Structural Characterization of Pandoraea pnomenusa B-356 Biphenyl Dioxygenase Reveals Features of Potent Polychlorinated Biphenyl-Degrading Enzymes

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Abstract

The oxidative degradation of biphenyl and polychlorinated biphenyls (PCBs) is initiated in Pandoraea pnomenusa B-356 by biphenyl dioxygenase (BPDOB356). BPDOB356, a heterohexameric (αβ)3 Rieske oxygenase (RO), catalyzes the insertion of dioxygen with stereo- and regioselectivity at the 2,3-hydroxyls of biphenyl, and can transform a broad spectrum of PCB congeners. Here we present the X-ray crystal structures of BPDOB356 with and without its substrate biphenyl 1.6-Å resolution for both structures. In both cases, the Fe(II) has five ligands in a square pyramidal configuration: H233 N2, H239 N2, D386 O1 and O2, and a single water molecule. Analysis of the active sites of BPDOB356 and related ROs revealed structural features that likely contribute to the superior PCB-degrading ability of certain BPDOs. First, the active site cavity readily accommodates biphenyl with minimal conformational rearrangement. Second, M231 was predicted to sterically interfere with binding of some PCBs, and substitution of this residue yielded variants that transform 2,2'-dichlorobiphenyl more effectively. Third, in addition to the volume and shape of the active site, residues at the active site entrance also apparently influence substrate preference. Finally, comparison of the conformation of the active site entrance loop among ROs provides a basis for a structure-based classification consistent with a phylogeny derived from amino acid sequence alignments.

Introduction

Polychlorinated biphenyls (PCBs) are among the most pervasive and persistent chlorinated environmental pollutants despite long-term regulation of their manufacture and use [1]. The discovery that many bacterial strains are able to at least partially degrade PCBs has fueled research directed toward improving bioremediation strategies to clean-up contaminated sites. In aerobic bacteria, PCBs are degraded co-metabolically by enzymes of the biphenyl (Bph) pathway [2]. The first four Bph enzymes comprise a typical meta-cleavage pathway involving the initial generation and subsequent ring fission of a catecholic metabolite. Bacterial strains vary widely in their abilities to degrade PCBs. However, the most potent PCB-degrading organisms, exemplified by Burkholderia xenovorans LB400 [3], Rhodococcus jostii RHA1 [4] and Pandoraea pnomenusa B-356 (formerly Comomonas testosteroni B-356 [5]), are able to transform congeners containing up to 7 chloro substituents.

Biphenyl dioxygenase is the first enzyme of the Bph pathway and the major determinant of PCB degradation [2]. Indeed, the reported PCB-degrading abilities of bacterial isolates largely reflect the PCB-transforming potency of their biphenyl dioxygenase. The catalytic component of this enzyme is a Rieske-type oxygenase (RO), which catalyzes the highly regio- and stereoselective insertion of dioxygen into an aromatic ring, activating the latter for subsequent catabolism. In addition to the oxygenase component (BphAE or BPDO), biphenyl dioxygenase incorporates an FAD-containing reductase (BphG) and a “Rieske-type” ferredoxin...
(BphF). With biphenyl as substrate, the reaction product is phenyl-(1R,2S)-cyclohexa-3,4-dienediol or 2,3-dihydroxy-biphenyldiol (Figure 1).

Structural analyses of several ROs, including those of naphthalene dioxygenase (NDO<sub>B.16g4</sub>) [6], BPDO<sub>RHA1</sub> from <i>R. jostii</i> RHA1 [7], and BPDO<sub>B1</sub> from <i>Sphingobium yanoikuyae</i> B1 [8] have provided important insights into the architecture and reactivity of PCB-transforming enzymes. It should be noted that BPDO<sub>B1</sub> degrades naphthalene and phenanthrene in addition to biphenyl [9] and the PCB-degrading properties of <i>R. jostii</i> RHA1 have recently been attributed to another RO produced by the organism [10]. These ROs are heterohexameric proteins consisting of α- and β-subunits. The α-subunits contain two domains: a Rieske ferredoxin domain and a mononuclear Fe(II) catalytic domain. Overall, the αβ protomers are arranged around a 3-fold axis with the α-subunits stacked with the β-subunits. A functionally important consequence of this arrangement is that it places the Rieske domain from one α-subunit against the Fe(II) catalytic domain of an adjacent α-subunit.

Potent PCB-degrading BPDOs have been classified into two types based on their congener preference [11-13]. KF707-type BPDOs preferentially transform double para-substituted congeners, such as 4,4′-dichlorobiphenyl, while LB400-type enzymes preferentially transform ortho- and meta-substituted congeners [14-16]. BPDO<sub>B356</sub> is further distinguished by its ability to dehalogenate some ortho-substituted congeners, and to catalyze the 3,4-dihydroxylation of others, such as 2,5,2′,5′-tetrachlorobiphenyl.

Mondello and coworkers identified four regions in the α-subunit catalytic domain corresponding to BPDO<sub>LB400</sub> residues 239-239, 277, 335-341, and 379 that were proposed to confer substrate specificity for the KF707-type BPDOs [15]. BPDO<sub>B356</sub> from <i>P. putida</i> KF356 was classified as a KF707-type enzyme based on the analysis of its sequence within these regions. However, BPDO<sub>B356</sub> preferentially transforms ortho- and meta-substituted congeners [17]. More recent studies have revealed that BPDO<sub>B356</sub> appears to be an even more potent PCB-degrading enzyme than BPDO<sub>LB400</sub>, and catalyzes the 3,4-dihydroxylation of some congeners [18]. Structural data are clearly required to properly understand the determinants of congener preference and regioselectivity of BPDOs. Moreover, such data will facilitate the directed evolution and protein engineering efforts to augment the PCB-transforming potency of these enzymes [19-21].

We report herein the X-ray crystal structure of BPDO<sub>B356</sub> at 1.5 Å resolution, as well as the 1.6 Å structure of the BPDO<sub>B356</sub>-biphenyl binary complex. Detailed structural analyses in context of the other known RO structures enabled us to identify structural determinants of congener selectivity. One of these determinants was verified using directed mutagenesis to generate a variant BPDO whose activity against biphenyl and 2,2′-dichlorobiphenyl was tested. Overall, these studies provide a structure-based rationale for the PCB-degrading abilities of BPDOs facilitating the further engineering of these enzymes.

**Results**

**Crystallographic refinement and final model**

The final models include the complete β-subunit, but lack the 18 N-terminal residues of the α-subunit, which were never represented in the electron density and were assumed to be present and disordered. All structures were refined to between 1.5 and 1.6 Å resolution with final R<sub>free</sub> values less than 20%. Additional data and statistics are presented in Table 1.

**Quaternary Structure of BPDO and Phylogenetic Analysis**

BPDO<sub>B356</sub> is an αβ heterohexamer, which is similar to previously reported structures of ROs, such as NDO<sub>B.16g4</sub> [6] and Group II contains ROs responsible for hydroxylating nitro-containing aromatics, such as NbzA<sub>B.765</sub> [22]. The heterohexameric ROs have very similar three-dimensional structures with rmsds between 0.7-2.4 Å for the Cα atoms of the α-subunits and between 0.7-1.3 Å for the β-subunits.

The superposition of eight α-subunit crystal structures was used to generate a structure-based alignment profile used to guide the overall alignment of amino acid sequences for 25 homologous ROs. The phylogenetic tree generated using this alignment displays three distinct groups (Figure 3). The available functional data indicate that these groups reflect the substrate specificities of the ROs. For example, Group II contains ROs responsible for hydroxylating nitro-containing aromatics, such as NbzA<sub>B.765</sub> [22] and Group III contains ROs responsible for hydroxylating phthalate, such as PhtA<sub>BDF63</sub> [23].

In Group I, the potent PCB-degrading enzymes BPDO<sub>B356</sub> and BPDO<sub>LB400</sub> cluster together with cumene dioxygenase IP01 (CumDO<sub>IP01</sub>) and are distinct from the cluster of benzene dioxygenases that include BPDO<sub>RHA1</sub>. Our revised classification based on crystal structure-based sequence alignments and reliance on functional data, while similar to the scheme developed by Nam and coworkers, which was based only on sequences [24], adds a new group to their classification.

Whereas our Group I corresponds quite well with their Group IV, our classification divides their Group III into two groups presented as Group II and Group III in Figure 3. More recently, Kweon et al. reported an inclusive classification of Rieske oxygenase systems driven by primary sequence data and encompassing all protein components involved in electron delivery and catalysis [25]. Although the present approach and that used by Kweon et al. are distinctly different, the molecular phylogenies conform: Group I in Figure 3 maps to Type IV of Kweon et al., Group II maps to Type III, and Group III maps to Type V.

**Structure of the β-subunit**

Despite the global similarity of the known β-subunit structures, as demonstrated by the overall low rmsds of 0.7-1.3 Å (Cα atoms), distinctive structural features divide the structures into two categories, similar to those found based on the phylogenetic analysis of the α-subunit; those that resemble NDO<sub>B.16g4</sub> (Group II) and those that resemble BPDO<sub>B356</sub> (Group I). The fold and interactions of the N-terminal residues with a neighboring β-subunit constitute one of the differentiating features. In NDO, these residues form a two-turn α-helix, which interacts with helix 2β (α2<sub>β</sub>) and α3<sub>β</sub> of an adjacent β-subunit (Note: Elements of secondary structure are numbered sequentially with separate lists...
for helices and β strands in each subunit. Subscripts α and β identify the subunit: α2β is the second helix along the chain of the β-subunit. Residues are identified by the one-letter amino acid code with the residue number appended; when necessary, the subunit is indicated by a subscripted α or β. In BPDOB356, the observed residues meander across the outer surface of the central sheet of the neighboring β-subunit, interacting with and covering residues that are solvent-exposed in NDO.

Other differentiating features occur in loops that interact with the α-subunit. The loop connecting strands β1β and β2β packs more extensively against the Rieske domain in NDO9816-4 than in BPDOB356. There is also variation in the loop connecting β5β and β6β, which bends towards α1α in BPDOB356 and away from it in NDO9816-4. The structures of the β-subunits of BPDO_RHA1 and CumDO_IP01 are more similar to BPDOB356, while that of nitrobenzene dioxygenase JS765 (NBDO JS765), polyaromatic hydrocarbon ring-hydroxylating dioxygenase CHY-1 (RHDO CHY-1), BPDOB1, and NDO 12308 are more similar to NDO 9816-4, which is consistent with sequence-based phylogeny based solely on the α-subunit (Figure 3).

The BPDOB356 β-subunit α3β3 loop participates in a web of hydrogen bonds with side chains from α1α including Q384α and D385α, the residues immediately preceding the active site Fe ligand D386α. These interfacial interactions may couple α and β in a way that directly affects the ability of the active site to adjust to different substrates. Compared to BPDOB356, the corresponding loop in NDO 9816-4 is approximately 3.0 Å further away from the α-subunit, is not involved in a similarly extensive hydrogen-bonding network, and might not be expected to exert a similar influence on the adaptations of the active site during catalysis.

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<th>BPDOB356-biphenyl MES buffer</th>
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doi:10.1371/journal.pone.0052550.t001

Figure 2. Ribbon diagram showing the overall structure of BPDOB356. Two orthogonal views showing three α/β protomers arranged around the crystallographic three-fold axis to form the active hexamer. This arrangement allows the Rieske domain (green ribbons) from the tan α-subunit to interact with the catalytic Fe²⁺ (rust sphere) in the adjacent subunit (purple ribbons). All structural graphics were created using Pymol (www.pymol.org).

doi:10.1371/journal.pone.0052550.g002
Thus, variations in interactions at this interface could explain previously reported inconsistencies in substrate-profiling experiments based on limited mutagenesis or subunit exchange to probe the role of the subunit.

Several studies of α-β chimeric enzymes have established that the subunit plays a role in determining substrate specificity in ROs [26–28]. In studies of the BPDO subunit of BPDO B356 has two possible subunit catalytic domains more variable than those of the α-subunits or the β-subunit Rieske domains or the δ-subunit FeS2 cluster serving as an electron donor during the catalytic cycle (Figure 2).

In BPDOB356, the Fe-S cluster is linked to the mononuclear Fe(II) by a hydrogen bonding network comprised of cluster ligand H123 of one α-subunit through D230 to H233 of the adjacent α-subunit by extending its Rieske domain onto the neighboring α-subunit with the Rieske Fe2S2 cluster serving as an electron donor during the catalytic cycle (Figure 2).

The subunit catalytic domains are more variable than those of the α-subunit catalytic domains or the β-subunits, and hexameric RO structures can be subdivided into two groups based on these variable regions, with NDOαβ16, α-BPBDOαβ16, α-NBDODNTF, and NDOαβ16 clustered in one group, and BPDOαβ356, BPDOαβ16, and α-NDOαβ16 constituting the other. The two groups correspond to branches on the phylogenetic tree (Figure 3), even though the structures of the catalytic domains

Figure 3. Unrooted phylogenetic tree obtained from a crystal structure-based sequence alignment of 25 α-subunits of related Rieske Oxygenases. Bootstrap values out of 100 replicates are indicated. The proteins are abbreviated using the gene name and strain as follows: dibenzofuran dioxygenase from Pandoraea promenusa B-356 (BphA356, GenPeptID: AAC45526); Burkholderia xenovorans LB400 (BphA4LB400, GenPeptID: YP_556400); Rhodococcus globularus P6 (BphA1P6, GenPeptID: CAAS6346); Rhodococcus jostii RHA1 (BphA1RHA1, GenPeptID: BAA06868); and Sphingobium yanoikuyae sp. YK3 (DfdA1YK3, GenPeptID: BAC06602); diterpenoid dioxygenase from Pseudomonas arietanaphila BKM (DitA9BKM, GenPeptID: AAD21063); dinitrobenzene dioxygenase from Burkholderia cepacia R34 (DntA3R34, GenPeptID: AAL50021); dibenzox-p-dioxyn dioxygenase from Sphingomonas JS765 (DxnA1JS765, GenPeptID: CAA51365); ethylbenzene dioxygenase from R jostii RHA1 (EbdAaRHA1, GenPeptID: BAC92718); 3-phenylpropionate dioxygenase from E. coli K-12 (HcaE12, GenPeptID: AC803690); naphthalene dioxygenase from Rhodococcus sp. NCIMB 12038 (NarA12038, GenPeptID: AAD28100) and Pseudomonas putida putid 9816-4 (NdoA9816-4, GenPeptID: POA110); nitrobenzene dioxygenase from Comamonas sp. JS765 (NbzA JS765, GenPeptID: AAL76202); polyaromatic hydrocarbon dioxygenase from Mycobacterium vanbaalenii PYR-1 (NdrA1PYR1, GenPeptID: AAF75991, NdrA3PYR1, GenPeptID: AAY8176) and Burkholderia sp. RPO7 (PhnAcRPO7, GenPeptID: AAD09872); phthalate dioxygenase from R. jostii RHA1 (PadAaRHA1, GenPeptID: ABG99212) and Burkholderia sp. DBF63 (PhnAcDBF63, GenPeptID: BAC54156); phenanthrene dioxygenase from Nocardioideas sp. KP7 (PhdA1KP7, GenPeptID: BAA94708) and Sphingomonas sp. CHY1 (PhnAC1CHY1, GenPeptID: CAG17576); and tetratline dioxygenase from Sphingomonas macrogolitabidus TFA (ThnA1TFA, GenPeptID: AAN26443). Proteins for which the crystal structure was used for alignment are indicated in bold text in the figure. doi:10.1371/journal.pone.0052550.g003
are quite similar with catalytically important residues conserved in structurally equivalent positions.

The most dramatic of the structural variations involves residues of low sequence identity (Figure S1) corresponding to 249–262 in BPDOB356, which form the entrance to the active site. Other differences are found in the extended helix (α11a) and the C-terminal region, where NDO9816-4, NBDO JS765, RHDO CHY-1, and BPDOB1 have an extended helical tail.

**Coordination of the Mononuclear Fe**

BPDOB356 was purified anaerobically with Fe(II) in the mononuclear Fe site from the addition of (NH₄)₂Fe(SO₄)₂·6H₂O during purification and crystallization with the crystals being flash-frozen while maintaining anaerobic conditions [17]. Previously, this as isolated BPDOB356 was determined to have an oxidized Rieske cluster [17]. Further, X-ray absorption scans acquired in association with the diffraction experiments indicated an oxidized Rieske cluster prior to data collection and, qualitatively demonstrated X-ray induced reduction after data collection (data not shown). The as isolated mononuclear Fe site in BPDOB356 exhibits square pyramidal coordination by two histidines, a bidentate aspartate, and a water molecule. The BPDOB356 structures demonstrate 2.2 Å bonds to the Nε2 of both H233 and H239, as well as bidentate binding to Oε1 (2.2 Å) and Oε2 (2.4 Å) of D386 (Figure 4). A single water ligand (W1) at a distance of 2.0 Å is observed (Figure 4a).

The coordination sphere of the mononuclear iron is remarkably similar in the BPDOB356:biphenyl complex. As in the substrate-free enzyme, the iron is pentacoordinate and of square pyramidal geometry (Figure 4b). H239 is the axial ligand, and the Fe is displaced toward it out of the basal plane by 0.5 Å. The Fe(II) coordination and geometry is thus similar to a variety of non-RO enzymes that coordinate Fe with histidines and carboxylic acids [31–34].

**Structural Influences on Substrate Preference**

The structural analyses suggest that differences both at the entrance to and within the active site cavity of the α-subunit likely contribute to differences in substrate preferences among ROs. In BPDOB356, access to the mononuclear Fe is via a 20 Å L-shaped tunnel (Figure 5a,c). This entrance is formed by α6 residues 235–237, α7 residue 240, α7-β17a loop residues 253–259, and β24α-α13b loop residue 431a.

Residues analogous to the BPDOB356 loop residues 253–259a are key components of the active site entrance in all ROs. The location and form of key entrance loop residues are similar for BPDOB356 and CumDO IP01, and both correspond to the “loop 1” conformation defined for CumDO IP01 [35]. In contrast, for the ROs clustered with NDO9816-4 [6], the equivalent loop residues have a very different conformation, called “loop 2” by Dong and co-workers [35], where the loop is located at the opposite side of the active site entrance. Thus, different phylogenetic clusters of ROs may use corresponding loop residues differently to regulate access to the active site. Although the entrance residues are disordered in BPDOB1A1, the phylogenetic analysis predicts its association with the “loop 1” cluster, and a surface rendering of BPDOB1A1 (Figure 5c) confirms that its entrance and cavity are more similar to BPDOB356 (Figure 5c) than NDO9816-4 (Figure 5d).

In summary, we predict that the entrance loop favors the “loop 1” conformation in BPDOB356, which form the entrance to the active site. Other differences are found in the extended helix (α11a) and the C-terminal region, where NDO9816-4, NBDO JS765, RHDO CHY-1, and BPDOB1 have an extended helical tail.
NDO$_{9816-4}$ cavity appears relatively flat, consistent with the shape of naphthalene.

For other ROs, the planarity or non-planarity of the substrates is consistent with the architecture of their active sites. The active site of NBDO$_{76705}$ is similar to NDO$_{9816-4}$ and accommodates a planar substrate. On the other hand the active site architecture of CumDO$_{IP01}$ (Figure 5f), which presumably catalyzes the oxidation
of cumene, a molecule distinctly nonplanar although similar in size to nitrobenzene, is similar to that of BPDO B356.

A further comparison of the active sites of BPDO B356 and CumDO IP01 is also of interest. The source bacterial strain for CumDO IP01 can co-metabolize, but not grow on, biphenyl [56]. This preference for cumene versus biphenyl can be explained by the obstruction of the D subsite by residue A321 of CumDO IP01, thereby creating a smaller cavity (Figure 5f) than in BPDO B356 (Figure 5c) with its structurally analogous G319.

Comparison of the active sites of BPDO B356 and BPDO RHAI in substrate free and biphenyl bound states reveals a difference that is likely to be important in the context of ability to process larger substrates and a wide range of PCBs. In the BPDO B356-biphenyl complex, the 2,3-carbons are 4.3 Å from the Fe(II) and the dihedral angle between the two aromatic rings is 112˚ (Figure 4b). In the BPDO RHAI-biphenyl complex the 2,3-carbons are 4.5 Å from the Fe(II) and the dihedral angle is 124˚ [7]. Thus, within experimental error, the position and conformation of the substrate are not distinguishable and likely represent a productive binding mode. However, the adjustments in protein conformation that accompany binding of biphenyl are much less dramatic in BPDO B356 than in BPDO RHAI. In particular, upon binding of biphenyl to BPDO B356, the side chain torsion angles of I283 in the D subsite adjust slightly to move the G81 atom away from biphenyl. In contrast, upon biphenyl binding in BPDO RHAI, the Cz of the analogous residue, L274, shifts about 2 Å to withdraw the side chain from the D subsite. This movement is part of an overall shift of 26 Å to accommodate biphenyl [7]. A requirement for such conformational changes to bind biphenyl may translate to lower reactivity of BPDO RHAI towards substrates larger than biphenyl. This hypothesis is consistent with the placement of BPDO RHAI in a phylogenetic cluster occupied by ROs characterized as benzene transforming enzymes.

As a corollary, the less–restricted active site cavity of BPDO B356 may explain its greater reactivity to a broad spectrum of substituted biphenyls, such as PCB congeners [17,18]. Moreover, the arrangement of residues and overall dimensions of the BPDO B356 active site cavity may provide a structural explanation of why ROs that clustered with BPDO B356 include the well-characterized potent PCB degrading enzymes.

**Mutagenesis and Steady-state Kinetics**

The role of the conserved active site residue M231A on the selectivity of BPDO B356 was probed by site directed mutagenesis. M231A was chosen because of its unique location at the junction of the P and D subsites and the placement of the M231 S6 atom in the plane of the proximal ring of biphenyl and near an ortho carbon atom on that ring. Substitution of a chlorine at this ortho carbon position would result in a steric clash with the M231 S6 atom. Therefore, mutations were chosen to alter the steric limitations of the active site (M231A) as well as the polar influences of residues in the active site (M231T). Steady-state kinetic characterizations of the active site (M231A) as well as the polar influences of residues in the active site (M231T). Substituting M231A with either smaller side chain lowered the apparent specificity of the enzyme for both biphenyl (4- to 6-fold) and 2,2′-dichlorobiphenyl (≈3-fold; Table 2). In the event of unproductive catalytic turnover or uncoupling H2O2 would be generated during the assay and the addition of catalase was used to determine the amount generated. Hydroxylation of biphenyl was well-coupled to O2 consumption in the variants. Interestingly, the transformation of the dichlorobi-
ND048564, NBDO425765, RHDOCHY11, and BPDOB1 from Group II contain no such clear divisions.

The structure of BPDOB356 may illuminate active site structural factors required for potent PCB-degrading ROs in Group I. Although binding of biphenyl to BPDOB356 required only minor adjustments by the protein, biphenyl binding to BPDOHHA1 required extensive conformational changes that expand the active site. For CumDOH71, a constriction of the active site cavity due to sequence variation may dictate a preference for cumene over larger potential substrates, such as biphenyl and PCBs. These observations may explain the reactivity of BPDOB356 with a broad range of recalcitrant PCB congeners on the basis of facility of aromatic substrate binding alone. By extension, our comparative analysis of these active sites provides a structure-based explanation for the reactivity of related potent PCB degrading ROs such as BPDOB480 and BPDOB7707.

For dioxygenases, unhindered binding of the aromatic substrate has determining significance to the binding and activation of the dioxygen substrate. If binding of a particular aromatic substrate challenges the productive binding of dioxygen, the consequence could be increased uncoupling of electron consumption and oxygen activation from the desired reaction. The consequences of a highly uncoupled reaction are highly detrimental and include loss of reducing equivalents with release of reactive oxygen species, inhibition, and suicide inactivation [39].

Finally, as demonstrated by the effect of mutations at M231 on steady state kinetic parameters for the reaction with a representative ortho-chlorinated PCB, 2,2′-dichlorobiphenyl, we also showed that structural alterations of the active site cavity based on the crystal structure can improve the processing of specific PCB congeners. The effects of the M231A and M231T mutations resulted in improvements in turnover number and coupling with the dichloro-substituted substrate, and are consistent with a more active site structural arrangement. This is further supported by a previous study of BPDOB480, where the corresponding Met to Ala conversion resulted in a variant with significantly altered regioselectivity with two substrates, 2,3′-dichlorobiphenyl and 3,4′-dichlorobiphenyl, but the effects on the kinetic parameters and coupling were not reported [40]. Thus, this structural information may contribute to strategies for the engineering of improved bioremediation pathways.

### Materials and Methods

#### Phylogenetic Analysis of Rieske Oxygenase Sequences

Sequences used for the phylogenetic analysis were selected from ROs whose X-ray crystal structures have been determined with additional sequences selected from a subset of related sequences. A structure-based sequence alignment was first accomplished by pair-wise superpositions of proteins of known structure. Additional sequences were added and aligned using CLUSTALW [41]. The final alignment was manually adjusted using JalView [42]. This alignment was input into the PHYLIPI package [43] and PROML was used to calculate the phylogenetic trees. The best tree was obtained using 21 jumbles of the input alignment. In order to obtain bootstrap values, 100 datasets were generated using SEQBOOT; then the best tree was calculated from each dataset using three jumbles. The final consensus tree was calculated using CONSENSE.

#### Protein Purification and Directed Mutagenesis

BPDOB356 and its variants were heterologously produced and purified anaerobically as described previously for the wild-type RO [17]. Directed mutagenesis was performed using the QuikChange protocol (Stratagene) and the following oligonucleotides: 5′-GCAGTTCTGCAGCGAC CGGGTACCCGAGCCGCGG-3′ (M231A mutation) and 5′-GCAGTTCTGCAGCGACAG GT ACCAGCGCGG-3′ (M231T mutation) combined with their reverse complements. PfuI DNA polymerase was used amplify the plasmids following annealing of the primers at 52°C.

#### Crystallization

Crystals were grown by sitting drop vapor diffusion under anaerobic conditions within a N₂ atmosphere glove box (Innovative Technologies, Newburyport, MA). Two protocols were used. Crystallization from a solution containing 100 mM sodium citrate, pH 5.8; 10% v/v 2-propanol, and 24% w/v PEG400 at 20°C was described previously [17]. In the second protocol, protein (36 mg/ml) in 25 mM HEPES, pH 7.3; 2 mM DTT; 10% v/v glycerol; and 0.25 mM ferrous ammonium sulfate was diluted to 7 mg/ml by addition of a solution containing: 25 mM HEPES, pH 7.3; 10% v/v glycerol; 50 mM NaCl; and 0.25 mM ferrous ammonium sulfate. Crystals were obtained via sitting drop vapor diffusion methods by mixing 4 μl of protein solution with 4 μl of a reservoir solution containing: 100 mM MES, pH 6.0; PEG 4000 (18–28% w/v); 3.5 mM ferrous ammonium sulfate; and 16% v/v 2-propanol. In both cases, the best diffracting crystals grew in one to two weeks. The citrate-buffered crystals were typically 0.3 mm × 0.1 mm × 0.1 mm and belonged to the space group type P3 with cell dimensions \( a = 36.5 \text{ Å}, c = 107.0 \text{ Å} \) for the trilpy primitive hexagonal cell. Typical MES-buffered crystals were 0.3 mm × 0.2 mm × 0.2 mm, and belong to the same space group with similar cell dimensions, \( a = 134.6 \text{ Å}, c = 104.6 \text{ Å} \). The structure of the BPDOB356: biphenyl complex was obtained by adding a small amount of biphenyl powder to crystals and incubating for a period of 24 hours before harvesting.

### Table 2. Apparent steady-state kinetic parameters of BPDOB356 wild-type (wt) and variants (M231A and M231T) for biphenyl and 2,2′-dichlorobiphenyl.

<table>
<thead>
<tr>
<th></th>
<th>Biphenyl</th>
<th>2,2′-Dichlorobiphenyl</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( k_m ) (μM)</td>
<td>( k_{cat} ) (s⁻¹)</td>
</tr>
<tr>
<td>WT</td>
<td>6.2 (0.5)</td>
<td>7.3 (0.2)</td>
</tr>
<tr>
<td>M231A</td>
<td>9.4 (1.9)</td>
<td>2.1 (0.1)</td>
</tr>
<tr>
<td>M231T</td>
<td>11.1 (3.1)</td>
<td>2.9 (0.3)</td>
</tr>
</tbody>
</table>

Coupling parameters are given for 2,2′-dichlorobiphenyl only. Standard deviations are given in parenthesis.

These values were reported in [17].

doi:10.1371/journal.pone.0052550.t002
**Table 3. Summary of crystallographic data.**

<table>
<thead>
<tr>
<th></th>
<th>BPDO&lt;sub&gt;b356&lt;/sub&gt; Citrate Buffer</th>
<th>BPDO&lt;sub&gt;b356&lt;/sub&gt; MES Buffer</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Structure Solution</td>
<td>Structure Refinement</td>
</tr>
<tr>
<td>Wavelength (Å)</td>
<td>1.54</td>
<td>1.00</td>
</tr>
<tr>
<td>Data Range</td>
<td>40-2.2</td>
<td>50-1.5</td>
</tr>
<tr>
<td>Space Group</td>
<td>R3</td>
<td>R3</td>
</tr>
<tr>
<td>a, Å</td>
<td>136.5</td>
<td>136.6</td>
</tr>
<tr>
<td>c, Å</td>
<td>106.5</td>
<td>107.2</td>
</tr>
<tr>
<td>Completeness, %</td>
<td>99.4 (94.2)</td>
<td>96.7 (78.0)</td>
</tr>
<tr>
<td>Unique Reflections</td>
<td>74538</td>
<td>114874</td>
</tr>
<tr>
<td>R&lt;sub&gt;free&lt;/sub&gt;, %</td>
<td>4.9 (10.1)</td>
<td>7.1 (12.3)</td>
</tr>
<tr>
<td>Twin Fraction</td>
<td>0.28</td>
<td>0.00</td>
</tr>
<tr>
<td>f/σ</td>
<td>50.1 (24.1)</td>
<td>28.2 (7.4)</td>
</tr>
</tbody>
</table>

Values in parentheses pertain to the outermost shell of data.

Refinement of crystallographic models

Initial models for the structure of the citrate-buffered crystals were refined using the program CNS with automated parameter adjustment and electron density map calculations. Final models of BPDO<sub>b356</sub> and the BPDO<sub>b356</sub>-biphenyl complex for the structure of the MES-buffered crystals were refined using SHELX-97 [53] and REFMAC5 [54], respectively. O [52] was used for model building, electron density evaluation and superposition of models. Anomalous difference electron density maps were used to verify the presence of iron at the active site and to assess its occupancy by comparison to the density observed for iron in the Rieske cluster. Atomic models and structure factors have been deposited in the Protein Data Bank under the PDB IDs 3GZV (BPDO<sub>b356</sub>) and 3GZX (BPDO<sub>b356</sub>-biphenyl complex).

**Steady-state Kinetic and Coupling Measurements**

Enzyme activity was assayed by following O<sub>2</sub> consumption using a computer-interfaced Clark-type polarographic oxygen electrode essentially as described previously [17]. The standard reaction mixture contained 70 mM Fe(SO<sub>4</sub>)<sub>2</sub>(NH<sub>4</sub>)<sub>2</sub>, 280 μM biphenyl, 125 μM NADH, 1.2 μM BphGB356, 2.8 μM BphGLB400, and 0.36 μM BPDOB<sub>b356</sub> in air-saturated 50 mM MES buffer, pH 6.0. Initial velocity measurements were taken using concentrations ranging from 0.9–176 μM 2,2′-dichlorobiphenyl (Note: 2,2′-dichlorobiphenyl is a suspected cancer hazard and as described in the MSDS appropriate personal protection equipment and handling measures were followed). Coupling between O<sub>2</sub> consumption and biphenyl turnover was estimated by adding catalase to the assay 90 s after initiating the reaction. The amount of O<sub>2</sub> released was taken to reflect 50% of the hydrogen peroxide produced.

**Supporting Information**

**Figure S1** Sequence alignment showing low sequence identity in the region that defines the active site entrance to BPDO<sub>b356</sub> (EPS)

**Acknowledgments**

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Conceived and designed the experiments: CC NA PK MC SCS. Analyzed the data: CC

References


