Exploiting marine fungal biodiversity for the bioremediation of chlorinated aromatic pollutants and discovery of novel enzymes

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In everyday life, we come across over 60,000 chemicals in the types of consumer products, drugs, pesticides, food additives, fuels and industrial solvents (Das and Dash, 2014). Chlorophenols (CPs) are introduced in the environment as metabolites of herbicides and other chlorinated xenobiotics or through anthropogenic activities as effluent discharge of industrial processes; for instance pulp bleaching, dye manufacturing, water disinfection with chlorine, waste burning and wood waste incineration (El-Naas et al., 2017; Honda and Kannan, 2018). In particular 2,4-dichlorophenol (2,4-DCP) has been widely used as a fungicide, pesticide and wood preservative (Huang et al., 2015), being released in high amounts into the environment (ca 10,000 kg in the US during 2014) according to the United Stated Environmental Protection Agency (US EPA), which listed it as a priority pollutant among other chlorophenols (Honda and Kannan, 2018; Patel and Kumar, 2017). Polychlorinated biphenyls (PCBs) are produced through the fusion of two benzene rings in the presence of chlorine gas. There are 209 different PCB congeners which are considered persistent organic pollutants (POPs) (Nikolaivits et al., 2017). PCBs in wastewaters derive from leaching runoff, leaching from landfills, and improper disposal of chemical waste. Previously disposed capacitors, transformers, inks, lubricants, adhesives, and other PCB-containing products are present in unsecured landfills and currently leach toxic PCB waste into water systems during rain events (Fusi et al., 2017).

Bioremediation is the use of living organisms in order to remove pollutants from soil and water; a method that is considered more cost-effective and environmentally friendly than the conversional techniques (Patel and Kumar, 2017; Ren et al., 2016). Microorganisms – mainly bacteria and fungi – indigenous to the contaminated regions are potential candidates for the task, benefiting from their acquired enzymatic arsenal, aiming to use the contaminants as food, ideally towards their complete mineralization (Srivastava, 2015). Fungi are robust organisms and most of them are usually more tolerant to high concentrations of pollutants compared to bacteria (Srivastava, 2015).

The marine environment is an untapped source of microbial diversity, showing various characteristics valuable for biotechnological applications, including bioremediation (Nikolaivits et al., 2017), especially considering that a great part of the earth's pollution appears in the oceans. An exceptionally under-investigated source of marine biodiversity is the fungal symbionts of invertebrates (e.g. ascidians, cnidarians, and sponges) (Nikolaivits et al., 2017). The mesophotic zone, in particular, is an underexplored marine habitat, probably due to the fact that it is below depths (30-100 m) reached with traditional SCUBA diving techniques. The biodiversity of mesophotic coral systems is considered a potential source of novel symbiotic microorganisms, which can contribute to the enzymatic arsenal of Biocatalysis and specifically biodegradation of recalcitrant pollutants (Nikolaivits et al., 2017).

In the present work, we study the potential of 107 marine-derived symbiotic fungi that were isolated through TASCMAR H2020 project to bioconvert the aromatic chlorinated pollutants 2,4-DCP and PCB29. The metabolites of 2,4-DCP detoxification by the most efficient fungi were elucidated using mass spectrometry and activities of ring-cleaving dioxygenases were measured. Regarding PCB29 bioconversion, enzymatic activities implicated in this process were measured. In both cases, novel enzymes (catechol dioxygenase and laccase) were isolated and biochemically characterized.

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