

An Iron Carbonyl Pyridonate Complex Related to the Active Site of the [Fe]-Hydrogenase (Hmd)

Blaise V. Obrist,[†] Dafa Chen,[†] Anne Ahrens,[‡] Volker Schünemann,[‡] Rosario Scopelliti,[†] and Xile Hu^{*†}

Laboratory of Inorganic Synthesis and Catalysis, Institute of Chemical Sciences and Engineering, Ecole Polytechnique Fédérale de Lausanne (EPFL), ISIC-LSCI, BCH 3305, Lausanne CH 1015, Switzerland, and Fachbereich Physik, Technische Universität Kaiserslautern, D-67663 Kaiserslautern, Germany

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A mononuclear iron bis(carbonyl) pyridonate complex (**1**), which exhibits several common structural features with the active site of the iron–sulfur cluster-free [Fe]-hydrogenase, was synthesized and characterized. Spectroscopic data of **1** suggests a 2+ oxidation state for the Fe ion in the [Fe]-hydrogenase. Complex **1** serves as a precursor to other hydrogenase models.

Three classes of hydrogenases are now known: the iron–sulfur cluster-containing [FeFe]-hydrogenase and [FeNi]-hydrogenase and the iron–sulfur cluster-free [Fe]-hydrogenase.^{1,2} Phylogenetically unrelated, the three hydrogenases share common features. They all contain active sites made of first-row transition-metal ions (Fe, Ni) and sulfur, CO, and CN ligands.^{3,4} The [FeFe]- and [FeNi]-hydrogenases catalyze hydrogen evolution and/or oxidation. [Fe]-hydrogenase, or the H₂-forming methylenetetrahydromethanopterin dehydrogenase (Hmd), catalyzes the reversible reduction of methylenetetrahydromethanopterin (methenyl-H₄MPT⁺) with H₂ to form methylenetetrahydromethanopterin (methylene-H₄MPT) and H⁺ (Figure 1), an intermediary step in the reduction of CO₂ to methane by methanogens grown under nickel-limiting conditions.⁵

Compared to the prominent [FeNi]- and [FeFe]-hydrogenases, the newly discovered [Fe]-hydrogenase is unique. It is the only hydrogenase that requires one single metal (Fe)

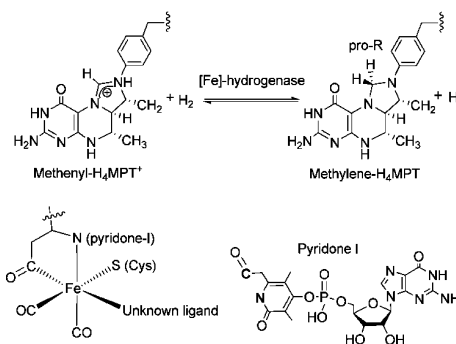


Figure 1. Top: Function of [Fe]-hydrogenase. The reaction is reversible with a ΔG° of -5.3 kJ/mol. Bottom left: Structure of the Fe-containing active site in [Fe]-hydrogenase. Bottom right: Structure for the pyridone I cofactor. The coordinating N and C atoms are highlighted in bold. Selected bond distances (Å): Fe–CO, 1.77; Fe–S, 2.34; Fe–N, 2.05; Fe–C(acyl), 1.88. Bond distances are taken from the 2009 EXAFS study (ref 7), which revised the 2008 crystal structure (ref 4).

for function.^{2,6} Spectroscopic measurements and especially two recent crystallographic studies^{4,7} suggest that the Fe ion is coordinated to a cysteine S atom, two cis-arranged CO ligands, a yet unidentified ligand, and a pyridone molecule (Figure 1).^{4,7–10} There is still ambiguity in the composition and binding mode of the pyridine ligand. According to the initial X-ray crystallographic study of the holoenzyme, the Fe ion is coordinated to the N atom of a 6-(carboxymethyl)-2-pyridone derivative that was identified as the light inactivation product of the Fe-containing cofactor.⁴ However,

* To whom correspondence should be addressed. E-mail: xile.hu@epfl.ch.
[†] EPFL.

[‡] Technische Universität Kaiserslautern.

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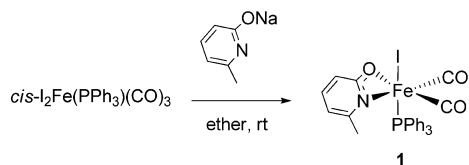


Figure 2. Synthesis of complex **1**. The pyridone is shown as a mixture of both pyridone and pyridinol resonance forms; see the text for details.

subsequent work showed that the X-ray crystallographic and EXAFS data fit better with the structure in which a 6-(formylmethyl)-2-pyridone cofactor coordinates to the Fe ion via both its N and acyl C atoms (Figure 1).⁷ Despite this uncertainty, the presence of such a six-membered-ring nitrogen ligand on a Fe center in a CO- and S-rich environment is unprecedented and intriguing.

Many useful model complexes for [FeNi]- and [FeFe]-hydrogenases are now available,¹¹ but few model complexes for [Fe]-hydrogenase are reported,^{12,13} and none of them contains a mimic for the unusual pyridone cofactor. One uncertainty of [Fe]-hydrogenase is the oxidation state of the Fe center. Mössbauer and IR data suggested that the Fe ion can be either low-spin Fe⁰ or Fe^{II}.^{8,9} A recent study suggested 2+ oxidation state for the Fe ion, but the conclusion was made on an iron(II) bis(carbonyl) aminopyridinebis(thiolate) model complex lacking a pyridone-type ligand.¹² It is thus interesting to probe how a pyridone ligand may influence the electronic properties of the Fe ion. Surprisingly, there are only a few reported iron pyridone complexes, and none of them contains one pyridone ligand coordinating to one single Fe center.¹⁴ Here we present a monomeric iron bis(carbonyl) pyridonate complex. The spectroscopic properties of the complex resemble those of [Fe]-hydrogenase and provide further evidence that the Fe ion in [Fe]-hydrogenase is Fe^{II}.

6-Methyl-2-pyridone was employed as a simple mimic of the pyridone cofactor found in the enzyme. The use of a triphenylphosphine coligand was critical to the stability of the resulting complex. Thus, the reaction of Fe(CO)₃(PPh₃)I₂¹⁵ with sodium 6-methyl-2-pyridonate (L) yielded a crystalline solid (**1**; Figure 2). IR and NMR spectroscopic

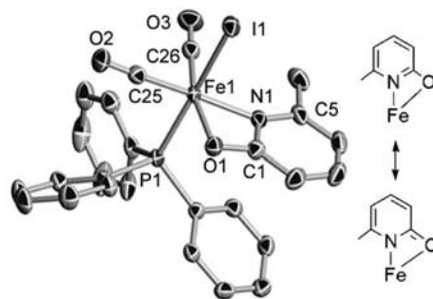


Figure 3. Solid-state structure of **1**. The iron–pyridone interaction is best described by two resonance forms as shown on the right. The thermal ellipsoids are displayed at 50% probability. Selected bond distances (Å) and angles (deg): Fe1–N1, 1.9612(19); Fe1–O1, 2.0106(14); Fe1–P1, 2.2652(6); Fe1–C25, 1.789(2); Fe1–C26, 1.768(2); Fe1–I1, 2.6450(3); C25–O2, 1.142(3); C26–O3, 1.140(3); C1–O1, 1.310(3); C1–N1, 1.351(3); C5–N1, 1.351(3); C25–Fe1–C26, 91.44(10); O1–Fe1–N1, 66.90(7).

data suggested a formula of Fe(CO)₂(PPh₃)IL for **1**, which was confirmed by elemental analysis and X-ray crystallography.¹⁶

The solid-state structure of **1** shows that the Fe^{II} ion is in a six-coordinate, pseudo-octahedral ligand environment (Figure 3).¹⁶ Two terminal CO ligands bind in a cis fashion, with an averaged Fe–C distance of 1.778(2) Å. The pyridonate ligand L is bidentate and coordinates to Fe via both the N and O atoms. The Fe–N and Fe–O distances are 1.9612(19) and 2.0106(14) Å, respectively. The C1–O1 and C1–N1 distances in L are between those of a single bond and a double bond.¹⁷ The Fe–L fragment is therefore best described by a mixture of two resonance forms, in which L exists in either deprotonated pyridinol or deprotonated pyridone form (Figure 3).¹⁸ The coordination sphere of Fe is completed by the axial iodide and triphenylphosphine ligands.

The structure of **1** and the active site of [Fe]-hydrogenase share some similarities. Both compounds contain two *cis*-carbonyls, and their Fe–CO distances are similar. Both contain a pyridone derivative. The pyridone ligand in the enzyme has an acyl group and coordinates to Fe via η^2 - κ -N,C; the pyridone in **1** is unfunctionalized and binds Fe via η^2 - κ -N,O. The Fe–N distances are comparable. Both pyridone rings are flat. In the crystallographic study of the holoenzyme, this arrangement was used as evidence for pyridinol from of the pyridone cofactor.⁴ The structure of **1** suggests that the pyridone ring remains planar even if it contains some components of the pyridone tautomeric form.

In the IR spectrum of **1**, two intense absorption bands were observed with $\nu(\text{max})$ of 2032 and 1987 cm⁻¹, revealing the presence of two terminal CO ligands (Figure S1 in the Supporting Information).¹⁶ The intensities of the two CO bands are nearly equal, consistent with a *cis* configuration. This IR spectrum is similar to those of [Fe]-hydrogenase and its extracted Fe-containing cofactor, which show CO bands

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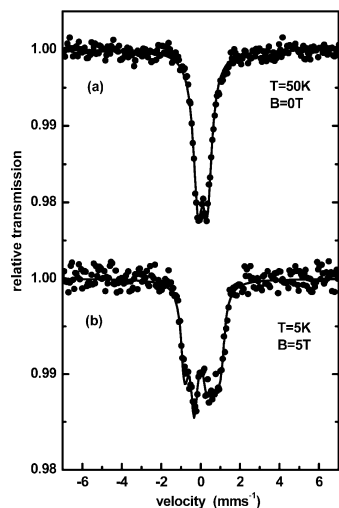


Figure 4. Mössbauer spectra of **1** obtained at $T = 50$ K (a) and at $T = 5$ K and an external field of $B = 5$ T applied perpendicularly to the γ -ray (b). The solid line represents a simulation assuming a diamagnetic ground state with parameters given in the text (except the line width used for the simulation displayed in part b, which was taken as $0.40 \text{ mm}\cdot\text{s}^{-1}$).

at $\nu(\text{max}) = 2011$ and 1944 cm^{-1} and 2031 and 1972 cm^{-1} , respectively.⁸

The average CO IR vibration frequencies can be correlated to the oxidation state of the Fe ions in monomeric iron bis(carbonyl) complexes.¹² For Fe^0 , $\nu_{\text{CO}}(\text{mean}) = 1862 \pm 23 \text{ cm}^{-1}$; for Fe^{II} , $\nu_{\text{CO}}(\text{mean}) = 2016 \pm 22 \text{ cm}^{-1}$. $\nu_{\text{CO}}(\text{mean})$ for [Fe]-hydrogenase is in the range for Fe^{II} ; therefore, a 2+ oxidation state should be expected. However, the Fe ion is in an unusual ligand environment, so a derivation of its ν_{CO} from the known trend is also possible. $\nu_{\text{CO}}(\text{mean})$ for complex **1** (2009 cm^{-1}) agrees with the norm for other iron(II) bis(carbonyl) complexes, suggesting that coordination of a pyridone ligand to a iron(II) bis(carbonyl) fragment does not result in a drastic change in the CO vibration frequencies. This reassures, albeit does not prove, the judgment from the IR study that the Fe center in [Fe]-hydrogenase is Fe^{II} .^{8,12,19}

The Mössbauer spectrum of the Fe^{II} model complex **1** displayed in Figure 4a shows a symmetric quadrupole doublet with an isomer shift $\delta = 0.10(2) \text{ mm}\cdot\text{s}^{-1}$, a quadrupole splitting $\Delta E_{\text{Q}} = 0.48(2) \text{ mm}\cdot\text{s}^{-1}$, and a line width of $\Gamma = 0.57 \text{ mm}\cdot\text{s}^{-1}$. Field-dependent Mössbauer studies of [Fe]-hydrogenase found $\delta = +0.06 \text{ mm}\cdot\text{s}^{-1}$ and a positive quadrupole splitting ($\Delta E_{\text{Q}} = +0.65 \text{ mm}\cdot\text{s}^{-1}$) for the diamagnetic Fe center.⁹ Whereas these Mössbauer parameters are consistent with a low-spin Fe^{II} or Fe^0 center, the very low isomer shift seems to favor Fe^0 .⁹ However, it was recently shown that a iron(II) bis(carbonyl) bis(thiolate) complex exhibits a similarly low isomer shift.¹²

The Mössbauer spectrum of **1** obtained in an external field of 5 T (Figure 4b) shows that **1** also has a diamagnetic

ground state as well as a positive sign of the quadrupole splitting. The asymmetry parameter of the electric field gradient used for the simulation displayed in Figure 4b has been taken as $\eta = 0$. The δ value of **1** and that of [Fe]-hydrogenase are very much comparable within the experimental accuracy of $\pm 0.02 \text{ mm}\cdot\text{s}^{-1}$. Also the positive sign of ΔE_{Q} is found in both cases, and the η values are comparable but the ΔE_{Q} values differ slightly. However, the free active Fe-containing cofactor of the protein itself exhibits $\Delta E_{\text{Q}} = 0.43 \text{ mm}\cdot\text{s}^{-1}$, which is in very good agreement with the ΔE_{Q} value of **1**.⁹ Thus, this work suggests that the Mössbauer parameters of the Fe ion in [Fe]-hydrogenase could arise from a Fe^{II} center in an octahedral environment with a pyridone and two CO ligands.

The redox properties of **1** were measured by cyclic voltammetry. **1** undergoes one nonreversible and one quasi-reversible reduction at -1.5 and -1.75 V in CH_2Cl_2 vs ferrocene/ferrocenium, respectively (Figure S2 in the Supporting Information).¹⁶ They are tentatively assigned to the Fe^{III} and $\text{Fe}^{\text{I/0}}$ couples.

Complex **1** serves as a precursor to other synthetic mimics of [Fe]-hydrogenase. A preliminary study shows that the salt metathesis reaction of **1** with PhSNa gave a mixture of complex $\text{Fe}(\text{CO})_2(\text{PPh}_3)(\text{SPh})\text{L}$ (**2**), free PPh_3 , and one or more paramagnetic species.¹⁶ Complex **2** is highly unstable, precluding purification by recrystallization. However, the reaction of **1** with sodium 2,6-dimethylphenylthiolate gave complex $\text{Fe}(\text{CO})_2(\text{PPh}_3)\{\text{S}(2,6\text{-Me}_2\text{C}_6\text{H}_3)\}\text{L}$ (**3**), which could be purified and isolated. Elemental analysis and ^1H and ^{31}P NMR and IR spectroscopic data are consistent with the formula of **3**.^{16,20}

In summary, we have prepared a monomeric iron bis(carbonyl) pyridonate complex as a synthetic model for the active site of [Fe]-hydrogenase. Spectroscopic studies of **1** complement earlier work on the enzyme and other model compounds and support the proposal that the Fe ion in [Fe]-hydrogenase exists as Fe^{II} . Reactions of **1** lead to new [Fe]-hydrogenase model compounds.

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Supporting Information Available: Experimental details, spectroscopic data, and a CIF file for **1**. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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