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HSF1-mediated oxidative stress response to menadione in *Saccharomyces cerevisiae* KNU5377Y3 by using proteomic approach

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ABSTRACT
The heat shock transcription factor HSF1 inthe yeast *Saccharomyces cerevisiae* regulates a wide range of genes and functions in diverse cellular reactions. To investigate the physiological response of HSF1 inthe presence of menadione (MD) in *S. cerevisiae* KNU 5377Y3, wild-type (k3wt) and isogenic *hsf*1 mutant (k3h1) cells were introduced. HSF1 was induced when k3wt cells were exposed to the superoxide-generating agent MD and k3h1 cells were hypersensitive to MD. Under MD stress, k3h1 cells down-regulated the expression of metabolic enzymes (Hxk, Fba1, Pgk1, Eno2, and Adh1), antioxidant enzymes (Trx2 and porin), and molecular chaperones and their cofactors (Hsp104, Ssb1, Hsp60, Hsp42, Hsp26, Hsp12, Cpr1, and Sti1). In addition, k3h1 cells increased cellular hydroperoxide levels and protein carbonylation under MD stress as compared to k3wt cells. However, there was a moderate difference in the wild-type (b3wt) and mutant (b3h1) cells derived from *S. cerevisiae* S288Cunder the same conditions. Thus, these results show that HSF1 is an important component of the stress response system, acting as an activator of cell rescue genes in *S. cerevisiae* KNU5377Y3, and its expression protects the cells from MD-induced oxidative damage by maintaining redox homeostasis and proteostasis in the presence of MD.

KEYWORDS
Saccharomyces cerevisiae KNU5377Y3; HSF1; Gene Expression; Menadione; Redox

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