Spectroscopic characterization of the coproporphyrin ferrochelatase from *Corynebacterium diphtheriae*

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Heme *b* is an iron porphyrin essential for bacterial pathogens to survive and infect the host. Unlike humans, monoderm (Firmicutes and Actinobacteria) Gram-positive bacteria produce heme *b* by using the coproporphyrin-dependent biosynthesis (CPD) pathway [1]. In the penultimate step of the CPD pathway, the coproporphyrin ferrochelatase (CpfC) catalyzes the insertion of ferrous iron into coproporphyrin III (cpIII), producing iron coproporphyrin III (coproheme). In the final step, the coproheme decarboxylase generates heme *b* by a two-step decarboxylation of the propionate groups at positions 2 and 4 of coproheme, forming vinyl groups [2]. Understanding the biosynthetic path of heme *b* in pathogens is essential for developing mechanism-based therapeutic drugs.

Our group previously investigated the CpfC of the firmicute *L. monocytogenes (Lm)* [3,4]. Here, the UV-vis electronic absorption and resonance Raman (RR) characterization of the wild-type (WT) CpfC from the actinobacterial *C. diphtheriae* (*Cd*CpfC) will be discussed.

Unlike *Lm*, but in common with the human ferrochelatase (fC), *Cd*CpfC contains a [2Fe-2S] cluster, a widespread inorganic iron cofactor whose role in fCs is still under debate. The apoprotein RR spectra are characterized by the bridging and terminal sulfur-iron stretching modes. Since these vibrations are sensitive to the type, configuration, symmetry, and nature of the ligands [5], insights into the structure of the cluster in solution have been obtained.

Moreover, the substrate (cpIII) and product (coproheme) are stabilized inside the active site of the protein by several hydrogen-bond interactions established between polar residues and the propionate groups of the porphyrin ring, in a similar way to *Lm* [3, 4].

Finally, the RR spectra of the CO adducts of the WT and selected variants of CdCpfC complexed with coproheme will be discussed in comparison with those of LmCpfC [6], providing information on the interactions of the distal polar residues with the iron-bound ligand.

References

[1] Dailey HA. et al., Noncanonical coproporphyrin-dependent bacterial heme biosynthesis pathway that does not use protoporphyrin, *Proc. Natl. Acad. Sci USA* (2015); **112**, 2210-2215.

[2] Sebastiani, F. et al., Reaction intermediate rotation during the decarboxylation of coproheme to heme b in *C. diphtheriae*, *Biophys. J.* (2021); **120**, 3600-3614.

[3] Gabler T., Dali A. et al., Substrate specificity and complex stability of coproporphyrin ferrochelatase is governed by hydrogen-bonding interactions of the four propionate groups, *Febs J.* (2022); **289**, 1680-1699.

[4] Dali A. et al., Active site architecture of coproporphyrin ferrochelatase with its physiological substrate coproporphyrin III: propionate interactions and porphyrin core deformation, *Protein Science* (2023); **32**, e453.

[5] Todorovic S. et al., Resonance Raman spectroscopy of Fe-S proteins and their redox properties, *J. Biol. Inorg. Chem.* (2018); **23**, 647-661.

[6] Dali A. et al., "Proximal ligand tunes active site structure and reactivity in bacterial L. monocytogenes coproheme ferrochelatase." Spectrochim. Acta (2024)