia including bacteria, actinomycetes, and fungi (Tuomela et al. 2000; Kellner and Vandenbol 2010).

A wide range of bacteria have been isolated from different compost environments, including species of *Pseudomonas*, *Klebsiella*, and *Bacillus*, e.g., *B. subtilis*, *B. licheniformis*, and *B. circulans* (Nakasaki et al. 1985; Strom 1985a, b; Falcon et al. 1987). Actinomycetes appear during the thermophilic phase as well as the maturation phase of composting and can occasionally become so numerous that they are visible on the surface of the compost. The genera of the thermophilic actinomycetes isolated from compost include *Nocardia*, *Streptomyces*, *Thermoactinomyces*, and *Micromonospora* (Waksman et al. 1939; Strom 1985a).

Lignin Degradation

Lignin-degrading Basidiomycetes, collectively referred to as white-rot fungi, are common inhabitants of forest litter and fallen trees. These are

Table 12.1 Ligninolytic enzymes produced by white-rot fungi

Enzyme	EC no.	Reaction catalyzed	Applications	References
Laccase	1.10.3.2	Phenol oxidation	Spore resistance; rhizomorph formation; pathogenesis; fruit bodies formation; pigments synthesis; lignin degradation	Yaropolov et al. (1994), Mayer and Staples (2002), Claus (2004), Minussi et al. (2007), and Maciel et al. (2010)
Lignin peroxidase	1.11.1.14	Phenol polymerization	Biodegradation of lignin defense of fungi against pathogens	Gold and Alic, (1993), Haglund, (1999), Piontek et al. (2001), Erden et al. (2009), Score et al. (1997), Trejo-Hernandez et al. (2001), and Maciel et al. (2010)
Manganese peroxidase	1.11.1.13	Phenol oxidation; oxidize Mn^{2+} to Mn^{3+}	Degradation of lignin interspecific fungal interactions	Hofrichter (2002), Score et al. (1997), Trejo-Hernandez et al. (2001), and Maciel et al. (2010)
Aryl-alcohol oxidase	1.1.3.7	H_2O_2 production		Martinez et al. (2009)
Glyoxal oxidase	1.2.3.5	H_2O_2 production		Martinez et al. (2009)
Manganese independent peroxidase	1.11.1.7	Activity on aromatic substrates		Wyatt and Broda (1995) and Ruiz-Dueñas et al. (2009)
Versatile peroxidase	1.11.1.16	Oxidizes Mn^{2+} ; high redox potential aromatic compounds	Able to efficiently oxidize phenolic compounds and dyes that are the substrates of generic peroxidases and related peroxidases	Ruiz-Dueñas et al. (2009)
Cellobiose dehydrogenase	1.1.99.18	Lignin degradation; unite the hydrolytic and oxidative systems; dispose manganese (MnII) for MnP through precipitate reduction from manganese oxide (MnO_2)		Henriksson et al. (2000a, b), Kersten and Cullen (2007), and Carvalho et al. (2009)

the only microbes that have been convincingly shown to efficiently depolymerize, degrade, and mineralize all components of plant cell walls including cellulose, hemicellulose, and the more recalcitrant lignin. As such, white-rot fungi play an important role in the carbon cycle (Kersten and Cullen 2007).

From the chemical point of view, lignin is a heterogeneous, optically inactive polymer consisting of phenylpropanoid interunits, which are linked by several covalent bonds (e.g., aryl-ether, aryl-aryl, carbon-carbon bonds) (Hofrichter 2002). The polymer arises from laccase- and/or peroxidase-initiated polymerization of phenolic precursors via the radical coupling of their corresponding phenoxy radicals. It is synthesized by higher plants, reaching levels of 20–30% of the dry weight of woody tissue. Because of the bond types and their heterogeneity, lignin cannot be cleaved by hydrolytic enzymes as most other natural polymers. Therefore, lignin is degraded with the help of different nonspecific oxidoreductases which specifically attack the aromatic moieties, preferably phenolic structures. The most widely studied enzymes in this group are laccase, LiP, MnP, and several other peroxidases such as VP (Sharma and Kuhad 2008).

Lignolytic Enzymes and Their Occurrence

Extracellular oxidative enzymes involved in lignin depolymerization include an array of oxidases and peroxidases. These enzymes are responsible for generating highly reactive and nonspecific free radicals that affect lignin degradation. The nonspecific nature and extraordinary oxidation potential of the peroxidases have attracted considerable interest in the development of several bio-processes.

Laccase

Laccase (benzenediol, oxygen oxidoreductases, EC1.10.3.2) is one of the few lignin-degrading enzymes that have been extensively studied since the eighteenth century. Laccases are majorly reported from eukaryotes, e.g., fungi, plants, and insects (Mayer and Staples 2002). However,

some evidences for its existence in prokaryotes, with typical features of multicopper oxidase enzyme family, have also been reported (Alexandre and Zulin 2000). The first bacterial laccase was detected in the plant root-associated bacterium, *Azospirillum lipoferum* (Givaudan et al. 1993), where it was shown to be involved in melanin formation (Faure et al. 1994). A typical laccase containing six putative copper binding sites was discovered in marine bacterium *Marinomonas mediterranea*, but no functional role was assigned to this enzyme (Solano et al. 1997; Sanchez-Amat et al. 2001). In insects, laccases have been suggested to be active in cuticle sclerotization (Dittmer et al. 2004). Two isoforms of *laccase 2* gene have been found to catalyze larval, pupal, and adult cuticle tanning in *Tribolium castaneum* (Arakane et al. 2005), and a novel laccase has been isolated and characterized from a bovine rumen metagenome library that neither exhibited any sequence similarity to known laccases nor contained hitherto identified functional laccase motifs (Beloqui et al. 2006).

Recently, Sharma and Kuhad (2009), has reported 22 COGs from Archaea, bacteria, and eukaryotes (<http://img.jgi.doe.gov> and <http://www.ncbi.nlm.nih.gov/cog>). Genome-specific best hit resulted in very exhaustive genomic information of diverse multicopper oxidases. Laccase (CotA) from *B. subtilis* 168 and *B. pumilus* SAFR-032 was found to share a common clade and close ancestry with multicopper oxidase from *Pyrobaculum aerophilum*, an Archaea. Moreover, *P. aerophilum* was also found to be evolutionary related to *E. coli* APEC O1 (laccase) and *Yersinia pestis* KIM (hypothetical protein). Well-known laccases from *T. versicolor* were found to be closely related to *Neurospora crassa* OR74A, *C. neoformans* var. *neoformans* JEC21, and *Drosophila melanogaster*, a common fruit fly. Multicopper oxidases from different yeast, i.e., FET3_Yeast, *Pichia stipitis* CBS6054 (FET3.1), and *Saccharomyces cerevisiae* (FET5), share a common phylogenetic position. An unusual evolutionary history was also established between pathogenic Proteobacteria, i.e., *Burkholderia mallei* and *Burkholderia pseudomallei*, and an archaeal species, i.e., *Haloarcula marismortui* ATCC 43049 and *Natronomonas pharaonis* DSM2160 (Sharma

and Kuhad 2009). Moreover, laccase has been extensively examined since the mid-1970s, and a number of reviews have appeared on the subject (Malkin et al. 1969; Malmstrom et al. 1975; Holwerda et al. 1976; Mayer and Harel 1979; Reinhammar 1984; Thurston 1994; Eriksson 2000; Xu 2005; Morozova et al. 2007; Sharma et al. 2007; Sharma and Kuhad 2008).

Lignin Peroxidase

Lignin depolymerization is catalyzed by extracellular peroxidases of white-rot Basidiomycetes such as *Phanerochaete chrysosporium* (Tien and Kirk 1983). Lignin peroxidase (LiP) was first discovered based on the H_2O_2 -dependent C_α - C_β cleavage of lignin model compounds and subsequently shown to catalyze the partial depolymerization of methylated lignin in vitro (Glenn et al. 1983; Tien and Kirk 1983; Gold et al. 1984; Tien and Kirk 1984). Due to their high redox potentials and their enlarged substrate range in the presence of specific mediators, LiPs have great potential for application in various industrial processes (Paice et al. 1995). LiP, being a heme-containing glycoprotein with an unusually low pH optimum (Glumoff et al. 1990), is able to catalyze the oxidation of a variety of compounds with reduction potentials exceeding 1.4 V (vs. normal hydrogen electrode) (Steenken 1998). Contrary to other heme peroxidases, ferric LiP is first oxidized by H_2O_2 to compound I, a two-electron-oxidized intermediate, which is then reduced by one substrate molecule to the second intermediate, compound II. Further reduction back to the resting enzyme can be accomplished either by the same substrate molecule or a second one.

Manganese Peroxidase

Manganese peroxidase (MnP) is considered to be the most common lignin-modifying peroxidase produced by almost all wood-colonizing Basidiomycetes (Tien and Kirk 1983; Martínez et al. 2005). Multiple forms of this glycosylated heme protein with molecular weights normally at 40–50 kDa are secreted by ligninolytic fungi into their microenvironment. There, MnP preferentially oxidizes manganese (II) ions (Mn^{2+}), always present in wood and soils, into highly reactive Mn^{3+} , which is stabilized by fungal chelators such as

oxalic acid. Chelated Mn^{3+} in turn acts as low-molecular-weight, diffusible redox mediator that attacks phenolic lignin structures resulting in the formation of instable free radicals that tend to disintegrate spontaneously (Kuwahara et al. 1984; Hofrichter 2002).

Versatile Peroxidase

Versatile peroxidase (VP) has been recently described as a new family of ligninolytic peroxidases, together with lignin peroxidase (LiP) and manganese peroxidase (MnP), both reported for *P. chrysosporium* for the first time. The complete genome of this model fungus has been recently sequenced revealing two families of LiP and MnP genes together with a “hybrid peroxidase” gene. Till date, VP has been reported from the genera *Pleurotus*, *Bjerkandera*, *Lepista*, *Trametes*, and *Panus* (Honda et al. 2006; Rodakiewicz-Nowak et al. 2006). The most noteworthy aspect of VP is that it combines the substrate specificity characteristics of the three other fungal peroxidase families. In this way, it is able to oxidize a variety of (high and low redox potential) substrates including Mn^{2+} , phenolic, and non-phenolic lignin dimers, α -keto- γ -thiomethylbutyric acid (KTBA), veratryl alcohol, dimethoxybenzenes, different types of dyes, substituted phenols, and hydroquinones (Ruiz-Deñás et al. 2009).

Glyoxal Oxidases

An important component of the ligninolytic system of *P. chrysosporium* is the H_2O_2 that is required as oxidant in the peroxidative reactions. Glyoxal oxidases have been proposed to play a role in this regard (Kirk and Farrell 1987). The temporal correlation of glyoxal oxidase, peroxidase, and oxidase substrate appearances in cultures suggests a close physiological connection between these components (Kersten and Kirk 1987; Kersten 1990). It is a glycoprotein of 68 kDa with two isozymic forms (pI 4.7 and 4.9). The active site of the enzyme has not been characterized, but Cu^{2+} appears to be important in maintaining activity of purified enzyme. Glyoxal oxidase is produced in cultures when *P. chrysosporium* is grown on glucose or xylose, the major sugar components of lignocellulosics. The physiological substrates for glyoxal oxidase, however, are not these

growth-carbon compounds, but their intermediates. A number of simple aldehyde, α -hydroxycarbonyl, and α -dicarbonyl compounds are the known substrates (Cullen and Kersten 1996).

The reversible inactivation of glyoxal oxidase is a property perhaps of considerable physiological significance (Kersten 1990; Kurek and Kersten 1995). Glyoxal oxidase becomes inactive during enzyme turnover in the absence of a coupled peroxidase system. The oxidase is reactivated, however, by lignin peroxidase and non-phenolic peroxidase substrates. Conversely, phenolics prevent the activation by lignin peroxidase. This suggests that glyoxal oxidase has a regulatory mechanism in the presence of peroxidases, their substrates, and their products (e.g., phenolics resulting from ligninolysis). Notably, lignin will also activate glyoxal oxidase in the coupled reaction with LiP (Cullen and Kersten 1996). Cellobiose oxidase (Ayers et al. 1978) and cellobiose: quinone oxidoreductase (CBQase) (Westermarck and Eriksson, 1974) may be involved in both lignin and cellulose degradation. Limited proteolysis of cellobiose oxidase indicates that CBQase is probably a breakdown product (Henriksson et al. 1991; Wood and Wood 1992). Cellobiose oxidase has two domains, one containing a flavin and the other containing a heme group. The flavin-containing domain binds cellulose and is functionally similar to CBQase. A role proposed for these oxidoreductases is to prevent repolymerization of phenoxy radicals produced by peroxidases and laccases during lignin oxidation (Eriksson and Goldman 1993; Cullen and Kersten 1996). Moreover the peroxide-generating enzyme, i.e., pyranose oxidase (glucose-2-oxidase), which is intracellular in liquid culture condition of *P. chrysosporium*, plays an additional important role in wood decay (Daniel et al. 1994).

Environmental Significance

Bioremediation technology utilizes the metabolic potential of microorganisms to clean up the environment (Watanabe 2001). Lignin peroxidase (LiP), manganese peroxidase (MnP), laccase, and versatile peroxidase (VPs) are the major LMEs of

WRF involved in lignin and xenobiotic degradation by white-rot fungi (Pointing 2001) (Table 12.1). Accessory enzymes such as H₂O₂-forming glyoxal oxidase, aryl-alcohol oxidase, oxalate producing oxalate decarboxylase (ODC), NAD-dependent formate dehydrogenase (FDH), and P450 monooxygenase have also been isolated from many white-rot fungal strains (Doddapaneni et al. 2005; Aguiar et al. 2006). Lignin peroxidases (LiPs) are capable of mineralizing a variety of recalcitrant aromatic compounds (Srivastava et al. 2005). Due to nonspecific nature, lignin-oxidizing enzyme is capable of mineralizing a wide variety of toxic xenobiotics and recalcitrant substrates. In recent years, a lot of work has been done on the development and optimization of bioremediation processes using WRF, with emphasis on the study of their enzyme systems involved in biodegradation of industrial waste (Thurston 1994; Eriksson 2000; Baldrian 2006; Sharma and Kuhad 2008) (Table 12.1).

Bioremediation of Industrial Pollutant

Bioremediation process employs microorganisms or plants to remove the contaminating organic compounds by metabolizing them to carbon dioxide and biomass (Alexander 1994). The purpose of bioremediation is to degrade pollutants to undetectable concentrations or to concentrations that are below the limits established by regulatory agencies. Bioremediation has been used to degrade contaminants in soils, ground water, wastewater, sludges, industrial waste, and gases (Alexander 1994).

Biodegradation of Synthetic Dye

Large amounts of structurally diverse dyestuffs are used for textile dyeing as well as other applications. Based on the chemical structure of the chromophoric group, dyes are classified as azo dyes, anthraquinone dyes, phthalocyanine dyes, etc. (Kuhad et al. 2004). Different dyes and pigments are extensively used in the textile, paper, plastic, cosmetics, pharmaceutical, and food industries (Levin et al. 2005). The involvement of LMEs in the dye decolorization process has been confirmed in several

independent studies using purified cell-free enzymes (Table 12.2). LiP of *P. chrysosporium* has been shown to decolorize azo, triphenylmethane, and heterocyclic dyes in the presence of veratryl alcohol and H₂O₂ (Cripps et al. 1990; Ollikka et al. 1993). Selected Basidiomycetes have been observed to decolorize PolyR-478 (Vasdev and Kuhad 1994) and various triphenylmethane dyes (Vasdev et al. 1995). Laccase can act on chromophoric compounds such as Remazol Brilliant Blue R or triphenylmethane dyes and suggests a potential application in bleaching or decolorization industrial processes (Vasdev et al. 1995).

Further, interest in the biodegradation of synthetic dyes has primarily been prompted by concern over their possible toxicity and carcinogenicity (Maas and Chaudhari 2005; Revankar and Lele 2007). White-rot fungi are better dye degraders than prokaryotes due to their extracellular nonspecific LME system capable of degrading a wide range of dyes (Christian et al. 2005). Most of the earlier dye decolorization studies were based mainly on *P. chrysosporium* and *T. versicolor* (Toh et al. 2003). However, other white-rot fungi including *Phellinus gilvus*, *Pleurotus sajor-caju*, *Pycnoporus sanguineus* (Balan and Monteiro 2001), *Dichomitus squalens*, *Irpex flavus*, *Daedalea flavida*, *Polyporus sanguineus* (Chander et al. 2004; Eichlerová et al. 2006; Chander and Arora 2007), *Funalia trogii* ATCC200800 (Ozsoy et al. 2005), *Ischnoderma resinosa* (Eichlerová et al. 2006), and *Ganoderma* sp. WR-1 (Revankar and Lele 2007) have been demonstrated to have higher dye decolorization rates than *P. chrysosporium* and *Trametes versicolor* (Table 12.2).

Biodegradation of Polycyclic Aromatic Hydrocarbon

Polycyclic aromatic hydrocarbons (PAHs) are ubiquitous environmental pollutants that occur in soils, sediments, airborne particles, freshwater, and marine environments (Bumpus 1989). PAHs are nonpolar, neutral, organic molecules that comprise two or more fused benzene rings arranged in various configurations, including linear, angular, and clustered alignments (Collins et al. 1996).

There have been several reports to use bioremediation of PAHs. Eukaryotic microorganisms,

such as fungi, cannot use PAHs as a sole carbon source for growth but usually co-metabolize the PAH to dead-end metabolites. In contrast, bacteria can completely degrade many PAHs and use them as the sole carbon and energy source for growth (Sutherland 1992). At present, many microorganisms are known to metabolize the lower-molecular-weight PAHs, but these PAHs tend not to be highly carcinogenic. Less is known about the potential for biodegradation of higher-molecular-weight PAHs, which tend to be more carcinogenic. A microorganism's ability to degrade PAHs is dependent on the bioavailability of the compound (Vandertol-Vanier 2000).

White-rot fungi can completely mineralize some polycyclic aromatic hydrocarbons (PAHs), indicating that complete oxidation of PAHs occurs. However, there are few examples of in vitro oxidation of PAHs by culture supernatants and purified enzymes. The oxidation of anthracene and pyrene by lignin and manganese peroxidases from *P. chrysosporium* and oxidation of many PAHs by the laccases of *T. versicolor* have been reported (Bumpus 1989; Collins et al. 1996). Pickard et al. (1999) have shown that previously uncharacterized fungal strains could metabolize selected PAHs in vivo. *C. gallica* was one of the strains studied and was found to degrade several PAHs. Anthracene concentration decreased by up to 90%; pyrene, up to 20%; and phenanthrene, up to 40% (Vandertol-Vanier 2000) (Table 12.2).

TNT and Other Explosives

The explosives TNT, HMX, and RDX are integral components of many armaments. Degradation of TNT was studied by Donnelly et al. in 1997, using four different strains of white-rot fungi *P. chrysosporium*, *Phanerochaete sordida*, *Phlebia brevispara*, and *Cyathus stercoreus* in liquid medium (Donnelly et al. 1997). They found that within 21 days of incubation, all fungi were able to reduce the TNT concentration (from 90 mg/L) in the liquid medium to below detection limits. *P. sordida* showed a relatively high growth rate and the fastest rate of TNT degradation. White-rot fungi were also found to degrade monoamino-dinitrotoluenes, the major chemical metabolites in the initial transformation of TNT. The studies

Table 12.2 Applications of ligninolytic enzyme producing organism in treatment of environmental pollution

Application	Organism	References
Decolorization of dyes	<i>Aspergillus</i> (recombinant)	Soares et al. (2001a)
	<i>Aspergillus</i> (recombinant)	Soares et al. (2001b)
	<i>A. niger</i>	Soares et al. (2002)
	<i>Cerrena unicolor</i>	Michniewicz et al. (2003)
	<i>Corioliopsis gallica</i>	Reyes et al. (1999)
	<i>C. rigida</i>	Gómez et al. (2005)
	<i>Funalia trogii</i>	Ünyayar et al. (2005)
	<i>Ganoderma</i> sp. WR-1	Revankar and Lele (2007)
	<i>Irpex lacteus</i>	Kasinath et al. (2003)
	<i>Laetiporus sulphureus</i> and <i>Coriolus versicolor</i>	Mazmanci et al. (2009)
	<i>Myceliophthora thermophila</i> , <i>Polyporus pinsitus</i> , <i>Trametes versicolor</i>	Claus et al. (2002)
	<i>Pleurotus eryngii</i> , <i>Pycnoporus cinnabarinus</i> , <i>T. versicolor</i>	Camarero et al. (2004)
	<i>Pleurotus ostreatus</i>	Hou et al. (2004), Palmieri et al. (2005)
	<i>P. cinnabarinus</i>	McCarthy et al. (1999) and Schliephake et al. (2000)
	<i>Sclerotium rolfsii</i> , <i>Trametes hirsute</i>	Campos et al. (2001)
	<i>Streptomyces cyaneus</i>	Arias et al. (2003)
	<i>Stereum ostrea</i>	Viswanath et al. (2008)
	<i>S. maltophilia</i> AAP56	Dube et al. (2008)
	<i>T. hirsuta</i>	Abadulla et al. (2000), Domínguez et al. (2005), Moldes et al. (2003), Rodríguez Couto et al. (2004b, 2005, 2006), Rodríguez Couto and Sanromán (2006), Couto and Toca-Herrera (2006a, b), Minussi et al. (2007), Nyanhongo et al. (2002), Levin et al. (2005), and Maceiras et al. (2001)
	<i>T. modesta</i>	Rodríguez Couto et al. (2002)
<i>T. trogii</i>	Kulys et al. (2003) and Peralta-Zamora et al. (2003)	
<i>T. versicolor</i>	Maceiras et al. (2001), Lorenzo et al. (2002), and Blánquez et al. (2004)	
<i>T. villosa</i>	Potin et al. (2004), Saito et al. (2004), Tavares et al. (2004), Zille et al. (2003), Knutson and Ragauskas (2004), Yamanaka et al. (2008), Ciullini et al. (2008), and Yang et al. (2009)	
<i>Trametes</i> sp. strain SQ01	Pickard et al. (1999)	
Strain I-4 of the family Chaetomiaceae	Vandertol-Vanier et al. (2002)	
Degradation of xenobiotics	<i>Cladosporium sphaerospermum</i>	Cho et al. (2002)
	<i>Coprinus cinereus</i> , <i>Myceliophthora thermophila</i> , <i>P. pinsitus</i> , <i>Rhizoctonia solani</i>	Itoh et al. (2000)
	<i>C. gallica</i>	Okazaki et al. (2002), Nicotra et al. (2004), and Casa et al. (2003)
	<i>Coriolus hirsutus</i>	Zavarzina et al. (2004)
	<i>Coriolus versicolor</i>	Eggen (1999) and Hublik and Schinner (2000)
	<i>Myceliophthora thermophila</i> , <i>Trametes pubescens</i>	Keum and Li (2004)
	<i>Panus tigrinus</i>	Mougin et al. (2002)

(continued)

Table 12.2 (continued)

Application	Organism	References
	<i>P. ostreatus</i>	Lante et al. (2000) and Carunchio et al. (2001)
	<i>P. ostreatus, T. versicolor</i>	Moeder et al. (2004)
	<i>P. cinnabarinus</i>	Niku-Paavola and Viikari (2000)
	<i>Pyricularia oryzae</i>	Böhmer et al. (1988) and Tanaka et al. (2001)
	<i>Rhus vernicifera</i>	Tanaka et al. (2003)
	<i>T. hirsute</i>	Collins et al. (1996) and Johannes et al. (1998)
	<i>Trametes</i> sp.	Majcherczyk et al. (1998) and Johannes and Majcherczyk (2000)
	<i>T. versicolor</i>	Majcherczyk and Johannes (2000) and Castro et al. (2003)
	<i>T. villosa</i>	Dodor et al. (2004), Fabbri et al. (2001), Fukuda et al. (2001), Kang et al. (2002), Cantarella et al. (2003), and Jung et al. (2003)
	<i>Trichophyton</i> sp. LKY-7	Steffen et al. (2007a, b), Cabana et al. (2007), and Cambria et al. (2008)
	<i>Stropharia rugosoannulata</i>	Calvo et al. (1998)
	<i>Stropharia coronilla</i>	Murugesan (2003)
	<i>Coriolopsis polyzona</i>	D'Annibale et al. (1999)
	<i>Rigidoporus lignosus</i>	D'Annibale et al. (2000)
	<i>Gliocladium virens</i>	D'Annibale et al. (2004)
Effluent treatment	<i>Lentinula edodes</i>	Tsioulpas et al. (2002), Aggelis et al. (2003), and Jaouani et al. (2005)
	<i>P. tigrinus</i>	Durante et al. (2004)
	<i>Pleurotus</i> spp.	Jolivald et al. (2000)
	<i>Pycnoporus coccineus</i>	Edwards et al. (2002)
	<i>R. vernicifera</i>	Lucas et al. (2003)
	<i>Trametes</i> sp. strain AH28-2	Pedroza et al. (2007)
	<i>T. versicolor</i>	Cordi et al. (2007)
	<i>Lentinula edodes</i>	Cordi et al. (2007)
	<i>Botrytis cinerea</i>	Ellouze et al. (2008), Bourbonnais et al. (1997), and Call and Mücke (1997)
	<i>Trametes trogii</i>	Archibald et al. (1997)
	<i>Lentinus tigrinus</i>	Crestini and Argyropoulos (1998)
	<i>Fomes fomentarius, Ganoderma callosum, Lentinus edodes, Merulius tremellosus, Phlebia radiata, P. ostreatus, T. versicolor</i>	Kandioller and Christov (2001)
	<i>C. versicolor</i>	Cordi et al. (2007)
	<i>T. versicolor</i>	Cordi et al. (2007)
Biopulping	<i>T. versicolor</i>	Paice et al. (1995) and Cordi et al. (2007)
	<i>Peniophora</i> sp., <i>Pycnoporus sanguineus, T. hirsuta, T. versicolor</i>	Oudia et al. (2008)
	<i>T. versicolor, T. villosa</i>	Balakshin et al. (2001)
	<i>Lentinula edodes</i>	Camarero et al. (2004)
	<i>Botrytis cinerea</i>	Georis et al. (2003)
	<i>C. versicolor</i>	Archibald et al. (1997)
	<i>P. eryngii, P. cinnabarinus, T. versicolor</i>	Bastos and Magan (2009)
	<i>P. cinnabarinus</i>	D'Souza-Ticlo et al. (2009)
Biobleaching	<i>T. versicolor</i>	Molina-Guijarro et al. (2009)
	<i>T. versicolor</i>	Punnapayak et al. (2007) and Zhao et al. (2010)

established that white-rot fungi are capable of metabolizing and detoxifying TNT under aerobic conditions in a non-ligninolytic liquid medium. The degradation of TNT by white-rot fungi is a two-step process: the first step was to be degraded to OHADNT and ADNT, and the second step was to DANT (Aken et al. 1999). As reported by Axtell et al. (2000), the strains of *P. chrysosporium* and *P. ostreatus* adapted to grow on high concentrations of TNT thus were able to cause extensive degradation of TNT, HMX, and RDX.

Bioremediation of Contaminated Sites

Many pesticides, xenobiotics, coal substances, and industrial products derived from polycyclic, aromatic, halogenated hydrocarbons, and other organic compounds are hazardous environment pollutants. Using oxidoreductases to detoxify and remove them is attracting active research efforts. Laccase and peroxidase have been used to transform (often in the presence of redox mediators) various xenobiotics, polycyclic aromatic hydrocarbons, and other pollutants found in industrial waste and contaminated soil or water (Xu 2005).

Contrary to most of the research on bioremediation using bacterial strains, fungal bioremediation has attracted in the past few years. White-rot fungi have potential to withstand toxic levels of most organopollutants. Five main genera of white-rot fungi have shown potential for bioremediation, viz., *Phanerochaete*, *Trametes*, *Bjerkandera*, *Pleurotus*, and *Cyathus* (Table 12.2). These fungi cannot use lignin as a sole source of energy, however, instead require substrates such as cellulose or other carbon sources. Thus, carbon sources such as corncobs, straw, and sawdust can be easily used to enhance degradation rates by these organisms at polluted sites. Also, the branching, filamentous mode of fungal growth allows for more efficient colonization and exploration of contaminated soil. The main mechanism of biodegradation employed by this group of fungi, however, is the use of lignin degradation system of enzymes. The enzymes LiP, MnP, and laccase involved in lignin degradation are highly nonspecific with regard to their substrate range; this is not surprising considering their mode of action via the generation of radicals (Reddy and Mathew 2001; Kapoor et al. 2005).

Degradation of Medical Waste

Exposure to alkyl-substituted polynuclear aromatic hydrocarbons, stilbenes, genistein, methoxychlor and endocrine-disrupting chemicals (EDC), nonylphenol (NP) and bisphenol A (BPA), and the personal care product ingredient triclosan (TCS) (Asgher et al. 2008) has been associated with a variety of reproductive responses in fish (Kiparisis et al. 2003). Degradation of genistein by *Phanerochaete sordida* YK-624 and detection of the activities of ligninolytic enzymes, MnP, and laccase during treatment show the involvement of WRF extracellular lignolytic system in disappearance of genistein (Tamagawa et al. 2005). MnP, laccase, and the laccase-HBT systems of WRF are also effective in removing the estrogenic activities of bisphenol A (BPA), nonylphenol (NP), 17 β -estradiol (E2), and ethinylestradiol (EE2) with production of high-molecular-weight oligomeric metabolites (Asgher et al. 2008; Lee et al. 2005). Further, removal of NP and BPA is associated with the production of laccase by *T. versicolor* and *Bjerkandera* sp. BOL13 (Soares et al. 2005, 2006). The enhanced biocatalytic elimination of nonylphenol (NP), bisphenol A (BPA), and triclosan (TCS) by *Coriolopsis polyzona* by the addition of ABTS (Cabana et al. 2007) also suggested the involvement of laccase-mediator system.

The ligninolytic enzymes of white-rot fungi catalyze the degradation of pollutants by using a nonspecific free-radical mechanism. When an electron is added or removed from the ground state of a chemical, it becomes highly reactive, allowing it to give or take electrons from other chemicals. This provides the basis for the nonspecificity of the enzymes and their ability to degrade xenobiotics, chemicals that have never been encountered in nature (Pointing 2001).

Biodegradation of Rubber Industry Waste

Recycling of spent rubber material is problematic due to the vulcanization, which creates strong sulfur bonds between the rubber molecules (Liu et al. 2000). Different processes for desulfurization of rubber material and to facilitate the reuse of waste rubber have been developed, including biotechnological processes (Bredberg et al. 2002). Microbial devulcanization is a promising way

to increase the recycling of rubber materials. However, several microorganisms tested for devulcanization are sensitive to rubber additives (Christiansson et al. 2000; Asgher et al. 2008). Most of the common rubber additives are aromatic compounds and can be effectively removed by LMEs of WRF. *Resinicium bicolor* is the most effective fungus for detoxification of rubber material, especially the ground waste tire rubber (Bredberg et al. 2002). Treatment of aromatic rubber additives with *R. bicolor* enhances the growth of *Thiobacillus ferrooxidans* bacterium as well as desulfurization compared to the untreated rubber (Asgher et al. 2008).

Control of Pitch in Paper Pulp Manufacturing

Wood extractives cause production and environmental problems in pulp and paper manufacturing. The lipophilic compounds, which form the so-called wood resin, are the most problematic, and they include free fatty acids, resin acids, waxes, fatty alcohols, sterols, sterol esters, glycerides, ketones, and other oxidized compounds. During wood pulping and refining of paper pulp, the lipophilic extractives in the parenchyma cells and softwood resin canals is released, forming colloidal pitch. These colloidal particles can coalesce into larger droplets that deposit in pulp or machinery forming “pitch deposits” or remain suspended in the process waters. Pitch deposition has a detrimental environmental impact when released into wastewaters (Gutiérrez et al. 2001).

The ability to colonize lignified plant material is a characteristic of wood decay fungi, which include white-rot, brown-rot, soft-rot, and sapstain species. The fungi that cause white rot and brown rot are Basidiomycetes and are characterized by their ability to degrade lignin and cellulose, respectively, resulting in white, i.e., cellulose or brown-colored, i.e., lignin-enriched decayed substrates. The typical sapstain fungi, also called “blue-staining fungi,” colonize wood vessels and rays (as well as softwood resin canals) penetrating through the cell-wall pits. The growth of sapstain fungi is supported by easily degradable extractives and causes discoloration and minimal weight

loss. Wood discoloration is caused by the presence of melanin that has a role in the protection of fungal hyphae against harmful radiation. Because most lipophilic compounds involved in the formation of pitch deposits are concentrated in wood rays and resin canals, the sapstain fungi were the first candidates for the biological control of pitch during wood pulping. Wood-rotting Basidiomycetes have also been investigated for biotechnological application in paper pulp manufacturing. Brown-rot fungi are of little applied interest because they degrade cellulose, the most valuable wood constituent for industrial utilization. Biopulping, in combination with chemical and mechanical treatments, represents an attractive alternative to reduce the consumption of pulping chemicals and energy. White-rot fungi and their enzymes are also of biotechnological interest for pulp bleaching. The advantages of WRF in the degradation of lipophilic extractives have also been realized. The main purpose of biobleaching is to reduce the consumption of the chlorinated reagents traditionally used to bleach pulp, which have a detrimental impact in the water environment (Gutiérrez et al. 2001).

Enzymatic Pulp Bleaching

New environmentally benign, elemental chlorine-free (ECF), and totally chlorine-free (TCF) bleaching technologies are necessary for minimizing the hemicellulose content in dissolving pulp, adjusting the brightness at a high level and improving, simultaneously, the quality of the effluent in terms of toxicity and absorbable organic halogen (AOX). Biological methods of pulp prebleaching using xylanases (Taneja et al. 2002) provide the possibility of selectively removing up to 20% of xylan from pulp and saving up to 25% of chlorine-containing bleaching chemicals. Alternatively, pulp can be bleached with white-rot fungi and their ligninolytic enzymes, enabling chemical savings to be achieved and a chlorine-free bleaching process.

Bjerkandera sp. strain BOS55, *Polyporus ciliatus*, *Stereum hirsutum*, *Phlebia radiata*, and *Lentinus tigrinus* have been found to be efficient biobleachers (Akhtar et al. 1992). Kirk and Yang

(1979) were the first to attempt to bleach pulp with *P. chrysosporium* and some other white-rot fungi. This could lower the kappa number of unbleached softwood kraft pulp up to 75%, leading to reduced requirement for chlorine during the subsequent chemical bleaching. *T. versicolor* could markedly increase the brightness of hardwood kraft pulp. The fungal treatment was carried out in agitated, aerated cultures for 5 days. The kappa number was decreased from 12 to 8, and the brightness increased by 34–48%. *P. cinnabarinus* was found to produce laccase and also its own laccase redox mediator, 3-hydroxy anthranilic acid (3-HAA) (Eggert et al. 1996). The presence of laccase is essential for lignin degradation by *P. cinnabarinus* and that in its absence pulp bleaching is greatly reduced. The biobleaching of kraft with laccase mediator continues to receive strong interest, in part due to the discovery of new mediators for laccase. A number of mediators have recently been used for the use of laccase enzyme in biobleaching, e.g., ABTS 2,2'-azino-bis(3-ethylbenzthiazoline-6-sulfonate) (Bourbonnais and Paice 1996), HBT, *N*-acetyl-*N*-phenylhydroxylamine (NHA) and violuric acid (VA) (Chakar and Ragauskas 2004). HBT oxidation leads to the discovery of a new class of mediators with NOH as the reactive species (R-NO). Kraft pulp treatment with laccase and ABTS was found to effectively demethylate and delignify hardwood kraft pulp when the mediator ABTS is present (Bourbonnais and Paice 1996).

Laccase, like other phenol-oxidizing enzymes, such as peroxidases (Huttermann et al. 1980; Haemmerli et al. 1986; Kern and Kirk 1987), preferentially polymerizes lignin by coupling of the phenoxy radicals produced by the oxidation of lignin phenolic groups. When laccase is used alone, the only reaction that can be observed on kraft lignin is polymerization. The fact that ABTS prevents polymerization of kraft lignin by laccase cannot be explained only by inhibition or reduction of the lignin phenoxy radicals produced by laccase, because when ABTS was added after lignin polymerization by laccase, the lignin was effectively depolymerized. It seems likely that ABTS functions as a diffusible electron carrier,

because laccase is a large molecule and therefore cannot enter the secondary wall to contact the lignin substrate directly.

Conclusion

The ligninolytic enzymes of white-rot fungi catalyze the degradation of pollutants by using a nonspecific free-radical mechanism. The enzymes LiP, MnP, laccase, and other ancillary enzymes involved in lignin degradation are highly nonspecific with regard to their substrate range. This is not surprising considering their mode of action via the generation of radicals. This provides the basis for the nonspecificity of the enzymes and their ability to degrade xenobiotics and other industrial waste that have never been encountered as a natural substrate and are deleterious to ecosystem. Lignolytic enzyme system holds potential for cleaning the degraded and contaminated sites, using combinatorial, holistic, and ecofriendly approaches.

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