Copper binding in IscA inhibits iron-sulfur cluster assembly in *Escherichia coli*

Guoqiang Tan[#,*], **Zishuo Cheng**[*], **Yilin Pang**[#], **Aaron P. Landry**[*], **Jianghui Li**[#], **Jianxin Lu**[#,2], and **Huangen Ding**[*,1]

[#]Laboratory of Molecular Medicine, Wenzhou Medical University, Wenzhou, Zhejiang, 325035, China

[*]Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA

Abstract

Among the iron-sulfur cluster assembly proteins encoded by gene cluster *iscSUA-hscBA-fdx* in *Escherichia coli*, IscA has a unique and strong iron binding activity and can provide iron for iron-sulfur cluster assembly in proteins *in vitro*. Deletion of IscA and its paralogue SufA results in an *E. coli* mutant that fails to assemble [4Fe-4S] clusters in proteins under aerobic conditions, suggesting that IscA has a crucial role for iron-sulfur cluster biogenesis. Here we report that among the iron-sulfur cluster assembly proteins, IscA also has a strong and specific binding activity for Cu(I) *in vivo* and *in vitro*. The Cu(I) center in IscA is stable and resistant to oxidation under aerobic conditions. Mutation of the conserved cysteine residues that are essential for the iron binding in IscA abolishes the copper binding activity, indicating that copper and iron may share the same binding site in the protein. Additional studies reveal that copper can compete with iron for the metal binding site in IscA and effectively inhibits the IscA-mediated [4Fe-4S] cluster assembly in *E. coli* cells. The results suggest that copper may not only attack the [4Fe-4S] clusters in dehydratases, but also block the [4Fe-4S] cluster assembly in proteins by targeting IscA in cells.

Keywords

IscA; copper toxicity; iron-sulfur cluster assembly

Introduction

IscA is a key member of the iron-sulfur cluster assembly machinery encoded by the housekeeping gene cluster *iscSUA-hscBA-fdx* in *Escherichia coli* (Zheng *et al.*, 1998, Roche *et al.*, 2013), and is highly conserved among aerobic organisms from bacteria to humans (Vinella *et al.*, 2009). Biochemical studies have shown that IscA may act as an alternative scaffold (Krebs *et al.*, 2001, Ollagnier-de-Choudens *et al.*, 2001) or intermediate carrier for iron-sulfur cluster biogenesis (Mapolelo *et al.*, 2012b, Mapolelo *et al.*, 2013, Vinella *et al.*, 2013). However, unlike other scaffold proteins such as IscU (Agar *et al.*, 2000, Unciuleac *et*

[1,2]Corresponding authors: Tel: 01 (225) 578 4797; Fax: (225) 578 2597 hding@lsu.edu. Tel: 86 (577) 8668 9805; Fax: 86 (577) 866 89805 jxlu313@163.com.

al., 2007, Raulfs *et al.*, 2008), *E. coli* IscA has a unique and strong iron binding activity *in vitro* (Ding & Clark, 2004, Ding *et al.*, 2005b, Yang *et al.*, 2006, Landry *et al.*, 2013) and *in vivo* (Wang *et al.*, 2010). Recent studies further showed that iron binding activity of IscA is conserved, as IscA homologues from *Azotobacter vinelandii* (Mapolelo *et al.*, 2012a), *Saccharomyces cerevisiae* (Muhlenhoff *et al.*, 2011), and humans (Lu *et al.*, 2010) also have a strong iron binding activity. Furthermore, the iron center in IscA can be mobilized by L-cysteine (Ding *et al.*, 2005a, Landry et al., 2013) and transferred for iron-sulfur cluster assembly in target proteins *in vitro* (Yang et al., 2006), suggesting that IscA may act as an iron chaperone to deliver iron for iron-sulfur cluster biogenesis. In human cells, depletion of IscA1 results in deficiency of iron-sulfur cluster assembly in mitochondria and cytosol (Song *et al.*, 2009). In *A. vinelandii*, depletion of IscA homologue leads to a null growth phenotype when cells are cultured under the oxygen-elevated conditions (Johnson *et al.*, 2006). In *E. coli*, deletion of IscA and its paralogue SufA also produces a null growth phenotype in M9 minimal media under aerobic conditions (Lu *et al.*, 2008, Mettert *et al.*, 2008). Further studies revealed that deletion of IscA and SufA blocks the [4Fe-4S] cluster assembly without significant effect on the [2Fe-2S] cluster assembly in *E. coli* cells under aerobic growth conditions (Tan *et al.*, 2009), suggesting that IscA/SufA has a crucial role for the [4Fe-4S] cluster assembly in *E. coli* cells. Consistent with this idea, other research groups have also reported that IscA homologues are essential for the [4Fe-4S] cluster assembly in *S. cerevisiae* (Muhlenhoff et al., 2011) and human cells (Sheftel *et al.*, 2012).

E. coli IscA is a homodimer with three conserved cysteine residues (Cys-35, Cys-99 and Cys-101) from each monomer forming a "cysteine pocket" between two monomers (Bilder *et al.*, 2004, Cupp-Vickery *et al.*, 2004). The site-directed mutagenesis studies showed that the "cysteine pocket" is essential for the iron binding activity *in vitro* (Ding *et al.*, 2004) and the physiological function of IscA in *E. coli* cells (Lu et al., 2008). The "cysteine pocket" in IscA appears to be highly flexible to accommodate a mononuclear iron or an iron-sulfur cluster without significant change of the structure (Wada *et al.*, 2005). The flexibility of the "cysteine pocket" led us to postulate that IscA may also bind other transition metal ions such as copper in its metal binding site. While copper is an essential element for all living cells, excess copper is highly toxic (Rodriguez-Montelongo *et al.*, 1993, Karlsson *et al.*, 2008). Recent studies further suggested that excess copper may disrupt the labile [4Fe-4S] clusters in dehydratases (Macomber & Imlay, 2009) and block iron-sulfur cluster biogenesis in *E. coli* (Fung *et al.*, 2013, Outten & Munson, 2013) and *Bacillus subtilis* (Chillappagari *et al.*, 2010). Since iron-sulfur proteins are involved in diverse physiological processes from energy metabolism to DNA repair and replication (Johnson *et al.*, 2005, White & Dillingham, 2012), the copper-mediated inhibition of iron-sulfur cluster biogenesis would have a broad impact on multiple cellular functions. Nevertheless, the molecular mechanism underlying the copper-mediated toxicity on iron-sulfur proteins has not been fully understood. Here, we report that among the iron-sulfur cluster assembly proteins encoded by the gene cluster *iscSUA-hscBA-fdx* (Zheng et al., 1998), IscA has a strong and specific copper binding activity in *E. coli* cells and *in vitro*. Copper and iron appear to share the same binding site in IscA, as mutation of the three conserved cysteine residues in IscA abolishes the iron and copper binding activities. Furthermore, excess copper can compete with iron for the metal binding site in IscA and effectively inhibit the IscA-mediated [4Fe-4S] cluster

assembly without significant effect on the [2Fe-2S] cluster assembly in *E. coli* cells. The results suggest that copper may not only attack the labile [4Fe-4S] clusters in dehydratases as reported previously (Macomber & Imlay, 2009), but also block the [4Fe-4S] cluster assembly in *E. coli* cells by targeting the iron-sulfur cluster assembly protein IscA.

Results

IscA has a unique and strong copper binding activity among the iron-sulfur cluster assembly proteins

To prevent or alleviate copper toxicity, *E. coli* has three copper homeostatic systems to maintain low intracellular copper content: CopA, a P-type ATPase that pumps copper ion out of the cytoplasm (Fan & Rosen, 2002); CueO, an oxidase that oxidizes Cu(I) to Cu(II) in the periplasm to prevent adventitious entry into the cytoplasm (Stoyanov *et al.*, 2001); and a copper pump that transports copper ion from the periplasm to the extracellular environment (Munson *et al.*, 2000). Deletion of CopA, CueO, and CusA, a subunit of the copper pump (Munson et al., 2000), results in an *E. coli* strain that is hypersensitive to copper in growth media (Grass & Rensing, 2001, Macomber & Imlay, 2009).

To explore the copper binding activity of iron-sulfur cluster assembly proteins *in vivo*, we expressed each protein encoded by the gene cluster *iscSUA-hscBA-fdx* in the constructed *E. coli copA/cueO/cusA* mutant cells grown in LB media under aerobic conditions. CuSO$_4$ (200 μM) was added to the cell cultures ten min before the expression of recombinant protein was induced. CuSO$_4$ at 200 μM was chosen as it reduced cell growth of the *E. coli copA/cueO/cusA* mutant in LB by about 20% and did not significantly affect protein synthesis in the cells. Each of the iron-sulfur cluster assembly proteins was produced in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with or without 200 μM CuSO4. Purified proteins were then subjected to the UV-visible absorption measurements and metal content analyses. As shown in Figure 1A, addition of CuSO$_4$ (200 μM) to LB media had little or no effect on the UV-visible absorption spectrum of IscS, a cysteine desulfurase that catalyzes desulfurization of L-cysteine and provides sulfide for iron-sulfur cluster assembly in proteins (Smith *et al.*, 2001, Marinoni *et al.*, 2012). Similarly, addition of CuSO$_4$ (200 μM) to LB media did not significantly change the UV-visible absorption spectra of the iron-sulfur cluster assembly scaffold protein IscU (Agar et al., 2000, Unciuleac et al., 2007, Raulfs et al., 2008) (Figure 1B), and heat shock cognate proteins HscB (Figure 1D) and HscA (Figure 1E) (Kim *et al.*, 2012). Ferredoxin (Fdx) [2Fe-2S] cluster (Ta & Vickery, 1992, Chandramouli *et al.*, 2007, Yan *et al.*, 2013, Kim *et al.*, 2013) was also not affected by addition of CuSO$_4$ (200 μM) in LB media (Figure 1F). Only IscA showed a new absorption peak at 258 nm (Figure 1C) when CuSO$_4$ (200 μM) was added to LB media. As the absorption peak at 258 nm has been attributed to the Cu(I) binding site with two cysteine residues as ligands in the Parkinsonism-associated protein DJ-1 (Puno *et al.*, 2013), we propose that IscA may bind Cu(I) via cysteine residues.

The copper content analyses using neocuproine or ICP-ES (the Inductively Coupled Plasma-Emission Spectrometry) showed that purified IscA contained 0.60±0.09 copper atoms per IscA dimer, while IscS, HscA and HscB had very little or no detectable amounts of copper (Figure 2A). IscU and ferredoxin retained a small but reproducible amount of copper (~ 0.1

copper atoms per dimer). However, unlike IscA, the copper content in IscU and ferredoxin was further decreased after additional purification steps, indicating that copper binding in IscU and ferredoxin was not stable. Thus, among the iron-sulfur cluster assembly proteins encoded by *iscSUA-hscBA-fdx*, IscA has a unique and strong copper binding activity.

As copper-binding proteins often have electron paramagnetic resonance (EPR) signals (Ve *et al.*, 2012), purified IscA was subjected to EPR measurements. As shown in Figure 2B, IscA purified from the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with $CuSO_4$ (200 μM) had no EPR signal. However, when purified IscA was treated with 2.5% (v/v) nitric acid to oxidize Cu(I) in the protein as described in (Ve et al., 2012), an EPR signal representing a typical Cu(II) center (Smith *et al.*, 2008, Ve et al., 2012) appeared (Figure 2B), demonstrating that purified IscA indeed binds Cu(I) that can be oxidized by the strong oxidant nitric acid. Quantification of the Cu(II) EPR signal showed that purified IscA contained 0.55±0.12 copper atoms per IscA dimer, which is close to that determined using neocuproine (0.60±0.09 copper atoms per IscA dimer).

To further determine the copper binding activity of IscA *in vivo*, recombinant IscA was expressed in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with increased concentrations of $CuSO_4$. Figure 2C shows that as the concentration of $CuSO_4$ in LB media was gradually increased from 0 to 1.0 mM, the copper binding of IscA was progressively increased from 0 to about 1.4 copper atoms per IscA dimer. On the other hand, the cell growth of the *E. coli copA/cueO/cusA* mutant was gradually decreased to about 30% when the concentration of $CuSO_4$ in LB media was increased from 0 to 1.0 mM (Figure 2C). Because the cell growth of the *E. coli copA/cueO/cusA* mutant in LB media was severely inhibited by 1.0 mM $CuSO_4$ (Figure 2C), we were unable to obtain the maximum copper binding in IscA expressed in the *E. coli copA/cueO/cusA* mutant cells. Nevertheless, the results suggest that the copper binding in IscA inversely correlates with the cell growth when the concentration of $CuSO_4$ in LB media is increased from 0 to 1.0 mM.

The in vitro copper binding activity of IscA

To determine the *in vitro* copper binding activity of IscA, we prepared apo-IscA as described previously (Landry et al., 2013) and incubated apo-IscA (50 μM dimer) with increasing concentrations of $CuSO_4$ (0 to 200 μM) in the presence of dithiothreitol. Dithiothreitol was used to reduce Cu(II) to Cu(I) (Banci *et al.*, 2003) to emulate the intracellular redox state of copper ion (Macomber & Imlay, 2009) and to reduce thiol groups in IscA for copper binding. After incubation at room temperature for 15 min, IscA was re-purified by passing through a HiTrap Desalting column. As the $CuSO_4$ concentration in the incubation solution was increased, the amplitude of the absorption peak at 258 nm (Figure 3A) and the copper content (Figure 3B) of re-purified IscA were gradually increased and saturated at about two-fold excess of $CuSO_4$ in the incubation solution. It was reported that dithiothreitol and copper may generate hydroxyl free radicals in solution (Kachur *et al.*, 1997). However, production of hydroxyl free radicals in solution had a long delay (up to 5 hours) after dithiothreitol was mixed with copper under aerobic conditions (Kachur et al., 1997). Furthermore, similar results were obtained when apo-IscA was incubated with $CuSO_4$ (0 to 200 μM) and dithiothreitol (2 mM) under anaerobic conditions (data not

shown). Thus, it is unlikely that oxygen or hydroxyl free radicals are involved in the copper binding in IscA. Because the copper binding in IscA was almost linear at low concentrations of $CuSO_4$ (Figure 3B), we were unable to estimate the copper binding constant of IscA. Nevertheless, the result clearly showed that the maximum copper binding in IscA is 2.2 ± 0.4 copper atoms per IscA dimer (Figure 3B).

IscA proteins re-purified after incuabtion with $CuSO_4$ and dithiothreitol were also subjected to EPR measurements. Without any treatments, re-purified IscA proteins were EPR silent, similar to that purified from *E. coli* cells (Figure 2B). However, when re-purified IscA proteins were treated with 2.5% (v/v) nitric acid to oxidize Cu(I) (Ve et al., 2012), a typical Cu(II) EPR signal appeared, indicating that IscA also binds Cu(I) *in vitro*. The amplitude of the Cu(II) EPR signal of IscA was proportionally increased as the concentration of $CuSO_4$ was increased in the incubation solution (Figure 3C), and was closely correlated with the copper content in IscA (Figure 3B).

To further explore the property of the copper-bound IscA, re-purified IscA proteins were analyzed using an anion exchange Mono-Q column which separates proteins based on their net charge and protein conformation. Figure 3D shows that copper binding in IscA shifts the protein elution profile from fractions 10 and 11 (apo-IscA) to fractions 13 and 14 (the copper-bound IscA), indicating that copper binding has significantly changed the conformation of IscA dimer.

The conserved cysteine residues in IscA are required for the copper binding activity

The three conserved cysteine residues (Cys-35, Cys-99 and Cys-101) are essential for the iron binding activity of IscA *in vitro* (Ding et al., 2004) and for its physiological function in *E. coli* (Lu et al., 2008). If copper and iron share the same binding site in IscA, mutation of the conserved cysteine residues would disrupt both the iron and copper binding in the protein. To test this idea, we constructed an IscA mutant in which all three cysteine residues (Cys-35, Cys-99 and Cys-101) were replaced with serine. Prepared apo-IscA and IscA mutant were then incubated with two-fold excess of $Fe(NH_4)_2(SO_4)_2$ or $CuSO_4$ in the presence of dithiothreitol, followed by protein re-purification to remove residual metal ions and dithiothreitol. As reported previously, incubation of the wild-type apo-IscA with two-fold excess of iron or copper produced the iron-bound IscA (with an absorption peak at 315 nm) (Figure 4A) (Ding & Clark, 2004) or the copper-bound IscA (with an absorption peak at 258 nm) (Figure 4B), respectively. In contrast, incubation of the IscA mutant with iron or copper did not produce any absorption peaks of the iron- or copper- binding in the protein. The iron and copper content analyses confirmed that unlike the wild-type IscA, the IscA mutant did not bind any detectable amounts of iron or copper under the same experimental conditions (data not shown).

The wild-type IscA and IscA mutant proteins were also expressed in the *E. coli copA/cueO/ cusA* mutant cells grown in LB media supplemented with $Fe(NH_4)_2(SO_4)_2$ (200 μM) or $CuSO_4$ (200 μM). Again, unlike the wild-type IscA, the IscA mutant failed to bind any iron (Figure 4C) or copper (Figure 4D) in the *E. coli* cells. Taken together, the results suggest that the three conserved cysteine residues in IscA are essential for its iron and copper binding activity *in vitro* and *in vivo*.

Copper competes with iron for the metal binding site in IscA

If iron and copper share the metal binding site, excess copper may compete with iron for the same binding site in IscA. Indeed, addition of $CuSO_4$ (200 μM) to LB media largely eliminated the iron binding peak at 315 nm of IscA expressed in the *E. coli copA/cueO/cusA* mutant cells (Figure 1C). The metal content analyses further showed that the iron content of IscA was decreased from 0.21±0.04 to less than 0.04 iron atoms with concomitant increase of the copper content from 0 to 0.60±0.09 copper atoms per IscA dimer when LB media were supplemented with 200 μM $CuSO_4$.

To further explore the copper and iron binding competition in IscA, purified apo-IscA was incubated with a fixed amount of iron and increasing amounts of copper in the presence of dithiothreitol, followed by re-purification of IscA. As shown in Figure 5A, incubation of apo-IscA (50 μM dimer) with 100 μM $Fe(NH_4)_2(SO_4)_2$ produced an iron-bound IscA with an absorption peak at 315 nm as reported above. However, when apo-IscA (50 μM dimer) was incubated with 100 μM $Fe(NH_4)_2(SO_4)_2$ and 100 μM $CuSO_4$, the absorption peak at 315 nm of IscA was significantly diminished (Figure 5A), and the iron content of IscA was decreased with concomitant increase of the copper content in the protein (Figure 5B). When apo-IscA (50 μM dimer) was incubated with 100 μM $Fe(NH_4)_2(SO_4)_2$ and 200 μM $CuSO_4$, the absorption peak at 315 nm of re-purified IscA was largely eliminated (Figure 5A), and the iron content of IscA was further decreased with the copper content increased to 1.81±0.15 copper atoms per IscA dimer (Figure 5B). Thus, excess copper can effectively compete with iron for the metal binding site in IscA.

Copper inhibits the [4Fe-4S] cluster assembly in the E. coli cells

Previous studies revealed that IscA and its paralogue SufA are essential for the [4Fe-4S] cluster assembly in *E. coli* cells under aerobic conditions (Tan et al., 2009). IscA and SufA share the similar crystal structure (Wada et al., 2005, Cupp-Vickery et al., 2004, Bilder et al., 2004) and iron binding activity (Lu et al., 2008). Parallel experiments showed that *E. coli* SufA also has a similar copper binding activity as IscA in the *E. coli copA/cueO/cusA* mutant cells grown in LB media (Supplementary Figure 1). Thus, if copper competes with iron for the metal binding site in IscA and SufA, copper may inhibit the IscA/SufA-mediated [4Fe-4S] cluster assembly in *E. coli* cells. To test this idea, we decided to analyze the [4Fe-4S] cluster assembly in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with or without $CuSO_4$ (200 μM).

E. coli dihydroxyacid dehydratase (IlvD) requires an intact [4Fe-4S] cluster for its catalytic activity (Flint *et al.*, 1993). Relative activity of IlvD has previously been used to assess the [4Fe-4S] cluster assembly in the protein in *E. coli* cells (Ren *et al.*, 2008). In this set of experiments, recombinant IlvD was expressed in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with or without $CuSO_4$ (200 μM). The cell extracts were prepared after the cells were passed through French press once, and immediately used for the IlvD activity assay. Figure 6A shows that addition of $CuSO_4$ (200 μM) to LB media before recombinant IlvD was expressed in the *E. coli* cells decreased the IlvD enzyme activity to about 10%. However, the enzyme activity of IlvD was largely recovered when the cell extracts were incubated with L-cysteine, cysteine desulfurase IscS, $Fe(NH_4)_2(SO_4)_2$,

and dithiothreitol to reconstitute the [4Fe-4S] clusters in IlvD under anaerobic conditions (Figure 6A), suggesting that $CuSO_4$ (200 μM) in LB media blocks the [4Fe-4S] cluster assembly in IlvD without inhibiting protein synthesis in the *E. coli* cells. Interestingly, when $CuSO_4$ (200 μM) was added to LB media after recombinant IlvD was expressed in the *E. coli* cells, over 85% of the enzyme activity of IlvD remained, indicating that copper at 200 μM in LB media does not significantly affect the pre-assembled [4Fe-4S] clusters in IlvD in *E. coli* cells.

To further explore the copper-mediated inhibition of the [4Fe-4S] cluster assembly in IlvD in the *E. coli copA/cueO/cusA* mutant cells, $CuSO_4$ (200 μM) was added to LB media when recombinant IlvD was expressed for one hour. As shown in Figure 6B, without any addition of $CuSO_4$, the active IlvD (IlvD with an intact [4Fe-4S] cluster) linearly accumulated in the cells. However, addition of $CuSO_4$ (200 μM) to LB media effectively blocked the new [4Fe-4S] cluster assembly in IlvD in the *E. coli* cells. Pre-assembled [4Fe-4S] clusters in IlvD decreased only slightly in the *E. coli* cells during incubation with LB media supplemented with $CuSO_4$ (200 μM). The Western blotting analyses of the cell extracts further confirmed that $CuSO_4$ (200 μM) did not significantly affect the protein expression of IlvD in the *E. coli* cells (Figure 6C). Thus, $CuSO_4$ (200 μM) can effectively inhibit the [4Fe-4S] cluster assembly in IlvD without significant effect on the pre-assembled [4Fe-4S] clusters in the protein in the *E. coli copA/cueO/cusA* mutant cells grown in LB media.

If copper blocks the [4Fe-4S] cluster assembly in the *E. coli* cells, it should also inhibit the activities of other proteins that contain [4Fe-4S] clusters. Indeed, similar results were obtained when recombinant aconitase B [4Fe-4S] cluster (Varghese *et al.*, 2003) or phosphogluconate dehydratase [4Fe-4S] cluster (Jang & Imlay, 2007) was expressed in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with $CuSO_4$ (200 μM) (data not shown). We also examined the effect of $CuSO_4$ (200 μM) on native NADH dehydrogenase I which requires multiple iron-sulfur clusters for its catalytic activity (Nakamaru-Ogiso *et al.*, 2008). Using deamino-NADH as specific substrate for NADH dehydrogenase I (Matsushita *et al.*, 1987), we found that addition of $CuSO_4$ (200 μM) dramatically inhibited the enzyme activity of NADH dehydrogenase I but without significantly affecting the activity of pre-existed NADH dehydrogenase I in the *E. coli copA/cueO/cusA* mutant cells (Figure 6D). Thus, copper can effectively inhibit the [4Fe-4S] cluster assembly in *E. coli* cells.

Excess copper emulates the phenotype of an E. coli mutant with deletion of IscA/SufA

Deletion of IscA and its paralogue SufA results in an *E. coli* mutant that fails to assemble [4Fe-4S] clusters (Figure 7A) but not [2Fe-2S] clusters in proteins (Figure 7B) under aerobic growth conditions (Tan et al., 2009). If the copper binding in IscA/SufA blocks iron-sulfur cluster biogenesis in *E. coli* cells, excess copper may emulate a phenotype of the *E. coli* mutant with deletion of IscA/SufA. To test this idea, we expressed the *E. coli* endonuclease III in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with $CuSO_4$ (200 μM). Endonuclease III hosts a stable [4Fe-4S] cluster (Thayer *et al.*, 1995) which should be resistant to disruption by copper (Macomber & Imlay, 2009). As shown in Figure 7C, addition of $CuSO_4$ (200 μM) to LB media largely blocked the [4Fe-4S] cluster

assembly in recombinant endonuclease III in the *E. coli* cells. In contrast, addition of $CuSO_4$ (200 μM) to LB media had very little or no effect on the [2Fe-2S] cluster assembly in ferric iron reductase FhuF (Muller *et al.*, 1998) in the *E. coli copA/cueO/cusA* mutant cells (Figure 7D). Similarly, addition of $CuSO_4$ (200 μM) to LB media did not affect the [2Fe-2S] cluster assembly in ferredoxin expressed in the *E. coli copA/cueO/cusA* mutant cells (Figure 1F). The selective inhibition of the [4Fe-4S] cluster assembly by $CuSO_4$ (200 μM) in the *E. coli* cells strongly suggests that copper in LB media may emulate the phenotype of the *E. coli* cells with deletion of IscA/SufA.

IscA acts as a primary target of copper toxicity

The proteins encoded by the gene cluster *iscSUA-hscBA-fdx* represent the house-keeping machinery for iron-sulfur cluster assembly under normal physiological conditions (Zheng et al., 1998). SufA and other proteins encoded by the alternative iron-sulfur cluster assembly gene cluster *sufABCDSE* (Takahashi & Tokumoto, 2002) are induced only under iron starvation (Outten *et al.*, 2004) or oxidative stress (Lee *et al.*, 2004). Thus, we postulate that IscA could be the primary target of copper toxicity in *E. coli* cells under normal growth conditions. To test this idea, we deleted the gene encoding IscA in the wild-type *E. coli* cells and explored the copper toxicity on iron-sulfur cluster assembly in these mutant cells. Recombinant endonuclease III was expressed in the wild-type and the IscA-deleted mutant cells grown in LB media supplemented with or without $CuSO_4$ (2 mM). Protein was purified from the cells and subjected to UV-Visible absorption measurements. As shown in Figure 8A, deletion of IscA severely blocked the [4Fe-4S] cluster assembly in endonuclease III expressed in *E. coli* cells. In contrast, deletion of SufA had no noticeable effect on the [4Fe-4S] cluster assembly in endonuclease III expressed in *E. coli* cells (data not shown). While $CuSO_4$ (2 mM) in LB media largely inhibited the [4Fe-4S] cluster assembly in endonuclease III in the wild-type *E. coli* cells, $CuSO_4$ (2 mM) had very little or no additional inhibitory effect on the [4Fe-4S] cluster assembly in endonuclease III in the IscA-deleted cells. We also performed the same experiments in the *E. coli copA/cueO/cusA* mutant cells, and found that deletion of IscA also significantly inhibited the [4Fe-4S] cluster assembly in endonuclease III in the cells. Again, while $CuSO_4$ (200 μM) largely inhibited the [4Fe-4S] cluster assembly in endonuclease III in the *E. coli copA/cueO/cusA* mutant cells, $CuSO_4$ (200 μM) had very little or no additional inhibitory effect on the [4Fe-4S] cluster assembly in endonuclease III in the IscA-deleted *copA/cueO/cusA* cells (Figure 8B).

Discussion

It has been proposed that copper may mediate production of reactive oxygen species via Fenton reaction and contribute to copper-mediated toxicity in cells (Rodriguez-Montelongo et al., 1993, Karlsson et al., 2008). However, recent studies argued that copper does not promote oxidative damage in *E. coli* cells even under aerobic conditions (Macomber *et al.*, 2007). Instead, copper may directly disrupt the labile [4Fe-4S] clusters of dehydratases, inactivate these enzymes, and contribute to copper toxicity (Macomber & Imlay, 2009). In this study, we expand this view by showing that copper can effectively block the [4Fe-4S] cluster assembly in *E. coli* cells by targeting the iron-sulfur cluster assembly protein IscA. Among the iron-sulfur cluster assembly proteins encoded by the gene cluster *iscSUA-hscBA-*

fdx (Zheng et al., 1998), IscA has a strong and specific copper binding activity *in vivo* (Figures 1 and 2) and *in vitro* (Figure 3). Substitution of the three conserved cysteine residues with serine in IscA abolishes the iron and copper binding activities (Figure 4), indicating that copper and iron may share the same binding sites in the protein. In addition, excess copper can compete with iron for the metal binding site in IscA (Figure 5) and inhibit the IscA-mediated [4Fe-4S] cluster assembly in *E. coli* cells grown in LB media (Figures 6 and 7). Furthermore, deletion of IscA severely inhibits the [4Fe-4S] cluster assembly in *E. coli* cells under normal growth conditions and addition of copper to the IscA-deleted mutant cells has very little or no additional inhibitory effect on the [4Fe-4S] cluster assembly in the *E. coli* cells (Figure 8). These results led us to propose that copper can effectively block the [4Fe-4S] cluster assembly in proteins and that IscA is a primary target of copper toxicity in *E. coli* cells.

The crystallographic studies revealed that IscA has a "cysteine pocket" formed by the three conserved cysteine residues which may accommodate a mononuclear iron or iron-sulfur cluster (Bilder et al., 2004, Cupp-Vickery et al., 2004, Wada et al., 2005). The results from this study further suggest that the "cysteine pocket" in IscA can also facilitate the copper binding, as mutation of the cysteine residues to serine abolishes both the copper and iron binding activities of IscA. While each IscA dimer can bind one ferric iron atom (Ding & Clark, 2004, Mapolelo et al., 2012a), IscA appears to bind two Cu(I) atoms per IscA dimer (Figure 3), suggesting that copper and iron may have different ligand binding coordination in IscA. Perhaps, unlike the iron binding in IscA which likely has five coordinates with two or three cysteinate ligands (Ding & Clark, 2004, Mapolelo et al., 2012a), the copper binding may only need two cysteine residues to form linear biscysteinate coordination geometry as seen in the Parkinsonism-associated protein DJ-1 protein (Puno et al., 2013). Although we are unable to estimate the copper binding affinity of IscA from the copper titration experiments (Figure 3B), the results from the completion of iron and copper binding in IscA (Figure 5) suggests that IscA has similar binding affinities for iron and copper. Evidently, elucidation of the copper binding ligands in IscA requires additional experimentations. Nevertheless, the observed competition of iron and copper binding for the metal binding sites in IscA represents a dynamic interplay between intracellular copper content and iron-sulfur cluster biogenesis in cells.

The salient finding of this study is that copper can effectively inhibit the [4Fe-4S] cluster assembly (Figures 5 and 6) without significant effect on the pre-assembled clusters in proteins in *E. coli* cells grown in LB media. In *E. coli*, iron-sulfur clusters are assembled by two major iron-sulfur cluster assembly machineries, the house-keeping *iscSUA-hscBA-fdx* (Zheng et al., 1998, Roche et al., 2013) and the redundant *sufABCDSE* (Takahashi & Tokumoto, 2002) which is induced under iron starvation (Outten et al., 2004) or oxidative stress (Lee et al., 2004). Since increased expression of the second iron-sulfur cluster assembly gene cluster *sufABCDSE* is an indication of the iron-sulfur cluster assembly deficiency in *E. coli* cells (Jang & Imlay, 2010), we analyzed the expression of the *sufA::lacZ* operon in the wild-type *E. coli* cells (Jang & Imlay, 2010) in response to $CuSO_4$ in LB media, and found that expression of the *sufA::lacZ* operon was indeed induced by $CuSO_4$ (Supplementary Figure 2), suggesting that copper has a general inhibitory effect on

iron-sulfur cluster biogenesis. This is in agreement with the recent observation that inactivation of the copper efflux pump CusCFBA stimulates expression of the *sufA::lacZ* operon in *E. coli* cells (Fung et al., 2013). The apparent contradiction with the previous report that copper disrupts the labile [4Fe-4S] clusters in dehydratases (Macomber & Imlay, 2009) is likely due to the different growth media used in the experiments. While the wild-type *E. coli* cells are highly sensitive to copper in M9 minimal media (32 μM $CuSO_4$ completely inhibits the cell growth) (Macomber & Imlay, 2009), the wild-type *E. coli* cells are highly resistant to copper in LB media (cell growth is decreased by only about 20% when LB media are supplemented with 2 mM $CuSO_4$ (Supplementary Figure 2)). One possible consideration is that copper in M9 minimal media and LB media may interfere the iron transportation in *E. coli* cells differently. It is also possible that iron deficiency in M9 minimal media (Wang et al., 2010) may have already limited iron-sulfur cluster biogenesis in *E. coli* cells in such that the effect of copper on iron-sulfur cluster biogenesis could not be observed.

Among the iron-sulfur cluster assembly proteins encoded by *iscSUA-hscBA-fdx* (Zheng et al., 1998), only IscA has a specific and strong copper binding activity (Figure 1). The inverse correlation between the copper binding in IscA and the cell growth of the *E. coli copA/cueO/cusA* mutant cells in LB media supplemented with increased concentration of $CuSO_4$ (Figure 2C) indicates that the copper binding in IscA may directly contribute to the cell growth inhibition. More importantly, the observation that excess copper in LB media selectively inhibits the [4Fe-4S] cluster assembly without affecting the [2Fe-2S] cluster assembly in *E. coli* cells (Figure 7C and D) suggests that copper in LB media may emulate the phenotype of an *E. coli* mutant with deletion of IscA/SufA (Tan et al., 2009). Although SufA can also bind copper (Supplementary Figure 1), the gene encoding SufA is induced only under iron starvation (Outten et al., 2004) or oxidative stress (Lee et al., 2004). Thus, IscA could be the major target of copper-toxicity in *E. coli* cells under normal growth conditions. Indeed, we find that deletion of IscA largely inhibits the [4Fe-4S] cluster assembly in endonuclease III expressed in *E. coli* cells. Furthermore, while copper in LB media effectively inhibits the [4Fe-4S] cluster assembly in endonuclease III in the *E. coli* cells, copper has very little or no additional inhibitory effect on the [4Fe-4S] cluster assembly in the IscA-deleted cells (Figure 8), supporting the notion that IscA is the primary target of copper toxicity. Interestingly, copper has also been shown to inhibit iron-sulfur cluster assembly in *Bacillus subtilis* by binding to a *Bacillus*-specific iron-sulfur cluster assembly protein SufU (Chillappagari et al., 2010). We noticed the small amount of copper binding in IscU (Figure 2A) which could also contribute to the copper-mediated inhibition of iron-sulfur cluster assembly in *E. coli* cells. However, considering the relatively weak binding of copper in IscU, it is plausible that the copper-bound IscA may accidently transfer the copper to IscU in cells. The question on how the copper binding in IscA inhibits iron-sulfur cluster biogenesis can only be speculated. One explanation is that excess copper may compete with iron for the metal binding site in IscA, thus preventing the turnover of IscA for iron-sulfur cluster assembly. Alternatively, the copper-bound IscA may poison the iron-sulfur cluster assembly machinery and inhibit iron-sulfur cluster biogenesis in cells. Additional experiments are required to illustrate the mechanism underlying copper-mediated inhibition of iron-sulfur cluster assembly in cells.

Experimental Procedures

Gene knockout in E. coli cells

Genes encoding three major proteins regulating intracellular copper homeostasis: CopA, CueO and CusA, were deleted following the procedures described in (Datsenko & Wanner, 2000). Gene encoding IscA was also deleted from the wild-type and the *copA/cueO/cusA* mutant cells. The gene deletion was confirmed by PCR. All primers for the gene deletion and confirmation were synthesized by Takara co. (Dalian, P. R. China). The constructed *E. coli copA/cueO/cusA* mutant cells grow normally in LB media and are hypersensitive to copper in media, as reported previously (Grass & Rensing, 2001, Macomber & Imlay, 2009).

Enzyme activity assay for dihydroxyacid dehydratase (IlvD)

The cell extracts were prepared by passing the cells containing recombinant IlvD through French press once, followed by centrifugation at 34,000 g for 45 min. The specific enzyme activity was measured using substrate DL-2,3-dihydroxy-isovalerate which was synthesized according to the method of Cioffi et al. (Cioffi *et al.*, 1980). In the enzyme assay, 10 μL of the cell extracts (~5.0 mg total protein/mL) prepared from the *E. coli* cells containing were added to 390 μL pre-incubated solutions containing 50 mM Tris (pH 8.0), 10 mM $MgCl_2$, and 10 mM D, L-2,3-dihydroxy-isovalerate (Flint et al., 1993). The reaction product (keto acids) was monitored at 240 nm using an extinction coefficient of 0.19 $cm^{-1}mM^{-1}$ (Flint et al., 1993). The amount of recombinant IlvD in cell extracts was quantified by Western blotting using the antibody against His-tag (abcam co.) For the reconstitution of iron-sulfur clusters in recombinant IlvD, cell extracts were incubated with cysteine desulfurase (IscS) (1 μM), $Fe(NH_4)_2(SO_4)_2$ (100 μM), L-cysteine (1 mM), and dithiothreitol (2 mM) at 37°C under anaerobic conditions for 30 min.

Enzyme activity assay for the NADH dehydrogenase I

NADH dehydrogenase I activity of *E. coli* cells was measured following the procedures described in (Xu & Imlay, 2012). Briefly, cells were grown in LB media supplemented with different concentration of $CuSO_4$. Cells were harvested after three hours of growth, washed once with buffer containing Tris (20mM, pH 8.0) and NaCl (200 mM), and re-suspended to OD of 2.5 at 600 nm. Inverted membrane vesicles were prepared by passing the cells through French press once. Inverted membrane vesicles (10 μL) was added to the reaction solution (290 μL) containing Tris (20mM, pH 8.0), NaCl (200 mM) and deamino-NADH (50 μM). Damino-NADH was chosen as NADH dehydrogenase II does not act on this NADH analogue (Matsushita et al., 1987). The NADH dehydrogenase I activity was determined by measuring oxidation of deamino-NADH at 340 nm at room temperature.

Protein purification

Genes encoding the housekeeping iron-sulfur cluster assembly proteins IscS, IscU, IscA, HscB, HscA, and ferredoxin from *E. coli* were amplified using PCR, and cloned to an expression plasmid pBAD as described previously (Yang et al., 2006). The IscA mutant was constructed by the site-directed mutagenesis QuikChange kit (Agilent co.). The cloned genes

and mutants were confirmed by direct sequencing. The plasmids expressing *E. coli* dihydroxyacid dehydratase (IlvD), endonuclease III, and FhuF were previously prepared (Tan et al., 2009). Each plasmid was introduced into the *E. coli copA/cueO/cusA* mutant cells. Cells containing the protein expression plasmid were grown to OD of 0.6 at 600 nm. $CuSO_4$ was then added to cell cultures ten min before recombinant protein was induced with 0.02% arabinose. After three hours of induction at 37°C with aeration, cells were harvested and washed twice with protein purification buffer (NaCl (500 mM), Tris (20 mM, pH 8.0)). Proteins were purified to a single band on the SDS-PAGE gel as described in (Yang et al., 2006). The concentration of purified protein was determined from the absorption peak at 280 nm using the published extinction coefficients.

Copper and iron content analyses

The iron content of protein samples was determined using ferroZine (Cowart *et al.*, 1993) as described previously (Ding et al., 2005b). The copper content of protein samples was determined following the procedure described in (Tutem *et al.*, 1991) with slight modification. Briefly, protein samples (160 μL) were incubated with 10 μL neocuproine (5 mM in H_2O:ethanol (1:1)), 20 μL SDS (20%) and 10 μL sodium ascorbate (5 mM). Mixtures were incubated at room temperature for 20 min, followed by centrifugation. The amplitude of the absorption peak at 450 nm of supernatants was used for quantification of copper content in each protein sample. Freshly prepared $CuSO_4$ (10 μM) was used as a standard. The metal contents in proteins were also analyzed by the Inductively Coupled Plasma-Emission Spectrometry (ICP-ES). Both metal content analyses produced similar results.

EPR (Electron Paramagnetic Resonance) measurements

The EPR spectra were recorded at X-band on a Bruker ESP-300 spectrometer equipped with an Oxford Instruments 910 continuous flow cryostat. The routine EPR conditions were: microwave frequency, 9.45 GHz; microwave power, 10 mW; modulation frequency, 100 kHz; modulation amplitude, 2.0 mT; sample temperature, 30 K; receive gain, 1.0×10^5. A solution containing Cu(II)-EDTA (10 μM) was used as a standard for quantification of C(II) in the protein.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

References

Agar JN, Krebs C, Frazzon J, Huynh BH, Dean DR, Johnson MK. IscU as a scaffold for iron-sulfur cluster biosynthesis: sequential assembly of [2Fe-2S] and [4Fe-4S] clusters in IscU. Biochemistry. 2000; 39:7856–7862. [PubMed: 10891064]

Banci L, Bertini I, Del Conte R, Mangani S, Meyer-Klaucke W. X-ray absorption and NMR spectroscopic studies of CopZ, a copper chaperone in Bacillus subtilis: the coordination properties of the copper ion. Biochemistry. 2003; 42:2467–2474. [PubMed: 12600214]

Bilder PW, Ding H, Newcomer ME. Crystal structure of the ancient, Fe-S scaffold IscA reveals a novel protein fold. Biochemistry. 2004; 43:133–139. [PubMed: 14705938]

Chandramouli K, Unciuleac MC, Naik S, Dean DR, Huynh BH, Johnson MK. Formation and properties of [4Fe-4S] clusters on the IscU scaffold protein. Biochemistry. 2007; 46:6804–6811. [PubMed: 17506525]

Chillappagari S, Seubert A, Trip H, Kuipers OP, Marahiel MA, Miethke M. Copper stress affects iron homeostasis by destabilizing iron-sulfur cluster formation in Bacillus subtilis. J Bacteriol. 2010; 192:2512–2524. [PubMed: 20233928]

Cioffi EA, Shaw KJ, Bailey WF, Berg CM. Improved synthesis of the sodium salt of DL-alpha, beta-dihydroxyisovaleric acid. Anal Biochem. 1980; 104:485–488. [PubMed: 7004266]

Cowart RE, Singleton FL, Hind JS. A comparison of bathophenanthrolinedisulfonic acid and ferrozine as chelators of iron(II) in reduction reactions. Anal Biochem. 1993; 211:151–155. [PubMed: 8323027]

Cupp-Vickery JR, Silberg JJ, Ta DT, Vickery LE. Crystal Structure of IscA, an Iron-sulfur Cluster Assembly Protein from Escherichia coli. J Mol Biol. 2004; 338:127–137. [PubMed: 15050828]

Datsenko KA, Wanner BL. One-step inactivation of chromosomal genes in Escherichia coli K-12 using PCR products. Proc Natl Acad Sci U S A. 2000; 97:6640–6645. [PubMed: 10829079]

Ding B, Smith ES, Ding H. Mobilization of the iron centre in IscA for the iron-sulphur cluster assembly in IscU. Biochem J. 2005a; 389:797–802. [PubMed: 15828873]

Ding H, Clark RJ. Characterization of iron binding in IscA, an ancient iron-sulphur cluster assembly protein. Biochem J. 2004; 379:433–440. [PubMed: 14720122]

Ding H, Clark RJ, Ding B. IscA mediates iron delivery for assembly of iron-sulfur clusters in IscU under the limited accessible free iron conditions. J Biol Chem. 2004; 279:37499–37504. [PubMed: 15247288]

Ding H, Harrison K, Lu J. Thioredoxin reductase system mediates iron binding in IscA and iron delivery for the iron-sulfur cluster assembly in IscU. J Biol Chem. 2005b; 280:30432–30437. [PubMed: 15985427]

Fan B, Rosen BP. Biochemical characterization of CopA, the Escherichia coli Cu(I)-translocating P-type ATPase. J Biol Chem. 2002; 277:46987–46992. [PubMed: 12351646]

Flint DH, Emptage MH, Finnegan MG, Fu W, Johnson MK. The role and properties of the iron-sulfur cluster in Escherichia coli dihydroxy-acid dehydratase. J Biol Chem. 1993; 268:14732–14742. [PubMed: 8325851]

Fung DK, Lau WY, Chan WT, Yan A. Copper efflux is induced during anaerobic amino acid limitation in Escherichia coli to protect iron-sulfur cluster enzymes and biogenesis. J Bacteriol. 2013; 195:4556–4568. [PubMed: 23893112]

Grass G, Rensing C. Genes involved in copper homeostasis in Escherichia coli. J Bacteriol. 2001; 183:2145–2147. [PubMed: 11222619]

Jang S, Imlay JA. Micromolar intracellular hydrogen peroxide disrupts metabolism by damaging iron-sulfur enzymes. J Biol Chem. 2007; 282:929–937. [PubMed: 17102132]

Jang S, Imlay JA. Hydrogen peroxide inactivates the Escherichia coli Isc iron-sulphur assembly system, and OxyR induces the Suf system to compensate. Molecular Microbiology. 2010; 78:1448–1467. [PubMed: 21143317]

Johnson DC, Dean DR, Smith AD, Johnson MK. Structure, function, and formation of biological iron-sulfur clusters. Annu Rev Biochem. 2005; 74:247–281. [PubMed: 15952888]

Johnson DC, Unciuleac MC, Dean DR. Controlled expression and functional analysis of iron-sulfur cluster biosynthetic components within Azotobacter vinelandii. J Bacteriol. 2006; 188:7551–7561. [PubMed: 16936042]

Kachur AV, Held KD, Koch CJ, Biaglow JE. Mechanism of production of hydroxyl radicals in the copper-catalyzed oxidation of dithiothreitol. Radiat Res. 1997; 147:409–415. [PubMed: 9092919]

Karlsson HL, Cronholm P, Gustafsson J, Moller L. Copper oxide nanoparticles are highly toxic: a comparison between metal oxide nanoparticles and carbon nanotubes. Chem Res Toxicol. 2008; 21:1726–1732. [PubMed: 18710264]

Kim JH, Frederick RO, Reinen NM, Troupis AT, Markley JL. [2Fe-2S]-Ferredoxin binds directly to cysteine desulfurase and supplies an electron for iron-sulfur cluster assembly but is displaced by the scaffold protein or bacterial frataxin. J Am Chem Soc. 2013; 135:8117–8120. [PubMed: 23682711]

Kim JH, Tonelli M, Frederick RO, Chow DCF, Markley JL. Specialized Hsp70 Chaperone (HscA) Binds Preferentially to the Disordered Form, whereas J-protein (HscB) Binds Preferentially to the Structured Form of the Iron-Sulfur Cluster Scaffold Protein (IscU). J Biol Chem. 2012; 287:31406–31413. [PubMed: 22782893]

Krebs C, Agar JN, Smith AD, Frazzon J, Dean DR, Huynh BH, Johnson MK. IscA, an alternate scaffold for Fe-S cluster biosynthesis. Biochemistry. 2001; 40:14069–14080. [PubMed: 11705400]

Landry AP, Cheng Z, Ding H. Iron binding activity is essential for the function of IscA in iron-sulphur cluster biogenesis. Dalton Trans. 2013; 42:3100–3106. [PubMed: 23258274]

Lee JH, Yeo WS, Roe JH. Induction of the sufA operon encoding Fe-S assembly proteins by superoxide generators and hydrogen peroxide: involvement of OxyR, IHF and an unidentified oxidant-responsive factor. Mol Microbiol. 2004; 51:1745–1755. [PubMed: 15009899]

Lu J, Bitoun JP, Tan G, Wang W, Min W, Ding H. Iron binding activity of human iron-sulfur cluster assembly protein hIscA-1. Biochem J. 2010; 428:125–131. [PubMed: 20302570]

Lu J, Yang J, Tan G, Ding H. Complementary roles of SufA and IscA in the biogenesis of iron-sulfur clusters in Escherichia coli. Biochem J. 2008; 409:535–543. [PubMed: 17941825]

Macomber L, Imlay JA. The iron-sulfur clusters of dehydratases are primary intracellular targets of copper toxicity. Proc Natl Acad Sci U S A. 2009; 106:8344–8349. [PubMed: 19416816]

Macomber L, Rensing C, Imlay JA. Intracellular copper does not catalyze the formation of oxidative DNA damage in Escherichia coli. J Bacteriol. 2007; 189:1616–1626. [PubMed: 17189367]

Mapolelo DT, Zhang B, Naik SG, Huynh BH, Johnson MK. Spectroscopic and functional characterization of iron-bound forms of Azotobacter vinelandii (Nif)IscA. Biochemistry. 2012a; 51:8056–8070. [PubMed: 23003563]

Mapolelo DT, Zhang B, Naik SG, Huynh BH, Johnson MK. Spectroscopic and functional characterization of iron-sulfur cluster-bound forms of Azotobacter vinelandii (Nif)IscA. Biochemistry. 2012b; 51:8071–8084. [PubMed: 23003323]

Mapolelo DT, Zhang B, Randeniya S, Albetel AN, Li H, Couturier J, Outten CE, Rouhier N, Johnson MK. Monothiol glutaredoxins and A-type proteins: partners in Fe-S cluster trafficking. Dalton Trans. 2013; 42:3107–3115. [PubMed: 23292141]

Marinoni EN, de Oliveira JS, Nicolet Y, Raulfs EC, Amara P, Dean DR, Fontecilla-Camps JC. (IscS-IscU)2 Complex Structures Provide Insights into Fe2S2 Biogenesis and Transfer. Angewandte Chemie International Edition. 2012; 51:5439–5442.

Matsushita K, Ohnishi T, Kaback HR. NADH-ubiquinone oxidoreductases of the Escherichia coli aerobic respiratory chain. Biochemistry. 1987; 26:7732–7737. [PubMed: 3122832]

Mettert EL, Outten FW, Wanta B, Kiley PJ. The impact of O(2) on the Fe-S cluster biogenesis requirements of Escherichia coli FNR. J Mol Biol. 2008; 384:798–811. [PubMed: 18938178]

Muhlenhoff U, Richter N, Pines O, Pierik AJ, Lill R. Specialized Function of Yeast Isa1 and Isa2 in the Maturation of Mitochondrial [4fe-4s] Proteins. J Biol Chem. 2011; 286:41205–41216. [PubMed: 21987576]

Muller K, Matzanke BF, Schunemann V, Trautwein AX, Hantke K. FhuF, an iron-regulated protein of Escherichia coli with a new type of [2Fe-2S] center. Eur J Biochem. 1998; 258:1001–1008. [PubMed: 9990318]

Munson GP, Lam DL, Outten FW, O'Halloran TV. Identification of a copper-responsive two-component system on the chromosome of Escherichia coli K-12. J Bacteriol. 2000; 182:5864–5871. [PubMed: 11004187]

Nakamaru-Ogiso E, Matsuno-Yagi A, Yoshikawa S, Yagi T, Ohnishi T. Iron-sulfur cluster N5 is coordinated by an HXXXCXXCXXXXXC motif in the NuoG subunit of Escherichia coli NADH:quinone oxidoreductase (complex I). J Biol Chem. 2008; 283:25979–25987. [PubMed: 18603533]

Ollagnier-de-Choudens S, Mattioli T, Takahashi Y, Fontecave M. Iron-sulfur cluster assembly: characterization of IscA and evidence for a specific and functional complex with ferredoxin. J Biol Chem. 2001; 276:22604–22607. [PubMed: 11319236]

Outten FW, Djaman O, Storz G. A *suf* operon requirement for Fe-S cluster assembly during iron starvation in *Escherichia coli*. Mol Microbiol. 2004; 52:861–872. [PubMed: 15101990]

Outten FW, Munson GP. Lability and liability of endogenous copper pools. J Bacteriol. 2013; 195:4553–4555. [PubMed: 23913325]

Puno MR, Patel NA, Moller SG, Robinson CV, Moody PC, Odell M. Structure of Cu(I)-Bound DJ-1 Reveals a Biscysteinate Metal Binding Site at the Homodimer Interface: Insights into Mutational Inactivation of DJ-1 in Parkinsonism. J Am Chem Soc. 2013; 135:15974–15977. [PubMed: 24144264]

Raulfs EC, O'Carroll IP, Dos Santos PC, Unciuleac MC, Dean DR. In vivo iron-sulfur cluster formation. Proc Natl Acad Sci U S A. 2008; 105:8591–8596. [PubMed: 18562278]

Ren B, Zhang N, Yang J, Ding H. Nitric oxide-induced bacteriostasis and modification of iron-sulphur proteins in Escherichia coli. Mol Microbiol. 2008; 70:953–964. [PubMed: 18811727]

Roche B, Aussel L, Ezraty B, Mandin P, Py B, Barras F. Iron/sulfur proteins biogenesis in prokaryotes: formation, regulation and diversity. Biochim Biophys Acta. 2013; 1827:455–469. [PubMed: 23298813]

Rodriguez-Montelongo L, de la Cruz-Rodriguez LC, Farias RN, Massa EM. Membrane-associated redox cycling of copper mediates hydroperoxide toxicity in Escherichia coli. Biochim Biophys Acta. 1993; 1144:77–84. [PubMed: 8347663]

Sheftel AD, Wilbrecht C, Stehling O, Niggemeyer B, Elsasser HP, Muhlenhoff U, Lill R. The human mitochondrial ISCA1, ISCA2, and IBA57 proteins are required for [4Fe-4S] protein maturation. Mol Biol Cell. 2012; 23:1157–1166. [PubMed: 22323289]

Smith AD, Agar JN, Johnson KA, Frazzon J, Amster IJ, Dean DR, Johnson MK. Sulfur transfer from IscS to IscU: the first step in iron-sulfur cluster biosynthesis. J Am Chem Soc. 2001; 123:11103–11104. [PubMed: 11686732]

Smith SR, Bencze KZ, Wasiukanis K, Stemmler TL, Benore-Parsons M. Association of Copper to Riboflavin Binding Protein; Characterization by EPR and XAS. Open inorganic chemistry journal. 2008; 2:22–24. [PubMed: 19337565]

Song D, Tu Z, Lee FS. Human IscA1 interacts with IOP1/NARFL and functions in both cytosolic and mitochondrial iron-sulfur protein biogenesis. J Biol Chem. 2009; 284:35297–35307. [PubMed: 19864422]

Stoyanov JV, Hobman JL, Brown NL. CueR (YbbI) of Escherichia coli is a MerR family regulator controlling expression of the copper exporter CopA. Mol Microbiol. 2001; 39:502–511. [PubMed: 11136469]

Ta DT, Vickery LE. Cloning, sequencing, and overexpression of a [2Fe-2S] ferredoxin gene from Escherichia coli. J Biol Chem. 1992; 267:11120–11125. [PubMed: 1317854]

Takahashi Y, Tokumoto U. A third bacterial system for the assembly of iron-sulfur clusters with homologs in archaea and plastids. J Biol Chem. 2002; 277:28380–28383. [PubMed: 12089140]

Tan G, Lu J, Bitoun JP, Huang H, Ding H. IscA/SufA paralogs are required for the [4Fe-4S] cluster assembly in enzymes of multiple physiological pathways in Escherichia coli under aerobic growth conditions. Biochem J. 2009; 420:463–472. [PubMed: 19309314]

Thayer MM, Ahern H, Xing D, Cunningham RP, Tainer JA. Novel DNA binding motifs in the DNA repair enzyme endonuclease III crystal structure. Embo J. 1995; 14:4108–4120. [PubMed: 7664751]

Tutem E, Apak R, Baykut F. Spectrophotometric determination of trace amounts of copper(I) and reducing agents with neocuproine in the presence of copper(II). Analyst. 1991; 116:89–94.

Unciuleac MC, Chandramouli K, Naik S, Mayer S, Huynh BH, Johnson MK, Dean DR. In vitro activation of apo-aconitase using a [4Fe-4S] cluster-loaded form of the IscU [Fe-S] cluster scaffolding protein. Biochemistry. 2007; 46:6812–6821. [PubMed: 17506526]

Varghese S, Tang Y, Imlay JA. Contrasting sensitivities of Escherichia coli aconitases A and B to oxidation and iron depletion. J Bacteriol. 2003; 185:221–230. [PubMed: 12486059]

Ve T, Mathisen K, Helland R, Karlsen OA, Fjellbirkeland A, Røhr ÅK, Andersson KK, Pedersen RB, Lillehaug JR, Jensen HB. The *Methylococcus capsulatus* (Bath) Secreted Protein, MopE*, Binds Both Reduced and Oxidized Copper. PLoS ONE. 2012; 7:e43146. [PubMed: 22916218]

Vinella D, Brochier-Armanet C, Loiseau L, Talla E, Barras F. Iron-sulfur (Fe/S) protein biogenesis: phylogenomic and genetic studies of A-type carriers. PLoS Genet. 2009; 5:e1000497. [PubMed: 19478995]

Vinella D, Loiseau L, de Choudens SO, Fontecave M, Barras F. In vivo [Fe-S] cluster acquisition by IscR and NsrR, two stress regulators in Escherichia coli. Mol Microbiol. 2013; 87:493–508. [PubMed: 23320508]

Wada K, Hasegawa Y, Gong Z, Minami Y, Fukuyama K, Takahashi Y. Crystal structure of Escherichia coli SufA involved in biosynthesis of iron-sulfur clusters: Implications for a functional dimer. FEBS Lett. 2005; 579:6543–6548. [PubMed: 16298366]

Wang W, Huang H, Tan G, Si F, Liu M, Landry AP, Lu J, Ding H. In vivo evidence for the iron-binding activity of an iron-sulfur cluster assembly protein IscA in Escherichia coli. Biochem J. 2010; 432:429–436. [PubMed: 20942799]

White MF, Dillingham MS. Iron–sulphur clusters in nucleic acid processing enzymes. Current Opinion in Structural Biology. 2012; 22:94–100. [PubMed: 22169085]

Xu FF, Imlay JA. Silver(I), mercury(II), cadmium(II), and zinc(II) target exposed enzymic iron-sulfur clusters when they toxify Escherichia coli. Appl Environ Microbiol. 2012; 78:3614–3621. [PubMed: 22344668]

Yan R, Konarev PV, Iannuzzi C, Adinolfi S, Roche B, Kelly G, Simon L, Martin SR, Py B, Barras F, Svergun DI, Pastore A. Ferredoxin competes with bacterial frataxin in binding to the desulfurase IscS. J Biol Chem. 2013; 288:24777–24787. [PubMed: 23839945]

Yang J, Bitoun JP, Ding H. Interplay of IscA and IscU in biogenesis of iron-sulfur clusters. J Biol Chem. 2006; 281:27956–27963. [PubMed: 16877383]

Zheng L V, Cash L, Flint DH, Dean DR. Assembly of iron-sulfur clusters. Identification of an iscSUA-hscBA-fdx gene cluster from Azotobacter vinelandii. J Biol Chem. 1998; 273:13264–13272. [PubMed: 9582371]
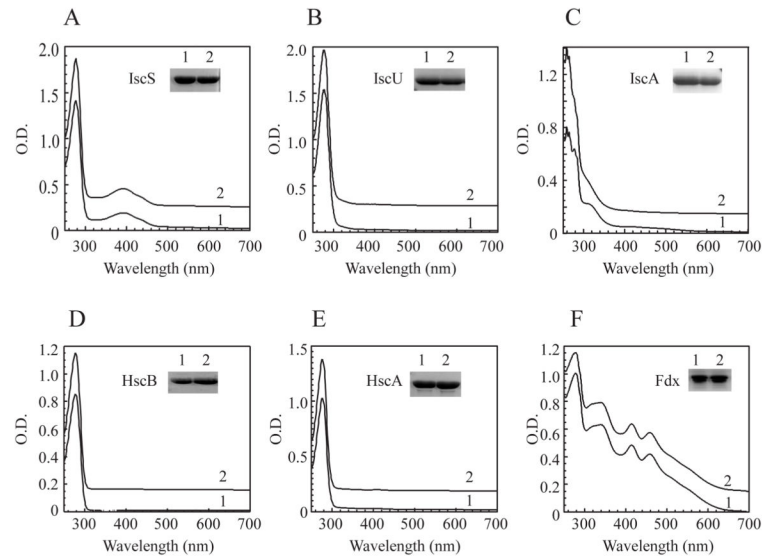
Figure 1. IscA has a unique copper binding activity among the iron-sulfur cluster assembly proteins

Each protein encoded by the gene cluster *iscSUA-hscBA-fdx* was expressed in the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with or without 200 μM $CuSO_4$. Proteins were purified from the cells and subjected to UV-visible absorption measurements. **A)**, IscS; **B)**, IscU; **C)**, IscA; **D)**, HscB; **E)**, HscA; **F)**, Ferredoxin. In each panel: spectrum 1, without $CuSO_4$ in LB media; spectrum 2, with $CuSO_4$ in LB media. Insert in each panel is a photograph of SDS-PAGE gel of purified proteins. The results are representatives of three independent protein preparations.
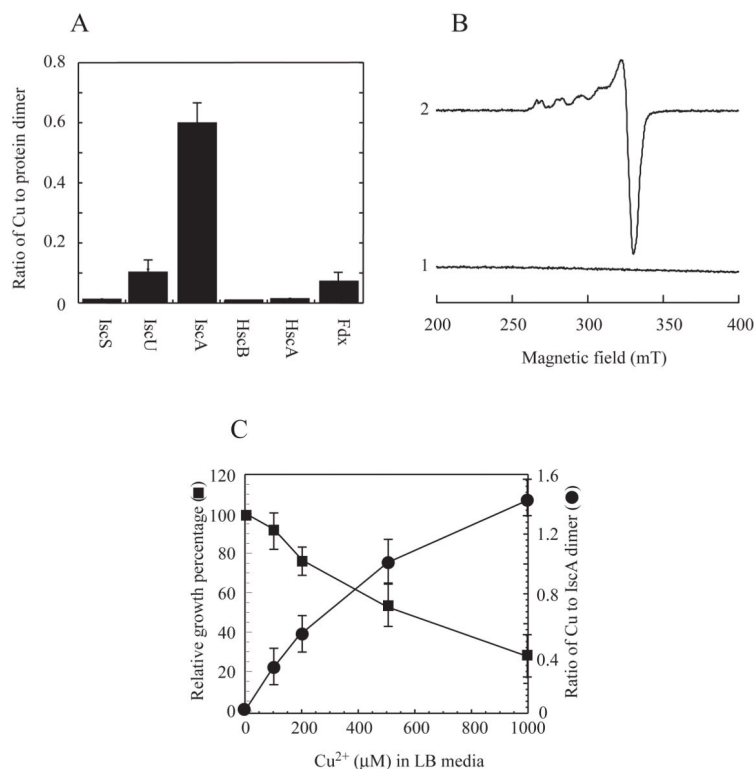
Figure 2. Relative copper binding activity of IscA in the *E. coli copA/cueO/cusA* mutant cells
A), the copper content of the iron-sulfur cluster assembly proteins encoded by the gene cluster *iscSUA-hscBA-fdx* purified from the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with 200 μM $CuSO_4$. **B),** the EPR spectra of IscA purified from the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with 200 μM $CuSO_4$. Purified IscA (50 μM) (spectrum 1) was treated with 2.5% nitric acid (spectrum 2). **C),** correlation of the copper binding in IscA and the relative cell growth in LB media supplemented with 0, 100, 200, 500, and 1000 μM $CuSO_4$. The copper content in purified IscA was plotted as a function of the $CuSO_4$ concentration in LB media (closed circles). The relative cell growth was defined as the percentage of the cell growth in LB media with $CuSO_4$ over that without $CuSO_4$, and was plotted as a function of the $CuSO_4$ concentration in LB media (closed squares). The 100% cell growth represented the cell density of O.D. at 600 nm of ~ 1.0 after 3 hours at 37°C in LB media with aeration. The results are the mean ± standard deviations from three independent experiments.
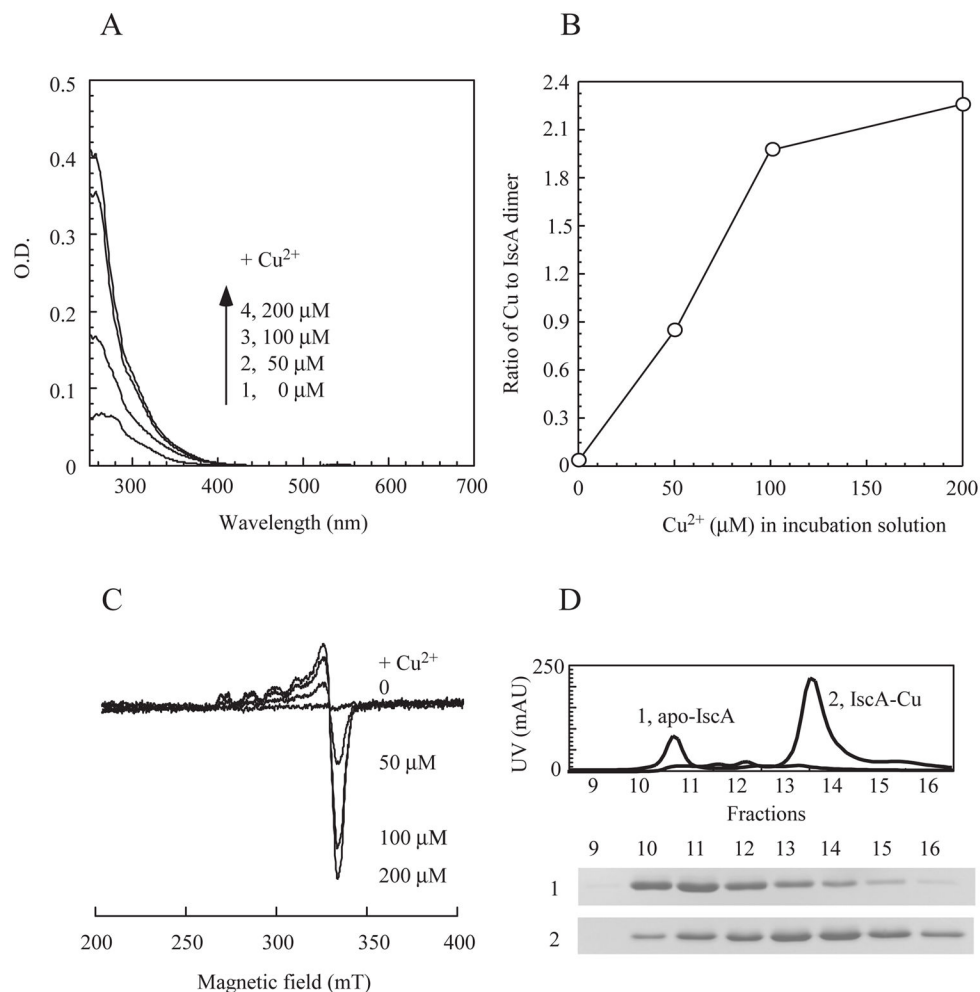
Figure 3. *In vitro* copper binding activity of IscA

Apo-IscA (50 μM dimer) was incubated with 0, 50, 100, and 200 μM $CuSO_4$ in the presence of dithiothreitol (2 mM). Protein was re-purified from incubation solutions by passing through a Hi-trap Desalt column. **A),** UV-visible spectra of re-purified IscA after reconstitution with the indicated concentration of $CuSO_4$. **B),** relative copper binding activity of IscA. The copper content of re-purified IscA was analyzed and plotted as a function of the $CuSO_4$ concentration in the incubation solution. **C),** the EPR spectra of the copper-bound IscA. Re-purified IscA proteins were treated with 2.5% (v/v) nitric acid and subjected to the EPR measurements. **D),** elution profiles of apo-IscA and the copper-bound IscA from a Mono-Q column. The copper-bound IscA was prepared after apo-IscA (50 μM dimer) was incubated with 200 μM $CuSO_4$ in the presence of dithiothreitol (2 mM). Top, elution profiles of apo-IscA (trace 1) or the copper-bound IscA (trace 2) using a linear gradient of NaCl (0 to 0.5 M). Bottom, photographs of the SDS-PAGE gel of the eluted fractions of apo-IscA (sample 1) and the copper-bound IscA (sample 2).
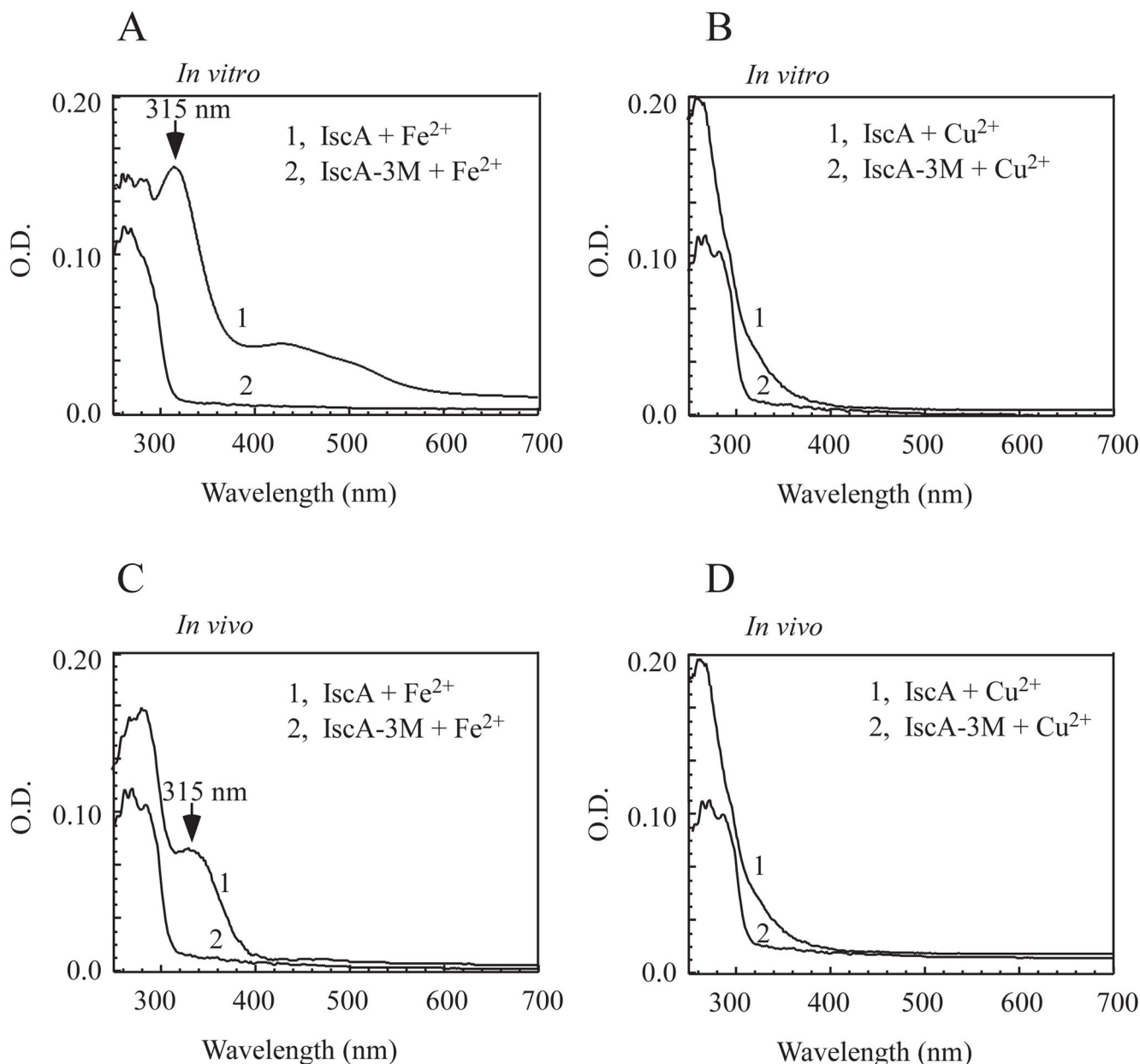
A

In vitro

B

In vitro

C

In vivo

D

In vivo

Figure 4. The conserved cysteine residues are essential for the copper binding in IscA

A), UV-visible spectra of IscA and the IscA mutant (IscA-3M) after incubation with iron *in vitro*. Apo-IscA and the IscA triple mutant (50 μM dimer) were incubated with $Fe(NH_4)_2$ $(SO_4)_2$ (100 μM) in the presence of dithiothreitol (2 mM) at room temperature for 15 min, followed by protein re-purification. **B)**, UV-visible spectra of IscA and the IscA mutant (IscA-3M) after incubation with copper *in vitro*. Apo-IscA and the IscA mutant (50 μM dimer) were incubated with $CuSO_4$ (100 μM) in the presence of dithiothreitol (2 mM) at room temperature for 15 min, followed by protein re-purification. **C)**, UV-visible spectra of IscA and the IscA mutant (IscA-3M) purified from the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with $Fe(NH_4)_2$ $(SO_4)_2$ (200 μM). **D)**, UV-visible spectra

of IscA and the IscA mutant (IscA-3M) purified from the *E. coli copA/cueO/cusA* mutant cells grown in LB media supplemented with $CuSO_4$ (200 μM).
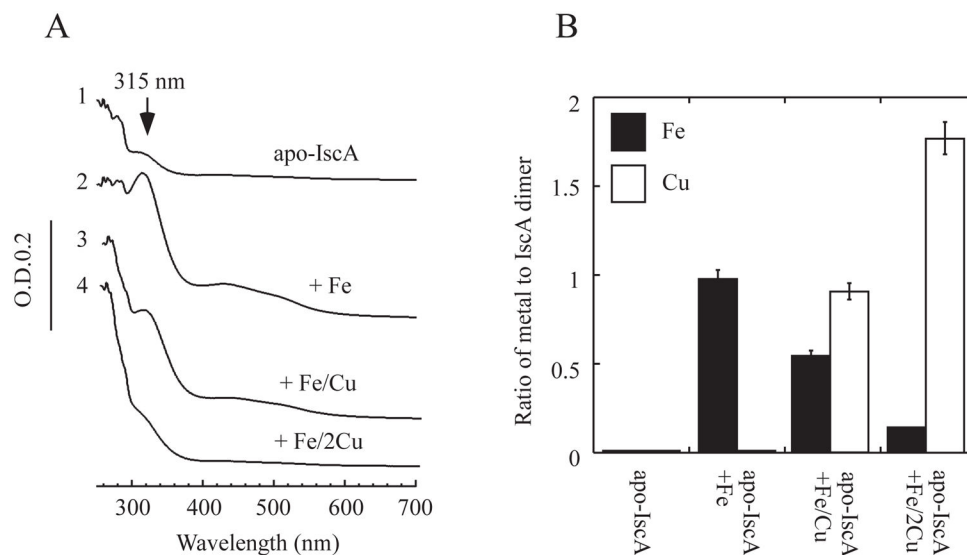
Figure 5. Excess copper competes with iron for the metal binding sites in IscA

A), copper competes for the iron binding site in IscA. Apo-IscA (50 μM dimer) (spectrum 1) was incubated with $Fe(NH_4)_2 (SO_4)_2$ (100 μM) (spectrum 2), $Fe(NH_4)_2 (SO_4)_2$ (100 μM) and $CuSO_4$ (100 μM) (spectrum 3), or $Fe(NH_4)_2 (SO_4)_2$ (100 μM) and $CuSO_4$ (200 μM) (spectrum 4) in the presence of dithiothreitol (2 mM) at room temperature for 15 min. IscA was re-purified from the incubation solutions and subjected to UV-visible absorption measurements. **B)**, iron and copper content analyses of re-purified IscA. The iron and copper content of re-purified IscA proteins from panel A) were analyzed and plotted as the ratio of metal to IscA dimer. The protein concentration was determined from the samples after incubation without metal ions. The results are presented as the mean ± standard deviations.
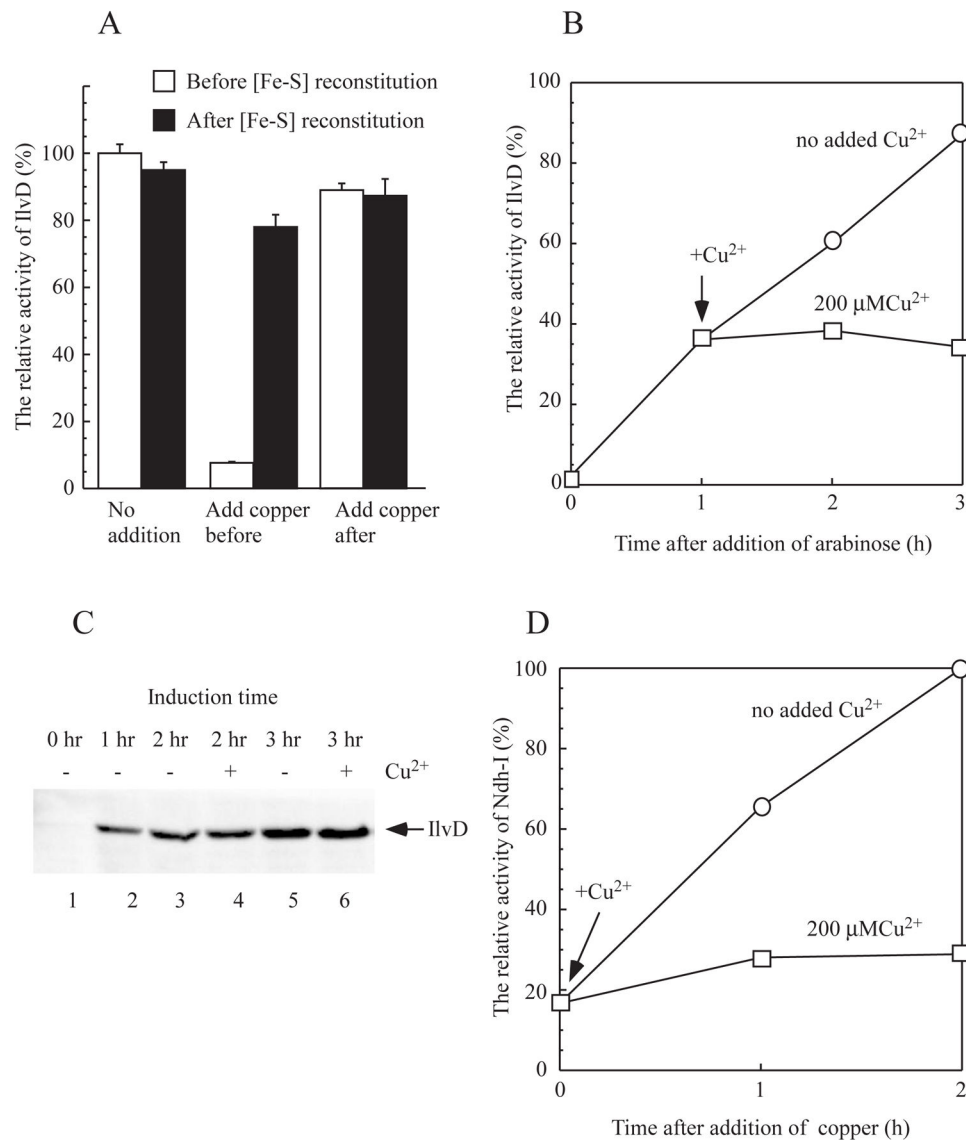
A

B

C

D

Figure 6. Copper largely blocks the [4Fe-4S] cluster assembly in the *E. coli* cells
A), inhibition of the [4Fe-4S] cluster assembly in recombinant dihydroxyacid dehydratase (IlvD) in the *E. coli* cells by copper. Recombinant IlvD was expressed in the *E. coli copA/ cueO/cusA* mutant cells grown in LB media. $CuSO_4$ (200 μM) was added to the cell culture before or after recombinant IlvD was produced in the cells. Cell extracts were prepared, and the enzyme activity of IlvD in the cell extracts was measured before (open bars) and after (closed bars) the cell extracts were incubated with L-cysteine (1 mM), cysteine desulfurase IscS (1 μM), $Fe(NH_4)_2(SO_4)_2$ (100 μM) and dithiothreitol (2 mM) under anaerobic conditions. **B),** effect of copper on the IlvD [4Fe-4S] cluster assembly in the *E. coli copA/ cueO/cusA* mutant cells. $CuSO_4$ (200 μM) was added to the cell culture after recombinant IlvD was expressed for one hour. Cell extracts were prepared at indicated time points, and the enzyme activity of IlvD in the cell extracts was measured and plotted as a function of cell growth time. **C),** effect of copper on the recombinant IlvD expression in the *E. coli*

copA/cueO/cusA mutant cells. The cell extracts were prepared and analyzed by Western blotting using the antibody against His-tag. Lane 1, at time 0; lane 2, after 1 hour induction; lanes 3 and 4, after 2 hours induction; lanes 5 and 6, after 3 hours induction. Lanes 3 and 5, with no copper addition; lanes 4 and 6, with $CuSO_4$ (200 μM). **D)**, effect of copper on NADH dehydrogenase I in the *E. coli* cells. Overnight cells of the *E. coli copA/cueO/cusA* mutant were grown for three hours, and treated with or without $CuSO_4$ (200 μM). The enzyme activity of NADH dehydrogenase I in the *E. coli* cells was measured at 0, 1 and 2 hours after addition of $CuSO_4$. The relative enzyme activity of NADH dehydrogenase I was plotted as a function of cell growth time. The results are the representatives from three independent experiments.
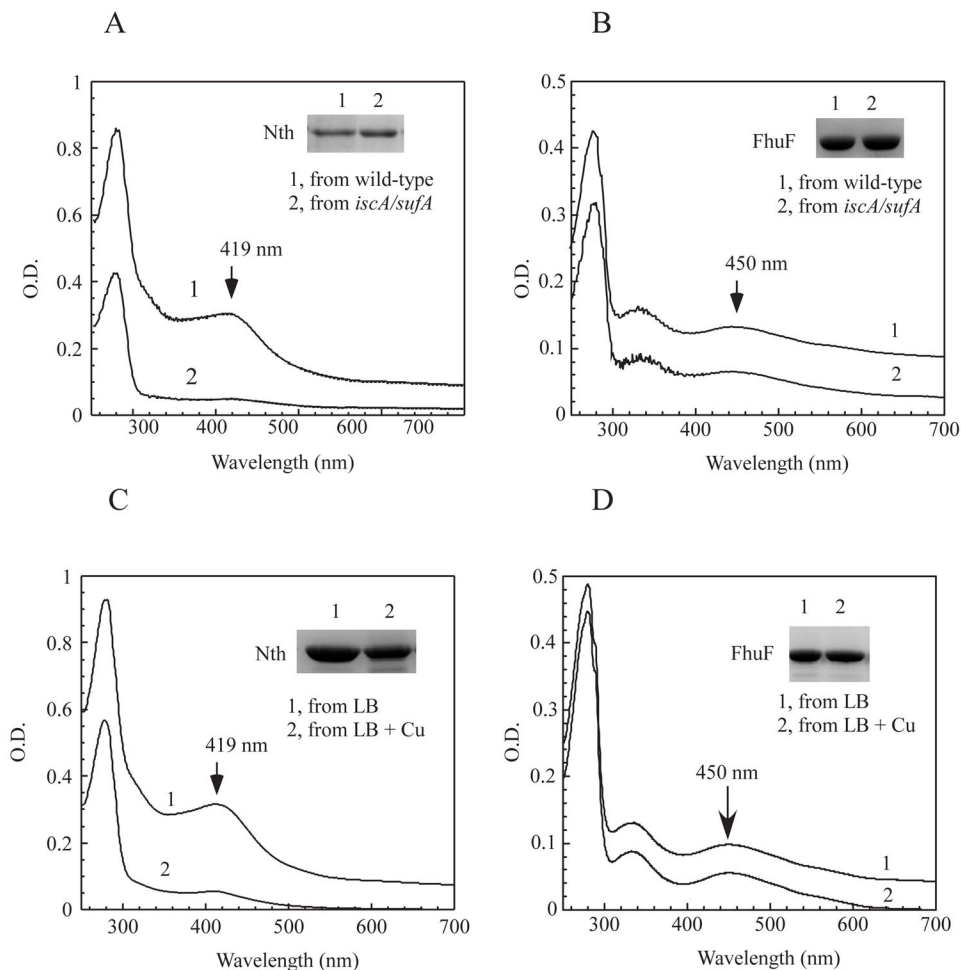
Figure 7. Copper selectively inhibits the [4Fe-4S] cluster assembly in the *E. coli* cells
A), UV-visible absorption spectra of recombinant endonuclease III (Nth) (~ 30 μM) purified from the *E. coli* wild-type cells (spectrum 1) and the mutant cells with deletion of IscA/SufA (spectrum 2) grown in LB media under aerobic growth conditions. The absorption peak at 419 nm indicates the [4Fe-4S] cluster of endonuclease III. **B)**, UV-visible absorption spectra of recombinant FhuF (~ 8 μM) purified from the *E. coli* wild-type cells (spectrum 1) and the mutant cells with deletion of IscA/SufA (spectrum 2) grown in LB media under aerobic growth conditions. The absorption peak at 450 nm indicates the [2Fe-2S] cluster of FhuF. **C)**, UV-visible absorption spectra of recombinant endonuclease III (Nth) (~ 22 μM) purified from the *E. coli copA/cueO/cusA* mutant cells supplemented with 0 (spectrum 1) or 200 μM (spectrum 2) $CuSO_4$ in LB media under aerobic growth conditions. **D)**, UV-visible absorption spectra of recombinant ferric iron reductase FhuF (~ 5 μM) purified from the *E. coli copA/cueO/cusA* mutant cells supplemented with 0 (spectrum 1) or 200 μM (spectrum 2) $CuSO_4$ in LB media under aerobic growth conditions. Insert in each panel is a photograph of SDS PAGE gel of purified proteins.
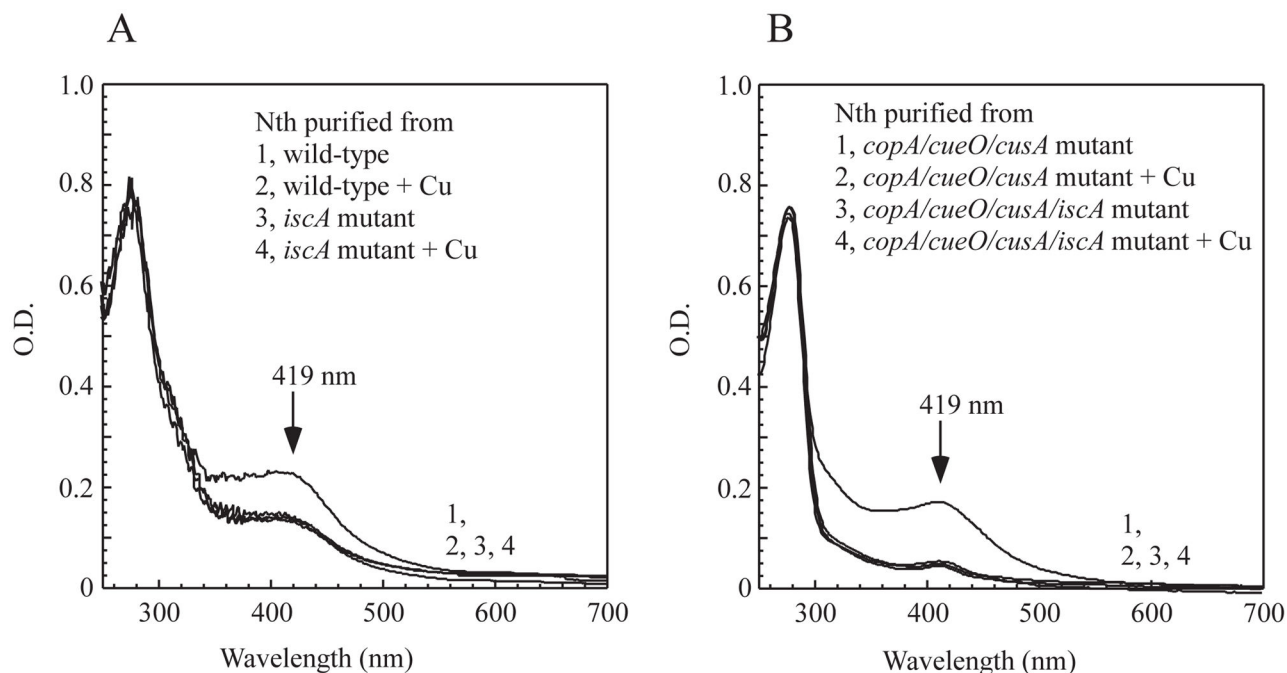
Figure 8. IscA is a primary target of copper toxicity

Recombinant endonuclease III was expressed in the *E. coli* cells grown in LB media supplemented with or without $CuSO_4$. Protein was purified from the *E. coli* cells and subjected to UV-visible absorption measurements. **A)**, effect of copper on the [4Fe-4S] cluster assembly in endonuclease III in the wild type and the *iscA* mutant cells. The *E. coli* cells were grown at 37°C in LB media with aeration for 3 hours. As indicated, $CuSO_4$ (2 mM) was added 10 min before expression of recombinant endonuclease III was induced. **B)**, effect of copper on the [4Fe-4S] cluster assembly in endonuclease III in the *E. coli copA/cueO/cusA* mutant and the *copA/cueO/cusA/iscA* mutant cells. The *E. coli* cells were grown at 37°C in LB media with aeration for 3 hours. As indicated, $CuSO_4$ (200 μM) was added 10 min before expression of recombinant endonuclease III was induced. The protein concentration was calibrated to ~ 40 μM for the UV-visible absorption measurements.