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High-throughput screening to identify regulators of meiosis-specific gene expression in *Saccharomyces cerevisiae*

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Transcriptional regulation is a key mechanism that controls the fate and response of cells to diverse signals. Therefore, the identification of the signal transduction pathways as well as the DNA-binding proteins, which mediate these signals, is a crucial step in elucidating how cell fate is regulated, and how can we perturb it. In the talk, I will discuss bioinformatics and functional high-throughput genomic approaches. Our model system is the budding yeast *Saccharomyces cerevisiae*, and the *IME1* gene that encodes the master regulator of meiosis. High throughput technology, based on fluorescent reporters (R-SGA), allows the screening of an array of all viable yeast gene deletion mutants. This protocol promoted the identification of too many potential transcription factors, and signal transduction factors. The main problem we faced was to discriminate between false and true regulators. Bioinformatic analysis identified potential cis-regulatory sequences with perfect homology to known transcription factors (TF). However, these consensuses and their corresponding TFs were found to be nonfunctional in the R-SGA analysis. Moreover, many TFS were shown to bind to a non-perfect site. The most rewarding approach was to examine a TF only if its known upstream regulators were also found in the screen. Specific examples will be given. In conclusion, our results support the view that although bioinformatic analysis can provide a useful guide, functional assays are required for accurate identification of TF-binding site interactions in complex promoters.

Biography

Yona Kassir is currently working as a Professor Emeritus at Technion-Israel Institute of Technology, Israel.

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