

Abstract

As the effector component of the Notch signaling pathway the transcription factors of the CSL family (CBF1/RBP-J κ /Suppressor of Hairless/Lag-1) are essential for many developmental processes in metazoan organisms, but they can function also independently of Notch. Recently, their presence was proved in fungal organisms lacking the Notch pathway as well as most of the known metazoan interacting partners. Cbf11 and Cbf12, the CSL proteins of the unicellular yeast *Schizosaccharomyces pombe*, were determined experimentally as non-essential nuclear transcription factors, which regulate cell adhesion, extracellular material production, colony morphology, septation and daughter cell separation, coordination of nuclear and cell division, and ploidy maintenance in an antagonistic way. The responsive genes of these factors are not known yet. In this study, genes of *S. pombe*, whose promoter regions represent potential direct targets for the Cbf proteins binding, were predicted. The binding of the Cbf11 and Cbf12 proteins, and of a truncated version Cbf12 Δ N to CSL response elements contained in the regulatory regions of selected *S. pombe* genes was tested *in vitro* by EMSA, and consequently, in the case of the Cbf11 protein, also *in vivo* by ChIP. Cbf11 and Cbf12 Δ N recognize specifically the response elements *in vitro*, but their affinity as well as their binding preferences differ among the sequences tested. The Cbf12 protein was not shown to bind to DNA, which might be an effect of the presence of the amino-terminal domain. The results obtained *in vitro* do not exclude our hypothesis that the Cbf11 and Cbf12 proteins bind the promoters of *S. pombe* responsive genes *in vivo* and, depending on context, act as negative and/or positive regulators of their transcription, however the binding of Cbf11 to selected gene promoter regions *in vivo* was not proved under the conditions used.