

Transcription Regulation

Cellular and developmental processes are controlled in large part by transcription factors. Chromatin immunoprecipitation and microarray are main methods involved in finding these regulatory elements *in vivo*¹. They were used previously to study protein-DNA interaction at a small number of specific sites *in vitro*. Nowadays researches are focused on yeast due to its relative genome simplicity comparing to higher eukaryotes.

Computational approaches are used to identify potential binding sites based on consensus sequences. The correlation is not absolute as many induced genes lack binding sites, suggestive of indirect modes of regulation.

The mentioned methods evolved and today genome-wide location analysis of DNA-bound proteins² made possible. Using these methods Ren B et al. revealed previously unknown functions for Gal4 and Ste12, transcription activators which control genes that are expressed in yeast as cells respond to changes in carbon source and mating pheromone.

Recently comparative genomics has been used to identify potentially *cis*-regulatory sequences within yeast on the basis of phylogenetic conservation, genome-wide location data and prior knowledge³. Harbison CT et al. studied transcription regulators under various conditions and that are conserved among the *Saccharomyces* species.

This study suggested 4 promotor architectures that provide clues to regulatory mechanisms and to 4 common patterns of regulator binding behaviour that were observed.

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1. Euskirchen G, Snyder M. A plethora of sites, (2004) *Nat Genet.* **36**(4):325-326.
 2. Ren B et al. (2000) Genome-wide location and function of DNA binding proteins. *Science* **290**(5500):2306-2309.
 3. Harbison CT et al. (2004) Transcriptional regulatory code of a eukaryotic genome. *Nature.* **431**(7004):99-104.