

## **Abstract**

The CSL family of transcription factors is essential for metazoan development, mostly due to their involvement in the Notch signaling pathway. We identified two novel classes of CSL genes in several fungal species, organisms lacking the Notch pathway. We characterized experimentally *cbf11*<sup>+</sup> and *cbf12*<sup>+</sup>, the two CSL genes of *Schizosaccharomyces pombe*, in order to elucidate the CSL function in fungi. We provide evidence supporting their identity as genuine CSL genes. Both *cbf11*<sup>+</sup> and *cbf12*<sup>+</sup> are non-essential; they have distinct expression profiles and code for nuclear proteins with transcription activation potential. Significantly, we demonstrated that Cbf11 recognizes specifically the canonical CSL response element GTG<sup>A</sup>/G<sub>G</sub>GAA *in vitro*. The deletion of *cbf11*<sup>+</sup> is associated with growth phenotypes and altered colony morphology. Furthermore, we found that Cbf11 and Cbf12 play opposite roles in cell adhesion, nuclear and cell division and their coordination. Disturbed balance of the two CSL proteins leads to cell separation defects, cut phenotype, and high-frequency diploidization. Our data show that CSL proteins operate in an organism predating the Notch pathway, which should be of relevance to the understanding of (Notch-independent) CSL functions in metazoans.