**Time series (GSE62120): (Dose not have paper published)**

Time dynamics of quantitative protein and mRNA levels reveals extensive translational regulation after stress (H2O2):  
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.

**(I used the first 11 samples for stressed time series)**

Treatment: 0.5mM H2O2

Time points: Cells were shaken at 160 rpm throughout the cultivation and samples were collected at 0, 5, 10, 15, 30, 50, 60, 90, 120, 180 and 240 minutes after treatment with 0.5 mM HP.

**Static (GSE19213):**

Paper: Yap1 activation by H2O2 or thiol-reactive chemicals elicits distinct adaptive gene responses.

Microarray analysis

The wild-type strain BY4741 and its isogenic single-deletion strain BY4741Δyap1 were used in this study. Four independent cultures of each strain grown to early exponential phase were harvested by centrifugation (12,000 g for 10 min at room temperature) and divided into four aliquots in 0.1 M sodium phosphate buffer, pH 7.0. One aliquot was the control, and the other three aliquots were treated with 0.3 mMH2O2, 0.05 mMacrolein, or 0.016 mMNEM, respectively, for 1 h at 30 °C. Total RNA was isolated using RNA STAT-60 (Tel-Test, Friendswood, TX, USA) and glass beads to disrupt the cell wall. All 32 RNA samples (n=4 per group) were analyzed using the Yeast 2.0 GeneChip from Affymetrix (Santa Clara, CA, USA). The microarray data have been submitted to the National Center for Biotechnology Information Gene Expression Omnibus repository, http://www.ncbi.nlm.nih.gov/projects/geo/ (Series Accession No. GSE19213).

(I used the wild-type H2O2 treated, replication 1-4 compared with wild-type control, replication 1-4 to get the top 5000 different expressed genes between treatment and control group)

Paper abstract: The yeast Saccharomyces cerevisiae transcription factor Yap1 mediates an adaptive response to oxidative stress by regulating protective genes. H2O2 activates Yap1 through the Gpx3-mediated formation of a Yap1 Cys303–Cys598 intramolecular disulfide bond.

The detailed mechanism of H2O2-induced Yap1 activation has been well studied. Oxidation of Yap1 leads to the formation of disulfide. bonds that are essential for its nuclear accumulation. However, Yap1 is not oxidized directly by H2O2. Instead, a glutathione peroxidase (GPX)-like enzyme, Gpx3, functions as the H2O2 sensor and transmits the oxidative signal to Yap1 by forming an intermolecular disulfide bond. This disulfide bond is later converted into an intramolecular disulfide bond between the Yap1 N-terminal CRD Cys303 and C-terminal CRD Cys598 [16]. A second intramolecular disulfide bond between Cys310 and Cys629 stabilizes the activated form of Yap1. Together, these two disulfide bonds cause an Nterminal α-helix to mask the nuclear export sequence in the c-CRD, resulting in nuclear accumulation of Yap1 [18]. In a single study investigating gene expression, researchers demonstrated that proper disulfide bond formation between the n- and the c-CRD is essential for activating the H2O2-responsive gene TRX2, by recruiting the mediator component Rox3 to the TRX2 promoter. Whereas Trx2 has been shown to be important to resistance to H2O2 [20], it also promotes the export of Yap1 from the nucleus by reducing the intramolecular disulfide bonds of Yap1, thereby unmasking its nuclear export sequence.

For the up-regulated genes, this analysis revealed 43 genes specifically responding to H2O2, 239 genes responding to both NEM and acrolein, and 214 genes responding to all three chemicals (Fig. 3A, left). By comparison to the corresponding responses in the Δyap1 strain, the Yap1-dependent genes were identified (Fig. 3A, right). (See Supplementary Tables S3 and S4 for the lists of Yap1-dependent genes up- or down-regulated, respectively, by the treatments and the expression profile of each gene.)