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Original Contribution

Protection against oxidative stress through *SUA7*/TFIIB regulation in *Saccharomyces cerevisiae*

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Abstract

The general transcription factor TFIIB, encoded by *SUA7* in *Saccharomyces cerevisiae*, is required for transcription activation but apparently of a specific subset of genes, for example, linked with mitochondrial activity and hence with oxidative environments. Therefore, studying *SUA7*/TFIIB as a potential target of oxidative stress is fundamental. We found that controlled *SUA7* expression under oxidative conditions occurs at transcriptional and mRNA stability levels. Both regulatory events are associated with the transcription activator Yap1 in distinct ways: Yap1 affects *SUA7* transcription up regulation in exponentially growing cells facing oxidative signals; the absence of this activator *per se* contributes to increase *SUA7* mRNA stability. However, unlike *SUA7* mRNA, TFIIB abundance is not altered on oxidative signals. The biological impact of this preferential regulation of *SUA7* mRNA pool is revealed by the partial suppression of cellular oxidative sensitivity by *SUA7* overexpression, and supported by the insights on the existence of a novel RNA-binding factor, acting as an oxidative sensor, which regulates mRNA stability. Taken together the results point out a primarily cellular commitment to guarantee *SUA7* mRNA levels under oxidative environments.

Abbreviations

- 5-FOA, 5-fluoroorotic acid;
- GTFs, general transcription factors;
- MOPS, 4-morpholinepropanesulfonic acid;
- PCR, polymerase chain reaction;
- PMSF, phenylmethylsulfonyl fluoride;
- SC, synthetic complete;
- SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis

Keywords

- TFIIB;
- Oxidative stress signaling;
- Yap1;
- mRNA stability

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