Abstract

Oxidative stress represents a complex and intensely studied phenomenon tightly linked to a range of human diseases, and to aging in many organisms. A plethora of key cellular regulators, including the Notch signaling pathway, have been recently described to respond to the cellular redox status. We have characterized the role of CSL (CBF1/Su(H)/LAG-1) proteins, the effectors of Notch signaling pathway in metazoa, in oxidative stress response in fission yeast. *Schizosaccharomyces pombe* contains two CSL paralogs, Cbf11 and Cbf12, that have antagonistic functions in the regulation of cell cycle and cellular adhesion. Both proteins are able to bind the canonical CSL motif and activate transcription and, thus, function as genuine CSL transcription factors. We have determined that the strain lacking *cbf11* is resistant to hydrogen peroxide but not to menadione, a source of superoxide anion radical. Using double knock-outs to assess genetic interactions we have revealed that the resistance of *cbf11* knock-out is dependent on the antioxidants catalase and sulfiredoxin. Genes encoding these antioxidants are under transcriptional control of the Sty1 MAP kinase pathway and the Pap1 transcription factor which are also required for the resistance of *Δcbf11* cells. Cbf12 is believed to play only a minor role in oxidative stress response, nonetheless, it was shown to genetically interact with Sck1 during oxidative stress. Furthermore, cells lacking *cbf11* display nutrient-dependent respiration defect accompanied with differential regulation of genes required for respiration control and energy metabolism. Our findings contribute to the understanding of stress response in the fission yeast and propose a novel role for the CSL proteins in regulation of cell respiration and oxidative stress response.

Key words: oxidative stress, genetic interactions, *Schizosaccharomyces pombe*, CSL proteins, Cbf11, Cbf12, cell respiration