Free Radical Biology and Medicine

Volume 34, Issue 3, 1 February 2003, Pages 385–393

Original contribution

Regulation of antioxidant enzymes gene expression in the yeast *Saccharomyces cerevisiae* during stationary phase

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Abstract

Gene expression of three antioxidant enzymes, Mn superoxide dismutase (MnSOD), Cu,Zn superoxide dismutase (Cu,ZnSOD), and glutathione reductase (GR) was investigated in stationary phase *Saccharomyces cerevisiae* during menadione-induced oxidative stress. Both GR and Cu,ZnSOD mRNA steady state levels increased, reaching a plateau at about 90 min exposure to menadione. GR mRNA induction was higher than that of Cu,ZnSOD (about 14-fold and 9-fold after 90 min, respectively). A different pattern of response was obtained for MnSOD mRNA, with a peak at about 15 min (about 8-fold higher) followed by a decrease to a plateau approximately 4-fold higher than the control value. However, these increased mRNA levels did not result in increased protein levels and activities of these enzymes. Furthermore, exposure to menadione decreased MnSOD activity to half its value, indicating that the enzyme is partially inactivated due to oxidative damage. Cu,ZnSOD protein levels were increased 2-fold, but MnSOD protein levels were unchanged after exposure to menadione in the presence of the proteolysis inhibitor phenylmethylsulfonyl fluoride. These results indicate that the rates of Cu,ZnSOD synthesis and proteolysis are increased, while the rates of MnSOD synthesis and proteolysis are unchanged by exposure to menadione. Also, the translational efficiency for both enzymes is probably decreased, since increases in protein levels when proteolysis is inhibited do not reflect the increases in mRNA levels. Our results indicate that oxidative stress modifies MnSOD, Cu,ZnSOD, and GR gene expression in a complex way, not only at the transcription level but also at the post-transcriptional, translational, and post-translational levels.

Keywords

- Mn superoxide dismutase;
- Cu,Zn superoxide dismutase;
- Glutathione reductase;
- Menadione;
- Oxidative stress;
- Proteolysis;
- Free radicals

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