A robust and extracellular heme-containing peroxidase from *Thermobifida fusca* as prototype of a bacterial peroxidase superfamily

Edwin van Bloois · Daniel E. Torres Pazmiño · Remko T. Winter · Marco W. Fraaije

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**Abstract** DyP-type peroxidases comprise a novel superfamily of heme-containing peroxidases which is unrelated to the superfamilies of known peroxidases and of which only a few members have been characterized in some detail. Here, we report the identification and characterization of a DyP-type peroxidase (*Tfu*DyP) from the thermophilic actinomycete *Thermobifida fusca*. Biochemical characterization of the recombinant enzyme showed that it is a monomeric, heme-containing, thermostable, and Tat-dependently exported peroxidase. *Tfu*DyP is not only active as dye-decolorizing peroxidase as it also accepts phenolic compounds and aromatic sulfides. In fact, it is able to catalyze enantioselective sulfoxidations, a type of reaction that has not been reported before for DyP-type peroxidases. Site-directed mutagenesis was used to determine the role of two conserved residues. D242 is crucial for catalysis while H338 represents the proximal heme ligand and is essential for heme incorporation. A genome database analysis revealed that DyP-type peroxidases are frequently found in bacterial genomes while they are extremely rare in other organisms. Most of the bacterial homologs are potential cytosolic enzymes, suggesting metabolic roles different from dye degradation. In conclusion, the detailed biochemical characterization reported here contributes significantly to our understanding of these enzymes and further emphasizes their biotechnological potential.

**Keywords** Peroxidase · Heme · Sulfoxidation · Enantioselective · Dye decolorizing

**Introduction**

Peroxidases (EC 1.11.1.x) represent a large group of oxidoreductases that catalyze the oxidation of substrate molecules using hydrogen peroxide as electron acceptor. The vast majority of peroxidases contain heme as cofactor (Banci 1997). These enzymes are consistently found in eukaryotic and prokaryotic cells and play a key role in important biological processes, such as biosynthesis of lignin, degradation pathways, and host-defense mechanisms (Passardi et al. 2005; Davies et al. 2008). Additionally, the chemical nature of peroxidase-catalyzed reactions, the oxidation of a wide variety of compounds with the help of hydrogen peroxide, has resulted in a wide range of peroxidase-based biotechnological applications. For example, peroxidases are utilized in biobleaching, wastewater treatment, and various analytical biosensors (Regalado et al. 2004).

Peroxidases are commonly subdivided into two superfamilies: the plant peroxidases and the animal peroxidases. The plant peroxidase superfamily also includes evolutionarily related, heme-containing peroxidases from fungi and bacteria and has been further subdivided into three classes based on cellular localization and function (Welinder et al. 1992). Class I plant peroxidases are intracellular peroxidases, including yeast cytochrome *c* peroxidase and chloroplast ascorbate peroxidase. Class II plant peroxidases are extracellular fungal peroxidases, like the lignin peroxidase and manganese peroxidase. Class III plant peroxidases represent extracellular plant peroxidases, such as horseradish peroxidase. The superfamily of animal peroxidases is not sequence-related to the group of plant...
peroxidases. Evolutionary relationships between different mammalian heme-containing peroxidase subclasses are just beginning to emerge (Loughran et al. 2008).

Recently, a novel superfamily of heme-containing peroxidases has been identified: the so-called dye-decolorizing peroxidase (DyP-type) superfamily (Sugano 2009). DyP-type peroxidases are not related in primary sequence, structure, and reaction characteristics to peroxidases belonging to the plant and animal peroxidase superfamilies. DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade homologs in bacteria. For example, DyP was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008). DyP-type peroxidases have been included as a separate superfamily in databases, such as PeroxiBase and Pfam (Passardi et al. 2007; Finn et al. 2008). DyP-type peroxidases were first discovered in fungi and were shown to be capable to degrade a wide range of dyes (Kim and Shoda 1999). This discovery was subsequently followed by the identification of some strains (Finne et al. 2008).

In the present study, we report the identification and characterization of a novel DY-type peroxidase (TfuDyP; accession number Q47KB1) from the thermophilic actinomycete Thermobifida fusca. Heterologous expression of TfuDyP in E. coli confirmed periplasmic export by the Tat system. The monomeric and robust enzyme contains non-covalently bound heme as cofactor, is most active at pH 3.5, is able to convert a large number of compounds, and catalyzes enantioselective sulfoxidations. Furthermore, we have been able to show that the conserved residues D242 and H338 are crucial for proper functioning of this type of peroxidases. In conclusion, the data show that TfuDyP is indeed a bona fide DY-type peroxidase and also represents the first characterized substrate protein of the T. fusca Tat system. Moreover, the detailed biochemical characterization reported here contributes significantly to our understanding of these enzymes.

Materials and methods

Reagents, enzymes, and sera

Restriction enzymes were from Roche Applied Science and New England Biolabs. GC-rich PCR system and Pfu DNA polymerase were from Roche Applied Science and Invitrogen. Enhanced chemiluminescence (ECL) Western-blotting detection reagent was from Amersham Biosciences. Reactive Blue 19 was from Acros Organics. All other chemicals were supplied by Sigma and were of analytical grade. Ni^{2+}–NTA agarose was obtained from Qiagen. Antiserum against the Myc sequence was from Abcam. DsbA and DnaK antisera were kind gifts of H. D. Bernstein and A. Mogk, respectively.

Strains, plasmids, and growth conditions

E. coli strain MC1061 (Casadaban and Cohen 1980) was used for routine cloning and maintenance of all plasmid constructs. This strain was also used for overexpression and purification of TfuDyP and its derivatives. E. coli strain BL1K0 (MC4100 ΔtatC) has been described previously (Bogsch et al. 1998) and was kindly provided by F. Sargent. BL1K0 and its isogenic control strain MC4100 (Casadaban 1976) was used for subcellular localization experiments. Cultures were grown to saturation at 37°C overnight. The following day, overnight cultures were back-diluted 1:100 into fresh media containing 0.2% l-arabinose to induce the expression of TfuDyP or its derivatives and grown to saturation at 37°C. All strains were routinely grown in Luria Bertani medium (LB; per liter, 10 g tryptone, 5 g yeast extract, 5 g NaCl) under aerobic conditions unless indicated otherwise. Where appropriate, ampicillin (100 μg/ml) was added to the culture medium.

The gene encoding TfuDyP was polymerase chain reaction (PCR) amplified from T. fusca genomic DNA thereby removing the original stop codon. The PCR fragment was cloned between the SacI and HindIII restriction sites of pBAD/Myc-His A (Invitrogen), resulting in pBAD/Myc-His A-TfuDyP. TfuDyP242A and TfuDyP338A were obtained by site-directed mutagenesis, using the QuikChange kit (Stratagene) and pBAD/Myc-His A-TfuDyP as template. Nucleotide sequences were verified by DNA sequencing (GATC, Konstanz). Primer sequences are available upon request.

Ni^{2+}–NTA agarose purification of TfuDyP

MC1061 cells expressing TfuDyP or its derivatives were grown in 0.5 L LB medium at 37°C to saturation. Cells were collected by centrifugation (5000×g for 10 min at 4°C) and resuspended in phosphate-buffered saline (PBS). Following addition of lysozyme (0.5 mg/ml), cells were disrupted by sonication. The cellular debris were removed by a short clarifying spin after which the supernatant was subjected to an ultracentrifugation step (100,000×g for 40 min at 4°C) to obtain the soluble fraction (containing the cytoplasmic and periplasmic fraction). The NaCl concentration was adjusted to 0.5 M, imidazole (15 mM) was added, and the samples were incubated with Ni^{2+}–NTA agarose for 120 min at 4°C. The slurry was loaded into a column and washed with buffer...
A (PBS with 0.5 M NaCl) supplemented with 15 mM imidazole followed by buffer A plus 30 mM imidazole. Samples were eluted with buffer A supplemented with 150 mM imidazole. To remove the imidazole and NaCl, the collected enzyme fraction was applied to a pre-equilibrated desalting column (Biorad). To monitor the purification procedure, samples were taken of each fraction and analyzed by sodium dodecyl sulfate-poly acrylamide gel electroforese (SDS-PAGE) and protein staining.

**Cell fractionations**

Cells expressing *Tfu*DyP were grown as described above. Twenty OD<sub>660</sub> units of cells were harvested and fractionated into a spheroplast and periplasmic fraction as described previously (Huber et al. 2005). The cytoplasmic fraction was obtained as follows. After disruption of the spheroplasts by sonication and a brief, clarifying spin, the clarified lysate was centrifuged (100,000×g for 40 min at 4°C), and the supernatant was taken as the cytoplasmic fraction. Subsequently, proteins were precipitated by trichloroacetic acid and analyzed by SDS-PAGE and immunoblotting.

**SDS-PAGE and immunoblotting**

Cellular fractions were normalized on the basis of the OD<sub>660</sub>, and samples of these fractions, containing equal OD<sub>660</sub> units, were analyzed on standard 12% SDS-PAGE gels. Proteins were transferred to nitrocellulose membrane (Amersham Biosciences) using a semidy apparatus from Biorad. Immunodetection was performed using the primary antisera described above, a secondary horseradish peroxidase-coupled antiserum (Rockland) and the ECL system from Amersham Biosciences (according to the instructions of the manufacturer). Proteins were visualized using the Fujifilm LAS-3000 imaging system. For native poly acrylamide gel electrophoresis (PAGE) gel electrophoresis, 3.6 μg of purified enzyme was analyzed on a 7.5% PAGE gel; SDS was omitted from all buffers, and samples were not reduced. Proteins were visualized by protein staining or stained for peroxidase activity, using 1.0 mM DAB and 0.03% H<sub>2</sub>O<sub>2</sub> in 25 mM citrate buffer pH 3.5.

**Enzyme assay and steady-state kinetic parameters**

*Tfu*DyP activity was measured spectrophotometrically (Perkin–Elmer Lambda Bio40) at ambient temperature in 25 mM citrate buffer pH 3.5, containing 35 nM of purified enzyme and 100 μM H<sub>2</sub>O<sub>2</sub>. The oxidation of the following substrates was tested at the indicated wavelength: Reactive Blue 19 (100 μM) at 595 nm (ε = 10 M<sup>-1</sup> cm<sup>-1</sup>), Reactive Blue 4 (100 μM) at 595 nm (ε = 4.2 M<sup>-1</sup> cm<sup>-1</sup>), reactive Black 5 (20 μM) at 597 nm (ε = 37 M<sup>-1</sup> cm<sup>-1</sup>), guaiacol (100 μM) at 465 nm (ε = 26.6 M<sup>-1</sup> cm<sup>-1</sup>), 2,6-dimethoxyphenol (100 μM) at 470 nm (ε = 49.6 M<sup>-1</sup> cm<sup>-1</sup>), veratryl alcohol (100 μM) at 340 nm (ε = 93 M<sup>-1</sup> cm<sup>-1</sup>) and o-phenylenediamine (100 μM) at 420 nm (ε = 31.3 M<sup>-1</sup> cm<sup>-1</sup>). Control reactions were included without enzyme, H<sub>2</sub>O<sub>2</sub>, or both. Conversion of substrates was only observed when both *Tfu*DyP and H<sub>2</sub>O<sub>2</sub> were present. The steady-state kinetic parameters of *Tfu*DyP were determined by analyzing the reactivity of the enzyme at different Reactive Blue 19 or H<sub>2</sub>O<sub>2</sub> concentrations. Data were fitted with Sigmaplot 10 software, using the Michaelis–Menten equation. Catalase activity of *Tfu*DyP in 25 mM citrate buffer pH 3.5 was analyzed spectrophotometrically by following the consumption of H<sub>2</sub>O<sub>2</sub> at 240 nm as described (Yumoto et al. 2000). All experiments were performed in duplicates, and the values obtained were within 10% of each other.

**Influence of pH and temperature on enzyme activity and stability**

The pH optimum of *Tfu*DyP was determined by measuring the Reactive Blue 19-decolorizing activity of the enzyme as described above in 25 mM citrate buffer adjusted to different pH values. To establish the optimum temperature of *Tfu*DyP, the activity towards Reactive Blue 19 was tested at temperatures in the range of 25–65°C. Before adding the enzyme, the assay mixture was equilibrated for 20 min at the appropriate temperature. The influence of the temperature on *Tfu*DyP stability was investigated by incubating 40-μl aliquots of the purified enzyme (19 μM) at ambient temperature, 30°C, 40°C, 50°C, and 60°C. Samples were taken, placed on ice, after which enzyme activity was analyzed as described above.

**Spectral assays**

Absorption spectra of purified *Tfu*DyP or its mutants were recorded on a Perkin–Elmer Lambda Bio40 spectrophotometer at ambient temperature. In reduction experiments, solutions were made anaerobic by flushing the cuvette with argon. Enzyme reduction was achieved by sodium dithionite or H<sub>2</sub>O<sub>2</sub>. The protoheme content was determined by the pyridine ferro-hemochrome method as described previously (Yumoto et al. 2000), and the heme content was calculated on the basis of the extinction coefficient (34.5 M<sup>-1</sup> cm<sup>-1</sup>) of pyridine hemochrome b (Berry and Trumpower 1987).

*Tfu*DyP catalyzed sulfoxidations

The enantioselectivity of *Tfu*DyP in sulfoxidations was determined as follows. Reactions were performed in Pyrex
tubes in a total volume of 1 ml. The reaction mixture typically contained 25 mM citrate buffer pH 3.5, 1 mM H$_2$O$_2$, 2.5 mM substrate, and 8 $\mu$M of $Tfu$DyP. Reactions were incubated for 36 h at 30°C at 200 rpm and were subsequently analyzed as previously described (van Hellemond et al. 2007; Torres Pazmiño et al. 2008).

### Analytical methods

Protein concentrations were determined using the Bradford method with BSA as standard. For enzymatic assays, the protein content was analyzed by Waddell’s method (Wolf 1983). The oligomeric form of $Tfu$DyP was investigated by gel permeation chromatography, using a Workbeads 40 SEC column (Bio-Works). The column was equilibrated with PBS and subsequently calibrated with a set of protein standards (6.5, 13.7, 29, 43, and 75 kDa).

### Sequence analysis

$Tfu$DyP was identified by PSI-BLAST searches of the NCBI bacterial genome sequence database. The presence of a potential Tat-dependent signal sequence was verified, using the TatP server (Bendtsen et al. 2005). Sequence alignment was performed using ClustalX version 2.0 (Larkin et al. 2007) with subsequent manual refinements.

### Results

#### Identification, expression, and verification of Tat-dependent periplasmic export of $Tfu$DyP

Using the protein sequence of Thanatephorus cucumeris Dec1 DyP, a prototype fungal DyP-type peroxidase (Kim and Shoda 1999), PSI-BLAST searches were performed to identify open reading frames (ORFs), encoding putative DyP-type peroxidases. This revealed a large number of ORFs encoding bacterial DyP-type peroxidases while relatively few homologs were found in sequenced genomes of fungi, other eukaryotes, or archaee. The bacterial hits were subsequently analyzed for the presence of signal sequences, and several were found to contain an N-terminal twin-arginine sequence motif which was indicative for a Tat-signal sequence. We chose to focus on a gene that encoded a potential Tat-signal sequence containing DyP-type peroxidase from *T. fusca* ($Tfu$DyP; Fig. 1a). We have shown before that this actinomycete can be a good source for robust enzymes (Fraaije et al. 2005). $Tfu$DyP consists of 430 amino acids with a calculated mass of 46 kDa for the unprocessed precursor protein. Sequence alignment showed that $Tfu$DyP is homologous to the Tat-dependently exported DyP-type peroxidases YwbN from *Bacillus subtilis* and YcdB from *E. coli* with a sequence identity of ~30% (Jongbloed et al. 2004; Sturm et al. 2006). The known fungal DyP-type peroxidases display sequence similarities of ~<20%. The so-called GXXDG motif, which represents a highly conserved cluster of residues in the heme-binding site of DyP-type peroxidases, was readily identified in the sequence of $Tfu$DyP (Sugano 2009) (Fig. 1a).

Next, the gene encoding $Tfu$DyP (including the signal sequence) was PCR-amplified from *T. fusca* genomic DNA and cloned into an arabinose-inducible expression plasmid. To aid in the detection and purification of the recombinant protein, a Myc–His$_6$ bipartite tag preceded by a flexible linker, was attached to the C-terminus of the protein. We first tested whether the *E. coli* Tat system is required for periplasmic export of heterologously expressed $Tfu$DyP. In *E. coli*, the membrane-bound Tat translocase is formed by TatABC subunits and is dedicated to the periplasmic transport of fully folded and often cofactor-containing substrate proteins (Lee et al. 2006). The TatBC subcomplex binds substrate proteins, which is believed to trigger subsequent recruitment of TatA to form the TatABC translocation complex (Lee et al. 2006). Consequently, the absence of TatC results in a block of Tat-dependent export as protein substrates are unable to associate with the receptor complex. The cellular localization of recombinant $Tfu$DyP was studied in wild-type *E. coli* cells and cells of a TatC null strain (ΔTatC). Cells expressing $Tfu$DyP were fractionated into a cytoplasmic and periplasmic fraction. The different subcellular fractions were analyzed by immunoblotting, using the indicated antisera. Figure 1b shows that in wild-type cells $Tfu$DyP is present as two forms (indicated by a closed circle and arrowhead, respectively). The upper band is found predominantly in the cytoplasmic fraction (C), unlike the lower form, which is mainly observed in the periplasmic fraction (P). Therefore, the upper band represents most likely the unprocessed precursor, whereas the lower band corresponds to the mature form. These data clearly show that, in wild-type cells, the precursor form has been exported to the periplasm and processed to the mature form. In the absence of TatC, periplasmic export of $Tfu$DyP is almost completely blocked as the vast majority of the protein is observed in the cytoplasmic fraction. Remarkably, under these conditions, $Tfu$DyP is mainly present as a cytoplasmic, mature-sized species, which may result from degradation of the signal sequence by cytoplasmic proteases as observed previously by us and others (Thomas et al. 2001; Sturm et al. 2006; van Bloois et al. 2009).

As controls to monitor the efficiency of the fractionation procedure, the levels of DnaK and DsbA, which serve as cytoplasmic or periplasmic marker, respectively, were analyzed in the same samples by immunoblotting. The data show that DnaK is restricted to the cytoplasmic fraction and
DsbA is mainly detected in the periplasmic fraction, demonstrating the efficiency of the fractionation procedure. These data show that TfuDyP requires the Tat system for periplasmic export as expected.

Purification of recombinant TfuDyP and spectral characterization of heme cofactor

To enable further biochemical characterization, TfuDyP was heterologously expressed in wild-type E. coli cells and subsequently purified from the soluble fraction (containing the cytoplasmic and periplasmic fraction) by one-step Ni$^{2+}$-NTA agarose chromatography under native conditions. This procedure yielded approximately 3 mg of purified enzyme from 1 L of culture broth. Samples were taken of the cell extract (CE), soluble fraction, containing cytoplasmic and periplasmic proteins, flowthrough (FT), wash steps (W1 and W2), and eluate and subjected to SDS-PAGE analysis followed by protein staining of the gel (Fig. 2a). As observed previously (compare Fig. 1a), TfuDyP is present as two forms in the eluate (indicated by a closed circle and arrowhead, respectively) of which the unprocessed precursor...
sor migrates in the gel at a position corresponding to 45 kDa. This corresponds nicely to the calculated mass of the unprocessed precursor of 46 kDa.

Several oligomeric states of DyP-type peroxidases have been reported, ranging from monomers to hexamers (Ebihara et al. 2005; Sugano et al. 2007; Zubieta et al. 2007b). Gel permeation experiments with purified TfuDyP revealed that this enzyme exists as a monomer in solution (data not shown). All hitherto characterized members of the DyP-type peroxidase family contain non-covalently bound heme as cofactor (Sturm et al. 2006; Sugano et al. 2007; Zubieta et al. 2007a, b). Therefore, we analyzed the spectral properties of recombinant TfuDyP to assess whether this enzyme also contains a heme cofactor. Notably, during purification of TfuDyP, a brown / reddish color of the soluble fraction was observed, which was more pronounced in the eluate, indicating that a chromogenic cofactor is associated with the enzyme. Figure 2b shows the spectral characteristics of purified TfuDyP. A large Soret band was observed at 409 nm together with two small absorbance maxima at 540 and 575 nm. The Reinheitzahl value (the ratio of $A_{409}/A_{280}$) for the purified enzyme was 0.90, which compares favorably with those reported for other DyP-type peroxidases (Kim and Shoda 1999; Sturm et al. 2006; Zubieta et al. 2007b). These data indicate that TfuDyP indeed contains a heme cofactor, which is in an oxidized state. A more detailed analysis of the heme cofactor was performed by determining the spectral properties of the enzyme after pyridine/NaOH treatment. This revealed a pyridine hemochrome spectrum (Fig. 2b inset) which is identical to that of protoheme IX (non-covalently bound heme b) (Berry and Trumpower 1987). From this spectrum, the heme content per mole of TfuDyP was estimated at 0.6, indicating that TfuDyP contains a single heme cofactor. Thus similar to other DyP-type peroxidases, TfuDyP protomers possess a non-covalently bound heme (protoheme IX) as cofactor and appear to be partly apo upon purification (Sturm et al. 2006; Sugano et al. 2007; Zubieta et al. 2007a, b).
Determination of enzymatic activity and substrate specificity

After having established that TfuDyP is a hemoprotein, we further delineated the biochemical characteristics of this enzyme. First, we tested whether TfuDyP can be reduced by dithionite. Anaerobic reduction of the enzyme with sodium dithionite altered the spectral shape significantly. The Soret band decreased and shifted towards 431 nm, and the two peaks at 540 and 575 nm condensed, resulting in a broad peak with a maximum at 560 nm (Fig. 2b). Also, the reactivity of the enzyme with H$_2$O$_2$ and the related observed spectral characteristics are fully in line with typical features of a heme-containing peroxidase.

To probe whether the purified enzyme displays (DyP-type) peroxidase activity, its reactivity towards a subset of well-known peroxidase substrates and anthraquinone and azo dyes was tested (Table 1). The oxidation of the indicated compounds was assayed spectrophotometrically at the appropriate wavelengths in 25 mM citrate buffer (pH 3.5) containing 100 μM H$_2$O$_2$. TfuDyP shows a modest activity towards substrates that are typical substrates for plant peroxidases, such as guaiacol and 2,6-dimethoxyphenol. Additionally, we found that TfuDyP is able to act on veratryl alcohol, o-phenylenediame, and 3,3-diaminobenzidine but not very efficiently (Table 1 and data not shown). The enzyme showed high reactivity towards the anthraquinone dyes, Reactive Blue 19, and Reactive Blue 4, whereas the azo dye Reactive Black 5 was poorly decolorized. The data also show that TfuDyP displays dye-decolorizing activity similar to related fungal and bacterial proteins (Kim and Shoda 1999; Zubieta et al. 2007a). Moreover, no catalase activity was detected under these experimental conditions, indicating that TfuDyP does not function as a catalase-peroxidase (data not shown).

Analysis of catalytic properties and steady-state kinetic parameters

Because the physiological substrate of TfuDyP is not known, we used Reactive Blue 19 as a representative substrate in subsequent experiments because of the high reactivity of the enzyme towards this dye. All DyP-type peroxidases characterized so far exhibit significant peroxidase activity at low pH. To determine the pH profile of TfuDyP, the decolorizing activity of the enzyme was analyzed spectrophotometrically in 25 mM citrate buffer adjusted at different pHs and containing 100 μM H$_2$O$_2$. We found that TfuDyP displayed the best Reactive Blue 19 decolorizing activity at pH 3.5 (Fig. 3a). A similar pH profile has been observed for fungal and bacterial DyP-type peroxidases (Kim and Shoda 1999; Stutzenberger and Lupo 1986; Antoine et al. 1999; Fraaije et al. 2005). After incubation for 2 h at 60°C, the enzyme lost 50% of its original activity, while at 30°C and 40°C, TfuDyP retained its activity after this period. This indicates that TfuDyP is a reasonable thermostable peroxidase.

For Reactive Blue 19 and H$_2$O$_2$, the steady-state kinetic parameters were determined. This revealed that TfuDyP displays a comparable affinity and turnover number for both substrates as $K_m$ values of 29 and 27 μM and $k_{cat}$ values of 10 and 9 s$^{-1}$ were found. The catalytic efficiency ($k_{cat}$/ $K_m$) for Reactive Blue 19 and H$_2$O$_2$ was 345 and 333 s$^{-1}$×mM$^{-1}$, respectively.

Enantioselectivity of TfuDyP

So far, no DyP-type peroxidase has ever been reported to be active with sulfides while (enantioselective) oxidations of sulfides have been extensively studied with plant and animal peroxidases. The enantioselective sulfoxidation of aromatic sulfides by plant peroxidases, such as HRP and LiP, is well established (van Rantwijk and Sheldon 2000; Klibanov 2003; Veitch 2004). To investigate whether TfuDyP is also able to catalyze this type of reaction enantioselectively, the sulfoxidation of several aromatic sulfides was tested followed by analysis of the products on a chiral GC column. All tested sulfides were enantioselectively converted into the corresponding sulfoxides by TfuDyP (Table 2). The best enantioselectivity was obtained with methyl phenyl sulfide, which yielded the (R)-sulfoxide with 61% ee. Notably, this value represents a lower limit as a non-enantioselective background oxidation was also observed. Despite the enantioselective oxidation of the tested aromatic sulfides, the overall conversion was relatively poor, consistent with the observed modest activity of TfuDyP towards relatively small aromatic substrates (Table 1). Nonetheless, the enantioselectivity of TfuDyP also confirms that the observed oxidations are truly enzyme-catalyzed by enantioselective binding of the substrate near the oxidizing heme cofactor.
Identification of enzymatically active forms

*E. coli* YcdB is able to incorporate heme in the cytoplasm prior to translocation across the inner membrane. This indicates that the unprocessed precursor and the periplasmic mature protein are enzymatically active as both contain the heme cofactor (Sturm et al. 2006). To investigate whether the unprocessed precursor and mature form of *Tfu*DyP are enzymatically active, we subjected purified *Tfu*DyP to native gel electrophoresis. Staining of the gel with Coomassie Brilliant Blue (CBB) revealed three protein bands (Fig. 3b). When staining for peroxidase activity using

### Table 1 Enzymatic activity of purified *Tfu*DyP on various dyes and general peroxidase substrates

<table>
<thead>
<tr>
<th>Compound</th>
<th>Structure</th>
<th>Activity (U.mg⁻¹)</th>
<th>Relative activity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reactive Blue 19&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td>4.28</td>
<td>100</td>
</tr>
<tr>
<td>Reactive Blue 4&lt;sup&gt;a&lt;/sup&gt;</td>
<td></td>
<td>1.26</td>
<td>29.5</td>
</tr>
<tr>
<td>Reactive Black 5&lt;sup&gt;b&lt;/sup&gt;</td>
<td></td>
<td>0.06</td>
<td>1.4</td>
</tr>
<tr>
<td>Guaiacol</td>
<td></td>
<td>0.03</td>
<td>0.7</td>
</tr>
<tr>
<td>2,6-Dimethoxyphenol</td>
<td></td>
<td>0.17</td>
<td>4</td>
</tr>
<tr>
<td>Veratryl alcohol</td>
<td></td>
<td>0.01</td>
<td>0.2</td>
</tr>
<tr>
<td>α-Phenylenediamine</td>
<td></td>
<td>0.03</td>
<td>0.7</td>
</tr>
</tbody>
</table>

<sup>a</sup>Anthraquinone dye  
<sup>b</sup>Azo dye  
<sup>c</sup>Activity was calculated as specific activity in U.mg⁻¹ (1U=1 μmol/min)  
<sup>d</sup>Relative activity was defined as activity toward Reactive Blue 19
DAB only two bands appeared (Fig. 3b). The upper band, which only appeared after CBB staining, was not observed after staining for peroxidase activity. Most likely, this band represents the apo-precursor which may have a different conformation due to the absence of heme, explaining its different migration behavior in native gel electrophoresis. DAB staining identified two bands that could be assigned to the unprocessed precursor and mature form after comparison with the CBB stained gel. The peroxidase activity displayed by the unprocessed precursor and mature form of TfuDyP indicate that both forms contain the heme cofactor like YcdB (Sturm et al. 2006).

Role of D242 and H338

The heme-binding site of DyP-type peroxidases contains a cluster of highly conserved residues, which includes the so-called GXXDG motif (Sugano 2009). Structural and biochemical evidence suggests that the aspartate of this motif (D242 in TfuDyP) dictates that DyP-type peroxidases are most active at low pH (Sugano et al. 2007). Furthermore, all DyP-type peroxidases contain a highly conserved histidine residue in the C-terminal domain of the protein (H338 in TfuDyP), which is part of the active site (Sugano 2009). The available structures of DyP, BrDyP, and TyrA show that this histidine residue is an important heme ligand (Sugano et al. 2007; Zubieta et al. 2007a, b). To verify that D242 and H338 are essential for peroxidase activity and/or cofactor binding, site-directed mutagenesis was employed to replace these residues by alanine. The mutant enzymes were purified, and their UV-visible spectra were recorded. Figure 3c clearly shows that the H338A mutant lacks the heme cofactor as the diagnostic Soret band is not observed in contrast to the D242A variant and the wild-type protein. Interestingly, the spectral properties of the D242A mutant are significantly different when compared with the wild-type protein. These spectral changes may reflect structural changes in the heme-binding region of the D242A mutant or altered ligation of the heme iron atom. The mutant enzymes displayed 0.7% (D242A) and 3% (H338A) of the Reactive Blue 19-decolorizing activity of the wild-type protein. These data clearly show that D242 is important for enzymatic activity, and H338 is crucial for proper cofactor assembly.

Discussion

Although DyP-type peroxidases represent a novel superfamily of peroxidases, only a few members have been characterized in some detail (Sugano 2009). Hence, our understanding of these enzymes is limited. In the present study, we have used the available bacterial genome sequence information by searching for proteins with homology to a known fungal DyP-type peroxidase and identified an ORF in the genome of T. fusca encoding a putative DyP-type peroxidase bearing a Tat-signal sequence. Heterologous expression of TfuDyP in E. coli revealed that the protein is transported to the periplasm by the Tat system. Similar to other DyP-type peroxidases, TfuDyP contains non-covalently bound heme (protoheme...
IX) as cofactor; it is most active at low pH and shows high
reactivity towards anthraquinone dyes and a moderate
activity towards standard peroxidase substrates, aromatic
sulfides and azo dyes (Kim and Shoda 1999; Sugano et al.
2000, 2007; Johjima et al. 2003; Sturm et al. 2006; Zubieta
et al. 2007a, b). These data suggest that Tfu DyP is indeed a
bona fide DyP-type peroxidase. Similar to plant peroxi-
dases, Tfu DyP is able to oxidize aromatic sulfides enantio-
selectively, resulting in the corresponding (R)-sulfoxides.
Notably, we show for the first time that a DyP-type
peroxidase is able to catalyze this type of reaction. The
displayed enantioselectivity by Tfu DyP in sulfoxidations
suggest a selective binding of the substrate within the active
site. Moreover, Tfu DyP is quite robust as the enzyme lost
50% of its original activity after 2 h incubation at 60°C.

The most distinguishing features of DyP-type peroxi-
dases are their unique reaction characteristics and structure
(Sugano 2009). The activity of plant peroxidases against
standard peroxidase substrates and azo dyes has been well
documented in contrast to the degradation of anthraquinone
dyes by these enzymes (Burner et al. 2000; Reszka et al.
2001; Stolz 2001; Reszka et al. 2005; Chen 2006).
Conversely, the reported fungal DyP-type peroxidases are
known to be highly active against anthraquinone dyes and
display only modest activity against standard peroxidase
substrates and azo dyes (Kim and Shoda 1999; Sugano et
al. 2000). For Tfu DyP, we have now also established that
sulfides can be oxidized by a DyP-type peroxidase but with
a poor efficiency. These observations reveal a major
difference in substrate acceptance profiles for the different
peroxidase superfamilies. Structurally, DyP-type peroxi-
dases comprise two domains that contain α-helices and
anti-parallel β-sheets, unlike plant peroxidases that are
primarily α-helical proteins. Both domains adopt a unique
ferredoxin-like fold and form an active site crevice with the
heme cofactor sandwiched in between (Banci 1997; Sugano
2009). The molecular basis for the different and comple-
menting substrates profiles for plant and DyP-type perox-
idases most likely stems from their structural differences.

DyP-type peroxidases have been included as a separate
superfamily in databases, such as Peroxibase, Pfam, and
InterPro. The most comprehensive overview of the DyP-type
peroxidase superfamily is offered by the InterPro database.
According to this database, which surveys all available
genome sequences, the DyP superfamily comprises almost
1,000 members of which 881 members are found in bacteria,
11 in cyanobacteria, 39 in fungi, 19 in higher eukaryotes, and
one is unclassified. With regards to the remarkable abun-
dance of DyP-type peroxidases in bacteria, we propose that
the superfamily of DyP-type peroxidases should be renamed
into the superfamily of bacterial peroxidases in analogy and
addition to the superfamilies of plant and animal perox-
idases. Furthermore, DyP-type peroxidases are, according to
PeroxiBase, further subdivided into the phylogenetically
distinct classes A, B, C, and D.

Intriguingly, many of the putative bacterial DyP-type
peroxidases are predicted to be cytoplasmic enzymes
(PeroxiBase class B and C), which suggests that they play
a role in an intracellular metabolic pathway. The exact role
(s) of these cytosolic bacterial peroxidases have to be
established. In contrast, a small group of putative bacterial
DyP-type peroxidases contain a Tat-signal sequence (Per-
oxibase class A), indicating that these enzymes function
outside the cytoplasm and in the case of Tfu DyP extracel-
larly. This would fit in a role of this enzyme in dye
degradation, as for the sequence-related peroxidases in
fungi. Such an activity has not been described before for
this actinomycete but is in line with various reports that
indicate that actinomycetes have the capacity to degrade to
some extent complex molecules, e.g., lignin or lignin-

<table>
<thead>
<tr>
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<th>Structure</th>
<th>Time (h)</th>
<th>ee (%)</th>
<th>Configuration</th>
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<td>61</td>
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<td>R</td>
</tr>
<tr>
<td>Ethyl phenyl sulfide</td>
<td></td>
<td>36</td>
<td>50</td>
<td>R</td>
</tr>
</tbody>
</table>

Table 2: Enantioselective oxidation of aromatic sulfides by Tfu DyP.
derived compounds (Kirby 2006). Thereby, it would represent a bacterial counterpart of the fungal lignin peroxidases. It also complies with the finding that T. fusca harbors many genes that encode for enzymes involved in degradation of aromatic compounds.

The highly conserved heme-binding motif of plant peroxidases is not present in DyP-type peroxidases. Rather, the heme-binding site of DyP-type peroxidases contains a cluster of highly conserved residues, which includes the so-called GXDG motif (Fig. 1a; Sugano 2009). Recently, the importance of the conserved aspartate (D171) in the GXDG motif of a related protein, DyP of T. cucumeris, was investigated. It was found that replacement of aspartate by asparagine abolished enzymatic activity. This is in agreement with the proposed function as an acid–base catalyst in the catalytic mechanism at low pH, as indicated by structural data (Sugano et al. 2007). Consistent with these data, replacement of the aspartate in the GXDG motif of TfuDyP (D242) by alanine inactivated the enzyme but did not interfere with cofactor assembly, indicating that D242 of TfuDyP plays a similar role in the catalytic mechanism as D171 of T. cucumeris DyP.

Sequence alignments have also identified a conserved histidine residue in the N-terminal domain of fungal DyP-type peroxidases, such as H164 in T. cucumeris DyP. H164 was previously assigned as ligand of the heme but recent structural data demonstrated that this residue does not contribute to heme binding (Sugano et al. 2004, 2007). While this residue is not present in bacterial DyP-type peroxidases, all DyP-type peroxidases contain a highly conserved histidine residue in the C-terminal domain of the protein, which is part of the active site. The available structures show that this histidine residue is an important heme ligand and represents the proximal histidine residue (Sugano et al. 2007; Zubieta et al. 2007a, b). However, the role of this residue in heme binding was never experimentally verified. To confirm whether the proximal histidine is indeed required for proper heme binding, we replaced the corresponding residue in TfuDyP, H338 (Fig. 1a), by an alanine. This abrogated heme binding and inactivated the enzyme, suggesting that the conserved H338 is indeed the proximal histidine of TfuDyP and other DyP-type peroxidases.

Taken together, our data show that TfuDyP is a novel member of the growing superfamily of bacterial peroxidases (previously DyP-type peroxidases) and represents the first characterized substrate protein of the T. fusca Tat system. The detailed biochemical characterization of TfuDyP reported here contributes significantly to our understanding of these enzymes and further underscores the biotechnological potential of TfuDyP because: (1) it was obtained mainly as a holoenzyme in contrast to other heterologously expressed bacterial DyP-type peroxidases (Zubieta et al. 2007a, b), (2) the enzyme appears to be robust, and (3) it accepts a broad range of substrates. Thereby, it is a promising alternative for other peroxidases, such as HRP, which are notoriously difficult to express in, e.g., E. coli. In addition, TfuDyP seems a good candidate for whole-cell biotransformations as it is transported to the E. coli periplasm, which increases its substrate accessibility as most substrates are able to enter the periplasm in contrast to the cytoplasm (Chen 2007).

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