IN BRIEF

TRANSLATIONAL CONTROL

A quantitative systems approach reveals dynamic control of tRNA modifications during cellular stress

Chan, C. T. Y. *et al. PLoS Genet.* **6**, e1001247 (2010)

A systems-level study in *Saccharomyces cerevisiae* highlights the functional role of tRNA post-translational modifications in cellular responses to stress. Mass-spectrometry-based methods were used to quantify the dynamic levels of 23 tRNA modifications in cells exposed to three doses of four mechanistically distinct toxicants: unique modification profiles were seen across doses and toxicants. Cells that lack the enzymes needed for tRNA modification in response to hydrogen peroxide are hypersensitive to the toxicant, thus establishing the biological importance of dynamically controlling the tRNA profile.

EVOLUTION

Widespread compensatory evolution conserves DNA-encoded nucleosome organization in yeast

Kenigsberg, E. *et al. PLoS Comput. Biol.* **6**, e1001039 (2010)

Compensatory evolution could be common in the yeast genome according to a study of the pattern of DNA sequence evolution at nucleosome-binding regions. An evolutionary sequence analysis of the *Saccharomyces cerevisiae* lineage reveals that the heterogeneous G + C content that preserves nucleosome organization results from the coupling between losses and gains of A/T bases at different locations. Weak selection in nucleosome-binding regions may be responsible for this evolutionary pattern, which might apply to the many examples in which fitness is encoded by dispersed sites.

TRANSCRIPTION

Recruitment timing and dynamics of transcription factors at the *Hsp70* loci in living cells

Zobeck, K. L. *et al. Mol. Cell* **40**, 965–975 (2010)

This study used live-cell imaging with high temporal resolution to provide new insights into the kinetics and dynamics of transcriptional control. The authors characterized the recruitment of GFP-tagged transcription factors to *Hsp70* genes in individual fruitfly salivary-gland cells after heat-shock induction. They found that factors are recruited individually and in a precise order, and that *Hsp70* loci are not recruited to a preformed transcription factory. Transcription factors were retained close to the loci, perhaps for 'recycling'.

DISEASE GENOMICS

Metabonomic, transcriptomic, and genomic variation of a population cohort

Inouye, M. *et al. Mol. Syst. Biol.* **6**, 441 (2010)

This study provides proof-of-concept evidence showing that combining metabonomic data sets with gene expression and genetic variation information can provide insights into links among disease-related traits. The authors' network analysis integrated 134 metabolic measures from a Finnish population of >500 individuals with transcriptomic and genomic data and revealed connections among lipids and immune response markers. These findings suggest clinically relevant relationships between obesity and inflammation and that systematic molecular investigation of populations can be more informative than focusing on individual metabolic traits.