The biosynthesis of rebeccamycin, an antitumor compound, involves the remarkable eight-electron oxidation of chlorinated chromopyrrolic acid. Although one rebeccamycin biosynthetic enzyme is capable of generating low levels of the eight-electron oxidation product on its own, a second protein, RebC, is required to accelerate product formation and eliminate side reactions. However, the mode of action of RebC was largely unknown. Using crystallography, we have determined a likely function for RebC as a flavin hydroxylase, captured two snapshots of its dynamic catalytic cycle, and trapped a reactive molecule, a putative substrate, in its binding pocket. These studies strongly suggest that the role of RebC is to sequester a reactive intermediate produced by its partner protein and to react with it enzymatically, preventing its conversion to a suite of degradation products that includes, at low levels, the desired product.

Results

Resemblance to Flavin Hydroxylases. RebC is a monomer with three distinct domains [Fig. 2 a and b and supporting information (SI) Fig. 6]. Domain I (residues 1–72, 104–190, and 279–354, in red), which binds the cofactor flavin adenine dinucleotide (FAD), is intertwined through four loops and one helix with domain II (residues 73–103, 191–278, and 355–398, in blue), which forms the base of a substrate-binding pocket. Domain III (residues 399–529, in green) is connected via an extended loop (residues 399–423) to domain II (residues 39–429) to domain III. This distance is from the active site, exhibits a typical thioredoxin fold (11), but lacks conserved cysteines and is of unknown function.

RebC exhibits overall structural homology to three proteins: phenol hydroxylase (12) (RMSD of 1.52 Å for 281 Cα carbon pairs), meta-hydroxybenzoate hydroxylase (13) (RMSD of 1.50 Å for 264 Cα carbon pairs), and para-hydroxybenzoate hydroxylase (14) (RMSD of 1.72 Å for 248 Cα carbon pairs) [Fig. 2 c; SI Fig. 7]. Structurally homologous residues are primarily located in domains I and III, with only 49 residues of domain II having structural homology to any Ca carbons of the three structural homologues. Each of these three homologues catalyze flavin-mediated hydroxylations on the ortho position of electron-rich phenol derivatives (SI Fig. 8) (13, 15, 16).

Further, the reduction potential of RebC is −179 ± 3 mV [Fig. 3], a value close to those reported for para-hydroxybenzoate hydroxylase (−163 mV) (17) and phenol hydroxylase (−213 mV) (18). By contrast, the reduction potentials reported for other well


The authors declare no conflict of interest.

Data deposition: The atomic coordinates and structure factors have been deposited in the Protein Data Bank, www.pdb.org (PDB ID codes 2R0C, 2R0G, and 2R0P).

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Crystallographic trapping in the rebeccamycin biosynthetic enzyme RebC

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Rebeccamycin (I, Fig. 1a) is a natural product isolated from Lechevaliera aerocolonigenes (1) and is a prototype for a class of compounds that bind to DNA–topoisomerase I complexes (2), preventing the replication of DNA and thereby acting as antitumor compounds (3). Rebeccamycin is synthesized by the action of eight enzymes, with the overall conversion of L-tryptophan, chloride, molecular oxygen, glucose, and a methyl group to the glycosylated indolocarbazole rebeccamycin (1) (4–9). One step in this pathway is the conversion of chlorinated chromopyrrolic acid (2) to the rebeccamycin aglycone (3) (Fig. 1b). Inclusion of RebC, an FAD-containing protein, in the reaction mixture results in near-exclusive production of arcyriaflavin A (5), 7-hydroxy-K252c (6), and K252c (7) at a 1:7:1 ratio (8) (Fig. 1b).

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studied nonhydroxylase flavoproteins can differ significantly from this value: for instance, lipoamide dehydrogenase (Escherichia coli) has a value of $-317$ mV, yeast glutathione reductase has a value of $-327$ mV (19), and the flavin of plant-type assimilatory nitrate reductase has a value of $-270$ mV (20). The structural homology and the close similarity of the reduction potential of RebC to flavin hydroxylase enzymes suggests that RebC is also a catalyst, functioning to carry out a flavin-mediated hydroxylation reaction on an electron-rich substrate.

**Flavin Shift upon Substrate Binding.** To identify the substrate-binding site of RebC, we soaked crystals with chromopyrrolic acid (4) to give three products, as shown. Addition of RebC leads to near-exclusive formation of arcyriaflavin A (5).

**Melting Helix of RebC.** One major difference between RebC and its structurally homologous flavin-dependent hydroxylases is the size of its putative substrates. Whereas para-hydroxybenzoate hydroxylase is thought to use a third conformation of the flavin (the OPEN conformation) to allow substrate to enter (23), any putative substrates of RebC would be too large to enter the active site through this conformation. Instead, our structural studies have revealed an alternative route for substrate entry. Density for residues 354–363, at the domain I–domain II interface, is absent in the native structure of RebC (Fig. 2a). In both the chromopyrrolic acid (4)- and K252c (7)-soaked structures, density for these residues appears as an extension into the substrate-binding pocket (Fig. 2b). We speculate that residues 354–363 may be a gateway for exchange of substrate and product: the exposure of the substrate-binding site to solvent in the native structure suggests that a substrate could easily enter the substrate-binding pocket when residues 354–363 are a mobile loop. Upon substrate binding, the helix could form, sealing the substrate from solvent and preventing its departure. This melting helix has not been observed in any other structural homologues of RebC and may represent a unique adaptation of this flavin hydroxylase for reaction with larger substrates.

**Identification of Compound Bound.** Although an authentic sample of chromopyrrolic acid (4) was used in our RebC crystal soaks, this compound is not a good fit to the experimental density (SI Fig. 10a–d), suggesting that during the week-long soak at room temperature, the integrity of the chromopyrrolic acid sample may have been compromised. In particular, although the experimental electron density is planar, modeling studies carried out by using the program Gaussian (24) show that the energetically favorable conformation of chromopyrrolic acid would be non-planar, with the indole rings turned out from one another to avoid steric clash. To eliminate difference electron density peaks beyond $\pm 3.0$ e in RebC, the indole rings of chromopyrrolic acid must be refined as planar, with a distance of 2.2 Å or less between the two indole C-2 carbons. Such a distance would imply an energetically destabilizing van der Waals clash between these two close carbon atoms, if this molecule were indeed chromopy-
rrolic acid. Analysis of the substrate-binding site of RebC reveals no mechanism for the stabilization of chromopyrrolic acid in such a high-energy conformation. Further, refining a distance of 1.43 Å (a covalent bond) between these two carbons atoms gives an even better fit to the observed density.

Although HPLC analysis of chromopyrrolic acid, as stored in a −20°C freezer, showed the presence of only one peak, corresponding to chromopyrrolic acid, similar analysis of a chromopyrrolic acid solution left at room temperature for 1 week, as occurs during the crystal-soaking experiment, showed the presence of multiple species including a major peak corresponding to chromopyrrolic acid and minor peaks corresponding to arcyriaflavin A (5), 7-hydroxy-K252c (6), and K252c (7) (SI Fig. 11). These results were confirmed by mass spectrometry and UV/visible spectroscopy (data not shown). The minor peaks indicate that, at low levels, chromopyrrolic acid spontaneously degrades under aerobic conditions at room temperature. This result suggests that the bound molecule in the RebC active site might be an intermediate or product of chromopyrrolic acid degradation rather than chromopyrrolic acid itself. A molecule other than chromopyrrolic acid in the active site is consistent with observed planar density as well as with the long soak times required to obtain electron density.

Fig. 2. RebC structural comparisons. (a) The structure of native RebC is shown with domain I (red), domain II (blue), domain III (green), and a flavin in the OUT conformation (green carbons). Density for residues 354–363 are missing in this structure; two arrows indicate the residues bordering the missing density. (b) The structure of chromopyrrolic acid-soaked RebC, also colored by domain, shows flavin in the IN conformation (green carbons), with $F_o-F_c$ omit density for the molecule captured in the substrate-binding pocket contoured at $\pm 3 \sigma$. The "melting" helix, which traverses from domain I to II, is visible in this structure, and two arrows indicate the residues bordering this helix. (c) Chromopyrrolic acid-soaked RebC (gray) is shown with aligned portions of para-hydroxybenzoate hydroxylase (pale blue, 1DOC, 248 of 394 residues), phenol hydroxylase (pale pink, 1PN0C, 281 of 664 residues), and meta-hydroxybenzoate hydroxylase (pale yellow, 2DKH, 264 of 639 residues). Aligned FAD molecules, which have been observed in the IN conformation, are shown in black (RebC), blue (para-hydroxybenzoate hydroxylase), and red (phenol hydroxylase).

Fig. 3. Reduction potential of RebC. The redox potential of RebC was determined by using the method of Massey (18) using 1-hydroxyphenazine ($E^\circ = -179$ mV) as a reference dye (see SI Methods).

Fig. 4. Mobile flavins. (a) Phenol hydroxylase (PDB ID code 1PN0) (12) has a mobile flavin, as seen from the superimposed structures of the FAD, which is found in both the OUT (light blue carbons) and IN (green carbons) conformations. The substrate phenol is also shown. (b) Two positions of FAD in RebC, manually superimposed from structures of native (light blue carbons, OUT) and chromopyrrolic acid-soaked structures (green carbons, IN), are shown. The 7-carboxy-K252c, which was refined into the chromopyrrolic acid-soaked structure, is shown with green carbons. (c) Cut-away view of FAD (light blue carbons) with a $2F_o-F_c$ omit map at 1σ shows that the flavin in the native structure is OUT, with a hydrogen bond between the isoalloxazine ring and Arg-239. The isoalloxazine ring is stacked between Arg-46 and Trp-276. Because FAD is thought to be reduced by NAD(P)H in the OUT conformation via a reaction at the re face of the isoalloxazine ring (23), Trp-276 would have to move aside for reduction to occur, just as proposed for the structurally homologous residue, Tyr-317 in meta-hydroxybenzoate hydroxylase, which also stacks on the re face of its isoalloxazine ring (13). (d) Cut-away view of FAD (green carbons) in the chromopyrrolic acid-soaked structure shows that the isoalloxazine ring in the IN conformation no longer stacks between Trp-276 and Arg-46, and the interaction with Arg-239 is lost. Arg-46 now interacts with FAD phosphate oxygens, and Arg-239 interacts with bound 7-carboxy-K252c (green carbons). The $2F_o-F_c$ omit map is contoured at 1σ.
Knowing that chromopyrrolic acid underwent spontaneous degradation during the week-long soak, we tried a series of crystallographic refinements to identify whether the molecule bound was a final product of degradation (5, 6, or 7) or an intermediate such as 9–11. Compound (9), which differs from chromopyrrolic acid in having an additional carbon–carbon bond and being planar, is a better fit to the overall density. Refinement of this compound, however, results in significant negative electron difference density at the C-5 carboxylate site, suggesting a substituent smaller than a carboxylate at the C-5 ring carbon. Electron difference density, however, shows an acceptable fit for a carboxylate at the C-7 carbon, when it is positioned out-of-plane to the plane of the indolocarbazole (SI Fig. 10e). We then refined arcyriaflavin A, which has ketone oxygen atoms in place of both carboxylates. The resulting \( F_0 - F_c \) maps show no difference density at the ketone of the C-5 carbonyl, suggesting a substituent smaller than a carboxylate at the C-5 ring carbon. Electron difference density, however, shows an acceptable fit for a carboxylate at the C-7 carbon, when it is positioned out-of-plane to the plane of the indolocarbazole (SI Fig. 10e).

Refinement of a molecule with a ketone at the C-5 carbon and an out-of-plane carboxylate at the C-7 carbon yields no significant electron difference density at either position (SI Fig. 10g). In summary, the experimental density is consistent with a compound containing an aryl–aryl bond between the indole C-2 carbons, with a single oxygen atom as a substituent at the C-5 carbon and a substituent larger than a single oxygen atom, such as an out-of-plane carboxylate, at the C-7 carbon. This density is most consistent with two tautomers (10 and 11) of 7-carboxy-K252c. Allowing the molecule to refine against the experimental electron density gives a short C–C bond (1.3 Å) from the C-7 carbon to the carboxylate, suggesting that tautomer 10 is bound, but also gives out-of-plane carboxylate density, suggesting that tautomer 11 is bound. It is likely that RebC is able to bind both 10 and 11 forms of 7-carboxy-K252c in its active site and that our final, refined 7-carboxy-K252c molecule reflects the presence of both tautomers. Given the observed degradation of chromopyrrolic acid to the products arcyriaflavin A, 7-hydroxy-K252c, and K252c, we postulate that an intermediate such as 7-carboxy-K252c must accumulate during the week-long crystal soak with chromopyrrolic acid and be “captured” by the RebC crystal.

Fig. 5. Substrate-binding site. (a) The 7-carboxy-K252c, which was refined in the chromopyrrolic acid-soaked structure, is bound at the interface of domain I (red) and II (blue), surrounded by a number of hydrophobic side chains, including Phe-227, which shifts conformation. Leu-358 is found on the helix that is disordered in the native structure. A loop (red, residues 303–306) from domain I interacts with one face of 7-carboxy-K252c. Hydrogen-bonding interactions with 7-carboxy-K252c include Glu-396, Arg-230, and Arg-239. An \( F_0 - F_c \) omit map is contoured at 3.0 σ. (b) Binding site of the K252c-soaked structure shows the isoalloxazine ring of flavin (green) locked in an OUT conformation. Trp-276 stacks on the re face of the isoalloxazine ring, Phe-227 is not shifted, and Arg-230 is too far to interact with K252c. Charged residue Glu-396 hydrogen-bonds with the indole nitrogens, and Arg-239 hydrogen-bonds with the FAD, and it does not interact with the substrate. K252c is contoured with an \( F_0 - F_c \) omit map at 3.0 σ. (c) The native structure of RebC shows the exposure of the substrate-binding pocket to solvent with the absence of the melting helix. Additionally, Glu-396 is disordered, Phe-227 is not shifted, and Phe-216 assumes two alternate conformations. FAD (green), as in the K252c-soaked structure, is positioned in the OUT conformation. (d) Cut-away view of 7-carboxy-K252c and FAD-binding site shows that one ring carbon of 7-carboxy-K252c is 5.1 Å from the C4a carbon of FAD. One oxygen of the carboxylate of 7-carboxy-K252c additionally has hydrogen bonds to both Arg-230 and Arg-239.
Table 1. X-ray refinement statistics

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The binding pocket of RebC is ideally suited for a molecule such as 7-carboxy-K252c. There are a series of hydrophobic side-chains to stabilize a poorly water-soluble molecule, and the three charged residues in the binding pocket interact with specific polar groups on the molecule: Arg-230 and Arg-239 are positioned to hydrogen bond with a negatively charged carboxylate (Fig. 5a and d) and may partially stabilize an out-of-plane carboxylate, and Glu-396 is within hydrogen-bonding distance of the two indole nitrogens (Fig. 5a). Interestingly, the side chain of Glu-396 is disordered in the native structure of RebC (Fig. 5c) and becomes ordered in the chromopyrrol acid- and K252c-soaked structures (Fig. 5a and b), suggesting that its role is to stabilize the indole nitrogens upon substrate binding. The arrangement of side chains in the active site may preclude the binding of chromopyrrol acid itself, due to its extended and twisted conformation. This idea is consistent with the previous observation that chromopyrrol acid itself is not turned over by RebC (8), and it is also consistent with our finding that experimental density in the chromopyrrol acid-soaked structure is not due to chromopyrrol acid itself.

Additional support for our assignment of a carboxylate-containing chromopyrrol acid-degradation intermediate, such as 7-carboxy-K252c, as the unknown compound bound in the chromopyrrol acid-soaked crystal, comes from the structure of K252c-soaked RebC (Fig. 5b, SI Fig. 12). Although K252c was found to bind in the same binding pocket as the molecule bound in the chromopyrrol acid-soaked structure (Fig. 5b), the flavin does not shift into the IN conformation in the K252c-soaked structure. Instead, the flavin assumes the OUT conformation seen in the native crystal (Fig. 5c). The flavin is locked into the OUT position through an interaction between the flavin N3 nitrogen and the ketone of K252c (Fig. 5b) as well as through interactions with Arg-239. Hence, the presence of a substrate carboxylate, which K252c lacks, appears to be key to the shift in the position of Arg-230, Arg-239, and the flavin. Structural differences between the two soaked structures rule out the possibility that we have captured K252c itself in our chromopyrrol acid-soaked structure and further predicts that the other two final products of chromopyrrol acid decomposition, 7-hydroxy-K252c and arcyriaflavin A, neither of which have carboxylates, will bind to RebC in a similar fashion as does K252c, with no shift of the flavin.

Flavin–Substrate Interactions. The distance from the C4a carbon of the FAD, the usual site for the generation of a hydroperoxy intermediate, to the C-7 of 7-carboxy-K252c, refined in the chromopyrrol acid-soaked structure, is 5.1 Å (Fig. 5d). Similarly, in phenol hydroxylase, the distance of the C4a of flavin to the site of hydroxylation of substrate is 5.3 Å in the IN conformation (12); in para-hydroxybenzoate hydroxylase, the distance of the C4a of flavin to the site of hydroxylation of the substrate is 4.5 Å in the IN conformation (14). The similar distance found between the C4a of the flavin and the C-7 of 7-carboxy-K252c suggests that the C-7 carbon is indeed the likely site of flavin-mediated hydroxylation by RebC. Furthermore, based on the arrangement of 7-carboxy-K252c relative to the flavin, hydroxylation is likely to occur on the exposed face of 7-carboxy-K252c (Fig. 5d, SI Fig. 13).

The favored binding of a planar molecule in the active site at an appropriate distance for flavin-based hydroxylation to occur suggests that the real substrate of RebC may be a compound such as 7-carboxy-K252c; that is, that 7-carboxy-K252c would have been made by StAP (or RebP) and presented to RebC as its substrate. Studies on synthetically isolated 7-carboxy-K252c have shown that the compound degrades within 30 min in DMSO, resulting in the production of both arcyriaflavin A and 7-hydroxy-K252c (25). Although this synthetic work further suggests that 7-carboxy-K252c is on the pathway to the desired final product, the spontaneous decomposition of 7-carboxy-K252c has precluded direct testing of its ability to serve as a substrate of RebC (25).

Discussion

Previous observations suggested that RebC might be a flavin hydroxylase: RebC contained three sequence motifs found in flavin hydroxylases, RebC-bound FAD, RebC was able to oxidize NAD(P)H in the presence of FAD, and the StAP/RebC tandem reaction showed FAD- and NAD(P)H-dependent effects (8). However, what role a flavin hydroxylase would play in the StAP/RebC-mediated catalysis of chromopyrrol acid (4) to the arcyriaflavin A (5) product was unknown (8). Furthermore, low levels of product (5) formation in a reaction mixture excluding RebC suggested that RebC might not need to have any enzymatic role at all. Finally, if RebC was an enzyme, its substrate was elusive: RebC did not react with chromopyrrol acid (4), arcyriaflavin A (5), 7-hydroxy-K252c (6), K252c (7), or arcyrubin A (8) (8).

Our work has provided strong evidence that RebC is indeed a flavin-dependent hydroxylase. It is a structural homologue of three known flavin aromatic hydroxylases, has a redox potential close to that of two known flavin aromatic hydroxylases, has the characteristic mobile flavin, and binds a putative substrate at an appropriate distance from the flavin C4a-carbon to be hydroxylated by a flavin C4a-hydroperoxide. Together, these findings make a strong case for the role of RebC in the use of flavin-based redox chemistry to hydroxylate a substrate en route to the production of arcyriaflavin A.

Our study further sheds light on the elusive nature of the substrate for RebC. Soaking RebC with chromopyrrol acid for >1 week gave experimental electron density that could not be accounted for by an energetically reasonable conformation of chromopyrrol acid. Therefore, based on electron-density arguments and HPLC studies, we have refined 7-carboxy-K252c in the active site. The ability of RebC crystals to purify this molecule from the suite of chromopyrrol acid degradation products and intermediates present after a week-long soak with chromopyrrol acid suggests that RebC has a unique affinity for this molecule and that 7-carboxy-K252c is likely to be a substrate of RebC.
Finally, our crystallographic study helps to explain the puzzle of why nature uses a two-enzyme system when one enzyme alone, RebP, appears to produce a small amount of the correct product. Our results suggest that RebP does not, in fact, produce the product arcyriaflavin A but, instead, converts chromopyrrolic acid to a reactive intermediate. This intermediate, without RebC present, spontaneously decomposes to a mixture of compounds, including a small quantity of product (25). With RebC present, the highly reactive intermediate is sequestered in the chiefly hydrophobic environment of its active site, where it is acted upon enzymatically, resulting in a single, correct product. Thus, both enzymes catalyze one or more reactions, and RebC is particularly well designed to stably bind a highly reactive intermediate, produced by RebP, on the pathway from chromopyrrolic acid to arcyriaflavin A. Using RebC as a crystallographic trap to purify product arcyriaflavin A but, instead, converts chromopyrrolic acid degradation products, we have provided strong evidence that RebC is a flavin hydroxylase, whose role is to hydroxylate a reactive intermediate, 7-carboxy-K252c, en route to production of the rebeccamycin precursor, arcyriaflavin A.

Methods

Crystallization, Data Collection, Structure Determination and Refinement, Reduction Potential Measurements, HPLC Analysis, and Structural Alignments. Crystallization, data collection, structure determination and refinement, reduction potential measurements, HPLC analysis, and structural alignments were carried out as described in SI Methods, and data refinement and collection statistics are presented in Table 1 and SI Table 2.


Final Protein Models. Crystallized RebC contains 529 residues with an N-terminal 20-amino acid tag. In all structures, the 20 residues of the N-terminal tag are disordered. In the native structure, residue 1, as well as residues 354–363 and residues 417–425, are missing from the density. In this structure, 91.0% of residues are in the most-favored region of a Ramachandran plot, with one residue in the disallowed region. In the K252c-soaked structure, residues 222–224, 246–250, and 417–425, are missing from the density, and 89.8% of residues are in the most-favored region of a Ramachandran plot, with no residues in the disallowed region. In the chromopyrrolic acid-soaked structure, residues 1 and 2, and 426–250 (of Chains A and B) and 418–421 (of Chain B) were not included in the model. In this structure, 88.3% of residues are in the most-favored region of a Ramachandran plot, with one residue in the disallowed region. Chloride ions were added to account for 9 σ positive difference density peaks in the native and K252c-soaked structures. When modeled as water, a positive difference density peak > 4.5 σ was present. Because this density peak is near an arginine, chloride was selected, because it is the only negatively charged ion in crystallization buffers.

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