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IN BRIEF

TECHNOLOGY

Sequencing transcriptomes *in situ*

The analysis of transcripts *in situ* provides valuable spatial information on gene expression at tissue-level and/or subcellular resolution. Approaches involving hybridization or sequencing have been developed, but these have been limited to characterizing the expression of only a few genes simultaneously. Lee *et al.* now present a new method of fluorescent *in situ* RNA sequencing (FISSEQ) that is applicable to various sample types from cultured cells to tissue sections and whole-mount embryos. All steps — reverse transcription, amplification and fluorescence-based sequencing — are carried out across the transcriptome at the cellular location of each transcript. Such an approach provides opportunities for spatially annotated global expression analyses.

ORIGINAL RESEARCH PAPER Lee, J. H. *et al.* Highly multiplexed subcellular RNA sequencing *in situ*. *Science* http://dx.doi.org/10.1126/science.1250212 (2014)

CHROMATIN

Chromosome roles for repetitive RNAs

To characterize the fate of transcripts from repetitive DNA (such as transposable elements), Hall *et al.* used a heterogeneous mix of repetitive DNA probes for fluorescence *in situ* hybridization in various mammalian cell types. They found that repetitive RNAs, particularly those derived from the long interspersed element LINE-1, were surprisingly abundant and acted in *cis* by stably associating with the chromosomes from which they were transcribed. Furthermore, the transcripts showed a particular association with active, euchromatic regions, where they inhibited chromosome condensation. These RNAs may thus antagonize the action of heterochromatin-associated *cis*-acting RNAs such as X inactive specific transcript (*XIST*).

ORIGINAL RESEARCH PAPER Hall, L. L. *et al.* Stable C_0T-1 repeat RNA is abundant and is associated with euchromatic interphase chromosomes. *Cell* **156**, 907–919 (2014)

GENE EXPRESSION

Global analyses of determinants of RNA decay

Two new studies have carried out analyses of RNA decay rates across the transcriptome in *Saccharomyces cerevisiae*. Both groups used strains with mutant forms of the RNA polymerase II subunit Rpb1 in order to inducibly block new transcription: Geisberg *et al.* used an Rbp1 fusion protein that is exported from the nucleus following rapamycin treatment, and Gupta *et al.* used a temperature-sensitive Rpb1 mutant. The subsequent decay of RNA was monitored using high-throughput sequencing of the 3′ ends of transcripts over time. Both teams found that even subtle alterations to the lengths of 3′ untranslated regions (through alternative polyadenylation of transcript isoforms) could alter mRNA stability. They then characterized the RNA sequence elements for which retention or exclusion during polyadenylation correlated with differential isoform stability. Geisberg *et al.* showed that a 20-nucleotide poly(U) sequence conferred stability by hybridizing with the poly(A) tail to disfavour binding of RNA-destabilizing proteins (such as poly(A)-binding protein (Pab1)). Gupta *et al.* showed that binding sites for the Fus3 RNA-binding protein destabilized transcripts. Thus, alternative polyadenylation has widespread roles in regulating mRNA stability through altering sites for RNA-binding proteins.

ORIGINAL RESEARCH PAPERS Geisberg, J. V. *et al.* Global analysis of mRNA isoform half-lives reveals stabilizing and destabilizing elements in yeast. *Cell* **156**, 812–824 (2014) | Gupta, I. *et al.* Alternative polyadenylation diversifies post-transcriptional regulation by selective RNA–protein interactions. *Mol. Syst. Biol.* **10**, 719 (2014)