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IN BRIEF

GENOMICS

Repetitive elements underestimated?

Repeat sequences — mainly transposable elements — have been estimated to comprise ~50% of the human genome. Typical approaches for identifying repeats are based on finding sequence similarity to a single consensus sequence for each repeat type. These authors re-examined the human genome using an algorithm that instead relies on relatedness within entire groups of evolutionarily diverged repeats. This led them to an increased estimate of 66–69% for the proportion of repeat-derived sequence in the human genome, after correcting for false positives. These results imply that repetitive DNA may have played a larger part in human evolution than was previously assumed.

ORIGINAL RESEARCH PAPER de Koning, A. P. *et al.* Repetitive elements may comprise over two-thirds of the human genome. *PLoS Genet.* **7**, e1002384 (2011)

NON-CODING RNA

Zebrafish provide insight into lincRNA evolution

Ulitsky *et al.* have identified >550 large intergenic non-coding RNAs (lincRNAs) in zebrafish using several different transcriptomic and chromatin data sets. Few of these lincRNAs have a detectable sequence similarity with mammalian lincRNAs, indicating rapid evolution of these RNAs. However, some of the lincRNAs have conserved functions despite having little sequence conservation. For example, injection of mouse or human orthologues could rescue developmental defects in zebrafish embryos that are depleted for certain lincRNAs. Zebrafish are therefore likely to be a useful model for exploring lincRNA function.

ORIGINAL RESEARCH PAPER Ulitsky, I. *et al.* Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. *Cell* **147**, 1537–1550 (2011)

EVOLUTION

Paths of antibiotic resistance

These authors developed a system to study the gradual evolution of antibiotic resistance. In their 'morbidostat' system, the amount of antibiotic in a bacterial culture is continuously adjusted to maintain an almost constant growth inhibition (that is, as resistance in the culture increases, so does the antibiotic concentration). Genome sequencing of *Escherichia coli* from parallel morbidostat cultures that were grown with one of three different drugs showed that the evolutionary trajectories for drug resistance are constrained. For example, resistance to trimethoprim evolves through sequential mutations in a target enzyme.

ORIGINAL RESEARCH PAPER Toprak, E. *et al.* Evolutionary paths to antibiotic resistance under dynamically sustained drug selection. *Nature Genet.* **44**, 101–105 (2012)

GENE EXPRESSION

A simple model for ensuring signalling specificity

This article reports that the specificity of a yeast cell's response to different environmental stimuli depends on the dynamics of nuclear translocation of a single transcription factor, Msn2. By artificially manipulating the amplitude, frequency and duration of Msn2 nuclear translocation and relating these parameters to the expression of an Msn2-dependent reporter gene in single cells, the authors developed a kinetic model that connects external inputs to differential gene expression via the dynamics of one signalling molecule.

ORIGINAL RESEARCH PAPER Hao, N. & O'Shea, E. K. Signal-dependent dynamics of transcription factor translocation controls gene expression. *Nature Struct. Mol. Biol.* **19**, 31–36 (2012)

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