Balanced Ero1 activation and inactivation establishes ER redox homeostasis

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The endoplasmic reticulum (ER) provides an environment optimized for oxidative protein folding through the action of Ero1p, which generates disulfide bonds, and Pdi1p, which receives disulfide bonds from Ero1p and transfers them to substrate proteins. Feedback regulation of Ero1p through reduction and oxidation of regulatory bonds within Ero1p is essential for maintaining the proper redox balance in the ER. In this paper, we show that Pdi1p is the key regulator of Ero1p activity. Reduced Pdi1p resulted in the activation of Ero1p by direct reduction of Ero1p regulatory bonds. Conversely, upon depletion of thiol substrates and accumulation of oxidized Pdi1p, Ero1p was inactivated by both autonomous oxidation and Pdi1p-mediated oxidation of Ero1p regulatory bonds. Pdi1p responded to the availability of free thiols and the relative levels of reduced and oxidized glutathione in the ER to control Ero1p activity and ensure that cells generate the minimum number of disulfide bonds needed for efficient oxidative protein folding.

Introduction

A key step in the maturation of many secreted proteins and extracellular domains of membrane proteins is the formation of disulfide bonds in the ER. Disulfide bonds, which stabilize native and functional conformations of proteins, are formed by pairing and oxidation of cysteines during the initial folding process in the ER. In Saccharomyces cerevisiae, most biosynthetic disulfide bonds are formed by dithiol/disulfide transfer reactions with the oxidized form of protein disulfide isomerase (PDI), Pdi1p (Sevier and Kaiser, 2002; Wilkinson and Gilbert, 2004). Pdi1p, in turn, requires other oxidizing molecules to be recycled because Pdi1p cannot generate disulfide bonds by itself. We and other colleagues identified the major disulfide-generating flavoenzyme Ero1p in S. cerevisiae (Frand and Kaiser, 1998; Pollard et al., 1998). In both yeast and mammalian cells, Ero1 directly transfers disulfide bonds to PDI (Frand and Kaiser, 2000; Mezghrani et al., 2001). The oxidative capacity of the yeast ER depends primarily on the activity of Ero1p: a temperature-sensitive ero1-1 mutation decreases the resistance of yeast to the reducing agent DTT and induces the unfolded protein response with accumulation of secretory proteins, and, after prolonged incubation at the restrictive temperature, a strain with this mutation loses viability (Frand and Kaiser, 1998, 1999; Cuozzo and Kaiser, 1999; Tu and Weissman, 2002), and overexpression of ERO1 from a multicopy plasmid increases the oxidizing capacity of yeast cells, as shown by their increased resistance to DTT (Frand and Kaiser, 1998).

The catalytic cycle of Ero1p depends on a relay of disulfide bonds from the conserved active-site cysteine pair, C352-C355, which is proximal to bound flavin adenine dinucleotide (FAD) to the second shuttle cysteine pair, C100-C105, which is responsible for direct disulfide transfer to Pdi1p (Frand and Kaiser, 2000; Gross et al., 2004; Sevier and Kaiser, 2006b). In addition to these two catalytic cysteine pairs, Ero1p contains three cysteine pairs (C90-C349, C143-C166, and C150-C295) that form regulatory bonds (Sevier et al., 2007). Several lines of evidence indicate that Ero1p is inactive with regulatory bonds formed, whereas it is active with regulatory cysteines in the reduced state. Ero1p is converted from an oxidized (inactive) state to the reduced (active) state in the presence of reduced thioredoxin-1 (Trx1) as a substrate; once Trx1 is fully oxidized through the action of active Ero1p, Ero1p returns to the oxidized (inactive) form (Sevier et al., 2007). A double mutant, Ero1p-C150A-C295A, which cannot form the crucial C150-C295 regulatory bond,

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Abbreviations used in this paper: BSO, buthionine sulfoximine; CPY, carboxypeptidase Y; FAD, flavin adenine dinucleotide; MBP, maltose binding protein; PDI, protein disulfide isomerase; SMM, supplemented minimal medium; TEV, Tobacco etch virus.

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exhibits increased Ero1p activity in vitro and in vivo (Sevier et al., 2007).

A byproduct of Ero1p activity is the generation of hydrogen peroxide as a result of a two-electron reduction of oxygen per disulfide generated. Thus, although Ero1p activity is essential for biosynthetic disulfide bond formation, uncontrolled Ero1p activity could produce too much reactive oxygen species that would be detrimental to the cell (Gross et al., 2006). Indeed, overexpression of the hyperactive Ero1p-C150A-C295A mutant inhibits cell growth, highlighting the physiological importance of the regulatory bonds in keeping Ero1p activity in check. Mammalian Ero1α has been shown to modulate its activity through a similar mechanism involving regulatory bonds, showing that autoregulation in response to the redox environment is a general property of Ero1 (Appenzeller-Herzog et al., 2008; Baker et al., 2008). An additional layer of protection against reactive oxygen accumulation in the ER of mammalian cells is provided by an ER resident, peroxiredoxin, which reduces hydrogen peroxide generated by Ero1 to limit peroxide accumulation (Tavender et al., 2008, 2010; Zito et al., 2010). An obvious sequence homolog to peroxiredoxin is absent in yeast; whether additional pathways functionally similar to the peroxiredoxin system exist in the ER of fungi remains to be explored.

The precise mechanism by which the regulatory bonds of Ero1 are reduced and then reoxidized will be crucial to understand how Ero1p activity is controlled and which features of the redox environment of the ER are sensed by Ero1p. Pdi1p is the most abundant oxidoreductase of the yeast ER and is the preferred physiological substrate for oxidation by Ero1p (Nørsgaard et al., 2001; Vitu et al., 2010); therefore, Pdi1p is likely to play an important part in regulating Ero1p. In the mammalian ER, the disulfide relay between Ero1α and PDI is regulated at least in part by the availability of PDI (Appenzeller-Herzog et al., 2010; Inaba et al., 2010). Interaction between Ero1α and PDI has been shown to be facilitated by a protruding β-hairpin in Ero1α and the β′ domain of PDI, which facilitates the interconversion between the Ox1 and Ox2 reductive-active forms of Ero1α (Masui et al., 2011). Differences between Ero1α and Ero1p, including the lack of a β-hairpin in Ero1p and the preference of Ero1p for the a domain of Pdi1p (versus the preference of Ero1α for the a′ domain), suggest that the yeast and mammalian Ero1-PDI systems may operate differently.

In vitro assays showing activation of Ero1p have typically used the nonphysiological substrate Trx1, which has a single CxxC-containing domain with a highly reducing redox potential rather than the physiological substrate Pdi1p because reduced Trx1 is more effective than Pdi1p at activating Ero1p by reduction of regulatory bonds (Sevier et al., 2007; Baker et al., 2008; Vitu et al., 2010). Here, we examine the role of Pdi1p in the reduction and reoxidation of the Ero1p regulatory bonds to reveal how the activity of Ero1p is set in a living cell. We have also sought to understand the role of glutathione in this process as the most abundant redox buffer of the ER. Although glutathione itself does not activate Ero1p nor is glutathione efficiently used as a substrate for Ero1p (Tu et al., 2000; Sevier and Kaiser, 2006b), reduced glutathione can stimulate Ero1p activity when used in conjunction with Pdi1p as a substrate (Sevier et al., 2007; Baker et al., 2008). We have reconstituted this coupled reaction in vitro and show that it recapitulates properties of the ER in vivo; as long as an excess of reduced glutathione is available, Pdi1p is maintained in a state enabled to activate Ero1p, which in turn provides oxidizing equivalents to oxidize glutathione.

**Results**

**Ero1p is capable of autonomous inactivation**

Because the regulatory bonds link distant sites of the Ero1p polypeptide chain, the presence or absence of these bonds can be readily discerned by mobility differences on nonreducing SDS-PAGE (Fig. 1 A). Activity of Ero1p can be inferred from the redox state of the regulatory bonds. In live yeast cells, Ero1p is converted to the reduced (active) form in cells treated with the reducing agent DTT and then returns to the oxidized (inactive) form after DTT removal (Fig. 1 B). Activation of Ero1p by reduction of the regulatory bonds and subsequent inactivation by reformation of the regulatory bonds could also be readily observed in an in vitro assay containing recombinant Ero1p (Ero1pc, 56–424, with an N-terminal (1–55) and a C-terminal (425–563) fragment removed) and an excess of reduced Trx1,
Fig. S1

![Image](https://example.com/image.png)

**Figure 2. Pathways for Ero1p inactivation.** (A) To test the ability of Ero1p to oxidize itself autonomously, 1 µM reduced (red) Ero1pc was prepared by incubation with 100 µM reduced His-s-tagged Trx1 for 2 min and then passage through Ni²⁺-tagged beads. The time course of Ero1pc inactivation was confirmed by SDS-PAGE (Mix; initial mixture: Ni²⁺-BF [beads bound fraction] + Ni²⁺-UF [unbound fraction]). (B) Autonomous reoxidation (ox) of Ero1pc after removal of Trx1 occurs rapidly and efficiently but depends on a functional active site (C355), and efficient reoxidation depends on the shuttle disulfide (C100-C105). The first lane in each time course (−) shows the oxidation state of Ero1pc before reoxidation by Trx1. (C) Ero1pc, expressed as an MBP fusion [MBP-Ero1p], can reoxidize Ero1pc-C355S in trans. An equal mixture of MBP-Ero1pc (or MBP-ero1-C100A-C105A; right) and Ero1pc-C355S was reduced by incubation with reduced Trx1 followed by Trx1 depletion. The time course of reoxidation of MBP-Ero1pc and Ero1pc-C355S was followed independently by separating MBP-Ero1pc and Ero1pc-C355S by size in SDS-PAGE and immunoblotting for MBP or Ero1.

serving as an effective substrate for Ero1p (Fig. 1 C). First, Ero1p is inactive with the regulatory bonds in a fully oxidized state. In ~0.5 min after addition of reduced Trx1, the regulatory bonds of Ero1p become reduced, and Ero1p is thus activated for the oxidation of Trx1. As a consequence of Ero1p, after ~60 min, all of the Trx1 is oxidized, and Ero1p returns to the oxidized inactive form (Fig. 1 C).

Activation of Ero1p by reduction of the regulatory bonds initiates on addition of reduced Trx1, indicating that the regulatory bonds can be reduced by direct dithiol/disulfide exchange with reduced Trx1. For the end phase of the reaction in which most of the Trx1 is oxidized and the regulatory bonds of Ero1p become reoxidized, we wished to know whether reoxidation of the regulatory bonds occurred by direct oxidation by oxidized Trx1 or instead by autonomous reoxidation by Ero1p when all of the reduced Trx1 had been consumed. To distinguish between these possibilities, we first tested the ability of active Ero1p to oxidize regulatory cysteines in the absence of Trx1. For this experiment, 1 µM Ero1pc was incubated with 100 µM His-s-tagged reduced Trx1 for 2 min, a time sufficient for complete activation of Ero1pc by reduction of the regulatory bonds. Subsequently, His-s-tagged Trx1 was removed by affinity to Ni²⁺ beads (Fig. 2 A). Trx1 depletion was confirmed by the significant absence of Trx1 in the Ni²⁺ unbound fraction and corresponding presence of Trx1 bound to the Ni²⁺ beads (unbound fraction; Fig. 2 A, bottom). A small amount of residual Trx1 was observed in the unbound fraction (Fig. 2 A, bottom), but it was anticipated that this limited fraction of Trx1 would be rapidly oxidized by Ero1p and not contribute to our Ero1p inactivation assay. After depletion of reduced Trx1, Ero1p was converted from a fully reduced to an oxidized form over a period of 60 min with a half time for completion of ~10 min (Fig. 2 B, top). The bands migrating between the fully reduced and oxidized forms likely correspond to partially oxidized states of Ero1pc. Parallel reactions using Ero1p mutants lacking the shuttle disulfide bond (Ero1pc-C100A-C105A) or the catalytic disulfide bond (Ero1pc-C355S) in the absence of Trx1 exhibited greatly slowed or no autonomous reoxidation of Ero1p, respectively (Fig. 2 B, middle and bottom). In addition, when the reoxidation reaction was performed in the absence of O₂ as an electron acceptor (Fig. S1 A, right), Ero1p exhibited slowed autonomous reoxidation. These observations show that Ero1p is capable of autonomous oxidation to form regulatory bonds and that this oxidation has catalytic requirements similar to biosynthetic disulfide bond formation.

We considered the possibility that autonomous oxidation of the Ero1p regulatory bonds was promoted by the hydrogen peroxide generated by Ero1p before removal of Trx1. Therefore, we examined the effects of hydrogen peroxide. Addition of catalase to the reaction, which should convert any hydrogen peroxide into water and oxygen (Fig. S1 B), did not significantly slow autonomous oxidation of the Ero1p regulatory bonds (Fig. S1 A, middle). Conversely, addition of 100 µM hydrogen peroxide, the maximum concentration that could be obtained from complete oxidation of 100 µM Trx1, did not enhance the oxidation of Ero1pc-C100A-C105A (Fig. S1 C).

**Autonomous oxidation of Ero1p occurs via an intermolecular reaction**

Autonomous oxidation of Ero1p could conceivably occur by intramolecular (in cis) or intermolecular (in trans) disulfide bond transfer. In the crystal structure of Ero1pc (Gross et al., 2004), one of the regulatory bonds, C90-C349, is close enough to the catalytic site to be oxidized in cis, whereas the other two regulatory bonds, C150-C295 and C143-C166, are located >20 Å away from the catalytic site, suggesting that the oxidation of these
bonds would require involvement of additional dithiol/disulfide exchanges with other cysteines. To determine whether one Ero1p protein can oxidize the regulatory bonds of another Ero1p, we asked whether Ero1pc-C355S, which is catalytically inactive and is not capable of autonomous oxidation, could nevertheless be oxidized in trans by active Ero1pc. A maltose binding protein (MBP) fusion to Ero1pc was used in this experiment so that MBP-Ero1pc and Ero1pc-C355SS could be distinguished by their distinct mobilities on SDS-PAGE. An autonomous oxidation assay was established by combining MBP-Ero1pc and Ero1pc-C355SS with reduced Trx1 to reduce the regulatory bonds on both forms of Ero1pc. After Trx1 was removed by Ni²⁺ affinity, both Ero1pc-C355S and MBP-Ero1pc were reoxidized at nearly equal rates, showing that efficient trans oxidation can occur (Fig. 2 C). Consistent with the oxidation of Ero1pc-C355SS being a product of MBP-Ero1pc catalytic function, disruption of the MBP-Ero1pc catalytic cycle by mutating the C100-C105 pair (MBP-ero1-C100A-C105A) prevented Ero1pc-C355SS oxidation (Fig. 2 C). We also tested the effect of dilution of Ero1pc in our autonomous oxidation assay and found that a fourfold dilution of Ero1pc slowed autonomous oxidation of Ero1pc (unpublished data). Together, the trans oxidation experiment and the dilution experiment show that autonomous oxidation of the Ero1p regulatory disulfides occurs predominantly, if not exclusively, by one Ero1p protein oxidizing the regulatory bonds of another Ero1p. The simplest mechanism for such dithiol/disulfide exchange would be for successive direct transfer of the C100-C105 shuttle cysteine disulfide bond to each of the three regulatory cysteine pairs. However, we cannot rule out the possibility that more complicated dithiol/disulfide rearrangements occur. Slow oxidation of Ero1pc facilitated by the Ero1pc-C100A-C105A (but not the Ero1pc-C355S) mutant could be observed also at late time points of the autonomous oxidation assay (>20 min), suggesting that the C352-C355 active site may contribute directly to oxidation of Ero1pc.

Ero1p is activated slowly but inactivated rapidly by Pdi1p
As we have shown, reduced Trx1 is a potent activator of Ero1p, and the use of Trx1 as an activator and substrate for Ero1p in in vitro assays made it possible to document the dramatic effect that reduction and oxidation of regulatory cysisteines have on Ero1p activity (Fig. 1 C; Sevier et al., 2007). However, Pdi1p is the major physiological substrate of Ero1p (Frand and Kaiser, 1999), and we were interested to use the in vitro assay for Ero1p regulation to make a comparable assessment of the ability of Pdi1p to either activate or inactivate Ero1p activity through reduction or oxidation of regulatory bonds.

First, we tested the ability of oxidized Pdi1p to inactivate Ero1p. We prepared activated Ero1pc-C100A-C105A by treatment with reduced Trx1 followed by removal of Trx1. The use of the Ero1pc-C100A-C105A mutant prevented efficient autonomous reoxidation of Ero1p, allowing us to test the ability of exogenous agents to reoxidize Ero1p. Oxidized Pdi1p and Trx1 were prepared by air oxidation during purification from *Escherichia coli*. The endpoint of air oxidation yielded Pdi1p that had the a domain almost fully oxidized and the a’ domain ~50% oxidized (Fig. S2) and Trx1 that was almost fully in the oxidized form (not depicted). We found that addition of a 20-fold molar excess of oxidized Trx1 had no effect on the rate of reoxidation of Ero1pc-C100A-C105A (Fig. 3 A, top), showing that oxidized Trx1 has little or no capability to oxidize the regulatory bonds of Ero1p. In contrast, oxidized Pdi1p dramatically increased the rate of Ero1pc-C100A-C105A reoxidation (Fig. 3 A, top right). The ability of oxidized Pdi1p to efficiently oxidize the regulatory bonds of Ero1p was not a peculiarity of the Ero1pc-C100A-C105A mutant, as we could also show that oxidized Pdi1p accelerated the oxidation of wild-type Ero1pc as well as Ero1pc-C355SS, which is unable to oxidize its regulatory bonds (Fig. S3). These results show that Ero1p can be inactivated by direct feedback from Pdi1p.

Next, we tested the converse process, the ability of reduced Pdi1p to reduce and thus activate Ero1p. To assess the activation process selectively, we again used Ero1pc-C100A-C105A because of this mutant’s greatly diminished capacity for autonomous oxidation of regulatory cysteines once reduced with an exogenous agent (Fig. 2 B, middle). Reduced Pdi1p requires 60 min to reduce the Ero1p regulatory bonds completely, whereas reduced Trx1 requires <5 min, indicating that Pdi1p is a relatively poor activator of Ero1p (Fig. 3 B, top). In summary, Trx1 is a potent activator but poor inactivator of Ero1p, whereas Pdi1p is a weak activator but potent inhibitor of Ero1p. These contrasting abilities to reduce or oxidize the regulatory bonds of Ero1p can be accounted for by the much greater reducing potential of Trx1 as compared with Pdi1p. By assaying the rate of activation or inactivation of Ero1p in separate reactions, we could show that reduced Pdi1p activates Ero1p more slowly than oxidized Pdi1p can inactivate Ero1p. This explains why in an in vitro Ero1p oxidation reaction that contains reduced Pdi1p as a substrate, Ero1p rarely, if ever, becomes fully activated, and the reaction proceeds relatively slowly.

The a and a’ domains of Pdi1p differ in their ability to regulate Ero1p
Yeast Pdi1p has two redox-active thioredoxin-like domains with different reduction potentials: the a domain (~195 mV) and a’ domain (~164 mV; Fig. 1 A; Tian et al., 2006; Vitu et al., 2010). We recently showed that Ero1p preferentially oxidizes the a domain (~164 mV; Fig. 1 A; Tian et al., 2006; Vitu et al., 2010). Thus, the a’ domain may play a lesser role in the oxidation of ER substrates despite its higher reduction potential than the a domain. To fully understand the interactions between Pdi1p and Ero1p, we wished to evaluate the contribution of each of the active Pdi1p domains to reduction and oxidation of Ero1p regulatory bonds.

Recombinant Pdi1p purified from *E. coli* had a fully oxidized domain and a partially oxidized a’ domain (Fig. S2), consistent with the different reduction potentials of the two domains. Moreover, naturally oxidized purified domain mutants Pdi1p-CCSS (a domain cysteines intact) and Pdi1p-SSSC (a’ domain cysteines intact) had similar oxidation states to the corresponding domains in wild-type Pdi1p (unpublished data). The same assay for Pdi1p oxidation of the Ero1p regulatory bonds was performed.
with Pdi1p-CCSS or Pdi1p-SSCC mutants. Both Pdi1p mutants accelerated oxidation of the Ero1p regulatory bonds. Despite the less-active disulfides, Pdi1p-SSCC reproducibly accelerated Ero1p oxidation more rapidly than Pdi1p-CCSS (Fig. 3 A), consistent with the higher reduction potential of the a’ CxxC. A Pdi1p-SSSS that lacked both redox-active sites did not accelerate oxidation of Ero1p regulatory bonds to the extent of the other Pdi1p variants, but a modest acceleration of Ero1p oxidation was observed (Fig. 3 A, bottom right). It is possible that the structural (CX6C) disulfide in Pdi1p (Fig. 1 A) has some effect or that Pdi1p may stabilize the oxidized form of Ero1p through a mechanism not involving disulfide exchange with the redox-active motifs.

Next, we compared the ability of reduced Pdi1p-CCSS or Pdi1p-SSCC to reduce the regulatory bonds of Ero1pc-C100A-C105A. Although reduction potentials measured against a glutathione standard suggest that the a domain is a better reductant, both reduced Pdi1p-CCSS and reduced Pdi1p-SSCC reduced Ero1p regulatory bonds at similar rates (Fig. 3 B, bottom). As expected, the single-domain mutants reduced the Ero1p regulatory bonds somewhat less efficiently than did wild-type Pdi1p, which has both active sites intact, and the double domain mutant Pdi1p-SSSS did not reduce the Ero1p regulatory bonds (Fig. 3 B, bottom right).

### The redox state of Ero1p can be set by a mix of reduced and oxidized Pdi1p

Reduced and oxidized Pdi1p promote activation and inactivation of Ero1p, respectively, suggesting that the activity of Ero1p in steady state may be set by the ratio of reduced to oxidized Pdi1p. By taking advantage of Ero1pc-C100A-C105A, which lacks the ability to oxidize Pdi1p efficiently, we could test admixtures of oxidized and reduced Pdi1p for their effect on the steady-state redox balance of the regulatory bonds of Ero1pc-C100A-C105A.
First, the autonomous oxidation of Ero1pc regulatory bond mutants Ero1pc-C150A-C295A, Ero1pc-C90A-C349A, or Ero1pc-C143-C166A was evaluated for their ability to undergo autonomous reoxidation after being reduced by Trx1. This comparison is complicated by differing band mobility for the oxidized and partially oxidized states of each of the mutants (Fig. 4A).

As a measure of the oxidation rate that could be consistently applied to each of the mutants, we represented the progression of the oxidation process as the decline in the fraction of Ero1p that was in a fully reduced state. All regulatory mutants showed similar overall autonomous oxidation rates (Fig. 4B), indicating that formation of the C150-C295 bond does not significantly affect oxidation of other regulatory bonds. Because the pattern of partially oxidized states was more complex for wild type (Fig. 2B) than for the mutants, it was not possible to make a precise quantitative comparison of rates.

Next, we tested each of the three regulatory bond mutants for their ability to be activated by reduced Pdi1p. This test required addition of the shuttle cysteine mutant to each of the three regulatory bond mutants. Reduction of Ero1pc-C100A-C105A-C150A-C295A by reduced Pdi1p was significantly faster than for Ero1pc-C100A-C105A or for the other regulatory bond mutants (Fig. 4, C and D). Ero1pc-C100A-C105A was oxidized more slowly than Ero1pc-C100A-C105A-C150A-C295A (Fig. 4B).

Although accurate quantitative amounts cannot be obtained as a result of the complications that oxidized Pdi1p contains a partially reduced domain and also nonlinear detection by immunoblot analysis, we found that when the fraction of reduced Pdi1p was >0.8, most Ero1pc-C100A-C105A was fully reduced, whereas when the fraction of reduced Pdi1p was <0.3, most Ero1pc-C100A-C105A was oxidized (Fig. 3C). In a steady state, in vivo Pdi1p is partially reduced (Vitu et al., 2010) like air-oxidized recombinant Pdi1p, and almost all Ero1p is in a fully oxidized form (see 0 time point of Figs. 1B and 5E). Therefore, we could conclude that partially reduced Ero1p is at least partially active and will continue to oxidize Pdi1p until a ratio of oxidized-to-reduced Pdi1p is achieved that no longer facilitates reduction and activation of Ero1p.

An Ero1p regulatory mutant is rapidly activated by Pdi1p

Previously, we showed that an Ero1p mutant that lacks only one of the three regulatory bonds, Ero1pc(c)-C150A-C295A, has high enzymatic activity both in vivo and in vitro (Sevier et al., 2007; Vitu et al., 2010). This suggests that in the absence of the C150-C295 regulatory bond, Ero1p is either more readily activated by reduced Pdi1p or less easily inactivated by reaction with oxidized Pdi1p or by autonomous oxidation.

First, the autonomous oxidation of Ero1p regulatory bond mutants Ero1pc-C150A-C295A, Ero1pc-C90A-C349A, and Ero1pc-C143A-C166A was evaluated for their ability to undergo autonomous reoxidation after being reduced by Trx1. This comparison is complicated by differing band mobility for the oxidized and partially oxidized states of each of the mutants (Fig. 4A). As a measure of the oxidation rate that could be consistently applied to each of the mutants, we represented the progression of the oxidation process as the decline in the fraction of Ero1p that was in a fully reduced state. All regulatory mutants showed similar overall autonomous oxidation rates (Fig. 4B), indicating that formation of the C150-C295 bond does not significantly affect oxidation of other regulatory bonds. Because the pattern of partially oxidized states was more complex for wild type (Fig. 2B) than for the mutants, it was not possible to make a precise quantitative comparison of rates.

Next, we tested each of the three regulatory bond mutants for their ability to be activated by reduced Pdi1p. This test required addition of the shuttle cysteine mutant to each of the three regulatory bond mutants. Reduction of Ero1pc-C100A-C105A-C150A-C295A by reduced Pdi1p was significantly faster than for Ero1pc-C100A-C105A or for the other regulatory bond mutants (Fig. 4, C and D). Ero1pc-C100A-C105A-C90A-C349A also
Pdi1p is the primary in vivo regulator of Ero1p

If Pdi1p regulates Ero1p through reduction and oxidation of its regulatory bonds, it should be possible to trap mixed disulfide complexes between Pdi1p and the regulatory cysteines of Ero1p in vivo. To specifically isolate mixed disulfides with regulatory cysteines, we used FLAG epitope–tagged Ero1p-C100A-C105A-C150A-C295A and Ero1p-C100A-C105A-C90A-C349A mutants that exhibited some reoxidation of Ero1p (Fig. 4 C) and oxidation of Pdi1p (not depicted) at the 60-min time point, suggesting that Ero1p may have alternative pathways to relay disulfide bonds to Pdi1p when the shuttle disulfide is unavailable (see Discussion).

do not hallucinate.

Figure 5. Pdi1p-mediated Ero1 regulation in vivo. (A) Pdi1p forms mixed disulfides with the Ero1p regulatory cysteines. Ero1p-C100A-C105A-Flag and its variants were immunoprecipitated (IP) by anti-Flag antibody and analyzed by immunoblotting against anti-Flag antibody and anti-Pdi1p serum. Lane 1, Ero1p-C100A-C105A-Myc; lane 2, Ero1p-C100A-C105A-Flag; lane 3, Ero1p-C100A-C105A-C90A-C349A-Flag; lane 4, Ero1p-C100A-C105A-C143A-C166A-Flag; lane 5, Ero1p-C100A-C105A-C150A-C295A-Flag. The single asterisk indicates a monomer of Ero1p mutants, and the double asterisks indicate mixed disulfides between Ero1p mutants and Pdi1p. Western blot. (B) Pdi1p was depleted by growing pdi1Δ covered with P_GAL1-Flag in SMM (glucose medium) for 16 h. (C) Immature CPY accumulates as Pdi1p is depleted. A control for fully reduced environment was prepared by treating cells with 1 mM DTT for 1 h. (D) Oxidation (ox) states of Ero1p after Pdi1p depletion (glucose medium) in a genetic background with pdi1Δ or with pdi1Δ with deletions of all PDI homologs (PDI homologΔ). red, reduced. (E) The roles of Pdi1p or glutathione in vivo activation of Ero1p. Pdi1p-depleted cells (middle) and glutathione-depleted cells (right) were prepared by growing CKY1081 in glucose medium and in galactose medium with 5 mM BSO, respectively. Cells were treated with 2 mM DTT for the indicated time.

exhibited slightly faster reduction than Ero1p-C100A-C105A or Ero1p-C100A-C105A-C143A-C166A (Fig. 4, C and D). These results suggest that removal of the C150-C295 regulatory bond lowers the threshold for Ero1p activation. Interestingly, both the Ero1pc-C100A-C105A-C150A-C295A and Ero1pc-C100A-C105A-C90A-C349A mutants exhibited some reoxidation of Ero1p (Fig. 4 C) and oxidation of Pdi1p (not depicted) at the 60-min time point, suggesting that Ero1p may have alternative pathways to relay disulfide bonds to Pdi1p when the shuttle disulfide is unavailable (see Discussion).

the crude immunoprecipitate by mass spectroscopy identified Pdi1p peptides but failed to identify additional PDI family members, including Eps1p, Eug1p, Mpd1p, or Mpd2p (unpublished data). This result suggests that Pdi1p is the primary oxidoreductase engaged in oxidation or reduction of the Ero1p regulatory bonds. Loss of any single regulatory cysteine pair in Ero1p-C100A-C105A did not prevent trapping of a mixed disulfide bond between Ero1p-C100A-C105A and Pdi1p, indicating that Pdi1p interaction with Ero1p-C100A-C105A is not limited to a single regulatory cysteine pair (Fig. 5 A). The mixed disulfides between Pdi1p and the various Ero1p-C100A-C105A regulatory bond mutants showed distinct mobilities on SDS-PAGE (Fig. 5 A), which likely corresponded to different variable combinations of cysteines in Ero1p and Pdi1p that engaged in oxidation and reduction of Ero1p regulatory bonds.

If reduced Pdi1p were essential for activating Ero1p, depletion of Pdi1p from the ER would be expected to decrease activation of Ero1p by reduction of regulatory bonds even under prevailing reducing conditions in the ER. We have established conditions to deplete a cell of Pdi1p, which is essential for viability, by glucose repression for 15 h of P_GAL1-PDI1 in a pdi1Δ genetic background (Fig. 5 B; Tachibana and Stevens, 1992; Frand and Kaiser, 1999). As expected, Pdi1p depletion disrupts folding in the ER, as shown by the accumulation of the ER form of carboxypeptidase Y (CPY), similar to that in cells that had been treated with DTT (Fig. 5 C). Radiolabeling of cells to specifically follow CPY synthesized after Pdi1p depletion confirmed a complete block of biosynthetic disulfide bond formation in newly synthesized CPY (Fig. S4). However, under the same conditions of Pdi1p depletion, most Ero1p remains oxidized (Fig. 5 D), indicating that the signal for an insufficiently oxidized ER...
cannot be transduced to activate Ero1p in the absence of Pdi1p. Pdi1p-depleted cells showed very slow activation of Ero1p even when they were treated with the reducing agent DTT, a condition that leads to rapid activation of Ero1p in Pdi1p-expressing cells (Fig. 5 E).

In the Pdi1p-depleted cells, a small amount of activated (reduced) Ero1p was detected (Fig. 5 D), and catalytically inactive Ero1 mutants Ero1p-C355S and Ero1p-C100A-C105A exhibited significantly more of the reduced forms (Fig. S5), suggesting that under conditions of Pdi1p depletion, although Ero1p can be reduced to some extent, most of the Ero1p remains in an oxidized state if autonomous reoxidation is possible. We tested the possibility that the residual reduction of Ero1p in cells that had been depleted for Pdi1p was catalyzed by another PDI homolog. By conducting the depletion experiment in a strain depleted for the other homologs (mpd1Δ, mpd2Δ, eug1Δ, eps1Δ, pdiΔ, and CEN-P GAL1-PDI1), we found that reduced Ero1p formed to at least the same extent as in a pdiΔ P GAL1-PDI1 strain (Figs. 5 D and S5), indicating that no other PDI family members contribute significantly to reduction of Ero1p regulatory bonds.

Glutathione acts synergistically with Pdi1p to activate Ero1p

The rapid Pdi1p-dependent reduction of Ero1p regulatory bonds that occurs in cells treated with DTT could be the result of a pool of reduced Pdi1p formed by direct reduction with DTT that had entered the ER. Alternatively, DTT treatment may produce a pool of reduced glutathione (GSH) in the ER, which in turn could lead to reduction of Pdi1p. To test the possibility that DTT acts indirectly through glutathione, we tested the effect of depleting cells of glutathione by treating cells with 5 mM buthionine sulfoximine (BSO) for 15 h, which blocks glutathione synthesis by inhibiting γ-glutamylcysteine synthetase. Reduction of Ero1p regulatory bonds by DTT treatment occurred more slowly in glutathione-depleted cells than in untreated cells (Fig. 5 E). This result suggests that the presence of a reducible pool of glutathione may accelerate the overall process of reduction of Pdi1p by DTT. Alternatively, depletion of glutathione by BSO treatment may subtly affect Pdi1p expression or have some other indirect effect on the redox state of the ER.

To address the role of glutathione in Ero1p activation more directly, we reconstituted Ero1p activation in vitro using both Pdi1p and GSH as substrates. By itself, Pdi1p is a poor activator of Ero1p because once Pdi1p has become oxidized through Ero1p oxidase activity, there is no longer sufficient reduced Pdi1p available to keep Ero1p in an active state, and oxidized Pdi1p can accelerate inactivation of Ero1p. Therefore, fully activated Ero1p was rarely observed during reaction with reduced Pdi1p (Fig. 6 A). Glutathione alone was also a poor activator of Ero1p. 10 mM GSH did not reduce regulatory bonds in either wild-type Ero1p (Fig. 6 B, left) or Ero1pc-C100A-C105A (not depicted). However, a mixture of 10 mM GSH and Pdi1p maintained a pool of at least partially activated Ero1p (Fig. 6 B, right). The basis of Ero1p activation in the presence of Pdi1p and GSH appeared to be that
provided by a pool of GSH in great stoichiometric excess to Pdi1p, which allowed for a significant pool of reduced Pdi1p to be maintained. This pool of reduced Pdi1p in turn could reduce the regulatory bonds of Ero1p, thus overcoming the kinetic barrier for GSH to reduce the Ero1p regulatory bonds. In this coupled reaction, oxidized glutathione (GSSG) was generated by the combined action of Pdi1p and Ero1p (Fig. 6 C), and production of GSSG depended on Ero1p enzymatic activity because even in the presence of Pdi1p, catalytically inactive Ero1pc-C100A-C105A did not produce GSSG actively, whereas hyperactive Ero1pc-C150A-C295A produced GSSG more rapidly than wild type (not depicted).

To investigate the effects of the balance of GSH to GSSG on Ero1p activity, we reconstituted an in vitro reaction in which recombiant Ero1p and Pdi1p were incubated in the presence of three different ratios of GSH/GSSG. When the reaction was begun in the presence of GSH only, the rate of glutathione oxidation was initially rapid but then slowed. Evidently, the concomitant generation of GSSG by the action of Ero1p and Pdi1p eventually leads to inactivation of Ero1p (Fig. 6 D, 5 mM GSH curve). Introduction of GSSG into the coupled reaction slowed the initial rate of GSH oxidation (compare the curves of 5 mM GSH with 8:1 and 3:1 GSH/GSSG; Fig. 6 D). Taking the background of slow nonenzymatic generation of GSSG into account, the Ero1p and Pdi1p catalyzed oxidation of GSH stops at when the molar ratio of GSH/GSSG is ~3:1. Thus, this ratio of GSH/GSSG appears to be the approximate steady-state set point for the coupled reaction.

**Discussion**

A conserved protein disulfide relay system of the ER, consisting of Ero1 and PDI, supports correct disulfide bond formation of secretory proteins (Sevier et al., 2001; Sevier and Kaiser, 2006a; Appenzeller-Herzog et al., 2008; Braakman, 2009). In *S. cerevisiae*, the Ero1-PDI relay is essential for biosynthetic disulfide bond formation and is thus essential for cell viability (Frand and Kaiser, 1998; Pollard et al., 1998; Vitu et al., 2010). We previously showed that the activity of *S. cerevisiae* Ero1p is controlled by an autoregulatory feedback loop that involves the reduction and the reoxidation of three regulatory disulfide bonds (Sevier et al., 2001). Here, we show that not only is Pdi1p the major substrate of Ero1p in the disulfide relay system but that Pdi1p is also the primary regulator of Ero1p activity by its ability carry out dithiol/disulfide exchange with the regulatory bonds. We also show that the redox state of glutathione in the ER is important for setting the regulatory state of Pdi1p, and, in this way, the disulfide bond–generating activity of Ero1p is controlled by the redox status of both Pdi1p and of glutathione.

In a reaction initiated by adding to Ero1p a stoichiometric excess of reduced Trx1, a model substrate, the regulatory bonds in Ero1p are rapidly reduced, and Trx1 is oxidized by active Ero1p. Once Trx1 has been oxidized, the regulatory bonds in Ero1p are reformed, and Ero1p returns to an inactive state. In this paper, we separated the activation and inactivation phases of this cycle to determine the biochemical requirements for each phase. As expected, the reduced form of Trx1 readily reduces regulatory bonds in Ero1p and is thus a potent activator of Ero1p. However, oxidized Trx1 has no capacity to reoxidize the regulatory cysteines of Ero1p. Instead, oxidation of the regulatory cysteines is accomplished by Ero1p itself in a reaction that probably involves the transfer of a disulfide bond from the shuttle cysteines of one Ero1p protein molecule to the regulatory cysteines of another. Thus, the inactivation phase occurs by autonomous oxidation of Ero1p once reduced Trx1 has been depleted by being converted to the oxidized form.

A similar analysis for a reaction that contains Ero1p and its natural substrate Pdi1p revealed that Ero1p is never fully activated in the presence of Pdi1p (Fig. 6 A). Whereas we initially thought that the inability of Pdi1p to activate Ero1p robustly was a consequence of some deficiency in the in vitro reaction, we now have evidence that the balance of the reduced and oxidized forms of Pdi1p is crucial in regulating Ero1p enzyme activity and faithfully reproduces the redox homeostasis set point of the ER.

Pdi1p has two redox-active domains containing the CxxC motifs. The a’ domain is not as efficiently oxidized by Ero1p as the a domain (Vitu et al., 2010). However, the a’ domain does appear to play a greater role than the a domain in oxidizing the Ero1p regulatory bonds; the partially oxidized a’ domain (Pdi1p-SSCC) accelerates oxidation of Ero1p regulatory bonds more rapidly than the fully oxidized a domain (Pdi1p-CCSS). Given the relative redox potentials of the two domains, their propensity to be oxidized by Ero1p and their relative ability to oxidize the regulatory bonds of Ero1p provide a consistent explanation for why the a’ domain is only partly oxidized, whereas the a domain is fully oxidized in cells under standard conditions (Vitu et al., 2010). In contrast to the yeast Pdi1p, the two active domains of the human PDI have similar reduction potentials, and the a’ domain is the one preferentially oxidized by Ero1p (Wang et al., 2009; Chambers et al., 2010). Therefore, it seems possible that the mechanism of Ero1p regulation via the two domains of the human PDI is distinct from the one in yeast. Specificity in interaction between human and yeast Ero1 and PDI proteins has been demonstrated (Vitu et al., 2010; Masui et al., 2011). Comparison of the activity of human and yeast proteins in vitro shows that the highest enzyme activity is achieved using protein combinations of Ero1 and PDI from the same species (Araki and Nagata, 2011). Low catalytic activity was traced in part to a weaker binding affinity between human Ero1p and yeast Pdi1p, relative to human PDI (Araki and Nagata, 2011). Whether the different redox potentials of the PDI domains in human and yeast PDI also contribute to the differences in Ero1 regulation between species remains to be assessed.

Several lines of evidence point to the existence of multiple disulfide relay pathways from Ero1p to Pdi1p. Best characterized is the flow of disulfides from the C352-C355 pair to Pdi1p via the C100-C105 shuttle cysteines. This pathway is necessary for full activity of Ero1p in vitro and is necessary for cell viability. Nevertheless, Ero1p-C100A-C105A retains some activity in vitro and shows slow autonomous reoxidation, showing that a disulfide bond can be transferred, albeit slowly, from the active site to the regulatory disulfides without the action of the C100-C105 shuttle (Fig. 2 B). Moreover, in vivo experiments have shown that yeast cells with an *ero1-C100A* mutation are
The thiol substrates (reduced protein thiols or reduced glutathione) present in the ER can be oxidized by Pdi1p, leading to formation of reduced Pdi1p. If sufficient reduced Pdi1p has formed, Ero1p is activated by direct reduction of the Ero1p regulatory bonds by reduced Pdi1p. Once activated, Ero1p oxidizes Pdi1p until a steady-state balance of oxidized and reduced Pdi1p is reestablished. The balance of reduced and oxidized Pdi1p determines the degree of Ero1p activation; once reduced Pdi1p has declined sufficiently, autonomous oxidation of the regulatory bonds of Ero1p will lead to Ero1p inactivation, preventing overoxidation of the ER. Under hyperoxidizing conditions, oxidized Pdi1p would rapidly inactivate Ero1p.

(Appenzeller-Herzog et al., 2010). It seems likely that ER redox homeostasis is maintained by the same basic mechanism in yeast and mammalian cells.

Materials and methods

Protein expression and purification

The sequence coding Ero1pc (56–424) or Ero1pc mutants (Ero1pc-C100A-C105A, Ero1pc-C355S, Ero1pc-C150A-C295A, Ero1pc-C90A-C349A, Ero1pc-C143A-C166A, and Ero1pc-C100A-C150A-C143A-C166A) was fused at the C terminus to His6-tagged MBP linked by the Tobacco etch virus (TEV) protease cleavage sequence (ENLYFQGS) inserted into the pET17b vector (EMD) between NdeI and XhoI restriction sites. We found that C355S was the only point mutation of the active-site cysteine pair (C352-C355) that could be produced in a soluble FAD-bound state. Ero1pc and all variants were overexpressed in Origami B(DE3) competent cells (EMD) by induction with 0.4 mM IPTG supplemented with 10 μM FAD overnight at room temperature. Ero1pc fusion proteins with His6-tagged MBP were purified from cell lysates by affinity to amylose (New England Biolabs, Inc.) and then dialyzed into TEV cleavage buffer (50 mM Tris, pH 7.8, 0.5 mM EDTA, and 0.5 mM tris[2-carboxyethyl]phosphine). MBF-fused Ero1pc (MBP-Ero1pc) and Ero1pc-C100A-C150A were also expressed and purified as described for Ero1pc purification. Ero1pc was cleaved from His6-tagged MBP by incubating with recombinant His6-tagged TEV protease (1:100 wt/wt protease to substrate; the TEV protease–encoding plasmid [pET17b] vector) with NdeI and XhoI restriction sites. We found that C355S was the only point mutation of the active-site cysteine pair (C352-C355) that could be produced in a soluble FAD-bound state. Ero1pc and all variants were overexpressed in Origami B(DE3) competent cells (EMD) by induction with 0.4 mM IPTG supplemented with 10 μM FAD overnight at room temperature. Ero1pc fusion proteins with His6-tagged MBP were purified from cell lysates by affinity to amylose (New England Biolabs, Inc.) and then dialyzed into TEV cleavage buffer (50 mM Tris, pH 7.8, 0.5 mM EDTA, and 0.5 mM tris[2-carboxyethyl]phosphine). MBF-fused Ero1pc (MBP-Ero1pc) and Ero1pc-C100A-C150A were also expressed and purified as described for Ero1pc purification. Ero1pc was cleaved from His6-tagged MBP by incubating with recombinant His6-tagged TEV protease (1:100 wt/wt protease to substrate; the TEV protease–encoding plasmid [pET17b] vector) with NdeI and XhoI restriction sites. We found that C355S was the only point mutation of the active-site cysteine pair (C352-C355) that could be produced in a soluble FAD-bound state. Ero1pc and all variants were overexpressed in Origami B(DE3) competent cells (EMD) by induction with 0.4 mM IPTG supplemented with 10 μM FAD overnight at room temperature.

In the mammalian cell, it has been suggested that oxidation of PDI and glutathione is well regulated by an equilibrium between Ero1-α and PDI.

Figure 7. A balance between reduced and oxidized Pdi1p determines ER redox homeostasis. The thiol substrates (reduced protein thiols or reduced glutathione) present in the ER can be oxidized by Pdi1p, leading to formation of reduced Pdi1p. If sufficient reduced Pdi1p has formed, Ero1p is activated by direct reduction of the Ero1p regulatory bonds by reduced Pdi1p. Once activated, Ero1p oxidizes Pdi1p until a steady-state balance of oxidized and reduced Pdi1p is reestablished. The balance of reduced and oxidized Pdi1p determines the degree of Ero1p activation; once reduced Pdi1p has declined sufficiently, autonomous oxidation of the regulatory bonds of Ero1p will lead to Ero1p inactivation, preventing overoxidation of the ER. Under hyperoxidizing conditions, oxidized Pdi1p would rapidly inactivate Ero1p.

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for SSSS] tagged with His6 at the N-terminus was inserted into pET20b between Ndel and SacI restriction sites. Recombinant His-tagged Pdi1p, Pdi1p variants, and His-tagged E. coli thioredoxin [Trx1; Sevier and Kaiser, 2000b] were overexpressed in B121(DE3)pLysS competent cells (EMD) by induction with 0.4 mM IPTG for 5 h at 37°C and purified from cell lysates by affinity to the HitTrap Ni2+ column. Puriﬁed, naturally oxidized Pdi1p and Trx1 were dialyzed into PBS. Reduced forms of Pdi1p and Trx1 were prepared by incubating with 10 mM DTT for 30 min at room temperature and removing DTT with Micro Bio-Spin 6 (Bio-Rad Laboratories).

Yeasts strains and plasmids

C. KY1044 and C. KY1045 and MaTα and MaTα strain pdi1Δ::KanMX strains covered by URA3 CEN PDI1 plasmid pCS213 have been previously described (Vitu et al., 2010). To facilitate scoring of crosses with the pdi1Δ strain, a NatMX-marked pdi1Δ strain was constructed by swapping the KanMX marker in C. KY1045 with a NatMX cassette by homologous recombination [Goldstein and McCusker, 1999]. Individual disruptions of the genes encoding the yeast Ero1 homolog proteins were made by one-step gene replacement of the entire ORF with KanMX by homologous recombination. The compound deletion strain C. KY1086 with the genotype MaTα GAL2 ura3-52 leu2-3,112 pdi1Δ::NatMX and pCS213 [C. KY1087, individual pdi1Δ and Bgl2::HA strains were mated, and an MaTα NatMX segregant was selected after sporulation. Viable disruption of C. KY1086 and C. KY1087 depends on a plasmid-Borne pdi1Δ gene provided by plasmid pCS213. C. KY1086 and C. KY1089 were generated by transformation of C. KY1086 or C. KY1087, respectively, with the pSK65 [CEN LEU2 PDS1-PDI1] followed by selection against pCS213 by plating on supplemented minimal medium (SMM) with 5-FOA. C. KY1090 was created by transformation of C. KY1044 with pSK2 [CEN LEU2 His6-PDI1] followed by selection against pCS213 with 5-FOA.

To create pSK2 [CEN LEU2 His6-PDI1], the sequence coding HHHH-HGGG was inserted right after the signal sequence (1–22) by introducing the Nhel restriction site in pCS463, which contains the PDI1 coding region and −875 and −150 bp of the 5′ and 3′ untranslated regions. Plasmid pSK65 [CEN LEU2 PDS1-PDI1] contains the PDI1 coding region and −60 and −150 bp of the 5′ and 3′ untranslated regions under the GAL1 promoter. ERO1-coding URA3 2 plasmids pSK64 [ERO1-Rag], pSK64 [ero1-C100A-C105A-FLAG], pDPS51 [ero1-C100A-C105A-C150A-C295A-FLAG], pDPS54 [ero1-C100A-C105A-C150A-C295A-FLAG], pDPS55 [ero1-C100A-C105A-C150A-C295A-FLAG], and pSK66 [ero1-C100A-C105A-C295A-FLAG] were generated by insertion of sequence-encoding tag fragment after the last codon using the NotI restriction site and subcloning or site-directed mutagenesis based on the previously reported plasmid pAF84 (Frands and Kaiser, 1998).

Analysis of protein oxidation states

For reduction of Ero1p regulatory bands in vitro, 1 μM Ero1p or its variants were incubated with 50 or 20 μM reduced Trx1, reduced Pdi1p, or reduced Pdi1p mutants in PBS containing 0.5 mM EDTA. After incubation at 25°C, the reactions were quenched by mixing with 1× SDS-AMS (4-acetamido-4′-maleimidylstilbene-2,2′-disulfonic acid) buffer (1× SDS sample buffer without reducing agent and 1 mM AMS [Invitrogen]), which alkylates free cysteine thiol and adds one ~500-D molecular weight to each free thiol. For reactions that contained glutathione or DTT, proteins were ﬁrst precipitated by oxidation states of Ero1p and Pdi1p were analyzed after oxidation by nonreducing SDS-PAGE followed by immunoblotting with anti-Ero1 serum or anti-HDEL (Santa Cruz Biotechnology, Inc.). The oxidation state of Trx1 was analyzed by nonreducing SDS-PAGE followed by immunoblotting with anti-Trx1 serum and oxidized band intensity.

To determine the effect of hydrogen peroxide on the oxidation state of Ero1p regulatory bands (Fig. S1), 1 μM Ero1p was incubated with 100 μM reduced His-tagged Trx1 in PBS containing 0.5 mM EDTA for 2 min, and Trx1 was selectively removed by afﬁnity for Ni2+ beads. To remove hydrogen peroxide generated during action of Ero1p oxidase, 80 μg/ml catalase was added to the reaction mixture after generation of hydrogen peroxide by catalase was conﬁrmed by measuring the amount of hydrogen peroxide in the reaction with Amplex UltraRed reagent (Invitrogen). 1 μM Ero1p was incubated with 100 μM reduced thioredoxin, 50 μM Amplex red, and 0.1 U/ml HRP in the presence or absence of 80 μg/ml catalase for 30 min at room temperature. Fluorescence was measured in a microplate reader with wavelength settings of 530/590 nm. Inactivation of Ero1p under anaerobic conditions was analyzed as described above except being performed in the anaerobic chamber ﬂowing N2 and CO2 gases. To test whether exogenous hydrogen peroxide or oxidized Pdi1p can promote inactivation of Ero1p, 100 μM hydrogen peroxide or 20 μM oxidized Pdi1p was added to Ero1p, Ero1p-C100A-C105A, or Ero1p-C35S55 after Trx1 depletion. Oxidation states of Ero1p and its mutants were analyzed after cysteine modiﬁcation with 1 mM AMS by nonreducing SDS-PAGE and immunoblotting with anti-Ero1p serum.

The oxidation states of each catalytic domain of recombinant Pdi1p were determined by introducing a thrombin cleavage site that allows separation of the two catalytic domains (Fig. S2). The sequence coding Nterminal His6-PDI1 of pCS213 [C100–C522] with a thrombin recognition sequence in the Xlinker was subcloned from pSK42 [Vitu et al., 2010] for E. coli expression. His6-Pdi1p thrombin was overexpressed in B121(DE3)pLysS competent cells by IPTG and puriﬁed from cell lysates with the HitTrap Ni2+ column. Puriﬁed His6-Pdi1p thrombin was dialyzed into PBS. 10 μg His6-Pdi1p thrombin was incubated with 1 mM AMS for 30 min at room temperature followed by treatment with 0.1 μg thrombin supplemented with 1 mM CaCl2 for 1 h at 37°C. Fully reduced Pdi1p control was prepared by treatment with 10 mM DTT for 30 min at room temperature. DTT was removed by using Bio-Spin 6. AMS-modiﬁed and thrombin-digested samples were analyzed by nonreducing SDS-PAGE.

The oxidation state of newly synthesized CPY in the Pdi1p-depleted ER was analyzed in pdi1Δ cells with galactose-inducible PDI1 grown to the exponential phase for 15 h in glucose medium to deplete Pdi1p. Cells were suspended in SMM-met, pulse labeled for 10 min at 30°C, and lysed in the presence of 10% chilled TCA to block disulﬁde exchange. After AMS modiﬁcation, CPY was immunoprecipitated and resolved by reducing SDS-PAGE. A fully reduced CPY control was prepared by treating cells with 10 mM DTT for 15 min before cell lysis.

Reoxidation of Ero1p after thioredoxin depletion

1 μM Ero1p was reduced by incubation with 100 μM reduced His-tagged Trx1 for 2 min and then passed through Ni2+ beads to remove Trx1. At times after Trx1 depletion, the reaction was quenched by mixing with SDS sample buffer containing 1 mM AMS. Depletion of Trx1 was conﬁrmed by analysis without reducing SDS-PAGE. When necessary, 40 μM oxidized Trx1, 20 μM oxidized Pdi1p, or 20 μM oxidized Pdi1p mutant was added into Ero1p or Ero1p mutants immediately after Trx1 depletion.

Puriﬁcation of mixed disulfides from yeast

C. KY1090 expressing His6-Pdi1p was transformed with pSK64 [ero1-C100A-C105A-FLAG], pDPS51 [ero1-C100A-C105A-C150A-C295A-FLAG], pDPS49 [ero1-C100A-C105A-C150A-C295A-FLAG], and pDPS50 [ero1-C100A-C105A-C143A-C166A], Exponentially grown cells were lysed by agitation with glass beads in the presence of chilled 10% TCA. TCA-precipitated protein pellets were washed with acetone and redisolved with 2% SDS and 50 mM Tris, pH 8.0, containing 50 mM NEM to block free cysteines. For efﬁcient afﬁnity puriﬁcation, SDS was removed by SDS-OUT reagent (Thermo Fisher Scientiﬁc). After clariﬁcation by centrifugation, Ero1p-C100A-C105A-FLAG was released from anti-FLAG afﬁnity beads using 100 μg/ml ﬂag peptide [Sigma-Aldrich] followed by deglycosylation with PNGaseF for 3 h at 37°C. Samples puriﬁed by afﬁnity to anti-FLAG beads were passed through an Ni2+ column to capture mixed disulﬁdes with His6-Pdi1p. Both Ni2+ unbound fraction and bound fraction were collected and analyzed by nonreducing SDS-PAGE and immunoblotting with anti-FLAG (Sigma-Aldrich) or anti-Pdi1p.

Depletion of Pdi1p and glutathione in yeast

To determine the oxidation states of Ero1p and mutants in Pdi1p- or glutathione-depleted cells, pSK63, pDPS49, and pSK66 were transformed into C. KY1088 and/or C. KY1089. Cells exponentially grown in SMM containing...
1.5% galactose and 1% raffinose were incubated in SMM containing 2% glucose for 15 h to shut off expression of Pdi1p. Glutathione was depleted by growing cells in the presence of 5 mM BSO, an inhibitor of glutathione biogenesis, for 15 h. Pdi1p depletion was confirmed by immunoblotting with anti-Pdi1p (Fig. 5 E), and glutathione depletion was confirmed using Ellman’s reagent.

The manipulation of CPY was performed in pdi1Δ cells with galactose-inducible PD1 grown to exponential phase for 15 h in glucose medium to deplete Pdi1p. For fully reduced cell environment, cells were incubated with 1 mM DTT for 1 h after a 14-h incubation in glucose medium. Cell lysates were prepared in the presence of chilled 10% TCA, and mature and immature CPY were analyzed by immunoblotting with anti-CPY serum.

Online supplemental material

Fig. S1 shows that autonomous oxidation and inactivation of Ero1p is not a side effect of hydrogen peroxide produced by aerobic catalysis by Ero1p. Fig. S2 shows that the endpoint of air oxidation yields a form of recombinant Pdi1p with the α domain almost fully oxidized, and the α’ domain is partially oxidized. Fig. S3 shows that air-oxidized Pdi1p can contribute to the oxidation of the Ero1p regulatory bonds. Fig. S4 shows that when cells are depleted of Pdi1p by growing pdi1Δ cells with glucose-repressible PD1 in glucose medium, newly synthesized CPY was recorded after adding 1 U of glutathione reductase.

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