ELSEVIER

Chemosphere 55 (2004) 487–491

CHEMOSPHERE

www.elsevier.com/locate/chemosphere

Short Communication

Degradation of the antifouling compound Irgarol 1051 by manganese peroxidase from the white rot fungus *Phanerochaete chrysosporium*

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Received 7 April 2003; received in revised form 31 October 2003; accepted 4 November 2003

Abstract

Irgarol 1051 (2-methylthio-4-*tert*-butylamino-6-cyclopropylamino-*s*-triazine), a derivative of *s*-triazine herbicide, is an antifouling compound used as an alternative to organotins. The compound is highly persistent and is known to be biodegraded only by the white rot fungus, *Phanerochaete chrysosporium*. We used partially purified manganese peroxidase (MnP) prepared from *P. chrysosporium* to evaluate its capacity to degrade Irgarol 1051. MnP degraded Irgarol 1051 to two major products, one identified as M1 (identical to GS26575, 2-methylthio-4-*tert*-butylamino-6-amino-*s*-triazine) and the other not identified but with same mass spectrum as M1 and a different ultraviolet spectrum. This report clearly demonstrates that this ligninolytic enzyme is involved in the degradation of Irgarol 1051.

Keywords: Antifouling compound; Biodegradation; Irgarol 1051; Manganese peroxidase; *Phanerochaete chrysosporium*; White rot fungi

1. Introduction

New antifouling compounds are required to protect ship hulls and fishing nets from biofouling, because organotin compounds have become strictly regulated internationally. Currently, approximately 18 compounds are used as antifouling biocides worldwide, and the environmental fates and behaviors of the eight biocides in common use have been reviewed (Thomas, 2001). Of these eight biocides, Irgarol 1051 (2-methylthio-4-*tert*-butylamino-6-cyclopropylamino-*s*-triazine), an analogue of *s*-triazine herbicides, has been used worldwide, and its residues have been detected in many coastal waters, lake waters, and sediments. Irgarol residues are frequently found in seawater along with the degradation product known as M1 (identical to GS26575, 2-methylthio-4-*tert*-butylamino-6-amino-*s*-triazine) because of their high persistence in aquatic systems (Okamura et al., 2000; Thomas et al., 2000; Ferrer and Barcelo, 2001). Three mechanisms of Irgarol degradation have been described to date: biodegradation by the white rot fungus (Liu et al., 1997), mercuric ion-catalyzed hydrolysis (Liu et al., 1999), and photodegradation by sunlight (Okamura et al., 1999). The appearance of M1 as the degradation product of the parent compound occurs in all three pathways.

A previous study of the biodegradation of Irgarol using the white rot fungus *Phanerochaete chrysosporium* suggested that the ligninolytic enzymes of the fungus were not involved but that constitutive enzymes possibly were (Liu et al., 1997). There currently exists great

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0045-6535/$ - see front matter
doi:10.1016/j.chemosphere.2003.11.012