Selective Oma1 Protease-mediated Proteolysis of Cox1 Subunit of Cytochrome Oxidase in Assembly Mutants

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Selective Oma1 Protease-mediated Proteolysis of Cox1 Subunit of Cytochrome Oxidase in Assembly Mutants*

Oleh Khalimonchuk, Mi-Young Jeong, Talina Watts, Elliott Ferris, and Dennis R. Winge

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Stalled biogenesis of the mitochondrial cytochrome c oxidase (CcO) complex results in degradation of subunits containing reduct cofactors. The conserved Oma1 metalloprotease mediates facile Cox1 degradation in cells lacking the Coa2 assembly factor, but not in a series of other mutants stalled in CeO maturation. Oma1 is activated in coa2Δ cells, but the selective Cox1 degradation does not arise merely from its activation. Oma1 is also active in cells with dysfunctional mitochondria and cox11Δ cells impaired in CeO maturation, but this activation does not result in Oma1-mediated Cox1 degradation. The facile and selective degradation of Cox1 in coa2Δ cells, relative to other CcO assembly mutants, is likely due to impaired hemylation and subsequent misfolding of the subunit. Specific Cox1 proteolysis in coa2Δ cells arises from a combination of Oma1 activation and a susceptible conformation of Cox1.

Cytochrome c oxidase (CcO,2 complex IV) is the terminal enzyme of the energy transducing respiratory chain in mitochondria. Eukaryotic CeO consists of 12–13 subunits, with three mitochondrial encoded subunits (Cox1–Cox3) forming the core enzyme with the redox copper and heme cofactors (1). The remaining nuclear encoded subunits form the periphery of the catalytic core (2). CeO is embedded in the mitochondrial inner membrane (IM) and exists as supercomplexes with respiratory complex III in yeast and in complexes I and III in metazoans (3). The biogenesis of CeO commences with the mitochondrial synthesis of Cox1–Cox3 subunits followed by the insertion of heme and copper cofactors and the addition of the imported nuclear subunits synthesized in the cytoplasm. A series of assembly factors facilitate Cox1 maturation and cofactor insertion. The process of CeO biogenesis is best defined in the yeast Saccharomyces cerevisiae. An IM-tethered translational activator Pet309 along with Mss51 stimulates COX1 translation (4–7). IM insertion of Cox1 occurs in a cotranslational manner with the Oxa1 translocase (8, 9). Mss51 has a second function in translational elongation of Cox1, and this occurs within a polypeptide complex consisting of Mss51, Cox14, Coa3, and Ssc1 (7, 10–13). Cox1 maturation involves progression from this Mss51-containing complex to downstream transient assembly complexes involving Coa1 and Shy1 (11, 14). Many CeO assembly mutants attenuate COX1 translation through sequestration of Mss51 within the Mss51-containing Cox1 complex (10). The C-terminal tail of Cox1, not embedded within the IM, mediates the formation of the sequestered Mss51-Cox14-Coa3-Ssc1 complex (15). This conformer of Cox1 is shielded from rapid proteolysis and may serve as a CeO storage reservoir poised to initiate CeO biogenesis. Mss51 release from this Cox1-containing complex is dependent on either association of two nuclear subunits Cox5a and Cox6 or the insertion of Shy1 into the complex (7, 10–13). Formation of the heme and copper centers in Cox1 occurs upon release of Mss51-stalled complex and likely within the Shy1-containing complex (16). The two heme groups in CeO are modified hemes containing a hydroxyethylfarnesyl group and oxidized pyrrole methyl substituent. These heme modifications are catalyzed by the Cox10 farnesyl transferase and Cox15 heme oxidase (17).

Coa2 is another factor participating in Cox1 maturation. Cells lacking Coa2 are stalled in CeO biogenesis and exhibit a rapid degradation of newly synthesized Cox1 leading to impaired CeO biogenesis (18). Cox1 translation proceeds normally, as does formation of the Mss51-Cox14-Coa3-Ssc1 complex with newly synthesized Cox1. However, Cox1 maturation is impeded by its facile degradation. The respiratory deficiency of coa2Δ cells is suppressed by one of two mechanisms (19). First, a N196K mutant allele of the Cox10 farnesyl transferase was found to be a robust gain-of-function suppressor of the respiratory deficiency of coa2Δ cells (19). The mutant Cox10 enzyme exhibits an unusually stable oligomeric complex that correlates with an active enzymatic state in catalyzing the farnesylation of heme b. Cox10 activation appears to be the rate-limiting step in the hemylation process (20). Enhanced catalytic activity of the mutant Cox10 is likely responsible for reversing the attenuation in Cox1 hemylation in coa2Δ cells.

The second mechanism that restores respiratory function in coa2Δ cells is by the disruption of the Oma1 IM protease (19). Oma1 is one of several quality control proteinases within the
Oma1-mediated Cox1 Degradation

### TABLE 1

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Mitochondria. Unlike two major quality control proteases in the IM, mAAA and iAAA, Oma1 contains only a metalloproteinase domain and lacks the ATPase function involved in extrusion of proteins from the membrane bilayer. The restoration of respiratory capacity in coa2Δ cells by elimination of Oma1 may occur by allowing more time for the inefficient Cox1 hemylation process. A similar situation has been recently described in which impairment in ER proteolysis rescues the activity of unstable lysosomal proteins by prolonging ER retention (21).

In the present study, we address the substrate specificity of Oma1 in the degradation of mitochondrially synthesized component of CoxO and the bc1 complex. We show presently that Oma1 protease mediates Cox1 degradation in coa2Δ cells but not other cells stalled in CO biogenesis. The facile degradation of Cox1 in coa2Δ cells arises not merely from Oma1 activation in the mutant but likely from the misfolded Cox1 conformer that is an efficient substrate for Oma1-mediated proteolysis.

### EXPERIMENTAL PROCEDURES

**Strains and Growth Media**—*S. cerevisiae* strains used in this study are listed in Table 1. Yeast cells were grown in YP (1% yeast extract, 2% bactopeptone) or SC minimal medium, supplemented with respective amino acids. The carbon source used was either 1% or 2% glucose, 2% galactose, or glycerol/lactate. The chromosomal loci of the respective genes in yeast cells were either tagged with a 13xMyc epitope tag at the 3′ position or disrupted by homologous recombination as described previously (11). Each disruption or gene modification was confirmed by PCR analyses of the respective locus. *Escherichia coli* DH5α cells, used for cloning and plasmid propagation, were cultured and handled as described previously (22).

**Vectors and Constructs**—Standard procedures were used for all manipulations with DNA fragments and plasmids (22). YEp352-MSSS1, pRS423-MSSS1, pRS426-SSCI, YEp352-MDJ1 (11), and pRS425-COA2 (18) plasmids were used in this study. All constructs were verified by sequencing. Plasmids were transformed into the yeast cells using lithium acetate procedure (23).

**Hydrogen Peroxide Sensitivity, Respiratory Growth, and Mitochondrial Reactive Oxygen Species Quantification Assays**—Sensitivities of the yeast strains and transformants to hydrogen peroxide were tested as described previously (24). For a large-scale treatment of the cultures with H₂O₂, the cells were grown overnight at 30°C in 1 liter ofYP with 2% glucose to an density of 2.0–3.0, diluted with the fresh medium to optical density of 1.0–1.5 and cultivated for 2 h with or without 6 mM H₂O₂ added. Followed the incubation, cells were harvested, and their mitochondria were isolated as described below. To test the respiratory competence, strains were grown overnight in selective medium containing 2% glucose, serially diluted, and spotted on glucose-containing medium (control) and 2% glycerol/2% lactate-containing rich or synthetic medium.

The levels of the reactive oxygen species generated by various yeast strains were quantified using the superoxide-sensitive fluorescent dye MitoSox (Invitrogen). Unsynchronized cultures were grown for 24 or for 48 h in the liquid YP medium with 2% glucose. An aliquot of each respective culture (5 × 10⁴ cells) was washed twice in PBS (0.137 mM NaCl, 2.7 mM

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KCl, 10 mM Na$_2$HPO$_4$, 2 mM K$_2$HPO$_4$, pH 7.4) and incubated with or without 5 μM MitoSox for 10 min at 37 °C in the dark. Following the incubation, samples were washed three times with PBS buffer and subjected to mild sonication for 1 min to disperse aggregated cells. FACS analysis of the stained samples was carried using FACscan flow cytometer (Becton Dickinson). MitoSox fluorescence was measured in FL-2H channel. FCS Express 3.0 program (DeNovo Software) was used for data analysis. Cell viability was assessed using cell staining with 1 μM Cytox Green fluorescent dye (Invitrogen) according to the manufacturer's instructions.

**Mitochondria Isolation and Assays**—Intact mitochondria were isolated from yeast cells as described (25). Mitochondrial protein concentrations were quantified by the Bradford assay (26). Specific CcO, aconitase, and succinate dehydrogenase enzymatic activities were determined as described (27–29). The specific activities were normalized to mitochondrial protein levels and presented as a percentage of wild-type activity. Separation of the intact mitochondrial protein complexes by blue-native PAGE (BN-PAGE) was performed as described previously (16). Complexes were resolved on a continuous 5–13% gradient gel, transferred onto a PVDF membrane, and analyzed by Western blot. For second-dimension SDS-PAGE analysis, lanes were cut out, incubated in 1% SDS-1% captoethanol for 1 h at 25 °C, run on a 12% denaturing SDS-PAGE gel, and assessed by immunoblotting. Fractionation of the mitochondrial complexes in the continuous 7–30% sucrose gradients by high-velocity centrifugation was conducted as described previously (16).

**Assessment of Proteolytic Activity**—Proteolytic activity in the mitochondrial membranes was measured following the method adapted from Bulska et al. (30). Mitochondria isolated from various strains were resuspended in hypotonic buffer (20 mM HEPES, pH 7.4) and gently sonicated (3 × 30 s with 50% duty cycle). Obtained mixtures were fractionated at 165,000 × g for 1 h at 4 °C, and pellet fractions were collected for further analysis. Resolated mitochondrial membranes (25 μg) were preincubated in 150 μl of the reaction buffer (10 mM MgCl$_2$, 1.0 mM DTT, 0.05% Triton X-100, 50 mM Tris-HCl, pH 7.9) with or without 8 mM ATP for 5 min at 25 °C. The reaction was then started by adding 5 μM (final concentration) FITC-casein (Sigma) to each sample. The samples were allowed to incubate at 25 °C for 35 min in the dark. Following the incubation, 100 μl of 50 mM Tris-HCl (pH 7.9) buffer were added and unhindered FITC-casein, and the membranes were removed by centrifugation at 20,000 × g for 20 min at 4 °C. The TCA precipitation step was omitted to increase the sensitivity of the analysis. Without 8 mM ATP for 5 min at 25 °C. The reaction was then performed for1 h at 2 °C, and pellet fractions were collected for further analysis.

**Preparation of Yeast Whole-cell Extracts**—Whole-cell extracts were prepared from the cells grown at 30 °C in 50 ml of YP with 2% glucose or raffinose to $A_{600}$ of 1.0–4.0. Cells were harvested by centrifugation at 20,000 × g for 5 min at RT, washed with distilled water and pelleted again. Collected cell pellets were resuspended in 250 μl of 50 mM Tris-HCl, pH 8.0, and mixed with 50 μl of lysis buffer (10 mM NaOH, 7.5% β-mercaptoethanol, 2 mM phenylmethylsulfonyl fluoride). Following the 10-min incubation on ice, cold TCA was added to a final concentration of 25%. Samples were vigorously mixed, kept on ice for 15 min, and centrifuged (15 min at 20,000 × g at 4 °C). Pellets were washed with 80% cold acetone, spun down for 10 min (20,000 × g at 4 °C), resuspended in 1× SDS-Laemmli buffer, and incubated at 56 °C for 15 min. A fraction of the each respective sample was subjected to SDS-PAGE followed by immunoblot analysis.

**Immunooassays**—For immunoblot analysis, mitochondrial or total TCA-precipitated proteins were loaded onto a denaturing 12% polyacrylamide gel, subjected to SDS-PAGE, and transferred onto a nitrocellulose or PVDF membrane. Transferred polypeptides were detected with indicated primary antibodies and visualized with either ECL reagents (Pierce) or the Odyssey Infrared Imaging System (LI-COR Biosciences), respectively, when horseradish peroxidase-conjugated or fluorescent secondary antibodies were used. Anti-Myc antibody was obtained from Roche Diagnostic. Antibodies to the mitochondrial outer membrane porin were from Invitrogen. Dr. Alex Tzagoloff kindly provided Atp2 (F$_1$) antiserum.

**RESULTS**

**Oma1 and Not mAAA Mediates Cox1 Degradation in coa2Δ Cells**—One dramatic phenotype of coa2Δ cells is the facile degradation of Cox1 (11). Cox1 is synthesized efficiently, and the disruption of the Oma1 metalloproteinase (19). The disruption of the ATP-dependent protease iAAA showed no effect, whereas the disruption of the mAAA with a hypomorphic mAAA mutant had a modest effect (18). Because the mAAA protease is known to mediate degradation of membrane proteins, we initially reassessed the role of mAAA in Cox1 degradation. The mAAA protease consists of hetero-oligomeric complex containing Yta10 and Yta12. Protease activity is abolished by the deletion of the Oma1 metalloproteinase (19). The disruption of the ATP-dependent protease iAAA showed no effect, whereas the disruption of the mAAA with a hypomorphic mAAA mutant had a modest effect (18). Because the mAAA protease is known to mediate degradation of membrane proteins, we initially reassessed the role of mAAA in Cox1 degradation. The mAAA protease consists of hetero-oligomeric complex containing Yta10 and Yta12. Protease activity is abolished by the deletion of either YTA10 or YTA12. Such mutants are impaired in the processing of the MrpL32 subunit of the mitoribosome and therefore exhibit an unstable mitochondrial genome (32). Respiratory function is restored by the expression of a MrpL32 variant that does not require mAAA processing (32). To reinvestigate the role of mAAA in Cox1 degradation in coa2Δ cells, we constructed a mutant lacking Coa2 and mAAA function.
Oma1-mediated Cox1 Degradation

**A**

![Figure 1](image_url)

**B**

Var1 -
Cox1 -
Cox2/Cyt. b -
Cox3/Atp6

**C**

WT
shy1 Δ
oma1 Δ
shy1 Δ oma1 Δ

**FIGURE 1. Oma1 specifically mediates Cox1 degradation in coa2Δ cells.**

*A* Respiratory growth of Coa2-deficient cells lacking various proteases. Cells were pregrown in complete liquid medium, serially diluted, and spotted onto plates containing 2% glucose or glycerol/lactate as a carbon source. *B*, in vivo labeling of mitochondrial translation products in the cells described in *A*. The cells were pulsed for 15 min with [35S]methionine at 30 °C. The reaction was stopped by addition of cold methionine. Following a 60-min chase at 30 °C, samples were subjected to 12% SDS-PAGE and analyzed by autoradiography. *C*, Respiratory growth of the shy1Δ and coa1Δ strains with and without Oma1. Cells were handled as described in *A*. Cyt. b, cytochrome b.

(yta10Δ with the heterologous MRPL32Δ). The elimination of all mAAA protease activity in coa2Δ cells did not restore any respiratory growth unlike the elimination of Oma1 (Fig. 1A). However, the addition of WT Coa2 to the coa2Δ yta10Δ mutant cells restored respiratory growth ruling out respiratory deficiency arising from loss of the mitochondrial genome (data not shown). We also tested whether the loss of mAAA activity restored levels of newly synthesized Cox1 using a mitochondrial protein translation assay in which cells were labeled with [35S]methionine in the presence of cycloheximide to block translation in the cytoplasm. Only mitochondrial translation products, including Cox1, are labeled in this protocol. Whereas the loss of Oma1 in coa2Δ cells restored newly synthesized Cox1, no appreciable restoration was apparent with the loss of mAAA function (Fig. 1B). These data confirm that Oma1 plays a major role in Cox1 degradation in coa2Δ cells.

Oma1-mediated Cox1 Degradation Is Restricted to coa2Δ Cells—Coa1 and Shy1 are two other CcO assembly factors that function in maturation of newly synthesized Cox1. Genetic analyses suggest these factors function in conjunction with Coa2. Cells lacking either Coa1 or Shy1 in certain *S. cerevisiae* genetic backgrounds exhibit a CcO deficiency and assembly intermediates are degraded. To assess whether Oma1 mediates the degradation of Cox1 in these mutant backgrounds, OMA1 was deleted in either coa2Δ or shy1Δ cells (Fig. 1C). The elimination of Oma1 from shy1Δ cells gave a very modest improvement in respiratory growth, but not with coa1Δ cells. Thus, the removal of Oma1 in coa2Δ cells is unique in yielding a dramatic improvement in respiratory function.

To address whether Oma1 is a general Cox1 quality control protease, we addressed the turnover of Cox1 in three mutants stalled in CcO biogenesis, namely cox14Δ, cox1Δ, and cox4Δ cells. These mutants stall Cox1 maturation at early to late steps, respectively. To monitor newly synthesized Cox1, we used the mitochondrial translation assay mentioned above. It should be pointed out that Cox1 translation is attenuated markedly in most CcO assembly mutants due to sequestration of Mss51 (10). This attenuation in Cox1 synthesis is apparent in cox11Δ and cox4Δ cells but pulse chase studies reveal that the newly synthesized Cox1 is still labile, relative to the pulse levels (Fig. 2A). Cox1 is equally labile in cox1Δ cells regardless of the presence or absence of Oma1 (Fig. 2A). The turnover of Cox1 in cox4Δ cells is likewise unaffected by the presence or absence of Oma1 (Fig. 2A). Cells lacking Cox14 do not exhibit the same attenuation in Cox1 synthesis (10). However, newly synthesized Cox1 is unstable in cox14Δ cells (12). The deletion of OMA1 in these cells does not alter the rate of Cox1 turnover (Fig. 2A).

It is difficult to compare Cox1 degradation rates in various CcO assembly mutants because Cox1 synthesis is attenuated in many but not all mutants due to sequestration of Mss51 (10). Therefore, we took advantage of the recently described genetic system involving the deletion of the C-terminal 15 residues in Cox1 (15). The C-terminal residues of Cox1 are important for the Mss51/Cox14 binding that is required for Mss51 sequestration (15). Although Cox1 synthesis proceeds normally, Cox1ΔC15 is partially labile and the cells are impaired in respiratory growth at elevated temperatures (data not shown). Cells containing the Cox1ΔC15 truncate were compared in the mitochondrial translation assay to deletion strains engineered in this background that lack either Cox11 or Coa2 (Fig. 3A). In the absence of Mss51 sequestration, the Cox1 synthesis rate is comparable in various mutants (Fig. 3A, lane 1), thereby allowing comparisons in turnover rates. The turnover of Cox1 is enhanced in coa2Δ cells relative to cox11Δ cells (Fig. 3B), highlighting the facile Cox1 degradation process in coa2Δ cells. To evaluate the role of Oma1 in Cox1 degradation in these strains, OMA1 was deleted in both coa2Δ and cox11Δ cells containing the C-terminal truncated Cox1. The elimination of Oma1 in coa2Δ cells stabilizes Cox1 during the chase (Fig. 3, bottom panel), whereas no appreciable change in Cox1 degradation occurred in cox11Δ cells upon loss of Oma1.

We evaluated whether Oma1 contributed to the degradation of an IM protein distinct from Cox1. We focused on the mitochondrial encoded cytochrome b subunit of the bc1 complex.
Oma1 contributes to the degradation of cytochrome b. The turnover of cytochrome b was assessed in cells lacking Qcr7. Cells lacking Qcr7 stall maturation of the bc1 complex leading to rapid cytochrome b degradation. To address whether Oma1 contributes to the degradation of cytochrome b, we compared qcr7Δ cells to qcr7Δ oma1Δ double null cells. The turnover of cytochrome b was unaffected by the presence or absence of Oma1. Thus, Oma1 exhibits selective proteolysis of Cox1 in coa2Δ cells.

Oma1-dependent Proteolysis Is Enhanced in coa2Δ Cell Mitochondria—The observed proteolysis of Cox1 in coa2Δ cells implies that Oma1 is active in the mutant cells. To test whether Oma1 activation occurs in such cells, we took advantage of two proteolysis assays. First, we isolated mitochondrial membranes from respective cells and monitored the proteolysis of FITC-casein. Casein is an efficient substrate for many proteases due to its non-compact structure. Mitochondrial membranes derived from coa2Δ cells showed a significant elevation in FITC-casein proteolysis, whereas it was attenuated in membranes isolated from wild-type cells (Fig. 4A). The assay was conducted in the presence or absence of ATP. Two major membrane proteases are the ATP-dependent mAAA and iAAA enzymes. AAA proteases are largely inactive without the addition of ATP. The effect of Oma1 on FITC-casein is readily apparent. The level of FITC-casein proteolysis in the double mutant was equivalent to the level with membranes isolated from wild-type cells. The second proteolysis assay involved the pre-isolation of the ~450 kDa Cox1-containing Shy1 complex from wild-type cells. The high mass Shy1 complex containing Cox1 was recovered from sucrose gradient ultracentrifugation. BN-PAGE was used to document the presence of the complex. Previous data revealed that the heme a and Cuβ cofactors sites are likely populated within this intermediate.

FIGURE 2. Cox1 degradation in CcO assembly mutants with and without Oma1. A, degradation kinetics of the newly synthesized Cox1 in wild-type, cox11Δ, cox4Δ, and cox14Δ strains with and without Oma1. Cells were pulsed with [35S]methionine as described in Fig. 1B. Aliquots were taken at indicated chase time points, and Cox1 degradation was assessed as a percentage of the signal abundance in each respective band. The intensities of Cox1 bands were normalized to the ones of the respective Var1 and cytochrome b (Cyt. b) signals. The data represent an average of three independent experiments; the error bars indicate S.D. B, in vivo labeling of mitochondrial translation products in the WT, qcr7Δ and qcr7Δoma1Δ cells. Cyt. b, cytochrome b.

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Oligomeric Oma1 Complex Altered in coa2Δ Cells—The facile Oma1-mediated degradation of Cox1 seen in coa2Δ cells suggests that a specific condition exists within the mutant cells leading to the degradation. This condition may activate Oma1 or result in a Cox1 conformer that is highly susceptible to degradation. We initially focused on the state of Oma1 in coa2Δ cells. In these studies OMA1 was chromosomally tagged with a C-terminal Myc epitope. The disruption of COA2 in these cells led to the same rapid Cox1 degradation suggesting the chimeric protein is functional (data not shown). The abundance and size of Oma1 was unperturbed comparing WT to coa2Δ cells on steady-state SDS-PAGE (Fig. 5A). Oma1 exists within a high mass complex that was postulated to be a homo-oligomeric species. The abundance of this complex observed on BN-PAGE is attenuated in coa2Δ cells (Fig. 5B). Steady-state levels...
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and the size of Oma1, as assessed by SDS-PAGE, were not altered in coa2Δ cells. Thus, neither the expression nor any proteolytic processing of Oma1 was apparent in coa2Δ cells. To assess why Oma1 was not visible on BN-PAGE of mitochondria of the mutant cells, we conducted a two dimensional BN-PAGE experiment to assess whether the epitope was less accessible. Separation of proteins in the second dimension by SDS-PAGE resulted in the appearance of Oma1 at a lower apparent mass on the native PAGE dimension in coa2Δ cells (Fig. 5C).

As we reported previously, coa2Δ cells exhibit limited sensitivity to hydrogen peroxide (18). To assess whether oxidative stress conditions may contribute to the change in Oma1, we tested WT cells treated with hydrogen peroxide. A similar perturbation in Oma1 was apparent in the treated WT cells (Fig. 5, D–F). Oma1 was not detected by single dimension BN-PAGE in peroxide-treated WT cells, but visible at a lower mass by two-dimensional PAGE. The same is true with chronically hyperpolarized mitochondria (data not shown). Steady-state levels of Oma1 and its size were also not altered by the peroxide treatment (Fig. 5E). Thus, the physical state of the Oma1 complex is altered in coa2Δ and stressed WT cells. Dual affinity purification of Oma1 from WT cells was carried out to ascertain if other proteins existed in the high mass complex, but Oma1 was the only major protein detected by mass spectrometry analyses.

Cox1 Degradation in coa2Δ Cells Is Not Primarily Related to Oxidative Stress—The peroxide sensitivity of coa2Δ cells is abrogated by the deletion of COX10 or COX15 suggesting this sensitivity arises from the very low levels of pro-oxidant heme a3Cox1 (Fig. 6A) (24). Because Oma1 exhibited a conversion to a lower mass complex in both coa2Δ cells and peroxide-treated WT cells, we addressed whether the Cox1 degradation in coa2Δ cells was due to oxidant-triggered activation of Oma1. We initially screened coa2Δ cells for additional markers of oxidative stress. Cells lacking Coa2 exhibited reduced levels of aconitase, but not succinate dehydrogenase activity (Fig. 6B). Aconitase, unlike succinate dehydrogenase, is highly susceptible to oxidative stress conditions due to the solvent-exposed iron atom in the iron-sulfur cluster (36). Another biomarker of oxidative stress is the mitochondrial MitoSox fluorophore that reports on levels of superoxide anion (37). Cells lacking Coa2 showed a marked elevation in MitoSox fluorescence by FACS analyses (Fig. 6C); this fluorescence is attenuated in coa2Δ cells lacking Cox10. The elimination of Cox10 in coa2Δ cells also partially reduces Oma1 proteolysis based on the FITC-casein assay, although the proteolytic activity is not returned to levels seen with WT membranes (Fig. 6D). The high mass Oma1 complex remains modified and cannot be observed by one dimensional BN-PAGE in coa2Δcox10Δ cells (data not shown). These studies suggest that Oma1 may be activated in coa2Δ cells primarily due to the mitochondrial dysfunction of the mutant cells rather than oxidative stress.

An independent test of whether stress activation of Oma1 is responsible for Cox1 degradation in coa2Δ cells was conducted. We investigated the state of Oma1 in cox11Δ cells that are COX-deficient and also are stressed oxidatively (24). Cox11 is a co-metallochaperone that mediates the copper metallation of the CuA site in Cox1 (38). Cells lacking Cox11 are sensitive to hydrogen peroxide due to the presence of the pro-oxidant heme a3Cox1 (24). The hydrogen peroxide sensitivity of cox11Δ cells is mitigated by the elimination of Cox10 (Fig. 7A). Cells lacking both Cox11 and Coa2 exhibit a peroxide sensitivity equivalent to the least sensitive of the two individual nulls, coa2Δ cells (Fig. 7B). In addition, cox11Δ cells exhibit elevated levels of super-

FIGURE 3. Cox1ΔC15 degradation in CcO assembly mutants with and without Oma1. Shown are representative chase autoradiograms (A) and degradation kinetics (B) of Cox1ΔC15 in WT, cox11Δ, coa2Δ, oma1Δ, coa2Δoma1Δ, and coa1Δoma1Δ cells. Lack of the 15 C-terminal residues in Cox1 relieves its translational attenuation in the respective mutants; however, the degradation rates of Cox1ΔC15 differ between coa2Δ and coa2Δ mitochondria. Intensities of Cox1ΔC15 were assessed as described in Fig. 2; error bars indicate S.D. (n = 3).
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FIGURE 4. Proteolytic activity of the mitochondrial membranes derived from coa2Δ cells. A, upper panel: proteolytic activities of mitochondrial membranes. Organelles isolated from indicated strains were disintegrated and fractionated. Mitochondrial membrane fractions were collected and preincubated in the reaction buffer with (+) or without (−) 8 mM ATP. The assays were initiated by addition of FITC-casein, followed by incubation at 25 °C for 35 min. Reactions were stopped by rapid cooling of the samples, and the membranes as well as unhydrolyzed substrate were removed by high speed centrifugation. Supernatants were diluted 10-fold, and the fluorescence intensity was measured at excitation wavelength of 445 nm and an emission wavelength of 515 nm. The intensities were normalized to the fluorescence of FITC-casein incubated without membranes. The data represent an average of three independent repeats; the error bars indicate S.D. Bottom panel: the same amount of isolated membrane fractions (25 μg) subjected to SDS-PAGE and visualized by Coomassie staining served as loading control for proteolytic reaction. B, upper panel: schematic description of the −450-kDa Shy1 complex isolation procedure. Lower panel, mitochondria (1.0 mg) from yeast strains expressing SHY1-Myc were lysed with 1% digitonin and clarified lysates loaded onto continuous 7–30% sucrose gradient and separated by the ultracentrifugation. Fractions were collected, and the distribution of −450 kDa Shy1 and 440-kDa Porin complexes was analyzed by BN-PAGE and immunoblotting. C, the respective mitochondrial membranes (25 μg) were lysed in 1% digitonin, and clarified lysates have been incubated with an aliquot (15 μl) of the isolated fraction 12 (fr. 12) containing a −450-kDa Shy1 complex. The mixtures were incubated as described in Fig. 3A. Following the 35-min incubation at 25 °C, samples were analyzed by either native or denaturing electrophoresis and immunoblotted with anti-Myc antibodies. Anti-F1 serum was used to visualize the monomeric form of complex V (V), which served as a loading control for BN-PAGE. Intensities of the Shy1 complex were assessed as described in the legend to Fig. 2.

oxide anion as monitored by MitoSox fluorescence in FACS analyses (Fig. 7B). Overexpression of Oma1 failed to reverse the peroxide sensitivity of cox11Δ cells (Fig. 7C), suggesting the newly synthesized Cox1 in cox11Δ cells is more protected from degradation than in coa2Δ cells.

Oma1 is also converted in cox11Δ cells to a conformer that is not detected by single dimension BN-PAGE (Fig. 7D) but is seen at the lower mass position after two-dimensional gel electrophoresis (data not shown). Steady-state levels of Oma1 are not altered in cox11Δ cells. Because a correlation exists between Oma1
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In support of this, membranes derived from cox11Δ/H9004 mitochondria exhibited elevated Oma1-dependent proteolysis of FITC-casein (data not shown). However, Cox1 is not degraded in cox11Δ cells to the same extent as in coa2Δ cells (Figs. 2A and 3). Thus, these studies suggest that the facile Oma1-mediated degradation of Cox1 seen in coa2Δ cells may correlate with a proteolytically susceptible conformer of Cox1 uniquely found in these cells.

Overexpression of Mitochondrial Chaperone Mdj1 Ameliorates Respiratory Defect in coa2Δ Cells—The folding of Cox1 is likely impaired in coa2Δ cells leading to a misfolded conformer that is an efficient substrate for Oma1. We tested whether respiratory growth of coa2Δ cells was enhanced by overexpression of the mitochondrial Hsp70 chaperone Ssc1 or DnaJ protein Mdj1. High levels of Mdj1 gave a modest enhancement in growth of coa2Δ cells on glycerol/lactate (Fig. 7E). Overexpression of Ssc1 did not enhance any growth of coa2Δ cells on glyco-
erol/lactate (data not shown). To assess whether increasing Cox1 synthesis would augment the Mdj1-mediated enhancement in respiratory growth, we tested the effects of co-overexpression of Mdj1 and Mss51 (Fig. 7E). No synergistic effect was observed. The respiratory deficiency of coa2Δ cells persists even with elevated levels of newly synthesized Cox1 and the protein chaperone Mdj1. Therefore, neither Mdj1 nor Ssc1 are efficient chaperones of the misfolded Cox1 in the mutant cells.

DISCUSSION

Oma1 is shown presently to be a dominant protein that mediates the degradation of Cox1 specifically in coa2Δ cells. Depletion of Oma1, but not the mAAA protease, leads to a selective enrichment in newly synthesized Cox1 in coa2Δ cells but not other CcO assembly mutants. We previously demonstrated that the respiratory defect of coa2Δ cells was reversed by the depletion of the Oma1 protease, but the specificity of Oma1 in Cox1 degradation was not addressed. In the present work, we focus on the substrate specificity of Oma1 in the degradation of mitochondrial synthesized component of CcO and the bc1 complex. In mutant strains stalled in CcO or bc1 assembly, Oma1 did not appear to have any appreciable role in subunit degradation apart from coa2Δ cells. Oma1 appears to be activated in coa2Δ cells and other CcO assembly mutants such as cox11Δ cells. However, the facile Cox1 degradation observed in coa2Δ cells does not arise merely from Oma1 activation. The observed depletion of newly synthesized Cox1 may relate to the state of Cox1 as a proteolytic substrate in the mutant cells.

We previously reported that respiratory growth of coa2Δ cells is also restored by the presence of a gain-of-function allele of the Cox10 farnesyl transferase (19). We postulated that coa2Δ cells were impaired in Cox1 hemylation, and this defect

FIGURE 6. Block of heme α synthesis in coa2Δ cells lowers reactive oxygen species (ROS) levels and proteolytic activity of mitochondrial membranes. A, cells were grown to mid-logarithmic phase and incubated with (+) or without (−) the 6 mM H2O2 for 2 h at 30 °C. Following incubation, the samples were serially diluted and plated onto the complete medium with 2% glucose. Plates were incubated for 36–48 h at 30 °C. B, enzymatic activities of mitochondrial aconitase (left panel) and succinate dehydrogenase (SDH, right panel) in mitochondria isolated from WT and coa2Δ cells. Activities are shown as a percentage of the WT activity. The data represent an average of three biological replicates, and the error bars indicate S.D. C, flow cytometric analysis of endogenous reactive oxygen species in WT, coa2Δ, cox10Δ, and coa2Δcox10Δ cultures stained with 5 μM MitoSox after 24 h of cultivation. The x axis indicates a log scale of the MitoSox fluorescence intensity, and the y axis represents cell counts. Any fluorescence outside of the gated area is indistinguishable from background and was not considered. The percentage of the cells within the gated area is indicated. D, proteolytic activities of the membranes from the strains listed above were tested as described in Fig. 3A.
could be suppressed by enhanced efficiency of hemylation by the mutant Cox10 enzyme or diminished proteolysis of the underhemylated Cox1. Impaired hemylation may result in a misfolded Cox1 that is a facile substrate for Oma1. The lack of an effect of Oma1 depletion in other CcO assembly mutants such as cox11Δ cells may relate to the population of the “heme a” subsite (as opposed to the heme a3 subsite) in these mutants but not coa2Δ cells. Cox1 spans the IM with 12 TM helices organized in six successive helical pairs forming a closed bundle (1). The farnesyl tail of the heme a in the heme a subsite is packed between helices 1, 11, and 12. The axial His ligands for heme a ligation come from His-62 in helix 2 and His-378 in helix 10. Thus, heme a binding in the a subsite is expected to stabilize the Cox1 helical bundle. The a3 subsite heme a does not appear to have the same stabilizing role. Thus, failure to hemylate the a subsite may be expected to destabilize Cox1 leading to rapid degradation. Coa2 is predicted to have a specialized role in mediating the population of the heme a subsite. Coa2 may be a Cox1 chaperone stabilizing a conformer competent for heme a insertion.

FIGURE 7. Cells lacking Cox11 show oxidative stress and modulation of Oma1. A, hydrogen peroxide sensitivity of indicated strains tested as in Fig. 6A. B, endogenous levels of reactive oxygen species in WT and cox11Δ cultures were analyzed by FACS as described in the legend to Fig. 6. C, sensitivity of either WT or cox11Δ cells transformed with an empty vector or Oma1-overexpressing plasmid. D, BN-PAGE (left panel) and SDS-PAGE (right panel) analyses of the Oma1::Myc complexes in the mitochondria isolated from WT or cox11Δ strains were carried out as described in the legend to Fig. 4. E, respiratory growth of the coa2Δ strain expressing Coa2, Mss51, Mdj1, or Mdj1 and Mss51. Cells were handled and tested as described in Fig. 1A, V, complex V.
Second, cells lacking Cox14 or Mss51 fail to form the Mss51 complex yet still do not show an Oma1-dependence in Cox1 degradation. Oma1 may not be fully active in cox14Δ or mss51Δ cells due to the lack of Cox10 activation (19). The rapid turnover of Cox1 in coa2Δ cells appears to arise from both the impaired hemylation of Cox1 and the heme α-mediated stress to activate Oma1.

The specificity of Oma1 for Cox1 degradation in coa2Δ cells is curious because iAAA and mAAA proteases are known to degrade misfolded mitochondrial proteins. Misfolded Cox1 in coa2Δ cells may exist within a particular subdomain of the mitochondrial IM accessible to Oma1 but not the ATP proteases. Alternatively, Oma1 may be important for initial cleavage and final proteolysis may be subsequently mediated by the AAA proteases. The recent cryo-EM reconstruction of the mAAA protease suggests that entry of a protein into the AAA hexameric ring may be restricted to unfolded polypeptide segments (39). Oma1 may function to generate a more unfolded state that can be accommodated by one of the AAA proteases. Oma1 is one of the mitochondrial proteases important in removing misfolded mitochondrial proteins. Yeast Oma1 was shown to be involved in the cleavage of the artificially misfolded polytopic IM protein Oxa1 (35). In mammalian cells, Oma1 functions in conjunction with the mAAA protease in stress-triggered processing of OPA1, a GTPase involved in mitochondrial membrane dynamics and genome maintenance (40, 41).

Oma1 activation was reported to occur in conditions in which mammalian mitochondria are dysfunctional (40, 41). Oma1 was reported to be proteolized within functional mitochondria precluding its function. Dissipation of the mitochondrial membrane potential blocked Oma1 cleavage thereby stabilizing the active state. We show presently that Oma1 is not regulated by proteolysis in yeast. Oma1 may be activated in cells with an impaired membrane potential through another mechanism such as protein modification. Oma1 was postulated to form a homohexameric structure that is independent of ATP (35). The observed change in mobility of the Oma1 complex in respiratory deficient or stressed mitochondria may relate to a change in the conformation or composition of the protein complex. Future studies will focus on the elucidation of the functional states and activation process of Oma1.

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