

Stress-Induced Post-Transcriptional Regulation in Yeast

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Background

Control of translational activity is an important part of post-transcriptional regulation (PTR), since it involves both global and transcript-specific mechanisms. Regulatory elements in untranslated regions (UTRs) of mRNAs are known to play a crucial role in PTR. In particular, indications that a majority of mRNAs in a cell are controlled by interactions between RNA binding proteins and regulatory elements exist. However, little is understood of what triggers the regulation system. In this survey we investigate the regulatory mechanisms by studying translation rates of mRNAs under different stress conditions. We also aim to clarify some open questions in PTR by studying overrepresentation of regulatory motifs among genes with translation rate changes under stress (Fig. 1).

Methods

Hybridization of polysome-associated mRNA and monosome-associated mRNA to microarrays can be used to measure translational activity for a large set of transcripts simultaneously. Polysome-to-monosome (PMF) log-fold changes between stressed and normal conditions were calculated from five microarray datasets.

A collection of known sequence motifs located in UTRs, from yeast as well as other species, were collected from the literature. Each motif was checked for overrepresentation within the set of differentially expressed genes. The enrichments were improved by phylogenetic filtering using six closely related yeast species.

A set of new sequence motifs, identified by alignment based filtering, were also checked for enrichment within the set of regulated genes.

Data

Five publicly available microarray datasets measuring translational activity under different stress conditions were analyzed in this survey. The datasets were made to study the effects of oxidative stress (H_2O_2), fusel alcohol stress, amino acid starvation, heat shock, and rapamycin stress on polysome association in *S. cerevisiae* [1, 2, 3].

Sequence data for the six species *S. Bayanus*, *S. Castellii*, *S. Kluyveri*, *S. Kudriavzevii*, *S. Paradoxus*, and *S. Mikatae* [4, 5] were used for phylogenetic filtering. UTR lengths for *S. cerevisiae* were extracted from tiling array data [6].

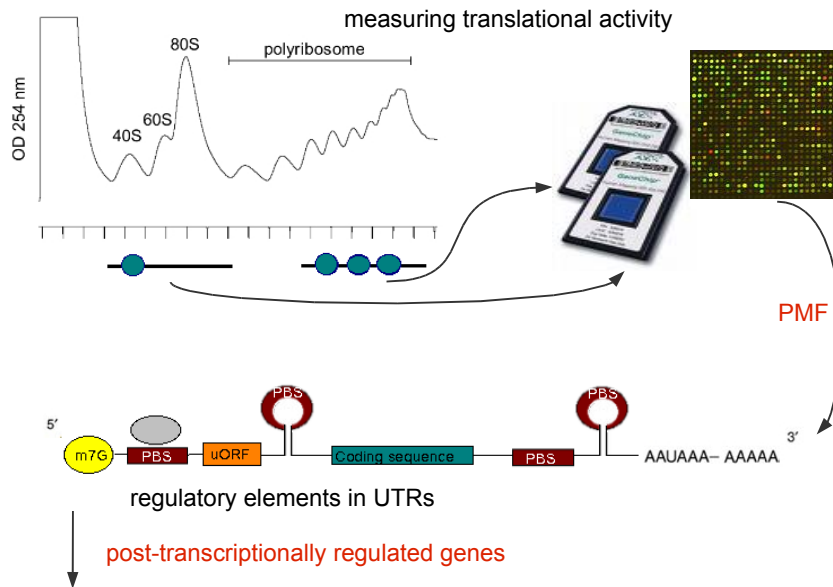


Figure 1: Survey of post-transcriptional regulation. Public microarray data measuring the expression from pooled monosomal and polysomal fractions of RNA were summarized in PMF. Genes ranked by the difference in PMF value between stress and control conditions were used in overrepresentation analysis of sequence motifs found in UTRs of mRNAs.

Results

Under the different stress conditions, a set of post-transcriptionally regulated genes were identified. Several de novo motifs, identified by alignment based phylogenetic filtering, and various known motifs were found to be enriched within the group of post-transcriptionally regulated genes, which might explain the regulatory responses.

Interesting differences between transcriptional and post-transcriptional control were also identified, indicating that post-transcriptional regulation in yeast seems to be more specific than transcriptional regulation.

References

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