Significant Increase of Oxidase Activity through the Genetic Incorporation of a Tyrosine–Histidine Cross-Link in a Myoglobin Model of Heme–Copper Oxidase**

Xiaohong Liu, Yang Yu, Cheng Hu, Wei Zhang, Yi Lu,* and Jiangyun Wang*
In aerobic respiration, heme–copper oxidase (HCO) performs efficient four-electron reduction of oxygen to water without releasing toxic, reactive oxygen species (ROS) such as superoxide and peroxide. Because of its importance in biogenetics, fascinating chemistry, and potential applications in fuel cells, HCO has been intensively investigated by structural biologists, enzymologists, and synthetic chemists. While tremendous progress has been made from the above studies, several important questions about the structural features and mechanism of HCO still remain. Of particular interest is the unique post-translationally modified covalent cross-link between carbon atom C6 of a tyrosine residue and nitrogen atom Nε2 of a nearby histidine residue (Tyr–His cross-link, Figure 1 A), which was first revealed by a high-resolution X-ray structure and then confirmed by biochemical and biophysical studies. Importantly, the Tyr–His cross-link is conserved in bacterial and mammal HCOs, thus implicating a strong evolutionary connection and the functional significance of the cross-link.

The presence of a covalent Tyr–His cross-link is firmly established in HCOs; however, its exact role in HCO function is still not fully understood. A major limitation of our understanding is that such a post-translational modification cannot be directly probed through traditional site-directed mutagenesis methods. To overcome this limitation, synthetic model compounds have been made, and studies of these model compounds have suggested that the cross-link between Tyr and His residues significantly decreased the pKₐ values of phenol and imidazole side chains. The decreased pKₐ value of phenol is believed to facilitate proton delivery and tyrosyl-radical formation. Despite these advances, questions about the roles of the Tyr–His cross-link still remain, because no study has been able to compare the functions of His and Tyr residues at the same positions in the same protein with and without cross-linking.

To answer the above question and to gain new insights into the HCO catalytic process, we report herein the genetic incorporation of the unnatural amino acid imiTyr (I; Figure 1 C), which mimics the cross-linked Tyr–His ligand, into a functional model of HCO in sperm whale myoglobin (Figure 1 B). The obtained enzyme model with the incorporated Tyr–His ligand imiTyr was termed imiTyrCuBMb. We then compared the activity of imiTyrCuBMb with a mutant that has His and Tyr residues at the same positions in the same protein but lacks such a cross-link (F33YCuBMb; F = Phe, Y = Tyr). Our results show that imiTyrCuBMb recapitulated important features of HCO; imiTyrCuBMb exhibited selective O₂-reduction activity while generating less than 6% ROS at more than 1000 turnovers. Importantly, incorporation of imiTyr in the HCO model resulted in eightfold increase in selectivity and threefold increase in catalytic turnover, thereby supporting that the Tyr–His cross-link is indeed essential for HCO function.

We chose myoglobin for genetic incorporation of the unnatural amino acids and to carry out functional studies, because the large (ca. 200 kDa) HCO membrane proteins consist of multiple subunits that are difficult to produce homogeneously in large amounts, whereas myoglobin is a much smaller (18 kD) water-soluble protein that can be expressed and purified easily in gram quantities. Previous biochemical and spectroscopic studies have indicated that the designed heme–copper center in myoglobin can be a functional model of HCOs.

We first synthesized (S)-2-amino-3-(4-hydroxy-3-(1H-imidazol-1-yl)phenyl)propanoic acid (I; hereafter termed imiTyr), which contains the ortho-imidazole–phenol linkage (Tyr–His ligand), and then we genetically encoded it into
myoglobin. The unnatural amino acid imiTyr (I) was synthesized by first protecting the amine group of 3-iodotyrosine using di-tert-butyl dicarbonate\[10\] to give Boc-t-3-iodotyrosine (Boc = tert-butoxycarbonyl), which was then heated to reflux with imidazole in the presence of Cs₂CO₃ and CuI in DMF to afford I in 50% yield\[7d\] (Figure 1 C).

To selectively incorporate imiTyr (I) at defined sites in proteins in \textit{E. coli}, a mutant \textit{Methanococcus jannaschii} tyrosyl amber suppressor tRNA (Mj\textit{tRNA}\textsubscript{Tyr}/tRNAs\textsubscript{Tyr} synthetase (MjTyrRS) pair was evolved that uniquely specifies I in response to the TAG codon. An MjTyrRS library, pBK-lib-jw1, in which six residues (Ty32, Leu65, Phe108, Gln109, Asp158, and Leu162) were randomized, and any one of the six residues (Ile63, Ala67, His70, Tyr114, Ile159, Val164) was either mutated to Gly or kept unchanged, was used to screen for active and selective mutants of tRNA synthetase MjTyrRS for I, as reported.\[11\] Nine MjTyrRS clones emerged after three rounds of positive selections and two rounds of negative selections (Table S1 in the Supporting Information). The best clone grew at a concentration of 120 µg mL\(^{-1}\) of chloramphenicol in the presence of 1 mM I, but only at a concentration of 20 µg mL\(^{-1}\) chloramphenicol in the absence of I, and the clone was named imiTyrRS. Sequencing of this clone revealed five mutations: Ty32Glu, Leu65Ser, His67Gly, Asp158Tyr, and Leu162Asn. Among the five mutations, the His67Gly mutation was required to create additional space to accommodate the imidazole group. The other four mutations may make specific hydrogen-bonding interactions to stabilize the imiTyr sidechain. Work is underway to obtain a structure of the imiTyrRS protein to gain insight into these interactions.

To determine the efficiency and fidelity for the incorporation of unnatural amino acid I into proteins, an amber stop codon was substituted for Ser4 in sperm whale myoglobin containing a C-terminal His tag. Protein expression was carried out in \textit{E. coli} in the presence of the selected synthetase (imiTyrRS), the tyrosyl amber suppressor tRNA Mj\textit{tRNA}\textsubscript{Tyr}/tRNAs\textsubscript{Tyr} and 1 mM I; as a negative control protein expression was also carried out in the absence of I. Analysis of the purified protein by SDS-PAGE showed that full-length myoglobin was expressed only in the presence of unnatural amino acid I in \textit{E. coli}, but not otherwise (Figure 2 A), thus indicating that tRNA synthetase imiTyrRS is specifically active for I but does not utilize any natural amino acid. The yield of the mutant myoglobin was 10 mg L\(^{-1}\). For comparison, the yield of wild-type sperm whale myoglobin (wtMb) under similar conditions was 50 mg L\(^{-1}\). ESI-MS spectrometric analysis of the mutant myoglobin gave an observed average mass of 18 497 Da, which is in close agreement with the calculated mass of 18 496 Da for the Ser4→I mutant myoglobin.

After we demonstrated the efficient genetic incorporation of imiTyr (I) into wtMb, we expressed myoglobin double mutant Leu29His/Phe33→I (called imiTyrCuMb) as a functional HCO model\[8\] with a yield of 5 mg L\(^{-1}\). The selective incorporation of imiTyr at position 33 was again confirmed by SDS-PAGE (Figure 2 A) and ESI-MS (Figure S2 in the Supporting Information). Together with distal residue His64 in sperm whale Mb, the newly introduced residues His29 and imiTyr33 constitute a Cu₄ binding site according to our model and place the copper ion in proximity to heme iron (Figure 1 B). The UV/Vis spectrum of imiTyrCuMb at pH 7.4 is similar to that observed for wtMb and is typical of a six-coordinate, H₂O-bound, high-spin heme with a Soret band absorption maximum at 408 nm (Figure S3 in the Supporting Information). The deoxy-imiTyrCuMb was obtained by reducing the purified met-imiTyrCuMb with excess dithiothreitol. The UV/Vis spectrum (Figure S3 in the Supporting Information) of deoxy-imiTyrCuMb exhibits a Soret band at 430 nm and a visible absorption band at 562 nm. This spectrum is nearly identical to that of deoxy-wtMb, thus indicating that mutation in imiTyrCuMb did not cause major structural changes of the protein. Addition of Cu\(^{2+}\) ions at pH 7.4 to imiTyrCuMb resulted in changes of the spectrum in the Soret region (Figure S4 in the Supporting Information), which was fitted to a double reciprocal plot and a Hill plot.\[9c\] These results indicate that a single Cu\(^{2+}\) binding site was present in imiTyrCuMb, with a \(K_D\) value of 1.6 µM.

Since the hallmark of native HCOs is the clean catalytic reduction of \(O_2\) to water without releasing ROS, we then measured the rate of oxygen reduction catalyzed by imiTyr-CuMb by using an \(O_2\) electrode in the presence of 1000 equivalents of ascorbic acid as the reductant and 100 equivalents of TMPD (tetrakis[methyl-\(p\)-phenylene]diamine dihydrochloride) as a redox mediator. A similar method was used to measure enzymatic activity of native HCO\[12\]. To differentiate between ROS and water products, we employed...
catalase, which selectively reacts with H$_2$O$_2$ to produce O$_2$, and superoxide dismutase (SOD), which selectively reacts with superoxide to produce H$_2$O$_2$ and O$_2$. If O$_2$ consumption results in release of ROS but not in formation of water, the apparent O$_2$-reduction rate will be lower in the presence of catalase and SOD, because they will convert ROS back into O$_2$. By comparing the rates of reduction in the absence and presence of catalase and SOD, the portion of O$_2$ reduction that is due to water formation (light gray, Figure 3 A) and due to ROS formation (dark gray, Figure 3 A) can be calculated. Not surprisingly, most of the O$_2$ consumed by wtMb lead to ROS, both in the presence and absence of Cu$^{2+}$ ions. By contrast, imiTyrCu$_{16}$Mb catalyzed O$_2$ reduction without generating more than 6% H$_2$O$_2$ in the presence of one equivalent Cu$^{2+}$ ions, with an oxygen-consumption rate of 12 $\mu$mol min$^{-1}$ (enzyme activity = 2 oxygen molecules/min). In the absence of Cu$^{2+}$ ions, however, more than 30% of O$_2$ was converted into ROS, thus indicating that Cu$_{16}$ is important for the catalytic turnover of O$_2$ into H$_2$O.

The myoglobin system described herein provides a unique possibility to directly compare the effect of His and Tyr residues with and without cross-linking. To take advantage of this unique feature, we also measured O$_2$ consumption for the myoglobin mutant Leu29His/Phe33Tyr/Phe43His (F33YC$_{16}$Mb). This mutant harbors a Cu$_{16}$ site consisting of residues His29, His43, and His64, as we have shown previously,[8b] and a tyrosine residue in position 33. While His43 and Tyr33 sidechains are in similar positions as the imidazole group and phenol group of imiTyr33, respectively (Figure 1 B), no cross-link is present between them. Not only was the overall activity of the F33YC$_{16}$Mb lower (ca. 40%) than that of imiTyrCu$_{16}$Mb, but more than 50% of the O$_2$ was also converted into ROS by F33YC$_{16}$Mb with or without Cu$^{2+}$ ions added, thus confirming that the cross-linked Tyr–His ligand plays a critical role for the selective reduction of O$_2$ into H$_2$O.

To test if imiTyrCu$_{16}$Mb is a robust O$_2$-reduction catalyst that is capable of performing many turnovers without self-destruction, we then measured O$_2$ consumption under multiple turnover conditions. TMPD (0.6 mM) and ascorbic acid (6 mM) were added to a solution containing imiTyrCu$_{16}$Mb (6 $\mu$m), CuSO$_4$ (6 $\mu$m), and O$_2$ (800 $\mu$m). O$_2$ reduction was then monitored by using an oxygen electrode until all the oxygen was consumed. Subsequently, a further addition of O$_2$ (800 $\mu$m) was carried out by purging the solution with pure oxygen, and then oxygen reduction was again measured until all the oxygen was reduced. These stepwise additions resulted in the multiple plateaus observed in the traces shown in Figure 3 B, and these processes were repeated until imiTyrCu$_{16}$Mb achieved more than 1000 turnovers. The turnover number reported here is an underestimate, because the extra turnovers occurring during oxygen addition were not included in the calculation. Notably, little decrease in the O$_2$-consumption rate was observed after the catalyst reached 1000 turnovers, thereby indicating that at this point the imiTyrCu$_{16}$Mb catalyst has remained intact. By contrast, F33YC$_{16}$Mb, the mutant without the cross-link, underwent less than 400 turnovers under similar conditions. These results again support that the cross-linked Tyr–His ligand is required for optimal O$_2$ reduction to H$_2$O. Here, the difference in catalytic activity between imiTyrCu$_{16}$Mb and F33YC$_{16}$Mb can also be attributed to the different geometries of the copper center. To further investigate the mechanism, we are currently working to solve the crystal structure of imiTyrCu$_{16}$Mb and examine the enzymatic property of another mutant having a Phe–His-type cross-linkage at the position 33.

In conclusion, by directly incorporating the unnatural amino acid imiTyr (I) into myoglobins in E. coli in response to the amber codon TAG, we have successfully designed a functional HCO model imiTyrCu$_{16}$Mb that catalyzes selective and efficient oxygen reduction to water. The HCO model imiTyrCu$_{16}$Mb bearing the Tyr–His cross-link is eightfold more selective with threefold more turnovers than F33YC$_{16}$Mb, which does not contain the cross-link but harbors His and Tyr residues at the same positions in the same protein. Since the synthesis of imiTyr contains only two steps with 50% overall yield, and mutant proteins bearing imiTyr (I) at any site can be easily obtained and purified in...
milligram quantities through site-directed mutagenesis and recombinant protein expression, further systematic investigation of the function of the Tyr–His cross-link is now possible. While imiTyrCu2Mb exhibits lower enzymatic activity (2 O2/min)[12] in comparison to native heme–copper oxidase (ca. 300 O2/s), it is possible to rapidly improve our HCO model to achieve higher activity through directed evolution and incorporation of unnatural amino acids. Our designed enzyme harbors the unnatural amino acid imiTyr, which is highly analogous to the post-translationally modified tyrosine–histidine ligand found in the Cu4 site of HCO; this designed enzyme serves as an ideal model for a more detailed understanding of HCOs and allows for potential applications in synthetic biology and alternative energy.[8,9,13]

**Experimental Section**

To express mutant myoglobin protein imiTyrCu2Mb, plasmid pBAD-JYAMB-His29TAG33 was cotransformed with pBK-imiTyrRS into GeneHog-Fis E. coli cells. Cells were amplified in LB (lysogeny broth) media (5 mL) supplemented with kanamycin (50 μg mL\(^{-1}\)) and tetracycline (Tris) buffer, pH 7.4. All experiments were performed three times to obtain standard deviations. The electrode was calibrated against air-saturated buffer and O2–chloride (Tris) buffer, pH 7.4. All experiments were performed at room temperature.

Oxygen consumption was measured by using an Oxygraph Clark-type oxygen electrode (Hansatech Instruments) at 25°C in 20 mM Tris(hydroxymethyl)aminoethane hydrochloride (Tris) buffer, pH 7.4. All experiments were performed three times to obtain standard deviations. The electrode was calibrated against air-saturated buffer and O2-depleted buffer prior to use. The protein was exchanged into 20 mM Tris buffer (pH 7.4), which was previously treated with chelax beads overnight to remove metal ions in the buffer.

The final protein concentration was adjusted to 6 μM. For the experiment with Cu\(^{2+}\), CuSO\(_4\) was added to a final concentration of 6 μM and stirred for 10 min. For the experiment with catalase and SOD, catalase (Sigma–Aldrich) was added to a final concentration of 7.3 U L\(^{-1}\), and SOD (Sigma–Aldrich) was added to a final concentration of 0.5 U mL\(^{-1}\). The reaction was initiated by adding TMPD and ascorbic acid to a final concentration of 0.6 mM and 6 mM, respectively. The oxygen concentration was read immediately after adding reductant. The turn-over experiment described in Figure 3B was performed similarly except that after the O2 in the reaction chamber was exhausted, the chamber was vented with pure O2 to boost O2 concentration to 800 μM. The concentration of ascorbic acid was kept at 6 mM.

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