
Determinants of RNA metabolism in the Schizosaccharomyces pombe genome

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Résumé

Decrypting the genomic regulatory code is important for our understanding of gene regulatory mechanisms and for interpreting genetic variants. The task however is challenging. Here we propose a systematic approach that combines 1) *in vivo* quantification of RNA synthesis, processing and degradation rates genome-wide using metabolically labelled RNA-sequencing, 2) identification of DNA elements predictive for these kinetic rates, and 3) testing for the causal role of these DNA elements by drawing on expression profiles of genetically distinct individuals. We demonstrate the power of this approach using fission yeast as a model system. This recovers known DNA and RNA motifs involved in RNA synthesis and degradation, quantifies the contributions of individual nucleotides to RNA synthesis, splicing, and degradation, and uncovers novel motifs that regulate RNA life time.

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