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**The adaptive response of a thermotolerant yeast
Saccharomyces cerevisiae KNU5377 to
menadione-induced oxidative stress**

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A thermotolerant yeast strain, *Saccharomyces cerevisiae* KNU5377 (KNU5377), was exposed to menadione stress as an oxidant. KNU5377 could survive under a menadione concentration of 680 μ M for 1 hr, however, the reference *S. cerevisiae* W303 could not survive even at a concentration of 400 μ M. To understand the stress tolerance of this strain, we analyzed the genome-wide gene expression of KNU5377 after the addition to 120 μ M of menadione with and without pretreatment, 6 μ M for 1 hr by using DNA microarray technology. Glutaredoxin 2 (*GRX2*), thioredoxin peroxidase 2 (*TSA2*), and thioredoxin reductase (*TRR1*) were up-regulated over 10-fold after treatment with 80 μ M of menadione for 1 hr. Genes including superoxide dismutase (*SOD1*), catalase (*CTA1*), glucose-6-phosphate dehydrogenase (*ZWF1*), glutaredoxin (*GRX1*), glutathione peroxidase (*GPX2*, *HYR1*), glutathione reductase (*GLR1*), thioredoxin peroxidase (*AHP1*), and thioredoxin 2 (*TRX2*) were also induced over two-fold induction under stress condition with pretreatment and treatment. In addition, transcriptional analysis of those genes showed good correlation with protein expressions and enzyme activity. These results suggest that *SOD1*, *CTA1*, *GPX2*, and *ZWF1* play crucial roles in the adaptive oxidative stress response of KNU5377.