

Abstract

Redox homeostasis maintenance is important for proper organism and cell function, for while relatively low amount of reactive oxygen (and nitrogen) species contributes to the fine tuning of signal transduction, excessive concentration of ROS (oxidative stress) has demonstrably harmful effects and is tightly connected to many pathological states. Cells therefore evolved broad palette of antioxidant mechanisms that express striking level of conservation among different species. Large, intricate stress response signaling networks have been already described; nonetheless, novel molecules employed in stress-related signaling are still being discovered. Several studies recently suggested transcription factors CSL, proteins essential for regulation of metazoan development as effectors of Notch signaling, are also involved in response to oxidative stress. The fission yeast *Schizosaccharomyces pombe*, well established model of response to various stresses, comprises two paralogs of CSL proteins – Cbf11 and Cbf12. We have found cells depleted of *cbf11* are highly resistant to hydrogen peroxide. This resistance appears to be caused by upregulation of important stress responsive genes including *ctt1*, *gst2*, *pyp2*, and *atf1*. Cbf11 is therefore negative regulator of these genes, which suppresses their expression probably indirectly through modulation of stress-response signaling. We have found Cbf11 is functionally connected with both Sty1/Atf1 and Pap1 pathways. Indeed, loss of Cbf11 resulted in increased activity of Pap1, which is known regulator of *ctt1* and *gst2*, and in remarkable alterations in Sty1/Atf1 signaling dynamics. The role of Cbf12 in regulation of *ctt1*, *gst2*, *pyp2*, and *atf1* transcript level was negligible. Our results identified new protein that participates in oxidative stress response regulation in fission yeast, determined signaling pathways that are influenced by Cbf11, provided foundation for upcoming research that should reveal exact mechanistic model of Cbf11 action, and might contribute to our knowledge of Notch independent CSL functions in metazoa, some of which have been already described in the scientific literature.