Chapter 8 Mycoremediation of Organic Pollutants: Principles, Opportunities, and Pitfalls

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Abbreviations

Ligninolytic enzymes
Lignin peroxidase
Manganese-dependent peroxidase
Versatile peroxidases
Dye-degrading peroxidases
Laccase
Tyrosinase
Unspecific peroxigenases
Cytochrome P450
Cellobiose dehydrogenase
Soft rot fungi
Brown rot fungi
White rot fungi
Litter-decomposing fungi
Polychlorobiphenyls
Polychlorinated dioxins
1,1-bis(4-chlorophenyl)-2,2,2-trichloroethane
Benzo[a]pyrene
Persistent organopollutants
Polycyclic aromatic hydrocarbons
Ligninolytic fungi
Non-ligninolytic fungi

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ROS	Reactive oxygen species
CBAs	Chlorobenzoic acids
EDs	Endocrine disruptors
ECMs	-
	Ectomycorrhizal fungal species
NADPH	I I I
PCDFs	Polychlorinated dibenzofurans
diCDD	Dichlorodibenzo-dioxin
OCDD	Octachlorodibenzo-p-dioxin
MPs	Micropollutants
PPCP	Pharmaceuticals and personal care products
NPs	Nonylphenols
BPA	Bisphenol A
DEHP	Diethylhexyl phthalate
EE2	17α-ethinylestradiol
WWTP	Wastewater treatment plant
HBT	Hydroxybenzotriazole
NSAID	Non-steroidal anti-inflammatory drugs
IBU	Ibuprofen
CA	Clofibric acid
CBZ	Carbamazepine
DBQ	Dimethoxy-1,4-benzoquinone
CLEAs	Cross-linked enzyme aggregates
TNT	Trinitrotoluene
TPH	Total petroleum hydrocarbons
qPCR	Quantitative PCR
PCP	Pentachlorophenol
SMC	Spent Mushroom Compost

8.1 Introduction

Fungi are a diverse group of microorganisms ubiquitously present in natural ecosystems and they are regarded as the major decomposers of complex biomaterials. Fungi can thrive in a huge variety of habitats, ranging from surface waters to terrestrial environments—including extreme zones of the biosphere like deserts or polar regions—and they use air to disperse their propagules. Regardless of their taxonomic classification, all fungi are essentially heterotrophic microorganisms, i.e., they assimilate nutrients by absorption from the extracellular environment. In general terms, they can be subdivided into biotrophic and saprotrophic organisms based on their ecophysiology. The first group encompasses symbionts and pathogens of other species, while the second is the group of "decomposers" of biomass.

Although several studies have highlighted the ecological importance of some biotrophic fungi (for example mycorrhizas associated with plant roots in polluted soils), for the rationale of this chapter, which deals with the importance of fungi in the decontamination of polluted environments, saprotrophic fungi are more significant.

Saprophytic fungi are able to decompose and transform a wide array of organic (and inorganic) substrates. In contrast to bacteria, which need to transport nutrients into their intracellular compartment prior to their utilization, fungal mycelia can be seen as "externalized stomachs" which secrete their hydrolytic enzymes and organic acids into the extracellular environment and transport digested substances and chelates inside their cell wall. Although bacteria are, to some extent, faster and more efficient than fungi in utilizing readily assimilable substrates (proteins, lipids, starch and free sugars), fungi have evolved extremely efficient enzymatic machineries for the degradation of complex nonprotein polymers, such as lignocellulose and chitin, which are inaccessible and/or recalcitrant to the majority of prokaryotes. Due to these unique capabilities, fungi are considered to play key roles in a number of biogeochemical processes and, more generally, in the cycling of carbon and other elements.

8.1.1 Lignocellulolytic Fungi and Their Enzymes¹

Lignocellulose is the most abundant renewable biomass on earth. All woody materials are composed mainly of complex carbohydrates (cellulose and hemicellulose) and lignin, the most complex and heterogeneous biopolymer known till date. Thanks to the production of lignocellulolytic enzymes, different saprotrophic fungi can degrade and utilize plant polymers. In general, extracellular lignocellulolytic enzymes from fungi can be subdivided into two major groups. The first one comprises a series of hydrolytic enzymes capable of breaking down polysaccharide constituents of the plant cell wall, namely cellulases (e.g., glucanases, glucosidases, cellobiohydrolases) and hemicellulases (xylanases, mannanases, xylosidase). The other group, referred to as ligninolytic system, promotes the radical-mediated nonspecific decomposition of lignin besides cleaving the aromatic moieties thereof. It includes heme peroxidases, (lignin peroxidase, LiP, E.C. 1.11.1.14; manganesedependent peroxidase, MnP, E.C.1.11.1.13; versatile peroxidases, VP, E.C. 1.11.1.16; dye-degrading peroxidases, DyP, E.C. 1.11.1.19), phenol oxidases (laccase, Lac, E.C. 1.10.3.2; tyrosinase, Tyr, E.C. 1.14. 18.1) and a series of accessory

¹Additional information on decomposition of lignocellulase redsidues and waste by white and brown rot fungi is presented in Chap. 9—White and brown rot fungi as decomposers of lignocellulosic materials and their role in waste and pollution control.

enzymes for the production of H_2O_2 (e.g., glyoxal oxidase, glucose oxidase and aryl alcohol oxidase). During the last decade, a new type of H_2O_2 -requiring enzyme has been described for the first time in the Basidiomycete *Agrocybe aegerita* (Ullrich et al. 2004) and, hence, in other fungi (Hofrichter and Ullrich 2014). These proteins are heme-thiolate haloperoxidases, nowadays classified as fungal unspecific peroxigenases (UPO, E.C. 1.11.2.1). Their catalytic cycle combines the typical pathways of extracellular heme peroxidases and intracellular monooxygenases (unspecific cytochrome P450 system, CYP450, E.C. 1.14.14.1), thus enabling them to catalyze an outstanding array of reactions (Hofrichter and Ullrich 2014).

By reason of the different strategy to decompose wood polymers—and owing to the appearance of the wood following the decay process—it is possible to distinguish soft rot (SRFs), brown rot (BRFs), and white rot fungi (WRFs). An additional group ecophysiologically close to the white rot is formed by litter-decomposing fungi (LDFs), which inhabit the organic horizon of forests and grassland soil. These basidiomycetes produce ligninolytic oxidases and peroxidases as WRFs, but their typical niche is soil, where they cause the decay of the leaf-litter and other plant-derived debris.

Ligninolysis per se does not support fungal growth, but fungi can cause a certain deterioration of the amorphous structure of lignin to access the carbohydrates intertwined in the lignin structure of the plant cell walls. To this end, SRFs almost exclusively produce cellulases that diffuse in the lignocellulose structure providing the fungus with nourishment, without significantly altering the structure of the cell wall. Ubiquitous SRFs include species of Chaetomium, Fusarium, Paecilomyces and other common soil genera-not typically wood-inhabiting fungi. Any timber which is in contact with the soil (for example, fence posts or telegraph poles) is ultimately attacked by these fungi, especially under condition of high moisture. SRFs such as Trichoderma spp. and Chaetomium spp. preferably attack plant biomass characterized by low lignin content. BRFs, instead, use a Fenton-type catalytic system to disrupt the lignin and holocellulose structure in wood (Rabinovich et al. 2004; Baldrian and Valášková 2008), thus facilitating the penetration of hydrolases in the plant cell wall. Strong and diffusible OH' radicals are produced starting from reduced iron (Fe²⁺) and H₂O₂, which are, in turn, produced either endogenously or via cellobiose dehydrogenase (CDH) catalyzed reactions, quinone-redox cycling or low molecular mass glycopeptides (Rabinovich et al. 2004; Baldrian and Valášková 2008). WRFs are also known to use Fenton-type reactions (Baldrian and Valášková 2008; Gómez-Toribio et al. 2009; Dashtban et al. 2010), although the distinctive feature of this fungal group is the production of extracellular high redox potential ligninolytic enzymes (LEs), which are responsible for the so called "enzymatic combustion" of lignin (Kirk and Farrell 1987). LDFs also produce ligninolytic enzymes and attack lignocellulose in a fashion very similar to that of wood-inhabiting white rots, although their niche is the superficial organic layer of soil.

8.1.2 Mycoremediation: Origin and Principles

The link between bioremediation potential of fungi and the decay of wood relies on the similarity between the components of the lignin macromolecules and the majority of aromatic pollutants. Indeed, the catabolic enzymes that fungi have evolved to access the cellulose and hemicellulose fibrils embodied in the wood structure were also found to be active towards a vast range of aromatic pollutants. Concerning this, an overview of the mechanism that ligninolytic and non-ligninolytic fungi use to attack both lignocellulose and organic contaminants is provided in Fig. 8.1.

The first evidence about fungal degradation of aromatic pollutants dates back more than 50 years (Anastasi et al. 2013), when Lyr (1963) reported the chlorophenol-removing potential of a wood-inhabiting fungus and awareness of fungal degradation of wood preservative agents had developed (Duncan and Deverall 1964). In the same period, the "kerosene fungus" Cladosporium resinae was also described for the first time upon its isolation from fuel tanks (Hendey 1964). However, the actual driving force which led to the birth of a new branch of bioremediation was the study of the model white rot fungus Phanerochaete chrysosporium. In fact, the ligninolytic machinery of P. chrysosporium became the focus of several researchers' attention in the early 1980s and a ligninase from the same fungus was characterized for the first time in 1984 (Tien and Kirk 1984). Driven by the capability of P. chrysosporium to degrade chlorinated lignin-derived by-products of the kraft pulping process, Bumpus and colleagues demonstrated one year later, in 1985, the ability of the same fungus to degrade (and partially mineralize) a set of persistent organopollutants, namely polychlorobiphenyls (PCBs), dioxins (PCDDs), lindane, 1,1-bis(4-chlorophenyl)-2,2,2-trichloroethane (DDT)

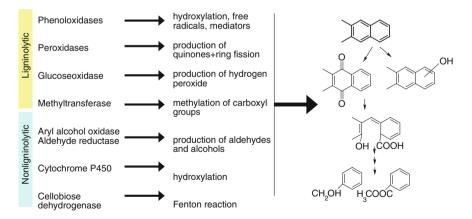


Fig. 8.1 Outline of the mechanisms used by ligninolytic and non-ligninolytic fungi to decompose lignocellulose and organic pollutants

and benzo[*a*]pyrene (BaP) (Bumpus et al. 1985). Since then, an intense period of research on the bioremediation potential of *P. chrysosporium* and other wood-degrading fungi has started (Hammel 1995; Rabinovich et al. 2004; Harms et al. 2011). Concerning this issue, the term "Mycoremediation" has been coined by the eminent mycologist Paul Stamets to specifically address the use of fungal mycelia and their enzymes in bioremediation. The majority of studies concerning fungal remediation have mainly considered the use of lignin degrading fungi (WRFs and LDFs) with typical target matrices being soils and sediments contaminated by persistent aromatic pollutants, such as wood preservatives, oil-derived products, explosives, dielectric fluids, pesticides and other man-made chemical products (Mougin 2002; Baldrian 2008; Cerniglia and Sutherland 2006; Cajthaml and Svobodová 2012).

Several physiological and biochemical features of ligninolytic fungi make them potential candidates for soil bioremediation strategies. As already mentioned, they produce a large number of oxidative enzymes, mainly Lac, LiP and MnP, which exhibit very low substrate specificity and, being active in the extracellular environment, are able to reach and attack scarcely bioavailable contaminants by nonspecific radical-based reactions. In addition to the extracellular one, WRFs possess an intracellular enzymatic system involving CYP450 monooxygenases (Črešnar and Petrič 2011). This intracellular pathway occurs in all eukaryotic organisms and it mainly regulates the bioconversion of hormones and the detoxification of drugs and xenobiotics (Bernhardt 2006). In wood rotting fungi, cytochrome P450 is supposed to cooperate with the ligninolytic system in the general mechanism of xenobiotic degradation (van den Brink et al. 1998). Moreover, white rots develop a spatially extensive hyphal growth, enabling them to penetrate across air-filled soil pores, air-water interfaces and even rock matrices (Bornyasz et al. 2005) and to act as dispersion vectors for bacteria (Kohlmeier et al. 2005; Bonfante and Anca 2009). Fungi can also tolerate high concentrations of organic contaminants and heavy metals with limited or no deleterious effects on their own enzymatic activities (Baldrian et al. 2000; Baldrian 2003; Tuomela et al. 2005). In spite of their extraordinary degrading capabilities, the vast majority of fungi cannot assimilate contaminants as a source of carbon and energy like bacteria, except in some cases of non-ligninolytic fungi. For this reason, lignocellulosic residues are used as amendants to support the fungal growth and, thus to improve the mycoremediation performances (Singh 2006). Furthermore, it is well known that fungi are involved in soil humification process: in this respect, the use of these organisms in soil remediation could lead, not only to the decontamination, but also to the reuse of the soil for agricultural purposes once the remediation goals are met (Bollag 1992; Michels 1998).

In the following sections, we present the principles and mechanisms behind fungal degradation of persistent organic pollutants (POPs) and other emerging organic micropollutants (MPs).

8.2 Polycyclic Aromatic Hydrocarbons

Polycyclic aromatic hydrocarbons (PAHs) are contaminants of great concern due to their worldwide distribution. Although they are natural compounds, PAHs also originate from incomplete combustion of fossil fuels and biomasses. For this reason, human activities are considered as the major source of PAH contamination of the environment. Chemically, PAHs consist of two or more fused benzene rings arranged either in a linear or a cluster mode and several members of this class—e.g., benzo[*a*]anthracene, chrysene and benzo[*a*]pyrene—have been included among priority pollutants owing to their toxic, mutagenic and carcinogenic properties (Haritash and Kaushik 2009). The persistence of PAHs in the environment is mainly due to their hydrophobicity, toxicity and recalcitrance to microbial degradation, which largely increase as the molecular weight of PAHs increases.

PAHs are, by far, the most extensively studied contaminants with respect to their susceptibility to fungal biodegradation. Owing to the chemical stability of PAHs, which is favored by the dense cloud of delocalized π electrons on the coplanar structure, the critical step for aerobic organisms is the initial incorporation of oxygen on the aromatic ring. In general, the way fungi use to attack PAHs is the same as that of mammalian and other eukaryotes, i.e., oxidation of PAHs to PAH trans-dihydrodiols by Phase I intracellular enzymes (CYP450 monooxygenases and epoxide hydrolase) followed by Phase II conjugation reactions mediated by transferases. This detoxification reaction was first described in Cunninghamella elegans by Cerniglia and Gibson (1977). Cerniglia (1997) also used this member of Mucoraceae as a model organism for subsequent PAH degradation studies, which prompted him to identify high molecular weight PAH-dihydrodiols, quinones and phenols metabolites. However, the above-cited study of Bumpus et al. (1985) about the xenobiotic degradation capabilities of P. chrysosporium, shifted the attention of many researchers towards ligninolytic fungi (LFs) and their powerful extracellular machineries. Since then, several other genera of LFs (mainly WRFs) such as Trametes, Pleurotus, Bjerkandera, Irpex, Phlebia, Nematoloma, and Lentinus have been demonstrated to metabolize PAHs efficiently under model liquid culture conditions or in the soil (Sack et al. 1997; Pointing 2001; Giubilei et al. 2009; Novotný et al. 2009; Baldrian 2008; Covino et al. 2010a, b, c). Additionally, it was proved that PAHs can be oxidized under in vitro conditions using Lac and peroxidases from LFs (Hammel et al. 1986; Majcherczyk et al. 1998; Eibes et al. 2006; Baborová et al. 2006; Covino et al. 2010c) and that the use of redox mediators can improve the rate of PAH degradation as well as expand the spectrum of substrates oxidized by such catalysts (Sack et al. 1997; Johannes and Majcherczyk 2000; Camarero et al. 2008; Cañas and Camarero 2010; Covino et al. 2010c). Besides, the involvement of CYP450 monooxygenase-epoxide hydrolase system was shown to be active in the initial degradation of PAHs also in LFs (Bezalel et al. 1997). Using ¹⁴C-labeled compounds, it was proved that LFs are able to completely mineralize PAHs to carbon dioxide (Bumpus et al. 1985; Bezalel et al. 1996a; Wolter et al. 1997; Sack et al. 1997). However, evidence for PAH ring-cleavage by fungi are poorly described. Hammel et al. (1991) showed that P. chrysosporium was able to decompose anthracene to phthalic acid while Bezalel et al. (1996b) presented the mechanism of 2,2'-diphenic acid production from phenanthrene. These authors suggested that CYP450 of Pleurotus ostreatus was responsible for the attack to phenanthrene, enabling further ring opening reactions. Moen and Hammel (1994) reported the formation of 2,2'diphenic acid from phenanthrene as a result of lipid peroxidation by MnP, while other authors found several ring-cleavage products of acenaphthylene and acenaphthene after incubation with Trametes versicolor Lac as well as a laccase-mediator system (Johannes et al. 1998; Majcherczyk et al. 1998). A few years later, Cajthaml et al. (2002) identified several PAH metabolites in Irpex lacteus axenic cultures spiked with phenanthrene, anthracene, fluoranthene and pyrene: the presence of ring-cleavage products and PAH-dihydrodiols reinforced the hypothesis that ligninolytic fungi use both the CYP450 system and extracellular ligninases. Baborová et al. (2006) not only confirmed that purified MnP from *I. lacteus* can attack recalcitrant representative of PAHs, but also that it can cleave the benzene ring to form 2-(2'-hydroxybenzoyl)benzoic acid. A pathway similar to that proposed for anthracene has been also hypothesized by Cajthaml and colleagues (2006) for benzo(a) anthracene, with emphasis on intermediates possessing two aromatic rings, e.g., 1,4-naphthalenedione, 1,4-naphthalenediol, and 1,2,3,4-tetrahydro-1-hydroxynaphthalene. The breakdown products in the metabolic pathway of benzo[a]anthracene by *I. lacteus* are shown in Fig. 8.2.

The WRF P. ostreatus, well known as oyster mushroom, is one of the most efficient degrader of PAHs (Bezalel et al. 1996b; Wolter et al. 1997). When it was grown in the presence of several PAHs (benzo[a]pyrene, pyrene, fluorene, phenanthrene, anthracene) metabolization and mineralization was shown to occur. The main PAH degradation products identified were: phenanthrene trans-9,10-dihydrodiol and 2,2'-diphenic acid, pyrene trans-4,5-dihydrodiol, anthracene trans-1,2-dihydrodiol, and 9,10-anthraquinone. For instance, the fungus was able to decompose phenanthrene, anthracene and pyrene by 50, 92 and 35 % in 5 days, respectively, in bran flakes media (Pickard et al. 1999). Schützendübel et al. (1999) found that Bjerkandera adusta removed 56 and 38 % of fluorene and anthracene 3 days after spiking these PAH in the fungal cultures, while P. ostreatus degraded 43 and 60 % of these compounds; other PAHs were degraded to a lower extent. All PAHs were removed uniformly during the period of incubation by P. ostreatus cultures, but fluorene and anthracene were degraded faster than other compounds in basidiomycete's rich media. The detected intermediates were mostly keto compounds (Schützendübel et al. 1999).

Another member of the Polyporales with remarkable PAH-degrading capabilities is the white rot fungus *Lentinus tigrinus* (Valentin et al. 2006; Covino et al. 2010a, c). Regardless of the N-content in the culture media, this fungus was able to remove up to 97 % of a mixture of 7 PAHs from 3 to 5 fused benzene rings. In addition, the major ligninolytic isoenzymes (Lac and MnP) from *L. tigrinus* were shown to efficiently degrade individual PAH congeners under in vitro conditions, either in the presence or in the absence of low molecular weight redox mediators, although MnP showed a wider PAH substrate range and faster oxidation rates than

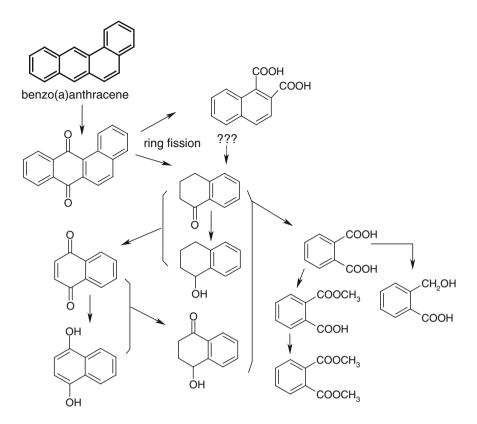


Fig. 8.2 Benzo[a]anthracene degradation by *I. lacteus*—adapted from Cajthaml et al. (2006)

the Lac produced by the same strain. When *L. tigrinus* was bioaugmented in a PAH-contaminated soil and in creosote wood, it removed PAHs to a higher extent than *I. lacteus* (Covino et al. 2010a). Moreover, Valentin et al. (2006) reported that *L. tigrinus*, *I. lacteus* and *B. adusta* were capable of growing and degrading PAHs under the typical halophilic conditions of a marsh soil.

Litter-decomposing fungi (LDFs) were claimed to have a greater potential than white rots in the mycoremediation of contaminated soil, mainly due to their innate capability to compete with natural soil microflora (Šašek 2003; Steffen et al. 2007). In addition to an early report on the BaP-degradation by *Marasmiellus troyanus* (Wunch et al. 1999), the first extensive screening of the PAH degrading potential of LDFs was performed by Gramss et al. (1999). Outstanding results in term of removal of a mixture of 5 PAHs were reported for two fungi, namely *Gymnophilus sapineus* and *Agrocybe praecox* (92 and 90 %, respectively, after 14 d). Steffen et al. (2002) reported the bioconversion of PAHs by nine litter decomposers in model liquid systems and concomitantly assessed the extent of ¹⁴C-benzo[*a*]pyrene (BaP) mineralization. The results showed that all fungi were capable of oxidizing PAHs, with two strains belonging to the genus *Stropharia* (*S. coronilla* and

S. rugosoannulata) that were more efficient than others. The authors also highlighted the positive correlation between Mn²⁺ supplementation, expression of MnP activity and overall degradation/mineralization of PAHs (Steffen et al. 2002). As a consequence, S. coronilla MnP was further purified and incubated under in vitro condition with¹⁴C-BaP. The results confirmed the involvement of this enzyme in the mineralization of BaP and a 12-fold higher increase in ¹⁴C-CO₂ production upon Mn²⁺ supplementation. In addition, the two *Stropharia* spp. mentioned above were the most efficient PAHs degraders among other litter decomposers in an artificially contaminated soil (Steffen et al. 2007). Similarly, Lac from the oak-litter decomposer Marasmius quercophilus was shown to degrade PAHs with ionization potential lower than 7.55 eV, i.e., anthracene and BaP (Farnet et al. 2009). As for the PAH degradation in real contaminated matrices, the shaggy mane mushroom Coprinus comatus was used in a laboratory-scale mycoremediation test targeting historically creosote-contaminated soil and wood. Regardless of lignocellulose support selected as growth substrate, the PAH degradation performances of this fungus were similar to that of representative white rots (Dichomitus squalens and P. ostreatus), and some high molecular weight PAHs were degraded by C. comatus beyond their threshold of bioavailability (Covino et al. 2010b).

Comparatively, BRFs were less investigated than ligninolytic fungi with respect to PAH degradation. However, in spite of early studies claiming the inadequacy of brown rots for mycoremediation applications (Martens and Zadrazil 1998), recent reports have highlighted the PAH biotransformation potential of the button mushroom *Agaricus bisporus* and the possible use of *A. bisporus* spent compost in soil decontamination (Mayolo-Deloisa et al. 2011; García-Delgado et al. 2015).

Soft-rotting fungi include common soil saprotrophs that usually grow on substrates other than wood, but they can occasionally cause its decay. Indeed, Ascomycetes such as Trichoderma, Chaetomium, Fusarium, Aspergillus, Penicillium and Paecilomyces are still regarded by many authors as non-ligninolytic fungi (Rabinovich et al. 2004; Marco-Urrea et al. 2015) although several SRFs genera are known to produce Lac (Verdin et al. 2004; Baldrian 2006; Wu et al. 2010; Cázares-García et al. 2013; Viswanath et al. 2014) and ligninolytic peroxidases (Yang et al. 2003, 2013; Silva et al. 2009). The redox potential of these enzymes, however, is lower than those typically produced by wood-rotting fungi and their role in lignin and PAH biotransformation has not yet been fully understood (Baldrian 2006). In general, WRFs and LDFs have attracted more attention than soft-rotters for their possible applicability in bioremediation. In spite of this, soil saprotrophs are frequently isolated from crude oil- and PAH-contaminated soils, where they constitute a large proportion of the fungal community (Rafin et al. 2000, 2012; Covino et al. 2015; Bourceret et al. 2015: Cébron et al. 2015). Very recently, an interesting review on NLFs with potential application in bioremediation of organopollutants has been published (Marco-Urrea et al. 2015) and an exhaustive list of species with reported PAH degrading capability can be found in the literature (Gadd 2001; Cerniglia and Sutherland 2006; Fernández-Luqueño et al. 2011; Harms et al. 2011; Marco-Urrea et al. 2015). The mechanism by which these fungi attack PAHs is the same as that described for C. elegans, i.e., via CYP450 monooxygenase-epoxide hydrolase system, which yields hydroxylated, (trans-) di-hydroxylated and transient dihydro-epoxide derivatives. These activated structures, that are capable of binding to nucleophilic groups of DNA, can be also transformed into sulfate-, methyl-, glucose-, xylose-, or glucuronic acid conjugates by Phase II enzymes (e.g., aryl sulfotransferase, glutathione S-transferase, UDP-glucuronosyltransferase and UDP-glucosyltransferase, methyl transferases). This step, followed by the excretion of these compounds into the extracellular environment, results in a significant detoxification with respect to both parent molecules and mutagenic dihydroxy-epoxides, as it is known to occur in higher eukaryotes (Cerniglia and Sutherland 2006; Marco-Urrea et al. 2015). Interestingly, some members of this group, e.g., the yeasts Pichia anomala and Rhodotorula glutinis or the hyphomycetes Fusarium solani, Trichoderma and Penicillium, possess the capability to use PAHs with up to 5 fused benzene rings as sole carbon source (Romero et al. 1998, 2002; Rafin et al. 2000; Pan et al. 2004; Verdin et al. 2004; Cerniglia and Sutherland 2006), and some of them can do so even in the presence of microaerobic $(5 < O_2 < 15 \%)$ or very-low oxygen conditions $(1 \% < O_2)$ (Silva et al. 2009). Detailed studies on BaP-degradation by F. solani demonstrated that this fungus (i) produces a surfactant-like hydrogel (polysaccharides and glycoproteins) to increase the BaP solubility and uptake; (ii) transports BaP in the intracellular environment and accumulate it in lipid vesicles; (iii) degrades the substrates by means of either CYP450 or reactive oxygen species (ROS) and (iv) mineralizes BaP to an extent similar to that reported for the white rot fungus P. ostreatus (Verdin et al. 2004, 2005).

8.3 Chlorinated Aromatic Pollutants

8.3.1 Polychlorinated Biphenyls

Polychlorinated biphenyls (PCBs) are synthetic compounds the structure of which consists of a biphenyl molecule (two aromatic rings linked by a C–C bond) carrying from one to ten chlorine atoms. Theoretically, the entire set of PCB homologs comprises 209 congeners. In the past, PCB mixtures were widely used for a number of industrial applications due to their thermal and chemical stability, flame resistance and dielectric properties. As a consequence, their use led to extensive environmental contamination either through accidental releases and/or inappropriate methods of disposal. Owing to their aforementioned inertness, PCBs are therefore still present in a number of areas where their production had been carried out for decades, although their application was drastically restricted long time ago. Nowadays, PCBs are considered among the most hazardous contaminants in the world, placing them at the forefront of public health concern. Indeed, the teratogenic, carcinogenic and endocrine disrupting effects of these xenobiotics have been widely reported in the literature (Crinnion 2011; Helmfrid et al. 2012; Kramer et al.

2012; El Majidi et al. 2013) especially for coplanar PCBs (not substituted at the ring positions *ortho*-) which exhibit "dioxin-like" toxicity features (US Environmental Protection Agency 2000; Van den Berg et al. 2006).

In the light of all these considerations, the cleaning-up of PCB-contaminated sites has become a global priority. Among diverse remediation approaches, the use of biological systems represents an efficient, cost-effective, and environmentally friendly alternative to the more commonly used thermal and physico-chemical technologies (Passatore et al. 2014).

Bacteria play a key role in PCB biodegradation processes: anaerobes can use highly chlorinated biphenyls as electron acceptors and convert them into less chlorinated congeners, while aerobic bacteria can co-metabolize lower chlorinated biphenyls (Pieper 2005; Field and Sierra-Alvarez 2008). However, the co-metabolism of PCBs *via* the biphenyl pathway leads to the formation of chlorobenzoic acids (CBAs), which tend to be accumulated as dead-end products. The build-up of these metabolites exerts an inhibitory feedback effect on the upper biphenyl degradation pathway resulting in the impediment or slowing down of the PCB biotransformation process as a whole (Adebusoye et al. 2008; Furukawa and Fujihara 2008). Therefore, it is worthwhile to search for other microorganisms that are able to mineralize PCBs completely.

Due to their wide metabolic capabilities, a large number of ligninolytic fungi belonging to the *Basidiomycota* phylum were tested in laboratory-scale model liquid systems for their ability to degrade technical PCB mixtures or single PCB congeners, notably: *P. chrysosporium* (Eaton 1985; Thomas et al. 1992; Vyas et al. 1994; Yadav et al. 1995; Kamei et al. 2006a) *T. versicolor* (Zeddel et al. 1993; Vyas et al. 1994; Cloete and Celliers 1999), *Lentinus edodes* (Ruiz-Aguilar et al. 2002), *P. ostreatus* (Kubátová et al. 2001; Čvančarová et al. 2012), *Grifola frondosa* (Seto et al. 1999), *Coriolopsis polyzona* (Vyas et al. 1994; Novotný et al. 1997), *Phlebia brevispora* (Kamei et al. 2006b), *I. lacteus* (Čvančarová et al. 2012); *B. adusta* (Beaudette et al. 1998; Čvančarová et al. 2012), *Pycnoporus cinnabarinus* (Čvančarová et al. 2012), *Phanerochaete magnoliae* (Čvančarová et al. 2012).

Generally, all these studies confirmed that the extent of degradation significantly decreases with increasing chlorine content. For instance, a negligible mineralization of individual tetra- and hexa-chlorobiphenyls was reported for *P. chrysosporium* (Dietrich et al. 1995), whereas the level of degradation remarkably increased for three- and di-chlorinated congeners. Similar trends were also observed with technical PCB mixtures. For example, Yadav et al. (1995) showed that *P. chrysosporium* was able to remove 60.9, 30.5, and 17.6 % of Aroclor 1242, 1254, and 1260 PCB mixtures (42, 54 and 60 % chlorinated), respectively, in 30 days.

Moreover, some fungal strains (e.g., *P. ostreatus*) have shown to selectively remove PCB congeners with a preference for compounds with chlorine atom in *ortho > meta > para* position (Kubátová et al. 2001), while others (e.g., *P. chrysosporium*) did not exhibit any noticeable specificity for the position of chlorine substitutions (Yadav et al. 1995).

A number of studies have dealt with the interpretation of PCB degradation mechanisms in fungi. A few works indicated that purified fungal extracellular phenoloxidases and peroxidases were unable to oxidize PCB congeners (Beaudette et al. 1998; Krčmar et al. 1999; Takagi et al. 2007). For instance, Krčmar et al. (1999) performed a biodegradation experiment with technical PCB mixtures containing low and high chlorinated congeners (Delor 103 and Delor 106) using *P. chrysosporium* mycelium, crude extracellular liquid and crude extract enriched in MnP and LiP activities. A decrease in the PCB concentration after 44 h of treatment with mycelium (74 %) or crude extracellular liquid (60 %) was observed whereas MnP and LiP isolated from the extracellular liquid did not catalyze any degradation.

Afterwards, based on the identification of PCB transformation products in liquid fungal cultures, the involvement of both extracellular ligninolytic system and intracellular CYP450 monooxygenases system in the degradation process of PCBs was hypothesized (Kamei et al. 2006a, b; Čvančarová et al. 2012). In this respect, other studies proved that the ligninolytic enzymes were able to breakdown some of the PCB degradation intermediates such as their hydroxylated derivatives, which are produced by CYP450 system (Keum and Li 2004; Takagi et al. 2007; Kordon et al. 2010).

Kamei et al. (2006a) investigated the transformation products of 4.4'-dichlorobiphenyl in *P. chrysosporium* in the attempt to determine its degradation pathway. Methoxylated- and hydroxylated-PCB derivatives were detected in P. chrysosporium liquid cultures and, thus the involvement of cytochrome CYP450 in the degradation process was supposed. The addition of piperonyl butoxide, a well-known CYP450 inhibitor, to fungal cultures prevented the formation of hydroxylated metabolites, further supporting the initial hypothesis. Chlorobenzoic acids, chlorobenzaldehydes and chlorobenzylalcohols were also identified as PCB degradation products. In particular, Cvancarová et al. (2012) reported the formation of chlorobenzoates from hydroxylated PCBs and hypothesized the further transformation via reductive pathways. Once CYP450 oxidizes the aromatic structure of PCBs, ring fission reaction can be mediated by other enzymatic systems (i.e., LEs) (Cajthaml et al. 2006; \check{C} vančarová et al. 2012); subsequently, a reductive mechanism can operate on the carboxyl group of CBAs leading to the formation of chlorinated aldehydes and alcohols (Muzikář et al. 2011; Stella et al. 2013). An overview of the PCB degradation pathway in ligninolytic fungi, including the formation and further biotransformation of CBAs, is provided in Fig. 8.3.

Despite the promising outcomes achieved in liquid cultures, few studies investigated the ability of white rot fungi to degrade chlorinated biphenyls either in artificially contaminated (Zeddel et al. 1993; Kubátová et al. 2001) or in actual PCB-contaminated soils (Borazjani et al. 2005; Federici et al. 2012). With regard to historically PCB-polluted matrices, a recent study demonstrated that a bioaugmentation approach based on the use of maize stalk-immobilized fungus *L. tigrinus* brought about 33.6 % of Aroclor 1260 depletion and 23.2 % of dechlorination in 60 days (Federici et al. 2012).

Compared to PCB biotransformation processes mediated by basidiomycetes, few studies investigated the PCB biodegradation potential of NLFs. One of the first

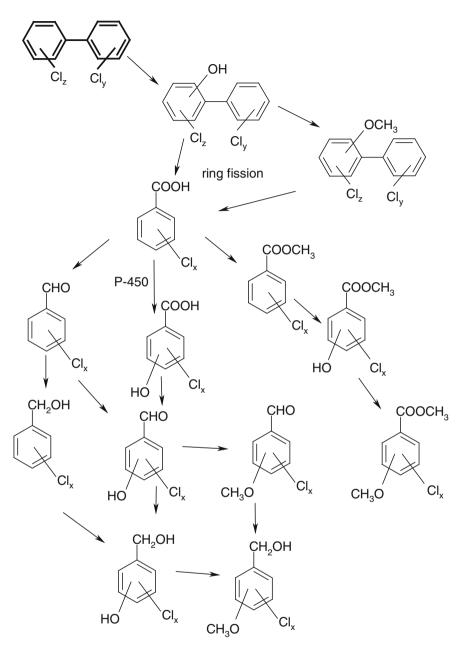


Fig. 8.3 Degradation pathway of PCBs and CBAs by *P. ostreatus*—adapted from Čvančarová et al. (2012) and Muzikář et al. (2011)

report (Dmochewitz and Ballschmiter 1988) revealed that the ascomycete Aspergillus niger was able to degrade a technical mixture of PCBs (Chlophen A) with a low chlorine content (42 %), while PCB mixtures with higher chlorination levels (54 and 60 %) remained untransformed. Recently, six fungal strains belonging to Aspergillus, Penicillium, Fusarium and Scedosporium genera were isolated from an aged contaminated soil (0.9 g kg⁻¹ PCB mixture Aroclor 1260) and tested for their ability to degrade three target congeners (2-monoCB, 4.4'-diCB and 2,2',5,5'-tetraCB) in liquid mineral medium in the presence of glucose (Tigini et al. 2009). The degradation experiments demonstrated that PCBs were cometabolically transformed by all the isolates at a similar rate, regardless of the number of halogenated substituents. A similar experimental approach was adopted by Mouhamadou et al. (2013). The PCB degradation ability of autochthonous fungal strains isolated from former industrial sites highly contaminated with PCBs was tested in liquid cultures. Among all the isolates, the ascomycetes Doratomyces nanus, Doratomyces purpureofuscus, Doratomyces verrucisporus, Myceliophthora thermophila, Phoma eupyrena, and Thermoascus crustaceus showed remarkable degradation ability (>70 %). As for the previous study, the number of chlorine substituents on the biphenyl nucleus did not affect the degradation rate. Thereafter, a consortium of the aforementioned fungal strains was used for the remediation of both PCB-contaminated soil and sediment (Sage et al. 2014). After 6 months of treatment, 18.7 and 33.3 % of 15 target PCBs were degraded in soil and sediment mesocosms, respectively. The fungal strains were re-inoculated and incubated for additional 2 months to further promote the biodegradation of PCBs. However, no additional PCB depletion was observed. This result suggested that the bioavailable fraction of PCB was completely removed after 6 months and the remaining fraction was inaccessible to fungi.

Research regarding the PCB degradation pathways in other non-white rot fungi, revealed that no dechlorination occurred during the transformation of 4-chlorobiphenyl by *Paecilomyces lilacinus*, but five chlorinated metabolites, including ring fission products, were identified (Sietmann et al. 2006). Another study by Tigini et al. 2009, where mitosporic fungi were incubated in the presence of PCBs, showed that no chloride ions were released. Moreover, peroxidase activities were not detected in the liquid cultures, either in the absence or in the presence of PCBs, providing further evidence that these extracellular enzymes were not involved in the biotransformation process. Only Lac activity was detected at significant levels, irrespective of the presence of PCBs, but the role played by this enzyme in the PCBs degradation process was not clarified.

In conclusion, despite the large number of studies regarding the mycoremediation of PCBs, further research is needed to explore the physiological and biochemical characteristics of fungi prior to any practical application. Moreover, as suggested in a recent study (Stella et al. 2015), a comprehensive evaluation of both physico-chemical factors (i.e., interaction of PCBs with soil organic matter) and biological factors (i.e., interaction with native microorganisms) is strongly required to develop an effective fungal-based remediation approach for the treatment of PCB contaminated matrices.

8.3.2 Chlorobenzoic Acids

Chlorobenzoic acids (CBAs) are a class of relevant environmental pollutants consisting of benzoic acid with different chlorination degrees of the aromatic ring. CBAs primarily result from bacterial biodegradation of polychlorinated biphenyls (PCBs) under aerobic conditions as reviewed by Field and Sierra-Alvarez (2008). During this process, CBAs tend to accumulate as dead-end products, acting as inhibitors for the upper biphenyl pathway and therefore restricts further PCB transformation (Pieper 2005; Adebusoye et al. 2008). Due to their relatively high solubility in water, CBAs are characterized by a mobility that is several orders of magnitude higher than that of PCBs. In addition, some of CBA isomers are highly toxic for aquatic organisms (Lee and Chen 2009), exhibit genotoxicity toward higher plants (Gichner et al. 2008) and act as endocrine disruptors (EDs) (Svobodová et al. 2009).

The number of publications dealing with the fungal degradation of CBAs is very limited. Four white rot fungi (*P. chrysosporium*, *P. ostreatus*, *T. versicolor*, *Heterobasidion annosum*) and two ectomycorrhizal (ECMs) fungal species (*Paxillus involutus*, *Suillus bovinus*) were tested for their capability to grow on different concentrations of 3-chlorobenzoic acid (0.1, 1, and 3 mM) and to degrade it in 4 weeks (Dittmann et al. 2002). Even low concentrations of 3-CBA led to a remarkable reduction in the growth of both ECMs and *P. chrysosporium*, whereas that of *P. ostreatus*, *T. versicolor* and *H. annosum* was not affected. This study showed, in particular, that the great ability of the latter group of white rot fungi to grow in the presence of 3-CBA correlated to the highest extent of degradation achieved at the end of incubation period.

Muzikár et al. (2011) performed a more comprehensive study dealing with fungal degradation of CBA. Eight ligninolytic fungal strains (I. lacteus, B. adusta, P. chrysosporium, P. magnoliae, P. ostreatus, T. versicolor, P. cinnabarinus and D. squalens) were tested for their ability to degrade a mixture of 12 CBAs (mono-, di- and tri-chlorobenzoates) in both model liquid systems and contaminated soils. In liquid media, I. lacteus, P. cinnabarinus and D. squalens were the most effective fungi in terms of CBA removal and toxicity reduction, whereas I. lacteus and P. ostreatus were the most efficient in an artificially ("ad hoc") contaminated soil. Analysis of the degradation products revealed that methoxy and hydroxy derivatives were produced along with reduced forms of the original acids (benzaldehydes and benzyl alcohols) and a general degradation pathway was proposed. However, the mechanism by which individual enzymes can degrade CBAs was not fully clarified. Subsequently, the white rot fungus L. tigrinus was selected for the evaluation of its efficiency in degrading a mixture of chlorinated benzoates (Stella et al. 2013). The in vivo degradation experiment showed that this organism was able to deplete most of the target CBA isomers within 20 days of incubation, with the exception of 2,6-diCBA, 2,3,6-triCBA and 2,4,6-triCBA. The authors suggested that the recalcitrance of these isomers might be due to the steric hindrance of the two chlorine substituents adjacent to the carboxyl moiety and to the general electron-withdrawing effect of halides. Furthermore, to gain insights into the CBA degradation pathway of *L. tigrinus*, in vitro experiments were performed with both extracellular LEs (Lac and MnP) and intracellular enzymatic systems (microsomal fraction containing CYP450 monooxygenases) extracted from *L. tigrinus* cultures. Lac and MnP were shown not to be involved in the initial transformation steps of CBAs, even in the presence of redox mediators, whereas CYP450 were able to oxidize chlorobenzoates. The key role played by CYP450 in the degradation of CBAs under in vitro condition was inferred by the NADPH-dependency of the reaction and by its susceptibility to piperonyl butoxide and carbon monoxide, two well-known CYP450 inhibitors (Stella et al. 2013). Additionally, the detection of a hydroxylated chlorobenzoic acid further supported the pivotal role of CYP450 system in the initial CBA bioconversion steps by *L. tigrinus*.

8.3.3 Chlorinated Dioxins and Furans

Polychlorinated dibenzodioxins (PCDDs) are a group of polyhalogenated organic compounds which consist of two benzene rings joined by two oxygen bridges (dibenzo-1,4-dioxin) with one or several of the hydrogens replaced by chlorines and polychlorinated dibenzofurans (PCDFs) are a group of organopollutants with properties and chemical structures similar to polychlorinated dibenzodioxins. PCDDs and PCDFs are released in the environment as by-products of several industrial processes, including incineration of waste, chemical and manufacturing of pesticides. Because of their lipophilic properties, they get accumulated in humans and wildlife causing developmental disorders and cancer as already reported several decades ago (Huff et al. 1980). For this reason, they were listed among the most persistent hazardous organic pollutants in the Stockholm convention. A large number of white rot fungi, namely P. chysosporium, Panellus stypticus, Phlebia spp., and Bjerkandera spp., were assessed as potential dioxin degraders. The capability of P. chysosporium to mineralize PCDDs was demonstrated in 1985 (Bumpus et al. 1985) without the elucidation of the metabolic pathway. Later, Valli et al. (1992) demonstrated that P. chrysosporium degraded 50 % of 2,7-dichlorodibenzo-*p*-dioxin (2,7-diCDD) under ligninolytic conditions while only 10 % was degraded under non-ligninolytic conditions, implying the involvement of LiP and MnP. The proposed pathway for 2,7-diCDD transformation involved oxidative cleavage of 2,7-diCDD by LiP resulting in the production of 4-chloro-1,2-benzoquinone and 2-hydroxy-1,4-benzoquinone. Afterwards, hydroquinones or catechols were produced via LiP and/or MnP mediated oxidation followed by methylation leading to the formation of methoxybenzenes. Interestingly, though the white rot fungus Panellus stypticus does not produce either LiP or MnP, it could transform 2,7-diCDD. The formation of 4-chlorocatechol as an intermediate and the inhibition of the degradation process upon addition of piperonyl butoxide, a well-known CYP450 inhibitor, suggested a degradation pathway involving CYP450 different from that described for P. chrvsosporium (Sato et al. 2002). The same degradation mechanism was proposed for several Phlebia species that mineralized 6.5 % of [¹⁴C]-2,7-diCDD producing hydroxylated and methoxylated intermediates (Mori and Kondo 2002a, b; Kamei and Kondo 2005), Moreover, Kamei et al. (2005) demonstrated that different Phlebia species were also able to degrade higher chlorinated dioxins, such as 2.3.7-triCDD, 1.2.8.9-tetraCDD and 1.2.6.7-tetraCDD. Several strains of the genus Bjerkandera were also screened for their ability to transform PCDDs and the production of key enzymes that catalyze the conversion of these pollutants was evaluated in either nitrogen-sufficient or -limited conditions (Manji and Ishihara 2004). Among the tested strains, Bjerkandera MS325, that could produce high levels of both MnP and LiP even under non-ligninolytic conditions, was proved to be the most efficient degrader of 1,3,6,8-tetraCDD (21 % of the original content removed in 10 days). Other WRFs were also studied for their ability to degrade dibenzo-p-dioxins as reviewed by Pinedo-Rivilla et al. (2009). In this respect, Trametes sp. CH2, Irpex sp. W3 and Pleurotus pulmonarius were reported for their capability to hydroxylate and methoxylate PCDDs (Yamaguchi et al. 2007; Nam et al. 2008).

In contrast to the above, evidence of PCDDs degradation by NLFs is limited to a few ascomycetes, but the enzymatic systems involved in such biotransformations remain unknown. A dioxin-degrading organism was isolated from the activated sludge of a landfill treatment plant and identified as Acremonium sp., (Nakamiya et al. 2002). This fungus (later identified as Pseudallescheria boydii) was able to remove 82 % of a mixture containing tetrachlorinated up to octachlorinated dioxins (2 ng/mL) under denitrifying conditions in 1 day. The incubation with octachlorodibenzo-p-dioxin (OCDD, 100 ng) under aerobic conditions led to the formation of 1- and 2-hydroxydibenzo-p-dioxin indicating that OCDD was transformed to non-chlorinated dibenzo-p-dioxins through a dechlorination process. However, the degradation mechanism of OCDD and other highly chlorinated dioxins was not described in detail. In another study, P. boydii was tested in a slurry bioreactor system for the treatment of dioxin-contaminated soils (Ishii and Furuichi 2007). Surprisingly, in spite of its great capability to remove dioxins, P. boydii failed to lower the dioxins level to the environmental standard in this particular experimental setup and, thus the biological treatment was coupled with a physico-chemical process (ethanol extraction) to reach the required quality standard. Two years after, the same authors clarified that P. boydii use glucose as carbon source to grow and degrade PCDDs during its logarithmic growth phase regardless of the concentration of dioxins (Ishii et al. 2009). Another study showed that the cyclic ether degrading fungus, Cordyceps sinensis, was able to degrade dibenzo-p-dioxin (DD), 2,3,7-trichlorodibenzo-p-dioxin (2,3,7-triCDD) and octachlorodibenzo-*p*-dioxin (OCDD) using either glucose or 1,4-dioxane as a carbon source (Nakamiya et al. 2005). Less chlorinated catechols and catechols themselves along with *cis*, *cis*-muconates were identified as by-products, this leading to the postulation of a new dioxin degradation pathway.

Considering the fungal degradation studies on PCDFs, the number of publications dealing with furans is very limited. A mixture of 10 of tetra- to octachlorodibenzofurans with chlorine substituents on the aromatic rings at 2-, 3-, 7-, and 8- positions was partially degraded by Phanerochaete sordida YK-624 stationary cultures in low-nitrogen medium and 4.5-dichlorocatechol and tetrachlorocatechol were formed from the degradation of 2,3,7,8-tetra- and octaCDD, respectively (Takada et al. 1996). The white rot fungus Phlebia lindtneri was able to degrade 2,8-diCDF producing hydroxyl-diCDF as an intermediate differently from P. sordida (Mori and Kondo 2002b). A yeast-like fungal strain was isolated from a dioxin-contaminated soil under selective conditions: the soil sample was suspended in a mineral salt medium supplemented with 1 g L^{-1} of dibenzofuran, a model compound for highly chlorinated dibenzofurans (Hammer et al. 1998). The yeast strain, identified as Trichosporon mucoides, metabolized dibenzofuran at fast rate (more than 50 % of the compound added was degraded within 8 h) and water-soluble intermediates were detected during the incubation period. In detail, different isomers of mono- and di-hydroxylated dibenzofurans were observed, along with the ring-cleavage product (2-(1-carboxy methylidene)-2,3-dihydrobenzo [b]furanylidene glycolic acid). The ability of the imperfect soil fungus Paecilomyces lilacinus to transform dibenzofurans was also investigated and 14 degradation intermediates were identified by UV spectroscopy, mass spectrometry, and proton nuclear magnetic resonance spectroscopy (Gesell et al. 2004). According to this study, the biotransformation of dibenzofuran was initiated by two separate hydroxylation steps leading to the accumulation of monohydroxylated- and dihydroxylated-dibenzofurans. Further oxidation yielded to the ring-cleavage of dibenzofuran structure, which was not previously described for filamentous fungi. The ring fission products were identified as benzo[b]furo[3,2-d]-2-pyrone-6carboxylic acid and [2-(1-carboxy-methylidene)-benzofuran-3-ylidene]-hydroxyacetic acid and its derivatives hydroxylated at 7 and 8- positions on the non-cleaved ring. Riboside conjugates of 2-hydroxydibenzofuran and 3-hydroxydibenzofuran were also detected. These results suggested the involvement of CYP450 in the initial steps of the furans transformation process as already reported for other chlorinated environmental pollutants; the formation of the riboside conjugates that increased with the dibenzofuran concentration supported the common opinion that different types of conjugation (glycosylation, sulfate, or glutathion conjugation) are used by eukaryotic cells to encounter toxic hydroxylated compounds.

8.4 Emerging Organic Micropollutants: Endocrine Disruptors, Pharmaceuticals and Personal-Care Products²

In recent years, the presence of organic micropollutants (MPs) in the aquatic environment (i.e., surface waters, groundwaters and drinking water reservoirs) has become an issue of worldwide concern (Luo et al. 2014). The development of powerful and sensitive analytical techniques contributed to the detection and quantification of a large number of organic chemicals in the environment, thus compelling the scientific community to consider this type of contamination as a subject that merits attention (Santos et al. 2010). Such MPs, also termed as "emerging" organic contaminants (Gasser et al. 2014), encompass a vast and ever-expanding array of substances, mainly of anthropogenic origin, that are detected in surface waters at trace concentrations (ng to µg per liter). Among these substances, pharmaceuticals and personal care products (PPCPs) such as antibiotics, anti-inflammatories, cytostatic drugs, disinfectants, β-blockers, UV-filters, fragrances, and other compounds are common water MPs (Verlicchi et al. 2010; Luo et al. 2014). The other group is represented by endocrine disrupting compounds, i.e., chemical compounds that interfere with the endocrine system and therefore could be detrimental to human and wildlife health. The most studied and detected EDs are the natural hormones estrone and 17β -estradiol, the synthetic estrogen 17α -ethinylestradiol, industrial compounds and additives, nonylphenols (NPs), bisphenol A (BPA) and also the personal care product triclosan (Cajthaml et al. 2009a). Besides, endocrine disrupting effects have been reported for PAHs (Arcaro et al. 1999), PCBs, CBAs, PCDDs and other POPs (Cajthaml 2014).

The occurrence of emerging organic MPs in the environment has been associated with a number of negative effects, mainly regarding the aquatic ecosystems (see below). Till date, however, discharge guidelines and standards for most of the MPs do not exist. For example, environmental quality standards for a minority of MPs (e.g., NPs, BPA, diethylhexyl phthalate-DEHP and diuron) were stipulated in Directive 2008/105/EC (European Parliament and The Council 2008). Nonylphenol and nonylphenol ethoxylates were also recognized as toxic substances by the Canadian government (Canadian Environmental Protection Act 1999); but other potent MPs, such as PPCP and EDs have not been included yet in the list of regulated substances (Luo et al. 2014).

²Additional information on fungal treatment of emerging pollutant in municipal wastewater is presented in Chap. 5—Fungal bioremediation of emerging micropollutants in municipal wastewater.

8.4.1 Toxicity of Emerging Micropollutants

The adverse effects associated with the occurrence of MPs in the aquatic environment include short-term and long-term toxicity, endocrine disrupting effects and induced antibiotic resistance of microorganisms-although the latter phenomenon is still largely disputed (Luo et al. 2014). Some damaging health effects that occur in human and wildlife are due to the exposure to particular organic pollutants, many of which could be detected in all human beings, which cause damage or impairment of neural, immune and reproductive systems (Luo et al. 2014). Although the majority of EDs and PPCP are not considered as recalcitrant as other POPs (e.g., PAHs, PCBs, PCDDs, etc.), the widespread usage and continuous delivery of low concentration of contaminants to the receiving ecosystems might give rise to toxicity even without high rates of persistence (Santos et al. 2010). It has been demonstrated that environmental concentrations of EDs induce the "feminization" of male tissues and/or the presence of female reproductive organs in males, along with other dysfunctions of the reproductive systems in many aquatic animals (Liu et al. 2009; Santos et al. 2010; Eggen et al. 2014). Since the 1940s, decline in semen quality and increasing incidence of testicular cancer in humans has been observed, although a direct link between exposure to EDs and manifestation of negative effects could be proved only in model organisms (UNEP 2012), which is also applicable to a number of scientific studies that reported the thyroid-disrupting effects of EDs and other environmental MPs. (e.g., BPA, phthalates, and perfluorinated chemicals) (Boas et al. 2012).

The challenges facing environmental scientists are significant. However, it is essential to conduct research that increases our scientific knowledge on the wide range of water MPs, including a detailed understanding of their environmental cycling and toxicological impact. To understand the dimension and the importance of such problem, it is interesting to look at the strategies adopted by the leading EU countries. As an example, the Swiss Federal Office for the Environment (FOEN) conducted the project "Strategy Micropoll" in the period 2006–2010 in order to develop a strategy to reduce the input of organic MPs from domestic wastewater into Swiss surface waters. Results from this project led to the development of the VSA-Platform "Verfahrenstechnik Mikroverunreinigungen," for which the Swiss Federation is going to grant ca. 1 billion euro funds in the following years.

8.4.2 Fungal Biodegradation of EDs

The number of scientific contributions dealing with fungal degradation of EDs and other water MPs has been growing steadily through the last decades. The majority of such studies, although not all, focused on the groups of wood-rotting fungi, mainly because of their capability to produce unspecific, high redox potential LEs (Ashger et al. 2008; Cajthaml et al. 2009a). These potent biocatalysts can, bring

about the attack on the phenolic moieties present in the chemical structure of many of the MPs, resulting in the formation of phenoxyl radicals, which subsequently undergo oxidative coupling. Once dimers, tetramers or oligomers are formed, the overall biological and endocrine disrupting activity is significantly reduced or completely removed (Cabana et al. 2007b; Cajthaml 2014). Intracellular enzymatic complexes like CYP450 were also shown to be involved in the degradation of several compounds by the intact fungal cells, as well as Fenton-like reactions (Marco-Urrea et al. 2010d; Cajthaml 2014). Due to the number and diversity of compounds in the MPs family, we will only select some of the compounds which were extensively studied and provide a brief overview of the most significant results reported in the scientific literature.

Typical man-made EDs with estrogen-like action include NPs, BPA and 17α -ethinylestradiol (EE2). NPs isomers mainly occur in the environment as degradation products of nonylphenol-polyethoxylates which are widely used as nonionic surfactants in many industrial processes. BPA is a key building block for polycarbonate plastics and epoxy resins, but it is also used in a number of other materials and applications. Synthetic estrogens, such as EE2, are used worldwide as oral contraceptives. Non-metabolized EE2 and its conjugates are first excreted into the urban sewage systems and, after incomplete degradation in the wastewater treatment processes, they reach the surface water ecosystems. The capability of the above-cited compounds to bind human receptors and cause endocrine disruptions has been documented (Cabana et al. 2007b).

NPs: NPs were found to be very efficiently degraded by LF cultures and purified LEs (see Corvini et al. 2006; Cabana et al. 2007b; Cajthaml et al. 2009a; Cajthaml 2014). The intermediate steps of NPs biotransformation by LFs, including (C-O) coupling reactions and oxidation at the terminal carbon of the alkyl chain, are summarized in Fig. 8.4. Several studies reported the formation of dimeric and holigomeric NP transformation products using Lac of Coriolopsis gallica and C. polyzona (Cabana et al. 2007a; Torres-Duarte et al. 2012), a mechanism that is known to suppress the estrogenic activity of the parent compounds. Tsutsumi et al. (2001) suggested similar transformation products following oxidation with MnP of P. chrysosporium. This coupling metabolite is probably produced as a result of the action of LEs on phenolic hydroxyl groups that results in the formation of phenoxyl radicals which subsequently undergo different spontaneous reactions, including oxidative coupling (Hofrichter 2002; Dec et al. 2003). Dubroca et al. (2005) proposed the formation of a direct C-C bond between the phenolic rings and the analogous structure was finally identified by Wang et al. (2012) with respect to p-t-octylphenol. Production of NP oligomers was similarly observed by other authors who tested, e.g., the degradation abilities of Lac from the aquatic fungus Clavariopsis aquatica (Junghanns et al. 2005). Syed et al. (2011, 2013) investigated the involvement of CYP450 (CYP5136A3 and CYP63A2) from P. chrysosporium in the NP transformation mechanisms and discovered a very versatile function of these intracellular monooxygenases. They documented the oxidation of NP and other alkylphenols at the terminal alkyl chain carbon (omega oxidation) via alcohols resulting in aldehydes. Based on the literature and known pathway in

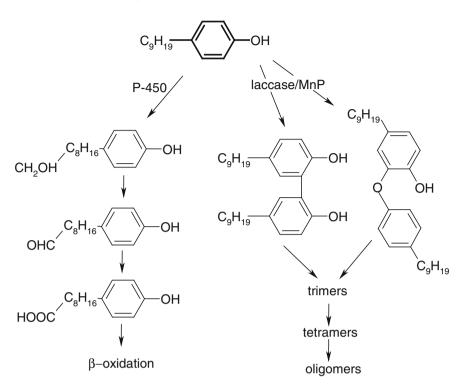


Fig. 8.4 Nonylphenols biotransformation by LFs-adapted from Cajthaml (2014)

yeasts/fungi for the degradation of an alkylphenol moiety, the authors concluded that the terminal oxidation of the alkyl side-chain is followed by the removal of the terminal carbons via the β -oxidation of NPs *via* carbon–carbon (C–C) and carbon–oxygen pathway as noted in other fungi, e.g., the yeast *Candida aquatextoris* (Vallini et al. 2001; Corvini et al. 2006; Rozalska et al. 2010). The possible entry into the basal metabolism is also supported by a study of Dubroca et al. (2005), who observed mineralization of NPs by a culture of *T. versicolor* using ¹⁴C-labeled NP. Surprisingly, the potentially anticipated metabolites following direct hydroxylation of NPs by CYP450 of LFs have not been detected yet (Corvini et al. 2006). It was shown that the production of the coupled NPs leads to a reduction of estrogenic activity (Tsutsumi et al. 2001), an aspect which has not been investigated with respect to alkylphenol carboxylic acids so far.

BPA: BPA has also been shown to be susceptible to biodegradation by several fungi and fungal enzymes. Fukuda et al. (2001) demonstrated that purified Lac from *Trametes villosa* efficiently transformed BPA under in vitro conditions without any requirement for electron-shuttling mediator. Structural analysis of the BPA degradation products using nuclear magnetic resonance spectroscopy indicated that the oligomers of BPA were formed as a result of successive oxidation–condensation entailing C–C coupling (Fukuda et al. 2004). The presence of oligomeric fragments,

each including a phenol moiety, suggested the cleavage of the oligomeric products to release 4-isopropenylphenol or simultaneous fission of the original BPA molecule. Neither the soluble nor the insoluble fractions of the BPA reaction products had estrogenic activity, even at high concentrations (Fukuda et al. 2004). Similar metabolites were also detected by Michizoe et al. (2005) who identified 4-isopropylphenol following the transformation of BPA by Lac (Trametes sp.) in a reverse micelle system in organic media, and by Cabana et al. (2007a), who detected BPA polymeric structures. Huang et al. (2005) proposed that the formation of C-O coupled polymer occurred via radical-mediated mechanisms triggered by horseradish peroxidase and reported the formation of 4-isopropenylphenol. Wang et al. (2012, 2013a) tested LiP from P. sordida and identified dimerized BPA with C-C coupling and also with a C-O bridge. The same authors also detected hydroxylated BPA and suggested the involvement of CYP450 in the transformation (Wang et al. 2013b). Hirano et al. (2000) used a MnP isoenzyme from *P.ostreatus* mostly breakdown products as and detected such phenol, *p*-cresol, 4-isopropenylphenol and its dimer. Structures akin to these were reported by Torres-Duarte et al. (2012) following the treatment of BPA with Lac of C. gallica. It is noteworthy that in all the studies where the authors monitored the estrogenic potency of samples after treatment, the removal of BPA by either purified LEs or fungal cultures was always accompanied by a simultaneous depletion of the estrogenic activity (Tsutsumi et al. 2001; Cabana et al. 2007b; Cajthaml et al. 2009a; Torres-Duarte et al. 2012).

EE2: Synthetic and natural estrogens are considered to be major contributors to the estrogenic activity associated with wastewater treatment plant (WWTP) effluents due to their incomplete removal in conventional wastewater treatment process (Clouzot et al. 2008). EE2 was generally reported to be more resistant to biodegradation than other natural estrogens (Cajthaml et al. 2009b; Tran et al. 2013). Numerous authors reported the high efficiency of LFs and LEs in biodegradation or transformation of EE2 (see reviews Cabana et al. 2007a; Cajthaml et al. 2009b; Demarche et al. 2012b) and effective EE2 degradation by whole cultures of several LFs has been described (Blánquez and Guieysse 2008; Cajthaml et al. 2009a). Estrogenic activity generally decreased with the progression of degradation. However, during EE2 biodegradation tests with I. lacteus, P. ostreatus, P. cinnabarinus and P. magnolia, residual or increased estrogenic activity was observed, suggesting the production of estrogen-like degradation products (Cajthaml et al. 2009a). Suzuki et al. (2003) investigated the removal of the steroidal hormones E2 and EE2 in organic solvent under biphasic conditions using MnP and the Lac-mediator (hydroxybenzotriazole—HBT) systems from P. chrysosporium ME-446 and T. versicolor IFO-6482. They also monitored the evolution of estrogenic activity and documented the high potential of LEs for the biodegradation of EE2. Similar results were obtained by other authors (Tanaka et al. 2001) who worked with Lac from Trametes sp. and Pycnoporus coccineus in a rotating reactor. Auriol et al. (2007) studied the T. versicolor Lac-catalyzed conversion of natural oestrogens and EE2 and showed that the Lac-catalyzed system was not significantly affected by the presence of a real municipal wastewater matrix. Moreover, when HBT was used as a mediator, the Lac-catalyzed system showed an improved efficiency. However, limited information is available about the fungal biotransformation products of EE2. Kresinová et al. (2012) published a study including a broad set of in vivo and in vitro experiments using sub-cellular and cellular fractions as well as purified LEs from P. ostreatus and suggested that the EE2 degradation mechanisms could involve intracellular microsomal enzymes, mycelium-associated laccase-like isoenzymes and extracellular ligninases (MnP and Lac). The synergic contributions of the individual transformation steps were documented and each phase of transformation was reported to individually reduce estrogenic activity. The authors also detected a set of intermediates clearly indicating that in spite of its recalcitrance, EE2 is efficiently transformed by the ligninolytic system and also by the CYP450 monooxygenase system. The intermediates included methoxylated estron (E1) and dioxo 17\beta-estradiol (E2), which were probably formed by the action of Lac, and dehydrogenated and hydroxylated EE2. Metabolites similar to the latter ones were also described by Choudhary et al. (2004) and Della et al. (2008) following the incubation of EE2 with the mucoromycete Cunninghamella elegans and microalgae, respectively. In a previous study, Tanaka et al. (2001) detected dimeric products of EE2 after treatment with Lac from *Trametes* sp.and observed a significant decrease in estrogenic activity but they did not perform any further analysis of the intermediates in detail. Other authors studied EE2 and natural estrogen biotransformation by Lac from the ascomycete Myceliphthora thermophila in a membrane bioreactor (Lloret et al. 2013) and detected two dimers and trimers of EE2 along with several transformation products of 17β-estradiol (E2). They identified E1 following Lac oxidation of E2 and characterized two C-C and two C-O dimers as well as four trimers with various coupling combinations and, concluding that the Lac transformation of E2 is analogous to that of EE2. The authors generally observed a decrease in the estrogenic activity during the course of the transformation. Similar results were achieved using Lac from Myceliophthora and Trametes pubescens, both adsorbed on glass beads. The enzymes were used for the transformation of natural estrogen E2 (Nicotra et al. 2004) and the reaction products were also tentatively identified as C-C dimeric compounds with coupling between either 4'-4 or 2'-2 and C-O (phenolic ring) at the 4' or 2' positions.

8.4.3 Fungal Degradation of Pharmaceuticals and Personal Care Products (PPCP)

The ability of fungi, especially belonging to the group of wood-inhabiting Basidiomycetes, to degrade PPCP detected in surface and process waters and sludge biosolids, has been demonstrated in recent years. In relation to this issue, non-steroidal anti-inflammatory drugs (NSAID) (e.g., diclofenac, naproxen, ibuprofen, ketoprofen), blood lipid regulators (clofibric acid), β -blockers (e.g.,

propanolol, atenolol), anti-epileptic drugs, (carbamazepine) and antibiotics (e.g., sulfamethoxazole, ciprofloxacin, erythromycin) are the most intensively studied pharmaceutical compounds (Marco-Urrea et al. 2009, 2010a, b, c, d; Accinelli et al. 2010; Rodarte-Morales et al. 2011, 2012; Domaradzka et al. 2015).

Marco-Urrea et al. (2009) screened four white rot fungi (T. versicolor, I. lacteus, G. lucidum and P. chrysosporium) for their ability to co-metabolize ibuprofen (IBU). clofibric acid (CA) and carbamazepine (CBZ) in model (glucose-supplemented) liquid systems. All strains efficiently removed IBU while the turkey-tail fungus T. versicolor was the most efficient in the biotransformation of the recalcitrant CA and CBZ. Failure of PPCP degradation by Lac and Lac-mediator systems under in vitro condition, reduced biotransformation rates in the presence of CYP450 inhibitors and the detection of hydroxylated and di-hydroxylated derivatives of IBU prompted the authors to conclude that CYP450 monooxygenase system is responsible for the initial oxidative attack to this NSAID. Further experiments in which T. versicolor was incubated in the presence of other NSAIDs (naproxen, ketoprofen and diclofenac) showed the involvement of intracellular (CYP450) and to a lesser extent, extracellular (Lac) enzymatic systems in pharmaceuticals degradation by this fungus (Marco-Urrea et al. 2010a, b, c). In all cases, the time course of the degradation of NSAIDs was accompanied by a significant drop in toxicity as assessed by the test with the luminescent bacterium Vibrio fisheri, and also by the presence of transient biotransformation products, the chemical structure of which had been elucidated by nuclear magnetic resonance techniques. The same authors took care to demonstrate whether T. versicolor could use mechanisms other than those reported above (CYP450-Lac) to oxidize representative PPCP (Marco-Urrea et al. 2010d). To rule this out, the fungus was incubated under conditions triggering the production of ROS (e.g., OH') via quinone-redox cycling (see also Gómez-Toribio et al. 2009). The degradation of CBZ, CA, and the β -blockers atenolol and propranolol occured (80 % of 10 mg L⁻¹ compounds initially added was removed after 6 h) only under 2,6-dimethoxy-1, 4-benzoquinone (DBQ) redox cycling conditions (i.e., fungus mediated Fenton-like mechanism) although the NSAID-bioconversion process was short-lived due to the depletion of DBQ by the same OH'. Several hydroxylated metabolites where reported for the first time, although the authors noted the complete disappearance of degradation products at the end of the incubation period (Marco-Urrea et al. 2010d).

Scale-up processes of *T. versicolor*-mediated degradation of PPCP from flasks to bubble column reactors were successful under both batch and continuous mode of operation (Blánquez and Guieysse 2008; Jelić et al. 2012), even in the presence of non-sterile real wastewaters from WWTP (Cruz-Morató et al. 2013), although sources of C and N (glucose and ammonium tartrate) were necessary for the growth of the fungus. In some cases, however, the production of hydroxylated metabolites with increased toxicity with respect to parent molecules has also been reported (Cruz-Morató et al. 2013).

8.4.3.1 White Rot Inocula for the Treatment of Sludge Biosolids³

Depending on their hydrophobicity, water MPs tend to partition in wastewater processes and adsorb onto sludges and therefore, considerable concentrations of PPCP and EDs are often detected in sludge biosolids (Cabana et al. 2007b; Clarke and Smith 2011). In consideration of this, Rodriguez-Rodriguez and colleagues (2012) tested a sludge-bioaugmentation approach using T. versicolor mycelia to remove the load of organic MPs therein. The fungus, pre-grown on lignocellulose-based pellets, was mixed (38 % w/w dry weight) with sewage sludge and control microcosms were set up with non-inoculated, sterile lignocellulose. The fungus was deemed responsible of a faster disappearance of some MPs (ranitidine and fenofibrate) and enhanced the removal of atorvastatin, diclofenac and hydrochlorothiazide in the initial phase of incubation. However, T. versicolor was rapidly overgrown by members of the sludge microflora and the overall degradation of several compounds at the end of the incubation period remained similar to that observed in the non-inoculated control. The authors therefore concluded that the bioaugmentation with white rot inoculant is feasible and advantageous with respect to the rates of contaminants removal but the biostimulation of the sludge microbiota, as assessed via denaturing gradient gel electrophoresis (DGGE), merits equal attention in the light of future applications (Rodríguez-Rodríguez et al. 2012).

8.4.3.2 Enzyme Aggregates and Immobilized Forms for the Treatment of Process Waters

The pollutant degradation potential of LEs was widely evidenced in the previous sections of this chapter. However, the application of fungal catalysts in free solution is unfeasible due to the denaturing and/or inactivating conditions (temperature, pH, metal ions etc.) often encountered in sewage or waste waters (Cabana et al. 2007b; Demarche et al. 2012a, b; Kües 2015). Therefore, for the optimal retention of catalytic properties and to promote an enduring reuse of such biocatalysts in continuous-flow processes, immobilization, encapsulation, and insolubilization are techniques of great interest nowadays.

Immobilization of Lac for its potential use in a variety of applications, including bioremediation, has been the subject of intensive research in the past decades (see the review Durán et al. 2002; D'Annibale et al. 1999, 2000). Among the carriers for the immobilization/encapsulation pre-activated for ionic or covalent binding with the enzyme, glass and mesoporous silica beads, ceramics and clay minerals, natural (chitin, chitosan, agarose, cellulose nanofibers) and synthetic (polystyrene, nylon 6, poly acrylamide) polymers were successfully used in a number of studies and

³Further information on the use of white rot and brown rot fungi in wastewater and sludge treatment can be found in Chap. 4—Application of biosorption and biodegradation function of fungi in wastewater and sludge treatment.

applications (Durán et al. 2002; Ba et al. 2013; Kües 2015). The only technical disadvantage of such immobilized or encapsulated forms is the low ratio of enzyme to support in the overall volume of biocatalyst (Cabana et al. 2007b; Ba et al. 2014). To overcome this, carrier-free insolubilization of laccase and other enzymes can be achieved by producing cross-linked enzyme aggregates (CLEAs). The technique relies on the precipitation of enzymes (e.g., Lac) and the subsequent addition of cross-linking agents, which bind together amino-acid residues of proteins to form stable and insoluble aggregates. The most widely used cross-linking agents are homobifunctional aldehydes (dialdehydes) such as glutaraldehyde, glyoxal and dextran polyaldehydes, although these chemical agents can have adverse effect on aquatic organisms (and humans) besides causing a certain loss of enzymatic activity during biocatalyst preparation (Ba et al. 2013). Chitosan represents a valuable alternative to dialdehydes as cross-linkers, provided that the carboxylic groups of the protein of interest are pre-activated by carbodiimides such as 1-ethyl-3-(3-dimethylaminoisopropyl) carbodiimide hydrochloride (EDC) (Zhang et al. 2009; Arsenault et al. 2011; Cabana et al. 2011; Ba et al. 2013).

Several studies reported that regardless of the cross-linker used, Lac- or peroxidases-based CLEAs are biocatalysts with improved properties (i.e., stability, catalytic efficiency and reiterate use) as compared to enzymes in their free-form and offer greater potential for applicability in the treatment of wastewater MPs (Cabana et al. 2007b; Taboada-Puig et al. 2011; Ba et al. 2013; Kües 2015). In an attempt to broaden the range of substrates oxidized by these biocatalysts, some authors have recently tested the co-aggregation of different type of enzymes, i.e., combi-CLEAs. For instance, Ba et al. (2014) characterized combi-CLEAs of T. versicolor Lac and mushroom-derived Tyr and then tested its efficiency for the removal of acetaminophen. Taboada-Puig et al. (2011) instead optimized the co-insolubilization of B. adusta VP and A. niger glucose oxidase (GOD), the latter serving as ancillary H₂O₂-producing enzyme. A good example of combi-CLEAs is represented by the concomitant aggregation of Lac, VP, and GOD from T. versicolor, B. adusta and A. niger, respectively (Touahar et al. 2014). This versatile combi-CLEA was able to oxidize a wider spectrum of MPs (pharmaceuticals) than Lac-based one, although the requirement of co-substrates (e.g., GOD substrates and Mn^{2+}) for its optimal activity might generate additional costs in case of practical applications.

Different types of reactors bearing immobilized or insolubilized enzymes have been tested for the removal of MPs from artificial or real wastewaters, although most of the research work has been carried out at bench-scale. Packed bed, fluidized bed, perfusion basket, and membrane reactors (Cabana et al. 2007a, 2009a, b; Taboada-Puig et al. 2011; Lloret et al. 2012a, b; Nair et al. 2013) were successfully used in batch or continuous mode of operation. Among these, membrane reactors appear to be the most promising for the treatment of micropollutant-containing waters under continuous-flow conditions since the porosity of the membrane allows the retention of biocatalyst while letting the permeate to flow through (Ba et al. 2013; Kües 2015).

The pilot-scale experiment of Gasser et al. (2014) demonstrated that a fluidized bed reactor (460 L total working volume) equipped with Thielavia (Myceliophthora thermophila) laccase immobilized on fumed silica nanoparticles (fsNP, 0.5 kg) and an ultra-filtration membrane unit (UF porosity 0.04 µm) could effectively and continuously remove BPA from wastewater treatment plant effluents. The experiment was conducted under field conditions, at a Swiss wastewater treatment plant, over a period of 45 days and the reactor was fed with WWTP effluents and operated continuously in a cyclic filtration mode which included membrane backwash in order to prevent clogging (net permeate production 78 L h^{-1}). At the end of the test, the Lac-fsNP biocatalyst retained around 30-40 % of its initial activity and approximately 66 % of BPA in the reactor's inlet was removed (Gasser et al. 2014). The authors also estimated the overall economic feasibility of this novel enzymatic treatment at WWTP and concluded that the costs for the Lac-fsNP bioreactor process $(0.130 \notin m^{-3})$ are just slightly higher than other suitable treatments, namely ozonation (0.078 \in m⁻³) and powdered activated carbon adsorption (0.114 \in m⁻³). Further improvement of the treatment efficiency and additional reduction of costs might be achieved by optimizing some of the running parameters of the process (e.g., mixing conditions, nanobiocatalyst load, and hydraulic retention time). Moreover, as already stated above for combi-CLEAs, the co-immobilization of enzyme mixtures on the same nano-carrier could widen the range of wastewater MPs removed by such bioreactor treatment, thus enhancing the overall applicability potential of enzymatic treatment technologies at WWTP.

8.5 Pilot- and Field-Scale Mycoremediation

Pilot- and full-scale applications are essential to evaluate the effectiveness and economic viability of fungal technologies. However, till date, there are few reports concerning the use of fungi in the treatment of contaminated matrices at field-scale and thus many technical and engineering challenges remained in the area of its application. For instance, the model WRF *P. chrysosporium* was very efficiently degrading organic pollutants in laboratory-scale experiments but never showed similar effectiveness in any field-scale tests.

In the early 1990s, *P. chrysosporium* was used in a pilot-scale treatability study at a trinitrotoluene (TNT) contaminated-site—a former USA Naval submarine base (Bangor, Washington). The initial TNT concentration of 1844 ppm was reduced to 1087 ppm in 120 days (degradation of 41 % of the original TNT content). However, the final concentration was still significantly above the target level of 30 ppm and thus the test was considered a failure (US EPA Handbook 1993).

A decade later, a field-scale trial for the remediation of crude oil-contaminated soil was performed using composting biopiles technology where the efficiency of the traditional process (soil aerated and amended with bulking agents, such as straw, sawdust, wood chips, etc.) was compared with that of a bioaugmentation approach (Li et al. 2002). In particular, three fungal strains characterized by high

lipase activities (*Mucor* sp., *Cunninghamella* sp. and *Fusarium* sp.) were isolated and reintroduced into the contaminated matrices either with or without *P. chrysosporium*. The results showed that the inoculum composed of only indigenous fungi remarkably increased the degradation rate of total petroleum hydrocarbons (TPH) with respect to non-inoculated soil, while the introduction of the allochthonous fungus did not improve the efficiency of TPH removal process.

A similar outcome was also achieved a few years later in a pilot-scale experiment for the treatment of soil contaminated by TNT, PAHs, PCDDs and PCDFs (Tuomela et al. 2012). Pine bark was selected as a substrate to support the growth of the litter-decomposing fungus Phanerochaete velutina. Once the inoculum was prepared, the allochthonous fungus was introduced into soil and the extent of degradation of the target pollutants was evaluated. P. velutina growth was completely inhibited when introduced in soil with high concentration of PAHs (5000 mg kg⁻¹) and TNT (>10 g kg⁻¹) and no degradation occurred, moreover, the presence of molds such as Trichoderma clearly prevented its growth. On the other hand, dilution of PAH and TNT-contaminated soil with garden compost significantly enhanced the degradation process. However, since the growth of both P. velutina and indigenous microorganisms was clearly stimulated under such conditions, the role of the litter-decomposing soil fungus in the removal of PAHs and TNT could not be clarified. These results were also confirmed two years later when a field-scale experiment (2 t) for the treatment of a PAH-contaminated soil was carried out (Winquist et al. 2014). At first, the degradation of PAHs was assessed in a laboratory-scale experiment where soil was mixed with composted green waste (1:1) and incubated with or without P. velutina. The higher extent of degradation (96 % for 4-ring PAHs and 39 % for 5- and 6-ring PAHs) observed in microcosms inoculated with the fungus after three months of incubation as compared to the biostimulated ones prompted the researchers to scale-up the process. Unfortunately, even if the percentage of degraded PAHs in soil under field condition was extremely high, the results obtained in the case of P. velutina-inoculated treatment (bioaugmentation) or non-inoculated treatment (biostimulation) were comparable. This again suggested that the degradation of PAHs could not be ascribed univocally to the exogenous fungus.

P. velutina inoculated on pine bark was also used to remediate a TNT-contaminated soil diluted with composted green waste (1:20) at pilot-scale level (0.3 t) (Anasonye et al. 2015). TNT was efficiently degraded up to 80 % in 107 days. The quantification of the fungal ITS region DNA copy number by quantitative PCR (qPCR) using specific primers for *P. velutina* proved that the fungus grew in such contaminated soil withstanding high concentration of TNT and autochthonous microorganisms. However, due to economical and practical issues, no control with non-inoculated soil was prepared and thus the real efficiency of the fungus in the removal of TNT could not be compared with the degradation ability of indigenous microbiota present in the green waste.

The capability of the white rot fungus *T. versicolor* to remediate a pentachlorophenol (PCP)-contaminated soil at field-scale level was also evaluated (Walter et al. 2005). The contaminated soil was collected at a timber treatment plant where PCP was widely used as a wood preservative. In a previous study performed at laboratory scale, PCP was removed from both biostimulated (soil mixed only with a lignocellulosic substrate) and bioaugmentated microcosms (T. versicolorcolonized lignocellulosic substrate) when the contaminated soil was diluted with uncontaminated soil. The role of the fungal inoculum versus indigenous microorganisms in the PCP degradation was not completely clarified, but complete mineralization of PCP was observed only in the presence of the allochthonous fungus. In view of this last result, soil "cells" (final volume approx. 500 L) were designed to carry out exclusively a T. versicolor-based treatment. The contaminated soil (1000 mg kg⁻¹) was diluted with non-contaminated soil and mixed with wood chips obtained from cuttings and shreds. Thereafter, such blended pile of material was mixed with a specific formulation composed of sawdust, cornmeal and starch previously inoculated with T. versicolor to obtain a final ratio of soil: woodchips: fungal inoculum of 40: 20: 40 or 60: 20: 20, respectively. After a rapid decline in PCP concentration within the first 25 weeks of incubation, the degradation rate remarkably decreased. Nonetheless, after 2.5 years, more than 90 % of the original PCP content was removed in both cells (20 or 40 % of fungal inoculum used) indicating that PCP levels at the end of treatment were not statistically different with respect to the differences in the amount of fungal inoculum.

P. ostreatus is one of the best candidates for potential applicability in mycoremediation of soils, therefore several field-scale tests based on the use of such were designed. This WRF was used for the filed-scale remediation of explosivecontaminated soil from the Yorktown Naval Weapons Station (Virginia, USA) where munitions manufacturing process was carried out for decades (Axtell et al. 2000). Two plots (6 cubic yards) of contaminated soil were blended with 3 cubic yards of a substrate mixture previously colonized by *P. ostreatus*. Concentrations of the target explosives, namely TNT, HMX (octogen) and RDX (cyclonite), were noticeably reduced during a 62-day incubation period. Nonetheless, in soil amended only with the substrate mixture, the concentrations of TNT, HMX, and RDX were also reduced substantially during the same period suggesting that the addition of amendments enhanced the growth and activity of indigenous microorganisms and thus sufficient to promote the degradation of these compounds in soil. However, the role of the *P.ostreatus* in this field-scale test was not elucidated.

Further application of fungal bioaugmentation was evaluated for the remediation of creosote-contaminated soil at a wood-preserving site in West Virginia (Lamar et al. 2002). After a preliminary bench-scale evaluation of the degradation capabilities of two WRFs, namely *P. ostreatus* and *I. lacteus*, *P. ostreatus* from a commercial spawn provider was selected to scale up the process. Two pilot-scale biocells comprising the contaminated soil, a sterile substrate (wood splinters or wood splinters with sawdust) and *P. ostreatus* spawn were monitored for 276 days. Concentration of all the 16 PAHs was reduced in both biocells below the industrial risk-based level with the exception of benzo[*a*]pyrene (Lamar et al. 2002). However, the involvement of indigenous microorganisms in the degradation process was not assessed.

The influence of *P. ostreatus* mycelia on the degradation of selected PAHs in soil was investigated under field conditions also in the Northern temperate zone (Hestbjerg et al. 2003). Homogenized *P. ostreatus* refuse from commercial mushroom production was added to PAH-contaminated soils collected from two sources: a former shipyard and coal tar storage from an asphalt factory. Treatments (soil control, soil mixed with autoclaved sawdust substrate and soil mixed with *P. ostreatus* refuse) were set up in concrete cylinders for both soils. In the case of the soil from the coal tar storage, the addition of the oyster mushroom significantly enhanced the degradation rate of 4-ring PAHs compared to the rate in either soil control or biostimulated cylinder, while 5- and 6-ring PAHs were only slightly degraded and no significant difference was observed between the two treatments. On the contrary, the growth and the activity of *P. ostreatus* were completely prevented when inoculated in the other soil, although the factors that resulted in its inefficacy were not clarified.

8.6 Mycoremediation of Soils: Opportunities and Pitfalls⁴

As it was evidenced in the previous sections, there is no doubt that both LFs and NLFs are potent biological tools for the degradation of persistent soil organopollutants and other emerging water MPs. Considering the soil compartment, fungal inoculants were successfully used since the 1980s for remediation studies at laboratory scale but only a limited number of field-scale trials, which were attempted in the past two decades, showed remarkable limitations with regard to the practical application of technologies based on the use of LFs. As a consequence, all the attempts to promote soil mycoremediation on the market and propose it as a valuable on-site bioremediation option have failed (Šašek 2003; Baldrian 2008).

The reasons that lie behind this failure are diverse, as it was already observed by several authors. The first and most important is, without any doubt, the competition between introduced fungi and the resident soil microflora. The idea that a single species, in most cases allochthonous to the soil, should bring about the complete restoration of a contaminated matrix is absolutely unrealistic and unsustainable. Fungi, like bacteria and plant roots introduced into the soil, are influenced by the type and activity of other resident soil organisms and this has a great influence on their colonization capacity. Moreover, the inoculation support onto which the fungi are immobilized prior to their introduction in non-sterile soil (e.g., straw, hay, corn cobs, seeds and seeds husks, wood chips or shavings, bark, etc.) represents a source of nutrients for the autochthonous soil microbiota, this generating divergent effects: an ensuing positive impact on bioremediation efficiency as has been reported in some cases (Lang et al. 2000; Steffen et al. 2007; Federici et al. 2012) and

⁴Additional information on using fungi and mycoaugmented compost to treat polyaromatic hydrocarbon can be found in Chap. 1—*Fungi in composting*.

growth-inhibition and mycophagy in other circumstances (de Boer and van der Wal 2008; Baldrian 2008).

The strict growth conditions required by most white rot fungi represent another significant constraint for the application of fungal technologies at field-scale. For example, *P. chrysosporium* requires high temperature to grow (37 °C) and to produce LEs (30 °C) making its application inadequate under actual environmental conditions (i.e., due to daily and seasonal fluctuations of temperatures) (Hestbjerg et al. 2003). On the other hand, several studies demonstrated that *P. ostreatus* was less affected by temperature and remained active in the degradation of organic pollutants even at very low temperatures (up to 8 °C) (Eggen and Sveum 1999; Lang et al. 2000; Hestbjerg et al. 2001). Moreover, in contrast to *P. chrysosporium* and other white rot fungi such as *D. squalens*, *Pleurotus* sp.was less affected by the presence of soil organisms and being highly competitive with soil microbiota, was more successful at colonizing the contaminated matrix (in der Wiesche et al. 1996; Lang et al. 1997, 1998).

One of the parameters which deeply influence the success of bioremediation application is the bioavailability of contaminants. In turn, this parameter depends on soil organic matter content, texture (e.g., percentage of clay minerals), structure (e.g., peds size, microporosity, etc.) and hydrophobicity of the contaminants. It has been claimed several times that biodegradation hardly ever reaches the complete removal of POPs, for example PAHs and PCBs, this being particularly valid in the case of historically contaminated matrices with high proportion of non-bioavailable compounds. It should be borne in mind that thorough extractions of lipophilic contaminants under harsh conditions that allow the quantification of total contaminant load in a defined matrix (soil) would also include the portion of "aged" pollutants tightly bound to soil components which are inaccessible to microbes in reality. Therefore, the concept of contaminant bioavailability is more readily accepted by decision makers and regulatory organizations (Naidu et al. 2013). Several authors in fact assert that bioavailability should be the underlying basis for risk assessment and in setting the remediation goals at contaminated sites (Latawiec et al. 2011; Naidu et al. 2013). In view of this, establishing contaminant bioavailability and careful testing of the treatability of contaminated matrices prior to field-scale application might help to clarify the feasibility of certain bioremediation interventions. Moreover, accurate compound-specific and ecotoxicological analyses (during and after mycoremediation trials) can help to assess whether the oxidized and more water-soluble derivatives are likely to exert a higher toxicity than parent molecules themselves, or if the residual portion of contaminants that has been immobilized in the soil humus, is inaccessible. In case polar metabolites are formed, as in the case of oxidized high molecular weight (HMW)-PAHs, it is of utmost importance to identify the members of the bacterial community which are able to cooperate with fungi and to consider their contribution.

Another critical factor that requires consideration while dealing with mycoremediation approaches is the formulation and the amount of inoculum which can favor an efficient and long-lasting colonization of the soil matrix. Ligninolytic fungi, both white rots and litter decomposers, are not endowed with intrinsic capabilities to grow in soil unless an external substrate is also provided. Therefore, lignocellulose pre-colonized by the fungus constitutes the inoculum/amendment for soil. However, using large amount of lignocellulose-immobilized fungi is not economically feasible and would significantly increase the volume of the soil after treatment. A valid alternative to bypass the high costs associated with the production of fungal inoculum is the reuse of Spent Mushroom Compost (SMC) which is a cheap and readily available source of both fungal mycelia and enzymes (Phan and Sabaratnam 2012). In fact, in recent years, the worldwide market of commercially grown edible fungi (i.e., *P. ostreatus*) has been growing exponentially and spent residues from mushroom industries are still considered as a waste to be disposed. In this respect, *P. ostreatus* refuse from commercial mushroom production was exploited as a source of viable mycelia to remediate contaminated soils under field conditions as reported in the previous section.

8.7 Conclusions

The potential of fungi in the remediation of contaminated matrices (soil, sediments, surface water) were highlighted and the shortcomings that make this technology not suitable yet for large-scale application were also analysed in this chapter.

A deeper understanding of the ecology of fungi in their natural environment and a detailed knowledge of the physiology of mycoremediation process, with specific regard to the condition when fungi come in contact with the recalcitrant organic pollutants, could enable us to take a step forward in the application of fungal-based technology for the treatment of polluted environmental matrices.

In this respect, advances in genomics have triggered a revolution in understanding even the most complex biological systems. Indeed, the composition of microbial community and its dynamics during the fungal colonization of contaminated solid matrices as well as the interactions between exogenously introduced mycelia and resident soil microorganisms can be described in depth by means of innovative molecular biology techniques.

Transcriptomics and proteomics are steadily progressing field of science and their application to study mycoremediation processes could clarify how the fungal gene expression and the production of enzymes involved in the degradation process are regulated in response to the variations of environmental condition (i.e., chemicals/pollutants concentration, physiological and nutritional stress condition, etc.). However, due to some methodological biases and the high costs associated to their applications, the analysis of metatranscriptome and/or metaproteome in contaminated/treated matrices is still limited to a few studies at bench-scale level. In the near future, as soon as these limitations could be surmounted, these approaches might be used as a tool for understanding the real potential of fungal inocula in the clean up of polluted environmental compartments.

Concerning this, mycoremediation cannot be considered as a method of choice nowadays, but it still deserves attention because the combination of fungal treatment with bacteria-based approaches or with phytoremediation could overcome the limitations associated with their stand-alone application. Moreover, despite the failure in the bioaugmentation of allochthonous species in soil, the importance of fungi in some widely accepted bioremediation approaches (e.g., co-composting of polluted matrices, biopiling, etc.) should not be overlooked. In some specific cases, such as low permeability clay soils where conventional (e.g., in situ) technologies are not applicable or ineffective, the mere addition of lignocellulose might represent a valuable alternative to stimulate the growth of resident mycoflora, and, in turn, bacterial populations that could attack the target pollutants.

On the other hand, the application of high redox potential fungal enzymes (laccases, peroxidases and peroxigenases) for the treatment of micropollutantcontaminated wastewaters appears more realistic and feasible than other approaches. In this respect, the development of bioreactors with immobilized/insolubilized biocatalysts appears to be at a technologically mature stage. In the authors' opinion, this is the most promising and likely fungal-derived technology that have a chance to be practically applied in the near future. The work of Gasser et al. (2014), along with a plethora of studies targeting the implementation of tertiary treatments at wastewater treatment plants, reinforces this assertion. Nonetheless, such biocatalyst-based bioreactors should not be viewed exclusively as an end-of-pipe (tertiary) treatment unit at urban WWTP because similar technologies might also be applied to reduce the chemical burden arising from critical point source of MPs contamination, such as chemical and pharmaceutical production plants effluents.

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