Characterization of 2,2',3-trihydroxybiphenyl dioxygenase, an extradiol dioxygenase from the dibenzofuran- and dibenzo-p-dioxin-degrading bacterium sphingomonas sp. strain RW1
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Characterization of 2,2',3-Trihydroxybiphenyl Dioxygenase, an Extradiol Dioxygenase from the Dibenzo-furan- and Dibenzo-p-Dioxin-Degrading Bacterium *Sphingomonas* sp. Strain RW1

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A key enzyme in the degradation pathways of dibenzo-p-dioxin and dibenzofuran, namely, 2,2',3-trihydroxybiphenyl dioxygenase, which is responsible for meta cleavage of the first aromatic ring, has been genetically and biochemically analyzed. The *dbf* gene of this enzyme has been cloned from a cosmid library of the dibenzo-p-dioxin- and dibenzofuran-degrading bacterium *Sphingomonas* sp. strain RW1 (R. M. Wittich, H. Wilkes, V. Sinnwell, W. Francke, and P. Fortnagel, Appl. Environ. Microbiol. 58:1005–1010, 1992) and sequenced. The amino acid sequence of this enzyme is typical of those of extradiol dioxygenases. This enzyme, which is extremely oxygen labile, was purified anaerobically to apparent homogeneity from an *Escherichia coli* strain that had been engineered to hyperexpress *dbf*. Unlike most extradiol dioxygenases, which have an oligomeric quaternary structure, the 2,2',3-trihydroxybiphenyl dioxygenase is a monomeric protein. Kinetic measurements with the purified enzyme produced similar *K*~m~ values for 2,2',3-trihydroxybiphenyl and 2,3-dihydroxybiphenyl, and both of these compounds exhibited strong substrate inhibition. 2,2',3-Trihydroxydiphenyl ether, catechol, 3-methylecathol, and 4-methylecathol were oxidized less efficiently and 3,4-dihydroxybiphenyl was oxidized considerably less efficiently.

Chlorinated dibenzo-p-dioxins (DBD) and dibenzofurans (DBF) are generated during the commercial production of chloroaromatic compounds as well as the incineration of industrial and domestic wastes. The exceptional toxicity and recalcitrance of these environmental pollutants have generated considerable interest in their possible destruction through microbial degradation, though the considerable efforts invested to isolate organisms with the desired catabolic activities, particularly since the Seveso accident, were signal unsuccessful. Recently, a bacterium, *Sphingomonas* sp. strain RW1 (36), that possesses the capability to completely mineralize DBD and DBF was isolated, which will enable the study of the mechanism of biological breakdown of such substances.

Thus far, studies on DBD and DBF degradation by this strain have revealed that metabolism is initiated by stereospecific dioxygenation of one of the aromatic rings. Following spontaneous chemical conversion of the dihydroxylated intermediates to 2,2',3-trihydroxybiphenyl (a DBF) and its corresponding ether (a DBD), extradiol dioxygenases *meta* cleave the hydroxylated rings (36). The similarity of the pathways raises the question of whether there are one or two sets of enzymes forming one or two pathways for the substrates.

Extradiol (*meta* cleavage) dioxygenases are a family of ferrous iron-containing enzymes that mediate aromatic ring cleavage in a wide variety of aromatic catabolic pathways, including those for naphthalene, benzene, biphenyl, and toluene (11). The pivotal role of these enzymes has been revealed by genetic studies on the TOL pathway, which indicates that its extradiol dioxygenase is a major determinant of substrate specificity of this pathway (27). Another critical aspect of these enzymes is their inhibition by some products (11), e.g., 3-chlorocatechol, which could be formed during the degradation of 4-chlorodibenzo-furan or 1-chlorodibenzo-p-dioxin. Despite their importance, extradiol dioxygenases remain poorly characterized, and to date, no detailed structural information exists for any member of this class of enzymes.

In order to address the question of whether one or two pathways for DBF and DBD exists in strain RW1 and to characterize the crucial *meta* cleavage enzyme(s) of this organism, we have begun to genetically analyze the DBF and DBD phenotypes. We report here the genetic and biochemical characterization of 2,2',3-trihydroxybiphenyl (2,2',3-THB) 1,2-dioxygenase, the second enzyme in the DBD and DBF catabolic pathway.

MATERIALS AND METHODS

Strains, plasmids, and media. *Sphingomonas* sp. strain RW1 was provided by R.-M. Wittich (36) and was grown at 30°C in M9 medium (20) supplemented with 0.1% (wt/vol) DBF (Aldrich) as the sole carbon source. Cloning procedures were performed with *Escherichia coli* CC118 (21). Hyperexpression of *dbf* was carried out with *E. coli* B121(DE3) (32). The cosmid library was infected in *E. coli* DK22 (18) and transformed into *E. coli* S17-1 (29). *E. coli* was routinely grown at 37°C in Luria broth (LB) medium (20) containing the appropriate antibiotics. Plasmids used in this study are described with the appropriate methods. 2,3-Dihydroxybiphenyl (2,3-DHB) for enzymatic tests was obtained from Wako Chemicals GmbH (Neuss, Germany), and 3,4-dihydroxybiphenyl (3,4-DHB) was obtained from Ultra Scientific (North Kingston, R.I.). 2,2',3-THB and 2,2',3-trihydroxydiphenyl ether were kindly provided by R.-M. Wittich.

Library construction and screening. Genomic DNA from cells of a 500-ml culture of *Sphingomonas* sp. strain RW1 was
FIG. 1. Proposed pathways for the degradation of DBD (compound A) and DBF (compound A') by Shingomonas sp. strain RW1 (36). Compounds: B and B', unstable hemiacetal; C, 2,2',3-THB ether; C', 2,2',3-THB; D, 6-(2-hydroxyphenyl)ester of 2-hydroxymuconic acid; D', 2-hydroxy-6-oxo-(2-hydroxyphenyl)-hexa-2,4-dienoic acid; E, salicylic acid; F, catechol.

prepared by standard procedures (3) and partially digested with Sau3A. Fragments between 10 and 30 kb in length were isolated from a sodium chloride gradient and ligated into the broad-host-range cosmid pLAFR3 (30). Recombinant cosmids were packaged in vitro with a packaging kit (Boehringer, Mannheim, Germany) and used for infection of E. coli DK22. The gene bank in DK22 was lysed by heat shock and transformed into E. coli S17-1. The library was screened by plating it on LB agar plates, incubating the plates overnight, and spraying the colonies the following day with a solution of 0.1% 2,3-DHB in 10% acetone-water.

**Sequencing of DNA.** Manipulation of the DNA was performed by standard procedures (20). DNA sequencing was performed by the method of Sanger et al. (28), using the T7 sequencing kit (Pharmacia, Uppsala, Sweden) according to the manufacturer's instructions. Overlapping subclones were generated by Bal 31 exonuclease (New England Biolabs) partial digests. Gel sequences were aligned and assembled with PC/GENE (IntelliGenetics Inc., Mountain View, Calif.). Homology searches were carried out on GENMON (GBF), using the EMBL and SWISS-PROT data bases.

**Hyperexpression of 2,2',3-THB dioxygenase.** The plasmid pT7-5RW, constructed by ligating a 1.4-kb PstI-SalI fragment containing the dbfB gene into the pT7-5 vector (33), was transformed into BL21(DE3). Cells were grown in LB containing 50 µg of ampicillin per ml to an optical density at 600 nm of 1. Expression of the T7 polymerase gene was induced by the addition of 1 mM isopropyl-β-D-thiogalactopyranoside (IPTG). Cells were harvested 3 h after induction.

**Preparation of crude extracts.** Crude extracts were prepared either aerobically and anaerobically at 4°C. Anaerobic procedures and buffer preparations were performed as described below. Cells were harvested by centrifugation for 10 min at 6,000 rpm in a Sorvall GSA rotor. Approximately 43 g (wet
weight) of cells was resuspended in 20 ml of 10 mM Tris–10% acetone, pH 7.5, and disrupted in a French pressure cell (Aminco Corp.) operated at 20,000 lb/in². Cell debris was removed by centrifugation at 60,000 rpm for 45 min (TLA 100.3; Beckman) at 4°C. Protein concentrations were determined by the method of Bradford (6), using bovine serum albumin (BSA) as the standard.

**Protein purification.** Purification of the 2,2′,3-THB dioxygenase was performed under strict anaerobic conditions. All buffers used were made oxygen free by boiling under a stream of nitrogen. The buffers were supplemented with 0.1 mM ferrous ammonium sulfate and 1 mM dithiothreitol and stored under N₂. During the preparation of crude extracts, all manipulations were carried out in the anaerobic chamber (Coy, Ann Arbor, Mich.) or in a N₂ atmosphere. Column chromatography was performed on a Pharmacia LKB Biotechnology fast protein liquid chromatography system in an anaerobic chamber. The chamber was filled with 95% N₂ and 5% H₂. Traces of oxygen were removed by a palladium catalyst. Protein was concentrated in an anaerobic chamber with an Amicon ultrafiltration cell containing a YM10 membrane.

The dioxygenase activity was precipitated from crude extracts by the addition of 1 volume of saturated ammonium sulfate solution in Tris-EDTA buffer (3). The mixture was stirred gently on ice for 30 min. The precipitate was collected by centrifugation at 50,000 rpm (Beckman, Ti 75 rotor) (4°C) under N₂, and redissolved in 20 ml of 50 mM potassium phosphate, pH 7.5. This solution was loaded on a Phenyl Sepharose HiLoad HR 16/10 column equilibrated with 50 mM potassium phosphate–1 M ammonium sulfate, pH 7.5. The enzyme was eluted with a linear gradient of 70 to 100% 50 mM potassium phosphate, pH 7.5. Fractions containing more than 400 U/ml were pooled and loaded onto a Mono Q HR 10/10 column equilibrated with 10 mM Tris–10% isopropanol, pH 7.5. The enzyme was eluted with a linear gradient of 4 to 20% 10 mM Tris–10% isopropanol–1 M sodium chloride, pH 7.5. Active fractions were combined, concentrated, and loaded onto a HiLoad 26/6 Superdex 200 gel filtration column equilibrated with a solution containing 10 mM Tris, 10% isopropanol, and 500 mM NaCl, pH 7.5. Fractions containing activity of more than 130 U/ml were combined and concentrated to a protein concentration of 9.5 mg/ml. 2,2′,3-THB dioxygenase was stored in liquid nitrogen and showed no loss of activity over a period of 4 months.

**NH₂-terminal sequencing.** The NH₂-terminal sequence was determined by automated Edman degradation on an Applied Biosystems model 470A protein sequencer.

**Electrophoresis and gel filtration.** The purity and size of the denatured protein were estimated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) performed on a Bio-Rad MiniProtein II essentially by the method of Laemmli (19). Gels were silver stained with the Bio-Rad (München, Germany) silver stain kit according to the manufacturer’s instructions. The molecular mass of the native protein was estimated by loading samples of purified protein (90 µg in 200 µl) and crude extracts of *Shingomonas* sp. strain RW1 and *E. coli* onto a Superose 6 HR10/30 column equilibrated with a solution containing 10 mM Tris, 0.5 M sodium chloride, and 10% isopropanol, pH 7.5. The following proteins were used as standards: thyroglobulin (669 kDa), ferritin (440 kDa), catalase (232 kDa), aldolase (158 kDa), BSA (67 kDa), ovalbumin (43 kDa), chymotrypsinogen (25 kDa), and ribonuclease A (13.7 kDa). A₂₈₀ and enzymatic activity were used to monitor the column fractions.

**Enzyme assays.** Dioxygenase activity was assayed by monitoring the formation of reaction products on a Beckman DU-70 spectrophotometer equipped with a Haake circulating water bath. The assay was performed in a total volume of 3 ml (pH 7.5, 25°C) containing 50 mM potassium phosphate and 1 µmol of 2,3-DHB. The reaction was initiated by the addition of 10 µl of appropriately diluted protein solution. The enzyme was diluted in anaerobic 50 mM potassium phosphate buffer supplemented with 0.5 mg of BSA, 0.1 mM ferrous ammonium sulfate, and 1 mM dithiothreitol to prevent oxidation. The reaction was monitored by following the production of HOPDA (2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid) at
The deduced amino acid sequence of the open reading frame is shown. The putative Shine-Dalgarno sequence is underlined. The totally conserved amino acids are printed in bold type.

434 nm (extinction coefficient \( [e] = 13.2 \text{ mM}^{-1} \text{ cm}^{-1} \) (pH 7.5). One unit of activity is defined as the amount of enzyme that converts 1 \( \mu \text{mol} \) of substrate per min. Initial velocity determinations were based on three trials.

The pH optimum of the purified 2,2',3-THB dioxygenase was determined over a pH range from 7.0 to 9.0 with extinction coefficients corrected for pH (8). The kinetic constants of 2,3-DHB cleavage by 2,2',3-THB dioxygenase were determined by measuring the initial rate of cleavage over a concentration range of 5 \( \mu \text{mol} \) to 2 mmol. The reaction was initiated with approximately 0.3 \( \mu \text{mol} \) of purified enzyme. Data were fitted to the substrate inhibition equation (1) with MINSQ (Micromath Inc.), a least-squares fitting routine.

The cleavage of catechol (375 nm; \( [e] = 36 \text{ cm}^{2} \text{\mu mol}^{-1} \text{ cm}^{-1} \)), 3-methylecatechol (382 nm; \( [e] = 16.8 \text{ cm}^{2} \text{\mu mol}^{-1} \text{ cm}^{-1} \)), and 4-methylecatechol (388 nm; \( [e] = 31.5 \text{ cm}^{2} \text{\mu mol}^{-1} \text{ cm}^{-1} \)) (35) were assayed in a similar manner, using the wavelengths and extinction coefficients shown in the parentheses.

The rate of cleavage of 2,2',3-THB was monitored at 434 nm. The extinction coefficient of 2'-OH-HOPDA was determined by incubating 50 \( \mu \text{mol} \) of 2,2',3-THB in 3 ml of potassium phosphate buffer containing 1.2 \( \mu \text{mol} \) of dioxygenase. This amount represents a sufficient quantity of enzyme to effect the complete cleavage of THB in less than 1 s. The initial velocity determinations were corrected for the spontaneous hydrolysis of 2'-OH-HOPDA to metabolite M (31). The rate
of hydrolysis of 2'-OH-HOPDA was determined with different concentrations of this compound. The reaction was monitored at 434 nm, and the data were fitted to the appropriate equations. The delay time between the starting of the reaction and the collection of data was measured and used to improve the estimate of the extinction coefficient of 2'-OH-HOPDA.

The cleavage of 2,2',3-trihydroxydiphenyl ether was monitored by monitoring the oxygen consumption during the dioxygenase reaction with an oxygen electrode (Bachhofer, Reutlingen, Germany).

Nucleotide sequence accession number. The nucleotide sequence of the 1.4-kb Psrl-Sall fragment (SPDDBF) was deposited in EMBL under accession number X72850.

RESULTS

Cloning and sequencing of dbfB. Screening of the cosmid library yielded 10 distinct clones that could convert 2,3-DHB to the bright yellow product HOPDA and that were classified according to the restriction patterns of their recombinant plasmids and the substrate specificities of the encoded dioxygenase activities. Four of the clones exhibited the ability to meta cleave 2,2',3-THB. The recombinant cosmids of these clones possessed a common 10-kb HindIII fragment which was subcloned into pUC18, yielding pRW201 (Fig. 2). Further restriction analysis and subcloning of this fragment resulted in the identification of a 1.4-kbp Psrl-Sall fragment that encoded the 2,2',3-THB meta cleavage activity (pRW2015).

Sequencing of this 1.4-kb fragment revealed an 885-bp open reading frame coding for a 32.46-kDa protein (Fig. 3) with an estimated pl of 4.96. The pl determined by electrofocusing of the purified enzyme (see below) was 4.55, a difference which could be due in part to the ferrous iron in the native enzyme. A purine-rich region, 5'-AAGGAGA-3', upstream of the putative start codon showed 100% identity to the Shine-Dalgarno sequences of two other extradiol dioxygenases (17)

and is assumed to be the ribosome binding site. The presence of a promoter on the Psrl-Sall fragment is indicated by the fact that this fragment could be cloned in either orientation with respect to the plac promoter of the pUC vector to give constructs exhibiting 2,2',3-THB dioxygenase activities.

Homology of 2,2',3-THB dioxygenase to other extradiol dioxygenases. No significant nucleotide sequence homologies between dbfB and other genes encoding extradiol dioxygenases were found: 55% homology to the 2,3-DHB dioxygenase of Pseudomonas sp. strain LB400 (15) was the best example. Comparison of amino acid sequences, however, revealed significant homologies (>30% of total identity) to the 2,3-DHB dioxygenases of Pseudomonas sp. strain LB400 (15), Pseudomonas pseudoalcaligenes (10), and Pseudomonas putida KF715 (14) (Table 1). Inclusion of the amino acid sequence of 2,2',3-THB dioxygenase in the alignment of 12 related extradiol dioxygenases performed by Hofer et al. (15) decreased the number of strictly conserved amino acids from 18 to 14. Of these 14 residues, 4 histidines (positions 146, 197, 208, and 241), 1 tyrosine (position 250), and 1 glutamate (position 260) (Fig. 3) are of particular interest, because they could function as ligands to the ferrous iron in the catalytic center.

Hyperexpression of dbfB in E. coli. Several different expression systems and strains were tested for hyperexpression of dbfB. The highest levels of activity were obtained from pT7-5RW in strain BL21 (data not shown). The highest specific activity was found 3 h after induction with IPTG and was approximately 30-fold higher than that of Sphingomonas sp. strain RW1 grown on DBF. SDS-PAGE analysis revealed most of the hyperexpressed protein present as inclusion bodies (data not shown). Attempts to solubilize the inclusion bodies did not yield active protein.

Enzyme purification and biochemical characterization. Purification of 2,2',3-THB dioxygenase in the soluble fraction resulted in an approximately 60-fold increase in the specific activity of the enzyme with a 15% yield. Essential details of the

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* One unit is defined as the amount of protein that converts 1 mmol of 2,3-DHB per min.

TABLE 2. Anaerobic purification of 2,2',3-THB dioxygenase from E. coli BL21(DE3)
purification are summarized in Table 2. The enzyme was purified to greater than 95% homogeneity, as indicated by silver-stained SDS-PAGE analysis (Fig. 4). The protein size was estimated to be about 32 kDa. The first 63 amino acids from the amino terminus, as determined by Edman degradation, were identical to those deduced from the amino acid sequence of dbfB (Fig. 3), except that the first methionine was absent, indicating that this N-terminal residue is posttranscriptionally removed.

The size of the native protein was calculated to be 34 ± 3.4 kDa by gel filtration of the purified protein, 30 ± 3 kDa from crude extracts of the E. coli clone, and 31.3 ± 3 kDa from extracts of Sphingomonas sp. strain RW1. These results indicate that the native enzyme is monomeric. The purified enzyme was observed to form higher-molecular-weight aggregates, corresponding to dimers and hexamers, within an hour of aerobic storage at 0°C. These oligomeric forms of the dioxygenase were considerably less active. Whether this lower activity is a function of the aggregation of the protein or oxidation of the active-site iron is not clear. However, because care was taken to handle the dioxygenase anaerobically and all kinetic measurements were performed within 25 min of thawing the enzyme, we believe that the kinetic parameters reported here reflect the properties of the native, monomeric form of the dioxygenase.

Attempts to purify the enzyme aerobically yielded preparations with specific activities of 0.9 U/mg of protein, which was less than 2 orders of magnitude lower than that of anaerobically purified enzyme (454 U/mg of protein), even with the addition of buffers containing various organic solvents, such as ethanol, glycerol, and acetone, known to stabilize other extradiol dioxygenases. Anaerobic reconstitution of aerobically purified material with dithiothreitol and ferrous ammonium sulfate was possible but could raise the yield only from 0.02% of the initial activity to 0.1%.

Kinetic characterization. At a substrate concentration of 0.33 mM, the pH optimum for the meta cleavage of 2,3-DHB by 2,2',3-THB dioxygenase was determined to be 7.5. All subsequent kinetic measurements were performed at this pH. The $K_m$ of the dioxygenase for 2,3-DHB was determined to be 8.5 ± 2 μM (Table 3). The enzyme displayed strong substrate inhibition ($K_{ss} = 914 ± 30 μM$).

The e at 434 nm of 2'-OH-HOPDA at pH 7.5 was calculated to be $22.4 ± 1.4 \text{mM}^{-1} \text{cm}^{-1}$. The nonenzymatic rate of conversion of 2'-OH-HOPDA to the colorless metabolite M (31) was determined to be first order with respect to 2'-OH-HOPDA over a concentration range of 5 to 200 μM. The half-life was determined to be $10.9 ± 0.08$ s. This rate permitted the estimation of initial velocities of cleavage of 2,2',3-THB by the dioxygenase (Fig. 5). The $K_m$ of the enzyme for this substrate was similar to that observed for 2,3-DHB.

The $K_m$ values of 2,2',3-THB 1,2-dioxygenase for catechol, 3-methylcatechol, and 4-methylcatechol were found to be approximately 1,000-fold higher than those of 2,3-DHB and 2,2',3-THB (Table 3). No substrate inhibition was observed with the monocyclic substrates. Cleavage of 3,4-DHB was observed but occurred too slowly for reliable data to be collected. Cleavage of 2,2',3-trihydroxydiphenyl ether by the purified dioxygenase could be detected by monitoring the oxygen consumption and showed a specific activity of approximately 15% of the specific activity for 2,3-DHB.

### DISCUSSION

Sphingomonas sp. strain RW1 exhibits the interesting properties of degrading DBF and DBD and of cometabolizing...
monochlorinated derivatives thereof. The genetical and biochemical analysis of this catalytic activity will undoubtedly advance efforts to develop biodegradative strategies for this class of serious environmental pollutants. Degradation of both DBF and DBD is initiated by a dioxygenase yielding 2,2',3-THB and 2,2',3-trihydroxydiphenyl ether (7). The following meta-cleavage step is also performed by a single enzyme, the 2,2',3-THB dioxygenase, which was characterized in this study. It seems that the broad growth substrate specificity of the strain reflects not the existence of multiple narrowly specific enzymes, but rather the existence of enzymes with broad substrate specificity.

Inspection of the polypeptide sequence of 2,2',3-THB dioxygenase revealed its primary structure to be that of a typical extradiol dioxygenase. In particular, strong homologies to 2,3-DHB 1,2-dioxygenases from biphenyl-degrading strains were found, which is perhaps not surprising, given the structural relatedness of the substrates of these enzymes. The additional hydroxyl substituent of 2,2',3-THB is present on the other aromatic ring which is not meta cleaved and should thus minimally influence the steric and electronic interactions of the substrate with the enzyme. This is also consistent with the similar $K_m$ values of 2,2',3-THB dioxygenase for 2,2',3-THB and 2,3-DHB (Table 3). Thus, 2,2',3-THB dioxygenase may have been acquired from a biphenyl pathway. Although Sphingomonas sp. strain RWI does not grow on biphenyl, it can be readily adapted to do so within a few generations (36). Whether the dbfB gene product plays a role in this acquired catalytic activity is, however, not known.

Nevertheless, there are several characteristics of 2,2',3-THB dioxygenase which distinguish it from the DHB dioxygenases. First, THB dioxygenase is much more oxygen labile than DHB dioxygenases, and this lability cannot be stabilized by organic solvents. Second, 2,2',3-THB dioxygenase is monomeric. Although another monomeric extradiol dioxygenase has been reported (5), extradiol dioxygenases are generally either tetrameric, as in the case of catechol 2,3-dioxygenases (26, 35), or octameric, as in the case of 2,3-DHB 1,2-dioxygenases (8, 9, 34). The significance of these differences in quaternary structure is not clear.

In the absence of direct evidence of the identity of the amino acid residues that function as endogenous ligands to the iron in the extradiol dioxygenases, sequence homologies can provide a useful hint as to which residues may fulfill this role. Of the 14 strictly conserved residues among the 13 related dioxygenases, 6 residues (4 histidines, 1 tyrosine, and 1 glutamate) have been shown to be involved in iron coordination in other metalloproteins: e.g., the ferrous iron of isopentenil N-synthase has been shown to be coordinated to three histidyl residues and one aspartyl residue (23). Recent studies have suggested that the aspartyl ligand is displaced upon binding of the substrate. Magnetic circular dichroism measurements on catechol 2,3-dioxygenase (22) supported by earlier electron paramagnetic resonance measurements on protocatechuate 4,5-dioxygenase (2) have led to the proposal of an exchangeable coordination position at the ferrous center in these enzymes, which is activated upon substrate binding. It could be that glutamate functions in extradiol dioxygenases in the same manner as aspartate in isopentenil N-synthase and that the iron coordination of these enzymes in the resting state is very similar.

The 3,4-DHB cleaving activity of 2,2',3-THB dioxygenase is interesting. While the catabolism of biphenyl and its chlorinated derivatives (PCBs) is initiated by hydroxylation at positions 2 and 3 in most characterized aerobic biphenyl pathways, Pseudomonas sp. strain LB400 has been shown to hydroxylate some PCB congeners in positions 3 and 4 (24). Since the 2,3-DHB dioxygenase of LB400 cannot cleave 3,4-DHB, the PCB-degrading potential of LB400 might increase if a 3,4-DHB cleaving activity were acquired. While the 3,4-DHB cleaving activity of 2,2',3-THB dioxygenase is not very high, various strategies might be employed to improve this activity. A limiting factor in the rational modification of this enzyme is the lack of three-dimensional structure information, which is currently a problem for all extradiol cleavage enzymes. The relatively small native size of the 2,2',3-THB dioxygenase (32 kDa) presents the possibility of obtaining such information from nuclear magnetic resonance studies.

The availability of more detailed structure-function information on this enzyme would not only facilitate the manipulation of its catalytic properties but also increase greatly our understanding of extradiol dioxygenases in general.

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