An Artificial Heme Enzyme for Cyclopropanation Reactions

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Abstract: An artificial heme enzyme was created through self-assembly from hemin and the lactococcal multidrug resistance regulator (LmrR). The crystal structure shows the heme bound inside the hydrophobic pore of the protein, where it appears inaccessible for substrates. However, good catalytic activity and moderate enantioselectivity was observed in an abiological cyclopropanation reaction. We propose that the dynamic nature of the structure of the LmrR protein is key to the observed activity. This was supported by molecular dynamics simulations, which showed transient formation of open conformations that allow the binding of substrates and the formation of pre-catalytic structures.

Engineered heme proteins such as cytochrome P450 enzymes, myoglobin, and cytochrome C have emerged as excellent catalysts for new-to-nature reactions,[3,2] including carbene-transfer reactions such as cyclopropanations,[3–7] olefinations, and[8,9] N–H,[10,11] Si–H,[12] and B–H insertion reactions.[13] These enzymes have proven amenable to optimization by both genetic methods and co-factor replacement.[14–20] A common feature of these (designed) heme enzymes is that they contain a large hydrophobic substrate binding pocket orthogonal to the plane of the heme moiety. Alternatively, significant effort has been devoted to the de novo design of heme proteins, particularly based on 4-helix bundles,[21–25] antibodies, or other proteins,[26,27] yet none of these has found application in catalysis of new-to-nature reactions. A key difference is that these artificial heme enzymes generally do not present a defined binding site suitable for binding the often hydrophobic substrates. Here, we report a novel artificial heme enzyme based on the lactococcal multidrug resistance regulator (LmrR), which is capable of catalyzing abiological enantioselective cyclopropanation reactions. Moreover, we propose that the structural dynamics of the artificial heme enzyme are key to its catalytic activity.

LmrR is a homodimeric protein with a unique and highly dynamic structure that is key to its biological function.[28,29] It presents an unusually large hydrophobic and promiscuous binding pocket at the dimer interface, which has proven to be very suitable for the creation of a novel active site through anchoring of a catalytically active Cu(II) complex inside. The resulting artificial metalloenzymes have been applied successfully in enantioselective Lewis acid catalysis.[30–33] In particular, supramolecular assembly of the artificial metalloenzyme through combination with a Cu(II)-phenanthroline complex proved powerful, giving rise to excellent enantioselectivity in the Friedel–Crafts alkylation reaction.[34] The diversity of reactions catalyzed by LmrR-based artificial enzymes led us to believe that the LmrR scaffold could be extended to other catalyst types, including heme-based catalysts.

The design was based on an LmrR variant that includes a C-terminal strep-tag and has two mutations in the DNA binding domain (K55D and K59Q), which facilitates expression and purification.[11] A second mutant, LmrR_W96A, was prepared to assess the effect of the tryptophan residues in the hydrophobic pore (W96 and W96′, with the prime denoting the dimer related subunit), which are known to play a role in the binding of guest molecules.[20]

The artificial heme enzymes were created through self-assembly by adding iron (III) chloroproporphyrin IX (Hemin) to the corresponding protein LmrR variant in a buffered solution (50 mM KHPO₄, 150 mM NaCl, pH 7; Scheme 1). The interaction of hemin with LmrR was examined by electronic absorption spectroscopy. The visible spectrum of hemin at pH 7.0 (Figure 1a) exhibits a broad Soret band and a weak peak around 610 nm in the Q band region, which is characteristic of a π–π porphyrin dimer that was previously shown to predominate in aqueous hemin solutions at neutral pH.[35,36] Addition of LmrR caused a substantial sharpening in the Soret and Q-band regions, resulting in a spectrum that is similar to that of hemin in organic solvents.[36] Clearly, upon addition of the protein, the dimeric porphyrin structure is disrupted and the hemin is in

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Crystal structure of LmrR

The crystal structure of LmrR in a tetragonal crystal form with one polypeptide chain occupying the asymmetric unit; the functional dimer (here shown in cartoon representation) is formed by a crystallographic dyad. In the electron density maps, the polypeptide chain is well defined, except for the tip region of the β-wing (residues 70–73) and the N- and C-termini (residues 1–4 and 109–111, including the C-terminal stop-tag). These regions show a high degree of disorder and were excluded from the final model. The heme is stacked in between the side chains of W96/W96 (for clarity only one of the alternate heme binding orientations is shown).

K55 and K59 residues reintroduced. The overall conformation of LmrR is similar to that observed in previously published drug-bound complexes. Electron density in the bound heme as a function of added heme concentration. Buffer: 50 mM phosphate buffer/150 mM NaCl, pH 7.0. In all binding modes, the heme is shielded at either side of the heme by the indole ring of W96/W96 and lies at an average distance of around 4 Å from the carbon atoms, thus suggesting cation–π interactions.

The heme, lacking the axial chloride ligand, was modelled in the LmrR crystal structure with four alternate binding modes, differing by rotations around a central axis perpendicular to the plane of the heme, and by a flip of the heme due to the crystallographic 2-fold symmetry (Figure S6). In all binding modes, the heme is shielded at either side of the heme by the indole ring of W96 and W96 and lies at an average distance of around 4 Å from the carbon atoms, thus suggesting cation–π interactions. Further stabilization is provided by van der Waals contacts with hydrophobic residues in the vicinity of the central tryptophan pair, namely, M8, A11, and V15 (and their equivalents from the dimer mate). This structure is unlikely to allow catalysis since the catalytic iron is fully shielded and cannot be accessed by substrates. However, the crystal structure already suggests considerable dynamics in the binding of the heme, which may include catalytically viable conformations. This was supported by molecular dynamics (MD) simulations (see below).

The potential of the artificial heme enzymes in catalysis was examined in the cyclopropanation of o-methoxy styrene (1a) with ethyl diazoacetate (EDA, 2) under anaerobic conditions as the benchmark reaction (Table 1 and Figure S4). In the absence of LmrR, the reaction was sluggish, and diethyl fumarate (4), which results from the dimerization of EDA, was found as the major product (entry 1). The artificial heme enzyme (LmrR concomitant with heme) was assembled in situ by adding 1 mol% of heme to a slight excess (1.1 equiv) of LmrR in previously deoxygenated 50 mM KPi buffer pH 8.0. The LmrR concomitant with heme-catalyzed reaction requires addition of EDA, was found as the major product (entry 1).
sodium dithionate as a reductant to generate the Fe^II^ heme, which is the active complex required for carbene generation. The reaction was started by adding 30 mM of 1a and 10 mM of 2. After 18 h at 4°C, the trans isomer of the cyclopropanation product 3a (trans/cis = 92:8) was obtained as the major product in 25% yield, which corresponds to a total turnover number (TTN) of 247, and with an ee of 17%. (entry 2). The only detectable side product was diethyl fumarate (4), with 28 turnovers. These results clearly show the acceleration and chemoselectivity due to the LmrR scaffold compared to the reactions catalyzed by heme alone under the same conditions.

The role of the protein scaffold was explored further by mutagenesis of residues in and around the hydrophobic pore. In addition to W96 (see above), residues M8, V15, F93, and D100 were mutated to alanine (see the Supporting Information). With the exception of V15A, all mutants showed significant protein enhanced catalytic activity that was comparable or greater than LmrR itself (entry 3–7). Surprisingly, this was also the case for LmrR_W96A, albeit with a complete loss of enantioselectivity. We attribute this to heme-LmrR_W96A association away from the hydrophobic pore, which may result in assemblies that are catalytically active but lack the defined chiral interactions to induce enantioselectivity. A significant increase in activity was observed in case of the mutants D100A and M8A, with the latter also giving rise to the highest enantioselectivity of 44% ee (entry 7).

Further optimization of the reactions conditions was performed with this mutant (Tables S5,6). It was found that a threefold excess of styrene over EDA and pH 7.0 gave the optimal conditions in terms of activity and selectivity (entry 8).

The activity of LmrR_M8A_catalyzed reactions for substrates 1a–c was compared for entry 8. In all cases, the artificial heme enzyme significantly outperformed the free heme cofactor. The enantioselectivity observed ranged from 25% ee in the case of 3c (entry 12) to 51% ee in the case of 3a (entry 8).

The observed catalytic activity and enantioselectivity are difficult to rationalize based on the crystal structure, which shows the catalytic iron center sandwiched between the two tryptophan residues, where it is inaccessible for the substrates. To gain more insight into the origin of the catalytic activity, computational studies were performed.

Calculations were focused on determining the conformational rearrangement required for LmrR_catalyzed atto substrate binding and the reaction to take place. Local and global rearrangements of the protein were assessed for the binding of the heme as well as in presence of the substrates by combining protein–ligand docking, quantum mechanics calculations, and large-scale molecular dynamics simulations.

Protein–ligand dockings of both the heme (5) and its adduct with the carbene intermediate (6; Figure S6) were carried out on LmrR, starting from the LmrR_catalyzed crystal structure. Local rearrangements were assessed by introducing rotameric flexibility for all the amino acids at the dimer interface. For 5 and 6, four binding poses with good predicted affinity (ChemScore values higher than 50 units) were found for both cases (Table S3). They correspond to different orientations of the heme group as a result of rotations around the axis perpendicular to the average plane of the heme passing through the metal. The best docking solutions of LmrR<sub>C</sub> show the heme sandwiched between W96/W96', similar to the crystal structure. However, in the case of the carbene complex (LmrR<sub>C</sub>6), some low-energy solutions present W96' rotated towards the solvent, thus providing space to accommodate the co-substrate (Figure S1 in the Supporting Information). To assess the structural rearrangement of LmrR upon heme binding, the four predicted structures of LmrR<sub>C</sub>5 and LmrR<sub>C</sub>6 were submitted to 100 ns MD simulations.

Cluster analysis shows high stability for the LmrR<sub>C</sub> catalyzed complex (Figure S8), with W96 and W96' generating a hydrophobic patch that sandwiches the heme. Some of the most populated clusters of the LmrR<sub>C</sub>5 system (clusters 1 and 3–6) show high similarity with the crystal structure, with the iron atom inaccessible to solvent (Figure 3a). On the other hand, clusters 0 and 2 (see the Supporting Information for details) show changes in the orientation of the α helix containing W96' (c4) and a flip of the W96' indole towards the outside of the pore (Figure 3b and Figure S10). These predicted conformational changes are in agreement with previous reports in which it was suggested that flexibility in the orientation of α4 is a major contributor to the ability of LmrR to structurally adapt to different drug molecules. These changes in the protein structure are accompanied by a significant displacement of the heme towards the solvent. The result is an opened conformation that has significant free space on the axial face of the heme group. This appears to be of key importance to catalysis, since the iron site becomes accessible to bind the carbene, which allows the reaction occur.

MD simulations of the LmrR<sub>C</sub> catalyzed complex (LmrR<sub>C</sub>6) show that this opened conformation is indeed capable of accommodating the carbene moiety. The simulations further underline the importance of W96' in controlling the accessibility of the heme–carbene complex. With W96' pointing towards the hydrophobic core, the heme–carbene is directed towards the solvent, where it will be accessible for the styrene co-substrate (Figure 3c). Rotation of W96' to the
However, the artificial enzyme exhibits good activity and shows enantioselectivity in catalysis. This is attributed to the dynamic nature of the LmrR-based artificial heme enzyme, involving substantial geometric rearrangement of the heme environment to allow binding of the substrates and their interaction with the heme. Indeed, the MD simulations show that the LmrR–heme complex undergoes significant conformational changes, giving rise to transient open conformations that make it possible to reach a pre-catalytic state, thereby allowing the reaction to proceed.

In conclusion, we have created an artificial heme enzyme based on the protein LmrR, which shows good activity and moderate enantioselectivity in an abiological reaction, that is, the catalytic cyclopropanation of styrenes. This is the first example of organometallic catalysis with an LmrR-based artificial metalloenzyme and thus illustrates the versatility of LmrR as a scaffold for artificial metalloenzymes design. A key finding is that the enzyme is active despite the fact that the crystal structure shows a tightly bound heme that appears inaccessible to substrates. It is proposed that the artificial enzyme can open up to allow formation of precatalytic structures as a result of a dynamic protein–heme assembly. Molecular dynamics studies add support to this hypothesis. This work suggests that dynamics have to be taken into account in the design of artificial enzymes and may be key to achieving catalytic activity.

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Conflict of interest

The authors declare no conflict of interest.

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