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Title

[Regulation Of The Saccharomyces Cerevisiae INO1 Gene: Novel Insights Into A Hallmark Of Eukaryotic Transcription Regulation](#)

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Abstract

Transcription regulation in eukaryotes is a complex process governed by the concerted action of different factors. The work in this thesis is focused on transcriptional regulation in *Saccharomyces cerevisiae*. I analyzed the regulation of the phospholipid biosynthetic gene *INO1*, which has been a model gene for transcription studies for over three decades. Some major questions that I have addressed are: what kinds of cis regulatory sequences and trans factors are important for regulation of *INO1*? What is the sequence of events in this regulation? How is the recruitment of these *trans* factors consequential for *INO1* transcription? I present my results here for the role of the basic helix loop helix transcription factor (bHLH) family in coordinated regulation of *INO1* transcription. I report that the centromeric binding factor 1 (Cbf1p) together with two other members of the bHLH protein family, Ino2p and Ino4p, are required for efficient derepression of *INO1* transcription. Together these bHLH transcription factors recruit the ISW2 chromatin-remodeling complex onto the *INO1* promoter to drive productive transcription from the *INO1* locus. My efforts in studying the regulation of *INO1* led me to study the regulation of *SNA3*, a gene found in tandem upstream ([arrow right][arrow right]) to the *INO1* gene and regulated by the same environmental conditions as *INO1*. Studies on the mechanism of coregulation of adjacent genes in budding yeast have been largely speculative. I provide evidence that the same bHLH proteins which regulate *INO1* also regulate *SNA3*, albeit differentially. Significantly, my results also show that the regulation of both *SNA3* and *INO1* is dictated from the intergenic region between the two genes. This is a novel mechanism of transcription regulation in yeast as regulation from downstream of ORF is unknown in yeast. Thus, my results with both *SNA3* and *INO1* provide novel details on how the process of transcription is regulated in response to an environmental cue.

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