Nature Reviews Genetics | AOP, published online 16 January 2013

IN BRIEF

GENE REGULATION

Global translational pausing in response to stress

The ability of mammalian cells to respond rapidly to stress through global suppression of translation has mainly been attributed to inhibition of translation initiation. However, these papers show that pausing of ribosomes during elongation has an important role. These studies used deep sequencing of ribosome-protected mRNAs or ribosomal footprinting in cells that were subjected to heat shock or proteotoxic stress. In response to both types of stress, the authors found widespread pausing of ribosomes early in elongation and showed that chaperone proteins are involved in regulating this pausing.

ORIGINAL RESEARCH PAPERS Shalgi, R. *et al.* Widespread regulation of translation by elongation pausing in heat shock. *Mol. Cell* 3 Jan 2013 (doi:10.1016/j.molcel.2012.11.028) | Liu, B. *et al.* Cotranslational response to proteotoxic stress by elongation pausing of ribosomes. *Mol. Cell* 3 Jan 2013 (doi:10.1016/j.molcel.2012.12.001)

PATHOGEN GENETICS

Screening to resolve redundancy

Identifying pathogenicity genes can be difficult because redundancy means that perturbing the function of a single pathogen gene often fails to result in a phenotype. This paper describes a method called insertional mutagenesis and depletion (iMAD), in which pathogenic *Legionella pneumophila* bacteria are first subject to mutagenesis and are then screened for their ability to grow in *Drosophila* cells that are depleted, by RNA interference, of different components of the secretory system. This screening revealed pathogen genes that target overlapping host pathways, allowing virulence factors with redundant roles to be identified and enabling the authors to dissect the complex network of host–pathogen interactions.

ORIGINAL RESEARCH PAPER O'Connor, T. J. *et al.* Aggravating genetic interactions allow a solution to redundancy in a bacterial pathogen. *Science* **338**, 1440–1444 (2012)

CHROMATIN

Retrotransposons and heterochromatin spreading

Some retrotransposons spread their heterochromatic marks into neighbouring genes to regulate their expression, but how widespread is this phenomenon? Eichten *et al.* found that spreading of cytosine methylation and histone H3 dimethylated at lysine 9 (H3K9me2) was associated with only a minority of retrotransposon classes when studied genome-wide in maize. Among retrotransposon-proximal genes, those affected by heterochromatic spreading were expressed at lower levels, indicating that such spreading may have gene-regulatory roles across the genome.

ORIGINAL RESEARCH PAPER Eichten, S. R. *et al.* Spreading of heterochromatin is limited to specific families of maize retrotransposons. *PLoS Genet.* **8**, e1003127 (2012)

DISEASE GENETICS

Defective reading of 5hmC in Rett's syndrome

Mellén *et al.* classified mouse neuronal cell types on the basis of profiles of 5-hydroxymethylcytosine (5hmC), 5-methylcytosine (5mC) and gene expression. They concluded that 5hmC is associated with active gene expression and accessible chromatin structure in ways that are distinct from non-neuronal cells. They also found that a mutant form of methyl-CpG-binding protein 2 (MECP2) that is associated with the neurodevelopmental disorder Rett's syndrome was defective for 5hmC, but not 5mC, binding. Thus, impaired reading of 5hmC marks might contribute to Rett's syndrome neuronal pathology.

ORIGINAL RESEARCH PAPER Mellén, M. *et al.* MeCP2 binds to 5hmC enriched within active genes and accessible chromatin in the nervous system. *Cell* **151**, 1417–1430 (2012)