

Regulation of Manganese Antioxidants by Nutrient Sensing Pathways in *Saccharomyces cerevisiae*

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ABSTRACT In aerobic organisms, protection from oxidative damage involves the combined action of enzymatic and nonproteinaceous cellular factors that collectively remove harmful reactive oxygen species. One class of nonproteinaceous antioxidants includes small molecule complexes of manganese (Mn) that can scavenge superoxide anion radicals and provide a backup for superoxide dismutase enzymes. Such Mn antioxidants have been identified in diverse organisms; however, nothing regarding their physiology in the context of cellular adaptation to stress was known. Using a molecular genetic approach in Baker's yeast, *Saccharomyces cerevisiae*, we report that the Mn antioxidants can fall under control of the same pathways used for nutrient sensing and stress responses. Specifically, a serine/threonine PAS-kinase, *Rim15p*, that is known to integrate phosphate, nitrogen, and carbon sensing, can also control Mn antioxidant activity in yeast. *Rim15p* is negatively regulated by the phosphate-sensing kinase complex *Pho80p/Pho85p* and by the nitrogen-sensing Akt/S6 kinase homolog, *Sch9p*. We observed that loss of either of these upstream kinase sensors dramatically inhibited the potency of Mn as an antioxidant. Downstream of *Rim15p* are transcription factors *Gis1p* and the redundant *Msn2/Msn4p* pair that typically respond to nutrient and stress signals. Both transcription factors were found to modulate the potency of the Mn antioxidant but in opposing fashions: loss of *Gis1p* was seen to enhance Mn antioxidant activity whereas loss of *Msn2/4p* greatly suppressed it. Our observed roles for nutrient and stress response kinases and transcription factors in regulating the Mn antioxidant underscore its physiological importance in aerobic fitness.

ADAPTATION to life in oxygen has entailed evolution of numerous enzymatic and nonenzymatic methods for detoxifying reactive oxygen species and repairing damage. Much is known about the widely spread superoxide dismutase (SOD) enzymes that disproportionate superoxide anion into oxygen and hydrogen peroxide (McCord and Fridovich 1969; Abreu and Cabelli 2010). Less understood is the class of small molecule nonproteinaceous manganese (Mn) containing complexes that can substitute for SOD in a variety of organisms. So-called "Mn antioxidants" were first identified in *Lactobacillus plantarum* that lacks SOD enzymes, but is aerobically viable due to intracellular accumulation of millimolar Mn (Archibald and Fridovich 1981a,b, 1982a,b; Archibald and Duong 1984). High levels of Mn have also been shown to substitute for SOD in strains of *Escherichia*

coli (Al-Maghrebi *et al.* 2002), *Neisseria gonorrhoeae* (Tseng *et al.* 2001), and the yeast *Saccharomyces cerevisiae* (Chang and Kosman 1989; Sanchez *et al.* 2005; Reddi *et al.* 2009), engineered to lack SOD enzymes. Elegant work by Daly and colleagues has shown that tolerance to radiation and oxidative stress in a variety of bacterial species is due to accumulation of high levels of intracellular Mn, but low Fe (Daly 2006, 2009; Daly *et al.* 2007, 2010; Gross 2007; Granger *et al.* 2011). In higher organisms, Mn treatment can prolong the life span and oxidative stress resistance in the simple metazoan, *Caenorhabditis elegans*, and also defend against reactive oxygen species (ROS) in the cryopreservation of sperm (Lin *et al.* 2006; Bansal and Kaur 2009; Cheema *et al.* 2009).

The biochemical nature of the Mn antioxidant has been subject to much investigation. It has been defined as a Mn-dependent but SOD-independent superoxide scavenging activity in bacterial and yeast lysates. This activity is EDTA sensitive, dialyzable, heat and protease resistant, and was proposed to represent Mn complexes of small molecule cellular metabolite(s) (Archibald and Fridovich 1981a; Chang and Kosman 1989). A number of Mn-carboxylate complexes (Archibald and Fridovich 1982b), as well as Mn-orthophosphate

Copyright © 2011 by the Genetics Society of America
doi: 10.1534/genetics.111.134007

Manuscript received August 23, 2011; accepted for publication September 12, 2011
Supporting information is available online at <http://www.genetics.org/cgi/content/full/genetics.111.134007/DC1>.

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(Pi) (Barnese *et al.* 2008), have been shown to exhibit superoxide scavenging activity *in vitro*, and the extreme radio-resistance of *Deinococcus radiodurans* is associated with certain Mn–Pi and -peptide complexes (Daly *et al.* 2010). Moreover, our *in vivo* studies in the Baker's yeast have demonstrated a role for Mn–Pi as an important backup for Cu/Zn containing SOD (*SOD1*) (McNaughton *et al.* 2010).

Using ENDOR spectroscopy to monitor Mn speciation in intact yeast cells, we observed a close correlation between the cellular level of Mn–Pi in various yeast strains and their resistance to oxygen toxicity (McNaughton *et al.* 2010; Szuromi 2010). Of the strains tested, the most severe oxygen toxicity was observed when phosphate control was disrupted through mutations in the phosphate-sensing kinase complex *Pho80p/Pho85p* (Kaneko *et al.* 1982; Ogawa *et al.* 2000; Wykoff and O'shea 2001; Carroll and O'shea 2002; Lee *et al.* 2007; Wykoff *et al.* 2007). Deletion of either *pho80* or *pho85* rendered *sod1Δ* mutants lacking Cu/Zn *SOD1* inviable in air and cells seemed nearly devoid of Mn antioxidant protection (Reddi *et al.* 2009). By ENDOR spectroscopy, Mn–Pi levels were lowered in this strain (McNaughton *et al.* 2010), although not to a degree expected for the profound oxygen toxicity observed. Ablation of *Pho80/Pho85p* inhibited Mn antioxidant activity through a mechanism other than simple loss of Mn–Pi.

In the context of cellular physiology, what dictates formation of Mn antioxidants? Are these spontaneously formed complexes of Mn that incidentally scavenge superoxide, or does the cell tightly regulate Mn antioxidant activity in concert with protein-based antioxidants? Using the Baker's yeast *S. cerevisiae* as a model organism, we provide evidence for the latter. Namely, we find that the ability of cells to utilize Mn as an antioxidant can fall under control of *Rim15p*, a PAS-kinase that integrates phosphate, nitrogen, and carbon-nutrient sensing (Pedruzzi *et al.* 2003; Cameroni *et al.* 2004; Roosen *et al.* 2005; Wanke *et al.* 2005; Swinnen *et al.* 2006; Smets *et al.* 2010; Yang *et al.* 2010). Hyperactivation of *Rim15p* from genetic ablation of its *Pho80p/Pho85p* (phosphate sensing) or *Sch9p* (nitrogen sensing) upstream regulators results in strong downregulation of the Mn antioxidant, helping to explain the profound oxygen toxicity in the *pho80* (or *pho85*) *sod1* null mutants. In addition, transcription factors downstream of *Rim15p*, which include *Gis1p* and the redundant pair *Msn2p* and *Msn4p* (hereafter referred to as *Msn2/4p*) that typically regulate stress-response factors, likewise play a role in titrating the activity of the Mn antioxidant. Overall, this work demonstrates that the Mn antioxidant is controlled by the same pathways that sense nutrients and respond to stress.

Materials and Methods

Yeast strains, plasmids, and growth conditions

All yeast strains for this study were derived from BY4741 (MATa, *leu2Δ0*, *met15Δ0*, *ura3Δ0*, *his3Δ1*). A full listing, including descriptions on their source or construction, is included in Supporting Information, File S1. Details on

the construction of the *msn2::HIS3* disruption plasmid, pAR007, and the *sch9::HIS3* disruption plasmid, pAR009, are in File S1. All strains were verified by PCR and DNA sequencing.

In general, yeast cells were grown at 30° in enriched yeast extract, peptone, dextrose medium (YPD), or synthetic complete (SC) medium lacking lysine as needed (Sherman 1991). For anaerobic growth, YPD or SC media was supplemented with 15 mg/liter ergosterol and 0.5% Tween-80 (YPDE or SCE, respectively). All experiments employed cells freshly obtained from frozen stocks and cultured on YPDE in oxygen-depleted, CO₂-enriched culture jars (GasPak, Becton-Dickinson). Growth tests to assay oxygen resistance in SC complete medium were conducted under well-aerated (shaking at 220 rpm) conditions as described (Reddi *et al.* 2009); tests for aerobic lysine auxotrophy and Mn toxicity were conducted under micro-aerobic conditions (not shaking) as described (Reddi *et al.* 2009; Rosenfeld *et al.* 2010).

Biochemical assays

For all biochemical assays including phosphate and manganese measurements, superoxide scavenging activity and Fe/S enzyme assays, cells were pregrown in triplicate cultures in SCE media ≈16 hr under an anaerobic N₂ atmosphere prior to dilution to o.d._{600nm} = 0.25 and growth for 6 hr in air, shaking at 220 rpm. Cells were then harvested, washed three times in ice-cold TE buffer (10 mM Tris-hydrochloride and 1 mM EDTA, pH 8.0), and three times in ice-cold MiliQ water prior to further analyses.

Total cellular phosphates (orthophosphate and polyphosphates) were measured using the molybdate reactivity method (Ames 1966; Reddi *et al.* 2009; McNaughton *et al.* 2010). Cells were lysed by glass bead homogenization in 500 ml of 0.1% Triton X-100. Total phosphate was measured from boiling 3–30 μg of whole-cell lysates for 10 min in 1 N H₂SO₄. Phosphate was quantified using a calibration curve of 0–300 μM phosphoric acid. Total cellular manganese was measured using atomic absorption spectroscopy (AAS) as described previously (Reddi *et al.* 2009).

For superoxide scavenging-activity assays, cells were lysed in 50 mM MES, 100 mM KCl, 0.1% Triton X-100, pH 7.0 by glass bead homogenization and 10–300 μg of cell lysate protein was subject to the xanthine/xanthine oxidase/XTT (3'-1-(phenylamino)-carbonyl-3,4-tetrazolium]-bis(4-methoxy-6-nitro) benzene sulfonic acid hydrate) assay for superoxide generation and detection (Ukeda *et al.* 1997). The increase in absorbance at 470 nm over 60 min upon addition of xanthine oxidase, corresponding to the rate of reduction of XTT by superoxide, was read in a Biotek HT Synergy plate reader or in a Beckman-Coulter UV/vis spectrophotometer. The rate of XTT reduction by lysates in the absence of xanthine oxidase was subtracted from all measurements. One unit of superoxide scavenging activity was defined as a 50% decrease in the rate of XTT reduction.

For aconitase (*Aco1p*) and isopropylmalate isomerase (*Leu1p*) activity assays, cells were subjected to glass bead

lysis in 50 mM MES, 100 mM KCl, 0.1% Triton X-100, pH 7.0 under a nitrogen atmosphere in a COY chamber. *Aco1p* and *Leu1p* activity was determined spectrophotometrically using a Biotek HT Synergy plate reader (Wallace *et al.* 2004). The assay mixture contained 50–300 μ g of lysate protein in 200 μ l of a buffer containing 50 mM tris(hydroxymethyl)aminomethane (Tris)-HCl, pH 7.4, and 100 mM NaCl and supplemented with either 0.5 mM *cis*-aconitate (*Aco1p* activity) or 0.5 mM citraconitate (*Leu1p* activity). Activities were determined by monitoring the disappearance of *cis*-aconitate (*Aco1p*) or citraconitate (*Leu1p*) at 240 or 235 nm, respectively, over the course of 3 min. These species were quantified by generating calibration curves of standardized concentrations of *cis*-aconitate or citraconitate. In both cases, 1 U of activity is defined as 1 nmol of substrate consumed per minute per milligram of protein.

Results

Phosphate signaling through *Pho4p* is not responsible for the aerobic lethality of *sod1 Δ pho80 Δ* mutants

A loss of phosphate control in *S. cerevisiae* through disruption of *PHO80* or *PHO85* renders *sod1 Δ* cells inviable in air and unable to effectively utilize Mn for oxidative stress suppression (Reddi *et al.* 2009; McNaughton *et al.* 2010; Rosenfeld *et al.* 2010). As seen in Figure 1A, Mn supplements to the growth medium only partly restore aerobic growth to a *sod1 Δ pho80 Δ* double mutant. The limited efficacy of Mn in this regard might be explained by the intolerance of *pho80* mutants to Mn toxicity (Figure 1B). These mutants accumulate very high Mn (Figure 1C, note log scale) due to uncontrolled uptake of Mn–Pi by the *Pho84p* transporter (Wykoff and O'shea 2001; Jensen *et al.* 2003; Reddi *et al.* 2009; Rosenfeld *et al.* 2010). To remove effects of Mn toxicity, we disrupted *PHO84*, which reversed both the high Mn accumulation (Figure 1C) and Mn sensitivity (Figure 1B) of the *sod1 Δ pho80 Δ* mutant. However, the *pho84* mutation did not restore aerobic growth and most striking, Mn supplementation was ineffective at reversing the aerobic lethality of a *sod1 Δ pho80 Δ pho84 Δ* mutant (Figure 1A). Hence, *sod1 Δ pho80 Δ* cells require massive accumulation of Mn to rescue any oxygen toxicity, consistent with the low efficacy of Mn as an antioxidant in this strain.

The *Pho80p/Pho85p* kinase pair negatively regulates the *Pho4p* transcription factor for the induction of phosphate uptake and storage genes such as *PHO84* (Kaneko *et al.* 1982; Ogawa *et al.* 2000; Wykoff and O'shea 2001; Lee *et al.* 2007; Wykoff *et al.* 2007). We addressed whether hyperactive *Pho4p* in *pho80* mutants accounts for the severe oxygen toxicity of *sod1 Δ pho80 Δ* cells. As seen in Figure 2A, deletion of *PHO4* did not reverse the aerobic lethality of *sod1 Δ pho80 Δ* cells, despite lowering phosphate (Figure 2B) and intracellular (Mn) (Figure 2C) to levels that approximated the *sod1 Δ* control. Hence, hyperactivated *Pho4p* cannot account for the aerobic lethality of *sod1 Δ pho80 Δ* cells and another downstream effector molecule must be responsible.

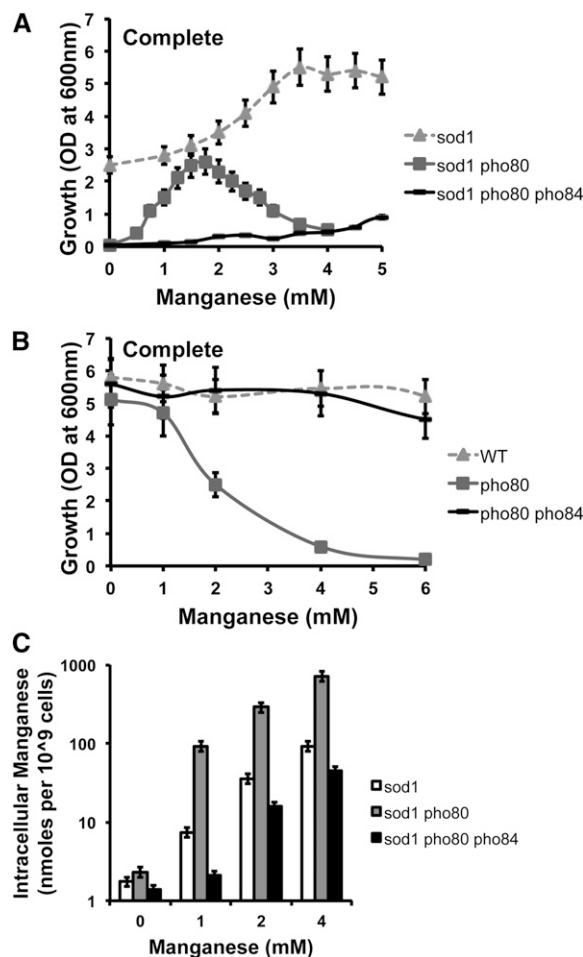


Figure 1 Loss of the Mn–phosphate transporter *Pho84p* enhances oxygen toxicity in a *sod1 Δ pho80 Δ* strain. (A) The indicated *sod1 Δ* strains were seeded in synthetic complete (SC) media at an optical density at 600 nm (o.d._{600nm}) of 0.05, and grown shaking for 16 hr with the indicated concentrations of MnCl₂. Total growth was determined by measuring the o.d._{600nm}. (B) Manganese toxicity of the indicated strains was determined by growing cells in SC medium supplemented with the indicated concentrations of Mn as described in A under nonshaking conditions. (C) Manganese accumulation of the indicated *sod1 Δ* strains was determined by atomic absorption spectroscopy (AAS) with cells grown in SC medium treated for 6 hr with the indicated concentrations of MnCl₂ as described in *Materials and Methods*. Manganese content is represented as nanomoles per 10⁹ cells. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: WT, BY4741; *pho80 Δ* , LR237; *pho80 Δ pho84 Δ* , LR154; *sod1 Δ* , AR203; *sod1 Δ pho80 Δ* , LR156; *sod1 Δ pho80 Δ pho84 Δ* , LR178.

Rim15p as a regulator of Mn antioxidant activity

A second target of the *Pho80p–Pho85p* cyclin–CDK complex is the PAS-kinase, *Rim15p* (Wanke *et al.* 2005; Swinnen *et al.* 2006). As with *Pho4p*, *Rim15p* is hyperactivated in cells lacking *pho80* or *pho85*. A deletion of *rim15* had no effect on the elevated phosphate (Figure 3B) or manganese (Figure 3C) of a *sod1 Δ pho80 Δ* mutant. Nevertheless, loss of *Rim15p* restored aerobic viability to these cells (Figure 3A). Thus, hyperactive *Rim15p* appears responsible for the severe oxidative stress of *sod1 Δ pho80 Δ* mutants under atmospheric oxygen.

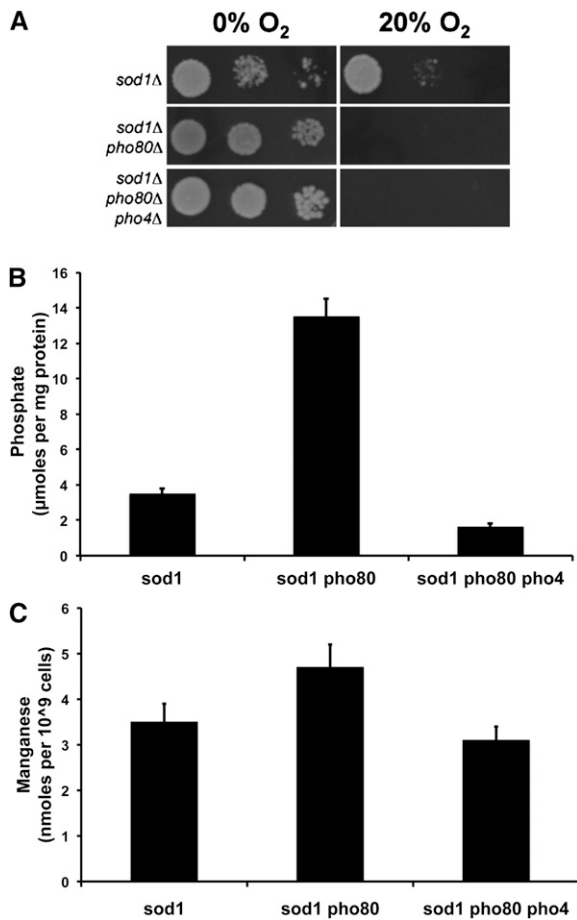


Figure 2 Activation of the Pho4p transcription factor is not responsible for the aerobic lethality of *sod1Δ pho80Δ* strains. (A) The effect of a *pho4Δ* mutation on the aerobic lethality of *sod1Δ pho80Δ* cells was tested by spotting 10^4 , 10^3 , and 10^2 cells of the indicated strains onto SCE plates and by growing in air or anaerobically for 3 days. (B) Phosphate content of the indicated strains was measured by molybdate reactivity of the indicated strains grown in SC medium as described in *Materials and Methods*. (C) Manganese content of the indicated strains was measured by AAS precisely as described in Figure 1C. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ*, AR203; *sod1Δ pho80Δ*, LR156; *sod1Δ pho80Δ pho4Δ*, AR106.

Another marker of *sod1Δ*-linked oxidative stress is an aerobic lysine auxotrophy resulting from superoxide damage to lysine biosynthetic enzyme(s) (Bilinski *et al.* 1985; Wallace *et al.* 2004). This defect can be reversed by Mn supplementation (Chang and Kosman 1989; Sanchez *et al.* 2005; Reddi *et al.* 2009). In comparing the dose response to Mn, the aerobic lysine auxotrophy of the *sod1Δ pho80Δ rim15Δ* triple mutant was more effectively rescued by Mn than the *sod1Δ pho80Δ* double mutant (Figure 3D), despite accumulating identical levels of the metal (Figure 3C). Thus, deletion of *RIM15* in *sod1Δ pho80Δ* cells not only promotes aerobic growth, but also lowers the intracellular dose of Mn required to protect against oxidative damage.

Rim15p is negatively regulated by a number of kinases downstream of nutrient sensing and signaling circuits. In

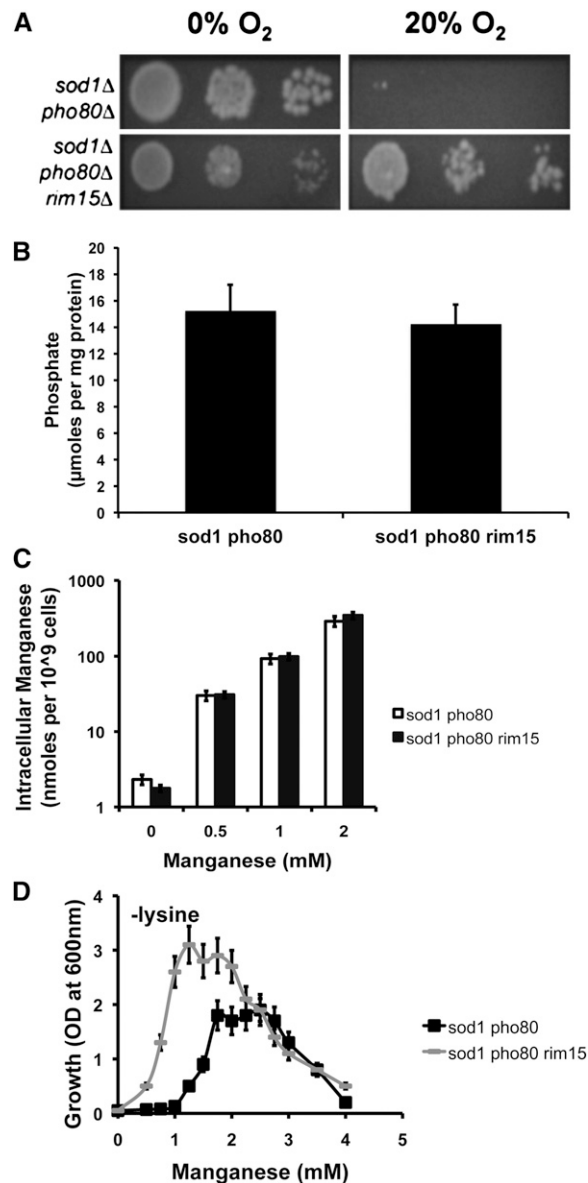


Figure 3 *RIM15* is responsible for the aerobic lethality and poor utility of Mn as an antioxidant in *sod1Δ pho80Δ* strains. Shown are the effects of a *rim15* mutation on (A) aerobic lethality of *sod1Δ pho80Δ* strains, (B) phosphate accumulation, and (C) Mn accumulation, as described in Figure 2, A, B, and C, respectively. (D) Manganese rescue of the *sod1Δ*-linked aerobic lysine auxotrophy was tested in SC medium lacking lysine and supplemented with the indicated concentrations of $MnCl_2$. Cells were grown as in A except under nonshaking conditions. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ pho80Δ*, LR156; *sod1Δ pho80Δ rim15Δ*, AR110.

addition to the aforementioned Pho80p–Pho85p cyclin–CDK pair (phosphate sensing), these kinases include *Tor1p* and the yeast Akt/S6K homolog, *Sch9p*, which are both involved in nitrogen sensing, and PKA, which senses carbon sources (Pedruzzi *et al.* 2003; Cameroni *et al.* 2004; Roosen *et al.* 2005; Wanke *et al.* 2005; Swinnen *et al.* 2006; Smets *et al.* 2010; Yang *et al.* 2010). We sought to determine if ablating the activities of any of these kinases in *sod1* cells

phenocopied the effects of a *pho80Δ* mutation. Toward this end, we deleted *TOR1*, *RAS2*, a positive regulator of PKA activity, and *SCH9* in *sod1Δ* cells. Of these, the *sch9* mutation conferred a severe aerobic growth defect to *sod1Δ* cells that was particularly profound in liquid cultures and was poorly rescued by Mn supplements (Figures 4A and 4B). This *sch9*-growth defect was indeed due to oxygen toxicity as it was abolished under anaerobic conditions or in strains with WT *SOD1* (Figure 4C). Moreover, *sch9Δ* conferred oxygen sensitivity to *sod1Δ* nulls without global changes in cellular phosphates or Mn (Figure S1A and Figure S1B). The ability of *sch9* mutations to phenocopy *pho80* mutations in terms of *sod1Δ* oxidative stress supports a role for Rim15p in negatively regulating the Mn antioxidant.

The downstream transcription factors *Gis1p* and *Msn2/4p* work in opposite to regulate the Mn antioxidant as a scavenger of superoxide in the cytosol

The downstream targets of Rim15p activation include the transcription factors *Gis1p* and the redundant pair *Msn2/4p*. All three transcription factors, which share ~95% of their gene targets, are thought to work in concert to activate cellular stress defense pathways, as well as metabolic adaptations to nutrient deficiency (Cameroni *et al.* 2004; Swinnen *et al.* 2006; Smets *et al.* 2010). We tested whether *Gis1p* and/or *Msn2/4p* activation was responsible for the aerobic lethality of the *sod1Δ pho80Δ* strain. As shown in Figure 5A, deletion of *gis1* rescued the aerobic lethality of *sod1Δ pho80Δ* cells, while *msn2/4* deletions did not. Moreover, in a dose-response study, extracellular Mn was more effective in suppressing the aerobic growth defect (Figure S2A) and aerobic lysine auxotrophy (Figure 5C) of *sod1Δ pho80Δ* cells when *gis1* was deleted, even though intracellular Mn (Figure 5B) and phosphate (Figure S2B) levels were unchanged. At equivalent intracellular concentrations of ~90 nmol Mn per 10⁹ cells achieved when *sod1Δ* cells are treated with 4 mM Mn or when *sod1Δ pho80Δ gis1Δ* cells are treated with 1 mM Mn (Figure 5B), the aerobic lysine auxotrophy of both strains is rescued by Mn to nearly the same degree (Figure 5C). Overall, the deletion of *gis1* phenocopies the effect of a *rim15* deletion in *sod1Δ pho80Δ* cells in terms of reversing the aerobic lethality and promoting Mn antioxidant capacity.

In stark contrast to a *gis1* deletion, the *msn2/4* mutations dramatically inhibited the ability of Mn to promote aerobic growth. Mn supplements were completely ineffective in suppressing the aerobic lysine auxotrophy of *sod1Δ pho80Δ msn2/4Δ* cells (Figure 5C) and also poorly reversed the aerobic lethality of *sod1Δ pho80Δ msn2/4Δ* in complete medium (Figure S2A). The differential effects of *gis1* vs. *msn2/4* mutations on the efficacy of Mn as an antioxidant were not due to differences in Mn accumulation (Figure 5B) or Mn toxicity (Figure S2C) or intracellular phosphate concentrations (Figure S2B). As a potential caveat to these studies, *sod1Δ pho80Δ msn2/4Δ* cells also grow poorly under anaerobic conditions (Figure 5A), due to a synthetic defect of combining *pho80* mutations with *msn2Δ msn4Δ*. How-

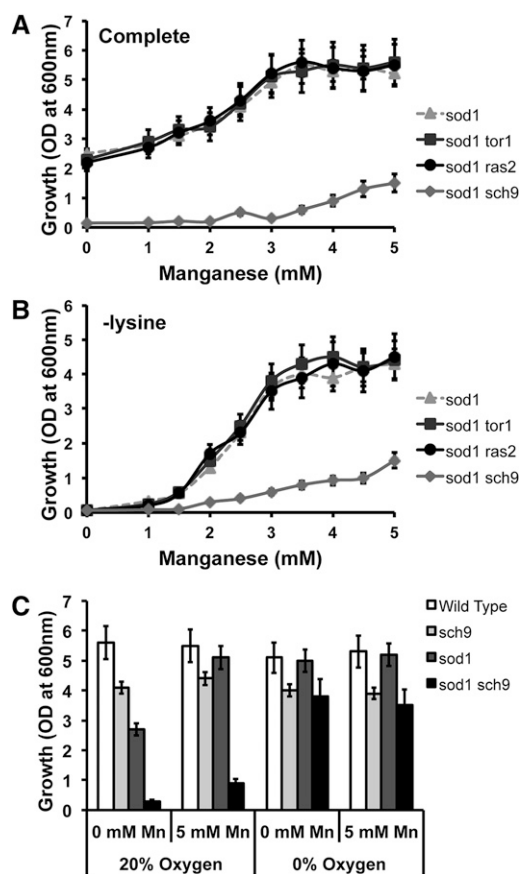


Figure 4 Deleting *sch9* renders *sod1Δ* cells oxidatively stressed and unable to utilize Mn for antioxidant protection. (A and B) The effect of *sch9Δ*, *tor1Δ*, and *ras2Δ* deletions on Mn promotion of aerobic growth was tested in (A) well-aerated SCE media and (B) media lacking lysine, as was done as in Figures 1A and 3D, respectively. (C) The effect of *sch9Δ*, *sod1Δ*, and *sod1Δ sch9Δ* mutations on growth in SCE media in the absence and presence of oxygen and manganese was determined by measuring the o.d._{600nm} values of shaking cultures after 16 hr of growth, as described in *Materials and Methods*. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ*, AR203; *sod1Δ sch9Δ*, AR163; *sch9Δ*, AR164. *sod1Δ tor1Δ*, AR120; *sod1Δ ras2Δ*, AR158.

ever, our other studies (see Figures 5D and 6) demonstrate that the inhibitory effects of *msn2Δ msn4Δ* mutations on the Mn antioxidant are also visible in a *PHO80+* strain.

We next assessed whether the effects of *gis1* and *msn2/4* mutations on the Mn antioxidant were evident without hyperactivation of Rim15p, *i.e.*, in a *PHO80+* strain. For these studies, *sod1Δ gis1Δ* double and *sod1Δ msn2Δ msn4Δ* triple mutants were generated. As seen in Figure 5D, the ability of Mn to support *sod1Δ* aerobic growth on media lacking lysine was significantly enhanced with a *gis1Δ* mutation and repressed with *msn2/4Δ* mutations without global changes in cellular phosphates or manganese (Figure S3). Even in the absence of hyperactivation conditions, these factors control the efficacy of Mn as an antioxidant.

To more directly study the differential effects of *Gis1p* and *Msn2/4p* on the Mn antioxidant, we used a biochemical assay to probe Mn-dependent superoxide scavenging activity. Figure

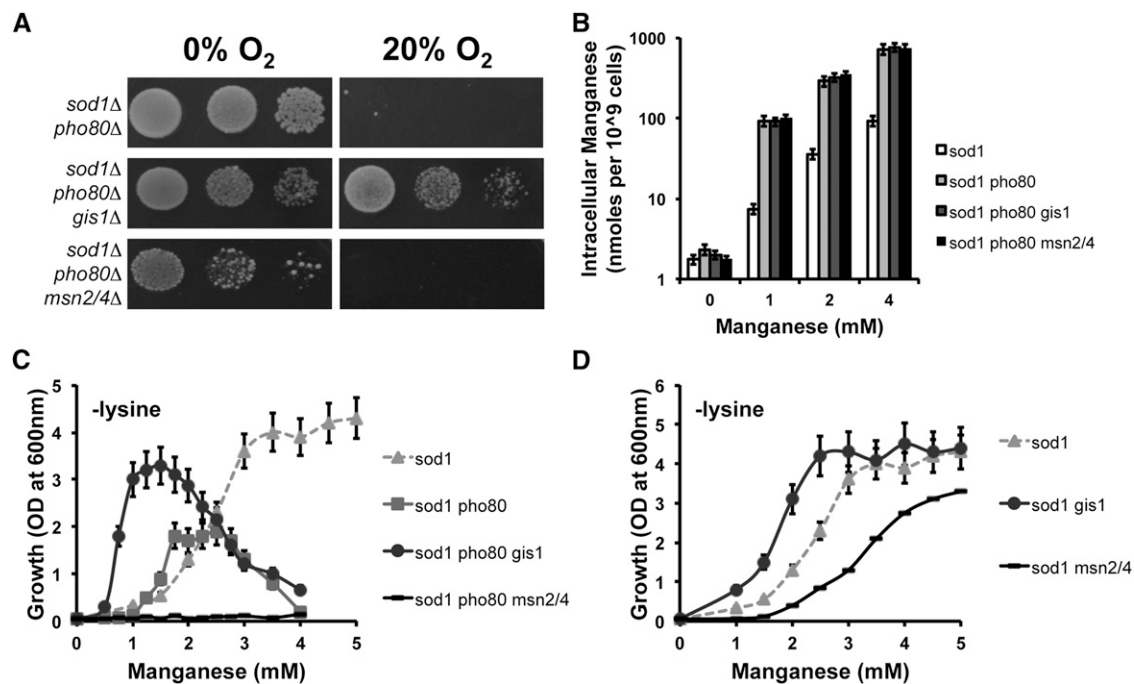


Figure 5 *GIS1* and *MSN2/4* have opposing effects on Mn antioxidant protection. The effect of *gis1* and *msn2/4* mutations on the (A) aerobic lethality of *sod1Δ pho80Δ* cells, (B) Mn accumulation in *sod1Δ pho80Δ* cells, and (C and D) Mn-mediated rescue of the *sod1Δ*-linked aerobic lysine auxotrophy in *sod1Δ pho80Δ* (C) and *sod1Δ* (D) cells were tested precisely as in Figure 3, A, C, and D, respectively. Details on culture conditions and growth are described in *Materials and Methods*. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ*, AR203; *sod1Δ pho80Δ*, LR156; *sod1Δ pho80Δ gis1Δ*, AR138; *sod1Δ pho80Δ msn2/4Δ*, AR300; *sod1Δ gis1Δ*, AR121; *sod1Δ msn2/4Δ*, AR155.

6A shows the superoxide scavenging activity of cell lysates prepared from WT, *sod1Δ*, *sod2Δ*, and *sod1Δ sod2Δ* cells, based on the xanthine/xanthine oxidase/XTT assay for *in vitro* superoxide generation and detection (Ukeda *et al.* 1997). By comparing results from the different *sod* null strains, we estimated the activities of *Sod1p* and *Sod2p* to be ~154 and ~20 U/mg protein, respectively, as well as SOD-independent superoxide scavenging (SISS) activity as ~5 U/mg protein. Previous studies have implicated this SISS to be that of the “Mn antioxidant” (Chang and Kosman 1989). Indeed, consistent with previous studies, we determined SISS activity in the background of cells lacking the cytosolic Cu/Zn SOD1 and the mitochondrial Mn-SOD2 is specific for Mn and is EDTA sensitive and heat resistant (Figures 6B and 6C). We observed that the *gis1* and *msn2/4* mutations differentially affect Mn-dependent SISS activity *in vitro*. As shown in Figure 6D, the *gis1* mutation endows cell extracts with approximately twofold greater superoxide scavenging activity (~11 U/mg protein), whereas the *msn2/4* mutations reduce it by nearly the same factor (~2 U/mg protein). In addition, Mn supplemented to cells during growth is more effectively utilized by the *gis1* mutant and poorly utilized by the *msn2/4* mutant for superoxide scavenging (Figure 6D).

Finally, we sought to determine the cellular localization of *Gis1p* and *Msn2/4p*-dependent Mn antioxidant activity. To address this, we took advantage of the fact that Fe/S cluster proteins are specific targets of superoxide toxicity (Wallace *et al.* 2004) and examined activity of two highly

homologous dehydratase Fe/S enzymes that are differentially localized, namely aconitase (*Aco1p*, mitochondrial matrix) and isopropylmalate isomerase (IPMI) (*Leu1p*, cytosol). Figures 7A and 7B show that deletion of the SOD encoding genes result in ~30% and 75% reductions in aconitase and IPMI activities, respectively, and these losses in activities are fully restored by Mn supplements. Although *gis1* and *msn2/4* mutations had no effect on the Mn rescue of mitochondrial aconitase (Figure 7A), these same mutations had a significant impact on Mn-mediated protection of cytosolic IPMI activity (Figure 7B). The *gis1* mutation enhanced IPMI activity at 2 mM Mn, whereas the *msn2/4* mutations reduced IPMI activity at all Mn levels tested. Hence, *gis1* and *msn2/4* mutations affect Mn antioxidant activity in the cytosol.

Discussion

Intracellular Mn has long been known to suppress oxidative stress in a variety of organisms. In organisms that do not express SODs and/or naturally accumulate high Mn and low Fe (*e.g.*, *L. plantarum* and *D. radiodurans*), there is good evidence for nonproteinaceous complexes of Mn such as Mn–Pi serving as physiological antioxidants, primarily by protecting against protein oxidation (Daly *et al.* 2004, 2007, 2010; Daly 2006, 2009; Fredrickson *et al.* 2008). Mn may also act as an antioxidant by functionally substituting for some Fe enzymes, thereby mitigating the potential for deleterious Fenton

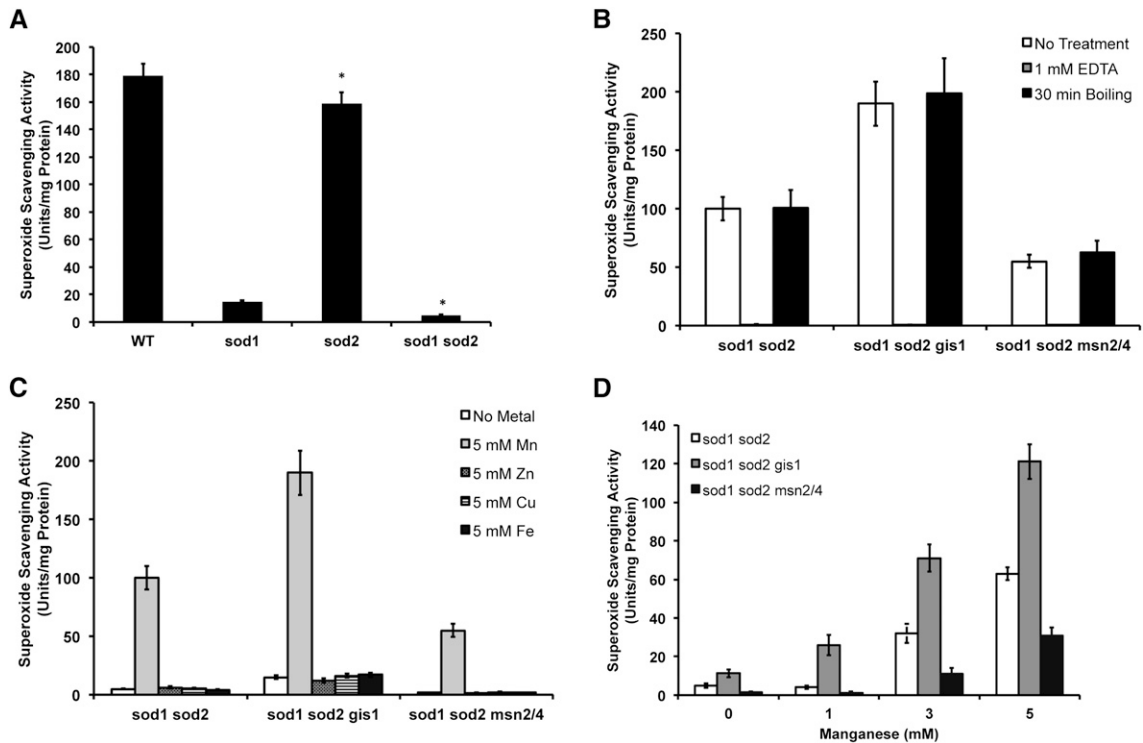


Figure 6 *GIS1* and *MSN2/4* differentially affect manganese-dependent superoxide scavenging activity in SOD-deficient cells. The indicated cells were grown for 6 hr in SC medium that was either (A) not supplemented with metals, or supplemented with (B) 5 mM $MnCl_2$, (C) 5 mM of $MnCl_2$, $ZnCl_2$, $CuCl_2$, or $FeCl_2$, or (D) the indicated concentrations of $MnCl_2$. Whole-cell lysates were prepared and analyzed for total cellular superoxide scavenging activity by the xanthine/xanthine oxidase/XTT assay described in *Materials and Methods*. One unit is defined as a 50% decrease in the rate of XTT reduction per milligram lysate protein. (A) The asterisk denotes a $P < 0.05$ and reflects the statistical significance in loss of activity upon a *sod2* mutation. (B) Where indicated, lysates were incubated for 30 min at room temperature with 1 mM EDTA or at 100° prior to superoxide scavenging activity assays to demonstrate metal chelator sensitivity and heat resistance of SISS activity. Details on culture conditions and the superoxide scavenging assays are described in *Materials and Methods*. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: WT, BY4741; *sod1* Δ , AR203; *sod1* Δ *gis1* Δ , AR121; *sod1* Δ *msn2/4* Δ , AR155; *sod1* Δ *sod2* Δ , AR142; *sod1* Δ *sod2* Δ *gis1* Δ , AR161; *sod1* Δ *sod2* Δ *msn2/4* Δ , AR160.

reactions at enzyme active sites (Anjem *et al.* 2009; Sobota and Imlay 2011). Regardless of the mechanism, it was unclear whether the protective effect of Mn is part of the cell's tightly

regulated battery of antioxidant responses or is a passive unregulated process. Using *S. cerevisiae* as a model organism, we provide the first line of evidence that the Mn antioxidant is

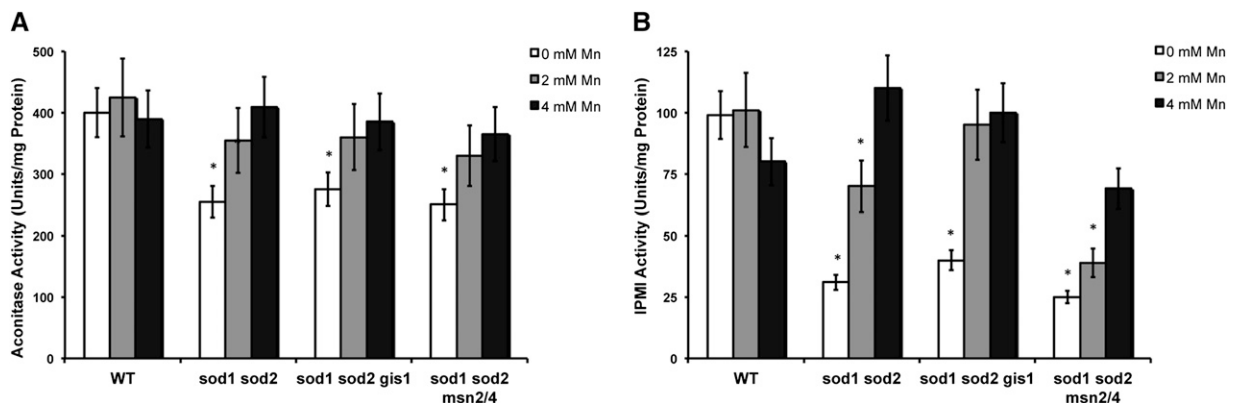


Figure 7 *GIS1* and *MSN2/4* differentially affect the ability of manganese to protect cytosolic but not mitochondrial Fe/S proteins. The indicated strains were grown in SC medium that was supplemented for 6 hr with the designated concentrations of $MnCl_2$ prior to cell lysate preparation and analysis of (A) aconitase and (B) isopropylmalate isomerase (IPMI) activity as described in *Materials and Methods*. Asterisk denotes a $P < 0.05$ and reflects the statistical significance between 4 mM Mn treatment and 0 or 2 mM Mn treatment. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: WT, BY4741; *sod1* Δ *sod2* Δ , AR142; *sod1* Δ *sod2* Δ *gis1* Δ , AR161; *sod1* Δ *sod2* Δ *msn2/4* Δ , AR160.

a component of the oxidative stress defense that is regulated through nutrient sensing pathways. Specifically, the nutrient signaling kinases *Pho80p*, *Sch9p*, and *Rim15p* as well as downstream regulators *Msn2/4p* and *Gis1p* can all regulate the efficacy of the Mn antioxidant in yeast cells.

We show herein that loss of *gis1* promotes the Mn antioxidant whereas mutations in *msn2/4* inhibit it; hence *Gis1p* and *Msn2/4p* negatively and positively regulate the potency of Mn as an antioxidant, respectively. Traditionally, these transcription factors are known for their regulation of genes involved in the response to stress and nutrients as well as genes for promoting longevity in response to calorie restriction (Reinders *et al.* 1998; Pedruzzi *et al.* 2000, 2003; Hasan *et al.* 2002; Cameroni *et al.* 2004; Fabrizio *et al.* 2004, 2001; Roosen *et al.* 2005; Swinnen *et al.* 2006; Medvedik *et al.* 2007; Wei *et al.* 2008; Zhang *et al.* 2009; Smets *et al.* 2010). The Mn antioxidant can now be added to this list of stress resistance and metabolism factors that are governed by such nutrient and stress signaling pathways.

Gis1p and *Msn2/4p* are reported to share a bulk of their gene targets (Cameroni *et al.* 2004; Swinnen *et al.* 2006; Smets *et al.* 2010); thus it is surprising that they have opposing effects on activity of the Mn antioxidant. It is possible that *Gis1p* and *Msn2/4p* negatively and positively regulate the same downstream target or coordinately regulate two distinct targets that have opposing actions on Mn as an antioxidant. While we still do not know the identity of the downstream factor(s), our data tentatively point to cytosolic target(s) for oxidative stress suppression. Specifically, *gis1* and *msn2/4* mutations affect the ability of Mn to protect the activity of the cytosolic Fe/S protein, *Leu1p* but not the homologous mitochondrial Fe/S protein, *Aco1p*. It is possible that the nature of the Mn antioxidant in the cytosol is distinct from that in the mitochondria and *Gis1p* and *Msn2/4p* signaling pathways only regulate the former.

Since Mn–Pi has been implicated as a key Mn antioxidant in yeast cells (Barnese *et al.* 2008; McNaughton *et al.* 2010) it is possible that *Gis1p* and *Msn2/4p* affect cellular phosphate interactions with Mn. However, we observed that *gis1* or *msn2/4* mutations have no effect on total phosphate or Mn. Moreover, we previously proposed that the lowering of Mn–Pi in *sod1Δ pho85Δ* mutants could not by itself explain the extreme oxidative stress of this strain (McNaughton *et al.* 2010). The activation of *Rim15p* and *Gis1p* in this mutant appears to inhibit the Mn antioxidant independent of Mn–Pi effects. Mn complexes to carboxylates (*e.g.*, lactate, succinate) can also act as antioxidants (Archibald and Fridovich 1982b) and it is possible that such compounds are targets for regulation by *Rim15p*, *Gis1p*, and *Msn2/4p*. This study also raises the intriguing possibility that phosphate can promote Mn antioxidant activity through *Pho80p*-mediated inhibition of *Rim15p* and *Gis1p* independently of phosphate-dependent chemical scavenging of superoxide by Mn–Pi complexes.

In conclusion, we demonstrate that *Rim15p*, *Gis1p*, and *Msn2/4p*, which are downstream of conserved nutrient sensing pathways, can regulate cytosolic Mn-mediated superoxide

scavenging activity. Unlike previous studies that have implicated *Gis1p* and *Msn2/4p* working in parallel gene activation pathways (Cameroni *et al.* 2004; Swinnen *et al.* 2006; Smets *et al.* 2010), we provide evidence that these factors can work in opposite with regard to the Mn antioxidant: *Gis1p* negatively regulates Mn antioxidant activity whereas *Msn2/4p* positively regulates it. In this manner, the two factors provide checks and balances for one another and together titrate the precise degree of oxidative stress protection required.

Acknowledgments

We thank Dr. Leah Rosenfeld for providing yeast strains. This work was supported by the Johns Hopkins University National Institute of Environmental Health Sciences center and by National Institutes of Health (NIH) RO1 grant ES 08996. A.R.R. was supported by NIH NIGMS fellowship F32 GM 093550.

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Communicating editor: M. D. Rose

GENETICS

Supporting Information

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Regulation of Manganese Antioxidants by Nutrient Sensing Pathways in *Saccharomyces cerevisiae*

Amit R. Reddi and Valeria C. Culotta

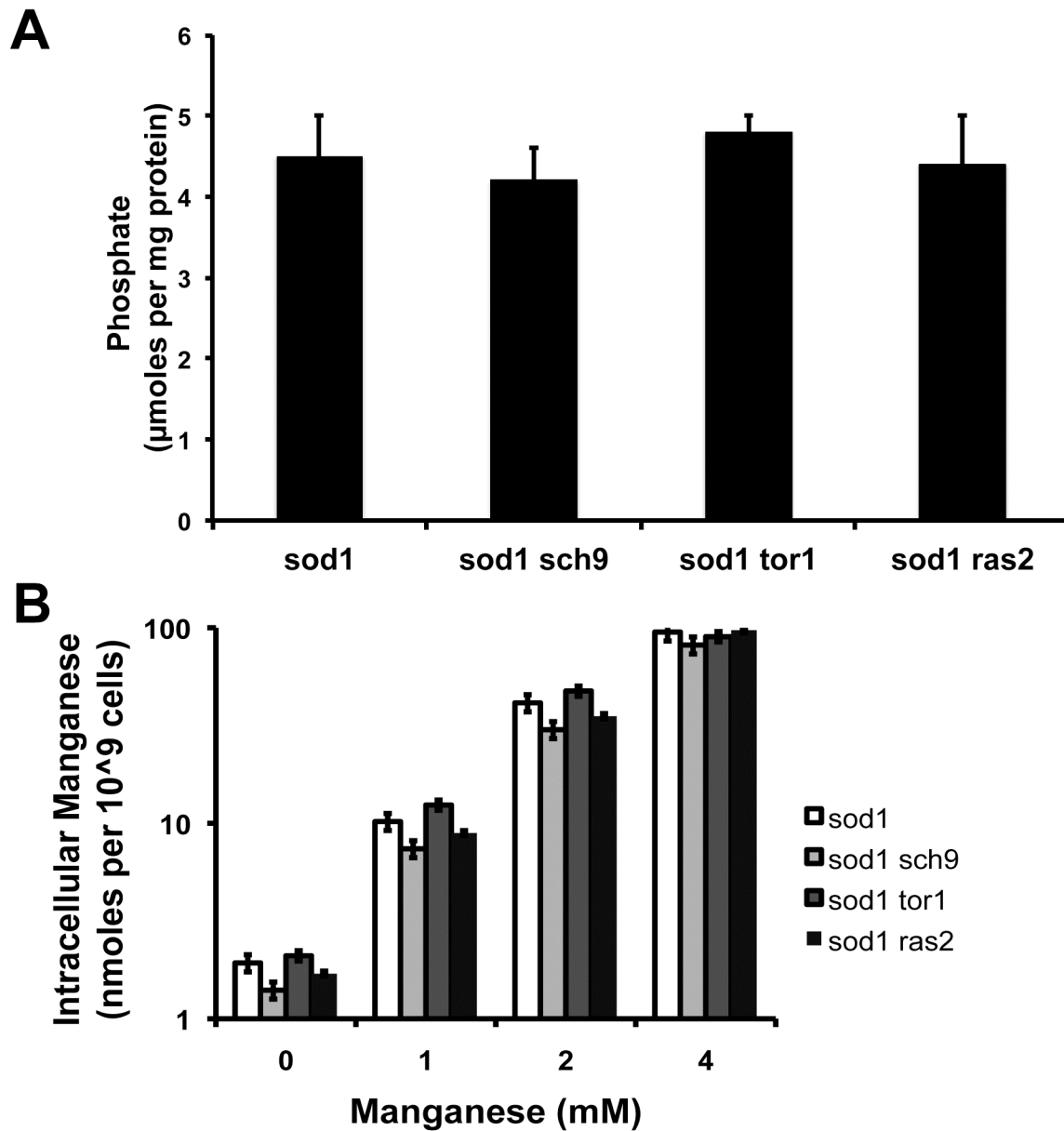


Figure S1 The effect of *sch9*, *tor1*, and *ras2* deletions on phosphate and manganese accumulation in *sod1* cells. **(A, B)** The effect of *sch9*, *tor1*, and *ras2* deletions on the **(A)** phosphate content of *sod1* cells and **(B)** Mn content of *sod1* cells, tested precisely as described in Figure 2B and 1D, respectively. Details on culture conditions and growth are described in the Materials and Methods. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1*Δ, AR203; *sod1*Δ *sch9*Δ, AR163; *sch9*Δ, AR164. *sod1*Δ *tor1*Δ, AR120; *sod1*Δ *ras2*Δ, AR158.

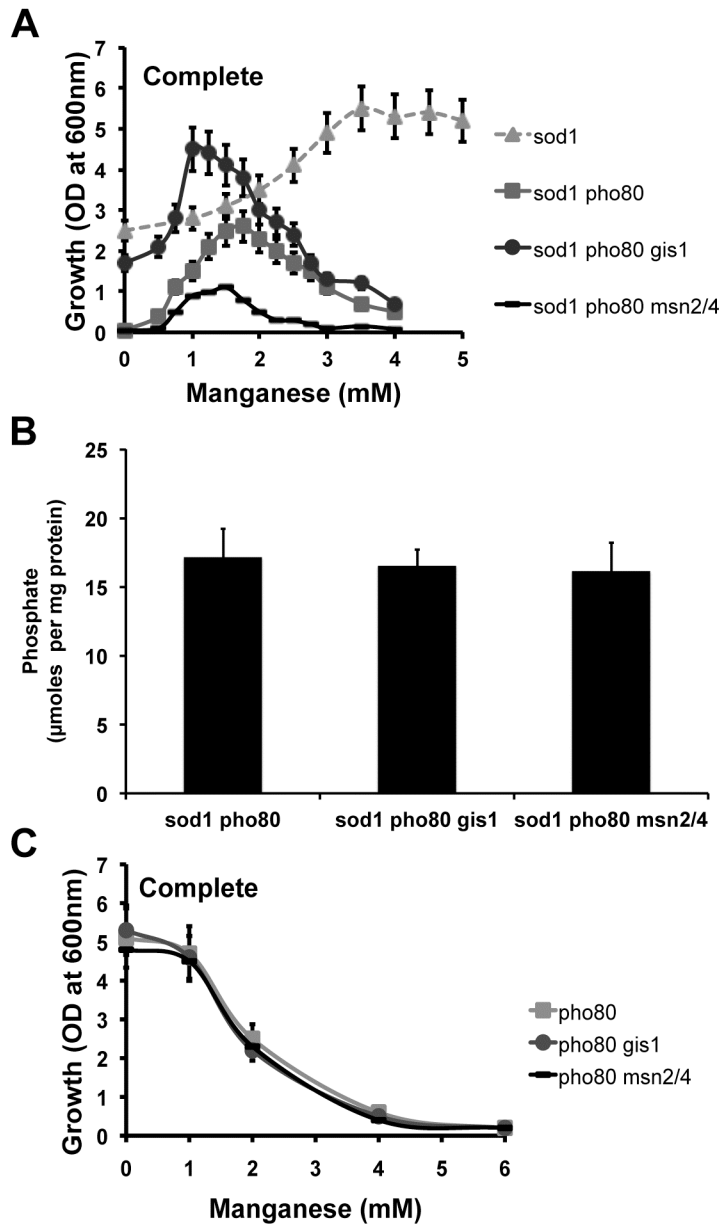


Figure S2 The effect of *gis1* and *msn2/4* mutations on aerobic growth, phosphate accumulation, and manganese toxicity in *sod1 pho80* cells. **(A-C)** The effect of *gis1* and *msn2/4* mutations on **(A)** aerobic growth as a function of Mn supplementation to SC media in *sod1Δ pho80Δ* cells, **(B)** phosphate content of *sod1Δ pho80Δ* cells and **(C)** Mn-toxicity of *pho80Δ* mutants grown in complete media. Experiments depicted in Figure S2 were performed precisely as described in Figures 1A, 2B, and 1C, respectively. Details on culture conditions and growth and analytical techniques are described in the Materials and Methods. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ*, AR203; *sod1Δ pho80Δ*, LR156; *sod1Δ pho80Δ gis1Δ*, AR138; *sod1Δ pho80Δ msn2/4Δ*, AR300; *pho80Δ*, LR237; *pho80Δ gis1Δ*, AR123; *pho80Δ msn2/4Δ*, AR156.

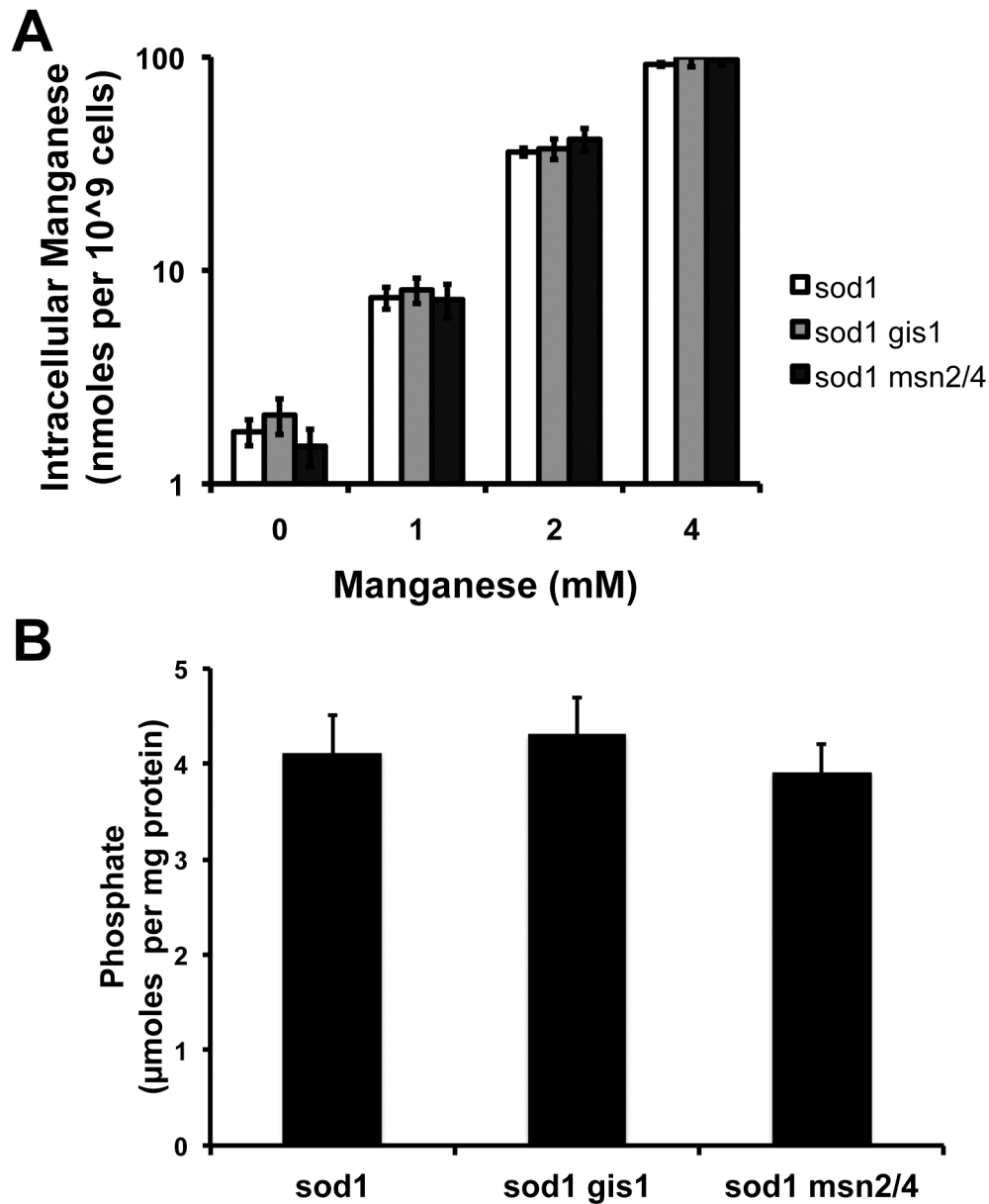


Figure S3 The effect of *gis1* and *msn2/4* mutations on manganese and phosphate accumulation in *sod1* cells. **(A,B)** The effects of *gis1* and *msn2/4* mutations on **(A)** manganese uptake as a function of manganese supplementation to SC media in *sod1Δ* cells and **(B)** phosphate content of *sod1Δ* cells. Experiments depicted in Figure S3 were performed precisely as described in Figures 1D and 2B, respectively. Details on culture conditions and growth and analytical techniques are described in the Materials and Methods. All reported values are averages based on triplicate cultures, with the errors representing the standard deviations. Strains employed: *sod1Δ*, AR203; *sod1Δ gis1Δ*, AR121; *sod1Δ msn2/4Δ*, AR155.

File S1

List of yeast strains and plasmids used in this study, including descriptions on their source and/or construction.

Strains and plasmids

All yeast strains for this study were derived from BY4741 (MATa, *leu2Δ0*, *met15Δ0*, *ura3Δ0*, *his3Δ1*) and include commercially available (Open Biosystems) *kanMX4* deletion derivatives of *sod1*, *sod2*, *pho80*, *rim15*, *gis1*, *msn2*, *msn4*, *tor1*, *ras2*, *pho4*, and *pho84*, which were all verified by colony purification and gene sequencing. We also utilized the previously reported strains LR156 (*sod1Δ::LEU2 pho80Δ::kanMX4*), RS001 (*sod1Δ::LEU2 pho84Δ::HIS3*) LR191 (*pho4Δ::LEU2 pho80Δ::kanMX4*), LR154 (*pho84Δ::HIS3 pho80Δ::kanMX4*), LR237 (*pho80Δ::LEU2*), LR122 (*pho84Δ::LEU2*), and LR181 (*pho4Δ::LEU2*) (Reddi *et al.* 2009; Rosenfeld *et al.* 2010). AR108 (*sod1Δ::LEU2 rim15Δ::kanMX4*), AR120 (*sod1Δ::LEU2 tor1Δ::kanMX4*), AR121 (*sod1Δ::LEU2 gis1Δ::kanMX4*), AR140 (*sod1Δ::LEU2 msn2Δ::kanMX4*), AR141 (*sod1Δ::LEU2 msn4Δ::kanMX4*), AR158 (*sod1Δ::LEU2 ras2Δ::kanMX4*), and AR203 (*sod1Δ::LEU2*) were obtained by deleting *SOD1* from the *rim15Δ::kanMX4*, *tor1Δ::kanMX4*, *gis1Δ::kanMX4*, *msn2Δ::kanMX4*, *msn4Δ::kanMX4*, *ras2Δ::kanMX4*, and BY4741 parent strains, respectively, as described previously (Culotta *et al.* 1995). LR178 (*sod1Δ::LEU2 pho84Δ::HIS3 pho80Δ::kanMX4*) was kindly provided by Dr. Leah Rosenfeld and was generated by deleting *SOD1* from LR154 as described previously (Culotta *et al.* 1995). AR142 (*sod1Δ::kanMX4 sod2Δ::URA3*) and AR161 (*sod1Δ::LEU2 sod2Δ::URA3 gis1::KanMX4*) were generated by deleting *SOD2* in the *sod1::KanMX4* and AR121 strains, respectively, as described previously (Culotta *et al.* 1995). AR151 (*msn2Δ::HIS3 msn4Δ::kanMX4*) and AR155 (*sod1::LEU2 msn2::HIS3 msn4::kanMX4*) were generated by deleting *MSN2* using the *msn2::HIS3* deletion plasmid, pAR007. AR160 (*sod1Δ::LEU2 sod2Δ::URA3 msn2::HIS3 msn4::KanMX4*) was generated by deleting *SOD2* in AR155, as described previously (Culotta *et al.* 1995). AR103 (*pho80Δ::LEU2 rim15Δ::kanMX4*), AR123 (*pho80Δ::LEU2 gis1Δ::kanMX4*), and AR156 (*pho80Δ::LEU2 msn2::HIS3 msn4Δ::kanMX4*) were generated by deleting *PHO80* in the *rim15Δ::kanMX4*, *gis1Δ::kanMX4*, and AR151 strains, respectively, as described previously (Rosenfeld *et al.* 2010). AR107 (*pho80Δ::URA3 rim15Δ::kanMX4*), AR134 (*pho80Δ::URA3 gis1Δ::kanMX4*), and AR299 (*pho80Δ::URA3 msn2::HIS3 msn4Δ::kanMX4*) were generated by allelic replacement of the *LEU2* selectable markers of AR103, AR123, and AR156, respectively, with *URA3* by transformation with pRS306 linearized with PvuII. AR110 (*sod1::LEU2 pho80Δ::URA3 rim15Δ::kanMX4*), AR138 (*sod1::LEU2 pho80Δ::URA3 gis1Δ::kanMX4*), and AR300 (*sod1::LEU2 pho80Δ::URA3 msn2::HIS3 msn4Δ::kanMX4*) were constructed by deleting *SOD1* in AR107, AR134, and AR299, respectively, as described previously (Culotta *et al.* 1995). AR010 (*sod1Δ::URA3 pho80Δ::kanMX4*) was generated by allelic replacement of the *LEU2* selectable marker of LR156 with *URA3* by transformation with pRS306 (Sikorski and Hieter 1989) linearized with PvuII. AR105 (*sod1Δ::kanMX4 pho4::LEU2*) and AR106 (*sod1Δ::URA3 pho80Δ::kanMX4 pho4::LEU2*) were constructed by deleting *PHO4* in the *sod1Δ::kanMX4* and AR010 strains, respectively, as described previously (Rosenfeld *et al.* 2010). AR164 (*sch9::HIS3*) was constructed by deleting *SCH9* with pAR009 in BY4741 cells. AR163 (*sod1::LEU2 sch9::HIS3*) was constructed by deleting *SOD1* in AR163, as described previously (Culotta *et al.* 1995).

The *msn2::HIS3* disruption plasmid, pAR007, was generated by first PCR amplifying the upstream (−743 to +27) and downstream (+2264 to +3037) sequences relative to the *MSN2* start site, introducing BamHI and Xho1, and Xba1 and BamHI restriction sites, respectively. The *MSN2* PCR products were digested with the enzymes indicated and ligated in a trimolecular reaction into the *HIS3* integrating plasmid pRS403 (Sikorski and Hieter 1989) digested with Xba1 and Xho1, resulting in pAR007.

Transformation of yeast strains with pAR007 linearized with BamHI resulted in deletion of *MSN2* sequences from +28 to +2263. The *sch9::HIS3* disruption plasmid, pAR009, was generated by PCR amplifying the upstream (-467 to -138) and downstream (+2485 to +3117) sequences relative to the *SCH9* start site, introducing BamHI and Xho1, and Xba1 and BamHI restriction sites, respectively. The *SCH9* PCR products were digested with the enzymes indicated and ligated in a trimolecular reaction into the *HIS3* integrating plasmid pRS403 (Sikorski and Hieter 1989) digested with Xba1 and Xho1, resulting in pAR009. Transformation of yeast strains with pAR009 linearized with BamHI resulted in deletion of *SCH9* sequences from -137 to +2484. Deletion of *MSN2* or *SCH9* was confirmed by PCR.

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