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Scope: [Self ▼]   Format: [HTML ▼]   Amount: [Quick ▼]   GEO accession: [GSE62120]   [GO]

Series GSE62120

Query DataSets for GSE62120

Status	Public on Mar 01, 2015
Title	Time dynamics of quantitative protein and mRNA levels reveals extensive translational regulation after stress
Platform organisms	Schizosaccharomyces pombe; Saccharomyces cerevisiae
Sample organism	Schizosaccharomyces pombe
Experiment type	Expression profiling by array

Summary — Eukaryotic cells are constantly challenged by the presence of reactive oxygen species, which play an important role in aging and human disease progression. In particular, acute oxidative stress can lead to extensive damage to cellular DNA, proteins, and lipids and can trigger a response that remodels the transcriptional and translational state of the cell. Although a number of previous studies have profiled the relative changes in mRNA and protein and more studies revealing the dynamics of transcription and translation in response to stress are starting to emerge, a quantitative view of this response has been lacking. Here, we have applied quantitative methods to characterize the time dynamics of mRNA and protein levels in the oxidative stress response of the fission yeast Schizosaccharomyces pombe, which has allowed us to perform dynamic modeling of responsive genes in units of copies per cell. Analysis of the resulting time dynamics provided a new genome-wide view of the scale, timing and rates of transcription and translation in the transient response. The majority of dynamic genes were observed to be responsive in their mRNA or protein levels alone implying extensive translational regulation. Nevertheless, modeling of genes with responsive mRNA and protein levels showed that protein levels could, in a majority of these cases, be accurately predicted with constant translation and decay rates while a minority benefited from explicit translation delay parameters. A number of independent features, e.g. measures of codon bias, ribosome occupancy, etc., were found to be less correlated to maximally perturbed protein levels than steady-state levels. Codon bias measures were more correlated than mRNA levels to quantitative protein levels at both perturbed and un-perturbed states. Measures of translation activity, on the other hand, were only significantly correlated at steady state.

Overall design	In total 32 samples: 11 for stressed time series R1, 11 for stressed time series R2, 5 for control time series C1 and 5 for control time series C2

Contributor(s)	Papadakis MA, Schmidt A, Marsellach FX, De Masi F, Pedersen HK, Slodkowicz G, Beyer A, Bähler J, Aebersold R, Workman CT
Citation missing	*Has this study been published? Please login to update or notify GEO.*
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Last update date	Mar 02, 2015
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Platforms (1)   GPL2529 [Yeast_2] Affymetrix Yeast Genome 2.0 Array

Samples (32)   GSM1519986 R1 Stress induced T=0
⊞ More...

GSM1519987 R1 Stress induced T=5

GSM1519988 R1 Stress induced T=10

Relations
BioProject   PRJNA263246

Analyze with GEO2R

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SOFT formatted family file(s)	SOFT ?
MINiML formatted family file(s)	MINiML ?
Series Matrix File(s)	TXT ?

Supplementary file	**Size**	**Download**	**File type/resource**
GSE62120_RAW.tar	30.6 Mb	(http)(custom)	TAR (of CEL)

Raw data provided as supplementary file

Processed data included within Sample table

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