<table>
<thead>
<tr>
<th>Title</th>
<th>Cysteine 295 indirectly affects Ni coordination of carbon monoxide dehydrogenase-II C-cluster.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Author(s)</td>
<td>Inoue, Takahiro; Takao, Kyosuke; Yoshida, Takashi; Wada, Kei; Daifuku, Takashi; Yoneda, Yasuko; Fukuyama, Keiichi; Sako, Yoshihiko</td>
</tr>
<tr>
<td>Citation</td>
<td>Biochemical and biophysical research communications (2013), 441(1): 13-17</td>
</tr>
<tr>
<td>Issue Date</td>
<td>2013-11-08</td>
</tr>
<tr>
<td>URL</td>
<td><a href="http://hdl.handle.net/2433/179795">http://hdl.handle.net/2433/179795</a></td>
</tr>
</tbody>
</table>

© 2013 Elsevier Inc.; This is not the published version. Please cite only the published version. この論文は出版社版でありません。引用の際には出版社版をご確認ご利用ください。

Type | Journal Article |

Textversion | author

Kyoto University
Title
Cysteine 295 indirectly affects Ni coordination of carbon monoxide dehydrogenase-II C-cluster

Author names and affiliations
Takahiro Inoue1, Kyosuke Takao1, Takashi Yoshida1, Kei Wada2, Takashi Daifuku1, Yasuko Yoneda1, Keiichi Fukuyama3, Yoshihiko Sako1*

1 Division of Applied Biosciences, Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan
2 Organization for promotion of Tenure Track, University of Miyazaki, Miyazaki 889-1692, Japan
3 Department of Biological Sciences, Graduate School of Science, Osaka University, Toyonaka, Osaka 560-0043, Japan

*To whom correspondence should be addressed. Tel: +81-75-753-6217; Fax: +81-75-753-6226; E-mail: sako@kais.kyoto-u.ac.jp

Abstract
A unique [Ni-Fe-S] cluster (C-cluster) constitutes the active center of Ni-containing carbon monoxide dehydrogenases (CODHs). His261, which coordinates one of the Fe atoms with Cys295, is suggested to be the only residue required for Ni coordination in the C-cluster. To evaluate the role of Cys295, we constructed CODH-II variants. Ala substitution for the Cys295 substitution resulted in the decrease of Ni
content and didn’t result in major change of Fe content. In addition, the substitution had no effect on the ability to assemble a full complement of [Fe-S] clusters. This strongly suggests Cys$^{295}$ indirectly and His$^{361}$ together affect Ni-coordination in the C-cluster.

**Keywords**

Carbon monoxide dehydrogenase; CODH; C-cluster; [Ni-Fe-S] cluster;

*Carboxydothermus hydrogenoformans*

**Abbreviation**

NH$_2$OH; hydroxylamine, CoA; coenzyme, PCR; polymerase chain reaction, IPTG;

Isopropyl β-D-1-thiogalactopyranoside
1. Introduction

Ni-containing carbon monoxide dehydrogenases (CODHs) are phylogenetically related; however, they vary in terms of their metabolic role, subunit composition, and catalytic activities [1,2]. CODHs physiologically catalyze oxidation of CO or reduction of CO$_2$ in an active center called the C-cluster [1-3]. The C-cluster is conserved in CODH structures from some bacteria, *Carboxythermus hydrogenoformans*, *Rhodospirillum rubrum*, *Moorella thermoacetica*, and an archaeon *Methanosarcina barkeri*. The C-cluster is composed of a unique [Ni-Fe-S] cluster that is linked by conserved ligands: five cysteines and one histidine residue (Fig. 1) [4-8].

The C-cluster ligands are important for their activity as well as metal coordination, e.g., the His$^{261}$ ligand is the central residue required for proper assembly of the Ni into the C-cluster [9]. Structural studies show His$^{261}$ directly coordinates one of the Fe atoms in the cluster (Fe1) with the Cys$^{295}$ in CODH-II (corresponding His$^{265}$ in CODH of *Rhodospirillum rubrum* (CODH$_{Rr}$)) [6]. Hereafter, residue numbers are based on the structure of *C. hydrogenoformans* CODH-II, unless otherwise noted. It is very unlikely that this His residue is a ligand for the Ni in all structures because it is over 4 angstroms away. In view of the importance of the His$^{261}$ for Ni coordination, the role of the ligand at position 295 is of interest to further understand of C-cluster.

*Carboxythermus hydrogenoformans* is a thermophilic anaerobic CO-utilizing bacterium. *C. hydrogenoformans* contains five genes encoding CODHs designated CODH-I to CODH-V on the genome [10]. Several functions for the enzymes are proposed based on their gene context and on physiological experiments [10–12]; CODH-I, energy conservation conjugated with a proton-pumping hydrogenase; CODH-II, NADH generation; CODH-III, carbon fixation in the acetyl-CoA pathway;
and CODH-IV, oxidative stress response. The physiological function of CODH-V remains unknown. In CODH-V, several alignment analyses suggest the conserved ligand Cys\textsuperscript{295} is replaced by Glu [3,13]. To evaluate the role of Cys\textsuperscript{295} in CODH-II, we constructed CODH-II variants of the Fe1 ligands (C295A, C295E mimicked for CODH-V and H261A) and compared their properties.

2. Materials and methods

2.1. Site-directed mutagenesis, heterologous expression and purification of recombinant CODH-II variants

The pET28-a based CODH-II expression plasmid used for mutagenesis experiments was previously described [14]. The Quick Change site-directed mutagenesis kit (Stratagene, La Jolla, CA) was used to introduce C295A, C295E, H261A and H261V mutations into the cooS-II gene. The oligonucleotide primer pairs were as follows: for C295A, 5'-TTAACGTGGTAGGTATTTTGCCACGGCAACGAGGTTTTGATGC-3' (forward), and 5'-GCATCAAAACCTCGTGGCCCCGTGGCACAATAACCTACCACGTTAAT-3' (reverse), C295E;

5'-ATTAACGTGGTAGGTATTTTGAAACGGGCAACGAGGTTTTGATG-3' (forward) and 5'-CATCAAAACCTCGTGGCCCCGTGGCACAATAACCTACCACGTTAAT-3' (reverse); H261A, 5'-GTGGCCGTTCATGGGGCTAACCCGGTCCTGTC-3' (forward), 5'-GACAGGACCGGGTTCATGGGGCTAACCCGGTCCTGTC-3' (reverse); and for H261V, 5'-AATGTGGCCGTTCATGGGGCTAACCCGGTCCTGTC-3' (forward) and 5'-TCGGACAGGACCGGGTTACCCCATGAACGCGCCACATT-3' (reverse).
Heterologous expression and purification of the CODH-II variants were performed as described previously [14]. Briefly, N-terminal (His)_6-tagged CODH-II variants were expressed in *Eschericia coli* Rosetta2 (DE3) (Novagen, Madison, WI) harboring the pRKISC plasmid [15]. *E. coli* cells were cultivated in TB medium at 30°C aerobically to an OD_{600} of 0.6 - 0.7. Then, 0.2 mM IPTG was added and the cells were cultivated anaerobically for 20 - 22h. The cells, 6-8 g (wt/vol), containing recombinant CODH-II variants were disrupted using a French press. The His-tagged enzymes were purified using a Cosmogel His-Accept column (Nacalai Tesque, Kyoto, Japan) in an anoxic glove box (COY Laboratory Products Inc., Grass Lake, MI) in an atmosphere of 95% N_2/ 5% H_2 at 25 ºC. Buffer A (50 mM Tris-HCl, pH 8.0, 300 mM NaCl) containing 20 mM imidazole and 2 mM dithionite was used for washing, buffer A containing 300 mM imidazole and 2 mM dithionite was used for elution.

2. 2. Metal analysis

Determination of the metal content of the enzyme solutions was performed at the Nitto Bunseki center (Osaka, Japan) by inductively coupled plasma mass spectrometry (ICP-MS). Enzyme samples were equilibrated in 50mM Tris-HCl buffer at pH 8.0 containing 2 mM sodium dithionite before shipment for metal analysis.

2. 3. Enzyme assays

CO and H_2 oxidation activity was assayed based on the CO and H_2 dependent reduction of oxidized methyl viologens at 70°C, respectively, as described previously [11]. One unit of activity was defined as the reduction of 1 µmol of CO per minute. NH_2OH reduction activity was assayed based on NH_2OH dependent oxidation of reduced methyl viologen at 40°C, according to a previous report with minor modification [16,17]. Assays were performed anaerobically in a 1.0 ml assay mixture.
containing 100 mM MOPS-NaOH (pH 7.5), 10 mM methyl viologen, and 100 mM NH₃OH. The assay solution was reduced to give an absorbance at 578 nm of near 1.0 with 100 mM sodium dithionite solution. The reaction was started adding the enzyme. A no-enzyme control assay was also performed with no significant decrease in A₅₇₈. One unit of activity was defined as the reduction of 1 μmol of NH₂OH per minute. CO₂ reduction activity was assayed at 25°C as described previously [14]. Briefly, production of CO from CO₂ with the enzyme was monitored with the formation of carboxyhemoglobin. One unit of activity was defined as 1 μmol CO production per minute. UV visible absorption spectra of the CODH-II variants were recorded at room temperature as described previously [11]. Enzyme samples were equilibrated in 50 mM Tris-HCl buffer at pH 8.0 before activity and UV-visible absorption analysis.

2. 4. Computational analysis

Multiple sequence alignments were constructed using CLUSTAL W [18]. The alignments were examined and columns with gaps were trimmed prior to phylogenetic reconstructions. Maximum-likelihood phylogenetic analysis was performed using PhyML ver. 3 [19].

3. Results

3.1. Metal analysis

The metal content of CODH variants were compared with that of wild type (Table 1). The amounts of Fe and Ni atoms per monomer of wild type in this study (7.5Fe and 0.90Ni, respectively) were lower than that expected from CODH-II structure (10Fe and 1Ni, respectively) [6]. C295A, C295E and H261A contained nearly the same amount of iron atoms respectively (Table 1). Wild type CO oxidation activity (8,900 U/mg)
obtained in this study was lower compared to that of the previous report (10,000-14,000U/mg), suggesting that on a part of recombinant enzymes, the [Fe-S] and/or [Ni-Fe-S] cluster degraded during purification process. The variants showed a very low level of nickel compared with wild type enzyme (Table 1).

3.2. UV-visible absorption spectra of CODH-II variants

UV-visible absorption spectra of CODH-II variants were recorded using several redox conditions, and were compared to the wild-type CODH-II. The spectra of as-isolated variants were identical to the wild-type (Fig. 2). The spectra of A420/A280, which is unique absorbance for CODH-II C-cluster, were similar to wild-type CODH-II [14]. For the wild-type CODH-II, bleaching of the [Fe-S] cluster shoulder occurs after treatment with CO or dithionite [14]. In contrast, the bleaching was observed when variants were treated with dithionite but not CO, e.g., CODH_{Rr} H265V (Fig. 2 insets), suggesting the [Fe-S] clusters of variants were not reduced by CO.

3.3. Activity of CODH-II variants

The activities of CODH-II variants were determined. All substitutions resulted in decreased CO oxidation activity and an increase in NH$_2$OH reduction activity (Table 2). C295A, H261A showed no CO oxidation activity and C295E showed 0.02% of the wild-type, respectively. The NH$_2$OH reduction activities of C295A, C295E and H261A were 171, 343, and 614% of the wild-type. Although the optimal growth temperature of C. hydrogenoformans is 70°C, we determined NH$_2$OH reduction activities of variants at 40°C, because reduced methyl viologen lacks stability at higher temperatures. And under the condition, all variants showed no CO$_2$ reduction and H$_2$ oxidation.

3.4. Distribution of the replacement at position 295

A phylogenetic tree was constructed using the sequence of Cdh from
Archaeoglobus fulgidus as an out group (Fig. 3). Protein phylogeny of the deduced amino acid sequence from the cooS genes, which is the catalytic subunit of CODHs, was divided into two major groups (Group 1 and Group 2) supported with robust (100%) bootstrap values (Fig. 3). Group 1 contained well-characterized CODHs including CODH-II and CODH_Rr. In contrast, Group 2 included CODHs like sequences whose properties and physiological functions are not known. Group 2 was further divided into two major clades (Clade A and Clade B) supported with robust (100%) bootstrap values (Fig. 3).

4. Discussion

In previous reports, several CODH_Rr variants of the C-cluster ligands were constructed and examined for the activities and metal contents [9,16,20,21]. Among the variants, only Val substitution for the His^{261} (corresponding His^{265} in CODH_Rr) resulted in a decrease in Ni content [9]. Therefore, His^{261} was thought to be the only critical residue required for proper assembly of the Ni into the C-cluster. The activity resulting from this substitution decreases CO oxidation activity, like other substitutions. In addition, this substitution results in an increase in NH$_2$OH reduction activity.

This study for the first time demonstrates that, Cys^{295} also plays a critical role in Ni coordination in the C-cluster where these ligands directly coordinate Fe1. ICP-MS analysis demonstrated the substitution revealed the decrease of Ni content and no major change of Fe content (Table 1). In addition, the UV-visible absorption spectrum of the as-isolated C295A in this study and C-cluster-miss CODH-II spectrum [22], where only C-cluster was missed and B and C clusters were assembled, suggests the substitution had no major effect on the ability of CODH-II to assemble a full complement of [Fe-S]
clusters (Fig. 2). Thus, Cys$^{295}$ and His$^{261}$ were strongly suggested to coordinate the Fe1 directly, playing central roles for Ni coordination together in the C-cluster. Interestingly, an Ala substitution for Cys$^{526}$, which seems to coordinate the Ni directly, did not have a major effect on Ni content [9]. The exact role of His$^{261}$ and Cys$^{295}$ in Ni coordination remains unknown. The lack of these Fe1 ligands probably alters the electronic structure as well as the geometry around the active site so that putting Ni into the cube is disrupted. The crystal structure presently reported provides for the common feature of C-clusters that allows the configurations of Fe$_3$-S$_4$-Ni moiety in the C-clusters to be asymmetric and apparently distorted by virtue of the link to Fe1 [4–8]. Our data suggest that the correct configuration of Fe1 coordinated by His$^{261}$ and Cys$^{291}$ is essential for Ni-insertion into the C-cluster.

CODH-II C295A exhibited no CO oxidation activity and, alternatively, exhibited an increased level of NH$_2$OH reduction activity (Table 2). This was similar to CODH-II H261A and previously from CODH$_{Rj}$ H265V [16]. C-cluster structure is similar to hybrid cluster structure of hybrid cluster proteins (HCPs), and HCPs show NH$_2$OH reduction activity [23,24]. These suggested the reactivity of Cys$^{295}$ or His$^{261}$ substituted C-cluster was similar to that of hybrid cluster.

CODH-II C295E showed similar properties compared to the variants, suggesting that the CODH-V C-cluster lacks Ni and consequently differs in its properties from well-characterized CODHs. Additionally, a few studies concerning Group 2 suggest the physiological function was different from the well-characterized CODHs [25,26]. This study would provide important insight into Group 2 CODHs like sequences whose property and physiological functions are not well known.
Acknowledgements

This work was supported by a Grant-in-Aid for Scientific Research (A) (No. 20248023 and 25252038) from The Ministry of Education, Culture, Sports, Science and Technology (MEXT) and Grant-in-Aid for JSPS Fellows (No. 24・4545) from the Japan Society for the Promotion of Science (JSPS).
References


[18] J.D. Thompson, D.G. Higgins, T.J. Gibson, CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting,


**Figure Legends**

**Figure 1**

**C-cluster structure of *Carboxydothermus hydrogenoformans* CODH-II.** The C-cluster is linked with residues His\(^{261}\), Cys\(^{295}\), Cys\(^{332}\), Cys\(^{446}\), Cys\(^{476}\) and Cys\(^{526}\). Fe atoms are colored in red, sulfur atoms are in yellow, and a Ni atom is in green.

**Figure 2**

**UV-visible absorption spectra of CODH-II variants.** The UV-visible absorption spectra of purified CODH-II variants in 50 mM Tris-HCl pH 8.0 are recorded. (a) CODH-II C295A, (b) CODH-II C295E and (c) CODH-II H261A. Conditions for each curve: blue line, as-isolated; red line, reduced with 2 mM dithionite under N\(_2\) for 2 minutes; green line, reduced with pure CO for 5 minutes; and purple line, oxidized with air for 5 minutes. Insets: a difference spectrum of condition as-isolated minus CO-reduced.

**Figure 3**

**Phylogenetic tree of CooS homologs.** A Phylogenetic tree of CooS homologs is constructed using the maximum-likelihood method. Major clades (labeled A) of CooS sequences are highlighted in gray boxes. CODHs biochemically or structurally characterized are indicated in bold letters. CODH-II and CODH-V from *C. hydrogenoformans* is highlighted by an asterisk. For species having more than one CODH, the number of the CODH out of the total is given parenthetically. Only bootstrap supports equal to or more than 80% are indicated.
<table>
<thead>
<tr>
<th>Recombinant protein</th>
<th>Metal content</th>
<th>Ni (mol/mol CODH)</th>
<th>Fe (mol/mol CODH)</th>
</tr>
</thead>
<tbody>
<tr>
<td>W.T.</td>
<td></td>
<td>0.90</td>
<td>7.5</td>
</tr>
<tr>
<td>C295A</td>
<td></td>
<td>0.078</td>
<td>8.9</td>
</tr>
<tr>
<td>C295E</td>
<td></td>
<td>0.076</td>
<td>9.2</td>
</tr>
<tr>
<td>H261A</td>
<td></td>
<td>0.082</td>
<td>8.8</td>
</tr>
</tbody>
</table>
Table 2 Specific activity of CODH variants

<table>
<thead>
<tr>
<th></th>
<th>CODH-II&lt;sub&gt;Ch&lt;/sub&gt;</th>
<th>CODH&lt;sub&gt;Rr&lt;/sub&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>W.T.</td>
<td>C295A</td>
</tr>
<tr>
<td>CO oxidation (units/mg)</td>
<td>8,900</td>
<td>N.D.</td>
</tr>
<tr>
<td>H&lt;sub&gt;2&lt;/sub&gt; oxidation (units/mg)</td>
<td>N.D.</td>
<td>N.D.</td>
</tr>
<tr>
<td>CO&lt;sub&gt;2&lt;/sub&gt; reduction (units/mg)</td>
<td>4.0</td>
<td>N.D.</td>
</tr>
<tr>
<td>NH&lt;sub&gt;2&lt;/sub&gt;OH reduction (units/mg)</td>
<td>0.7</td>
<td>1.2</td>
</tr>
</tbody>
</table>

CODH-II<sub>Ch</sub>; CODH-II from *C. hydrogenoformans*, CODH<sub>Rr</sub>; CODH from *R. rubrum*

N.D.; not detected

<sup>a</sup>; the values are taken from Ref. [9]
Fig. 1 C-cluster structure of *Carboxydothermus hydrogenoformans* CODH-II. Inoue et al. 2013
Fig. 2-A, B, C UV-visible absorption spectra of CODH-II variants.
Inoue et al. 2013
Fig. 3 Phylogenetic tree of CooS homologs.
Inoue et al. 2013