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IN BRIEF

GENE REGULATION

Key role for translation in cell cycle control

Stumpf and colleagues used ribosome profiling — deep sequencing of ribosome-protected mRNA fragments — to investigate the role of translational regulation of gene expression in the mammalian cell cycle. Working with human cells, they found that there is pervasive translational regulation of the expression of genes that have important roles in the cell cycle. In addition, functionally related genes, including those involved in metabolism, DNA repair and nuclear transport, were found to be translationally co-regulated, which indicates that translation mediates coordinated gene expression.

ORIGINAL RESEARCH PAPER Stumpf, C. R. *et al.* The translational landscape of the mammalian cell cycle. *Mol. Cell* http://dx.doi.org/10.1016/j.molcel.2013.09.018 (2013)

SYNTHETIC BIOLOGY

Recoding bacterial genomes

In two new studies, Lajoie and colleagues recode and expand the genetic code of the *Escherichia coli* genome by incorporating non-standard amino acids (NSAAs). This allows the production of novel proteins, which has potential applications in areas such as biosafety, agriculture and medicine. In their first study, Lajoie *et al.* replaced the UAG stop codon with the synonymous UAA codon. They subsequently deleted the gene that encodes release factor 1, which mediates translational termination at UAG. This allowed them to re-introduce UAG and re-assign its function from that of a stop codon to one that incorporates chosen NSAAs. The resulting genetically recoded organism had increased resistance to bacteriophage T7 and was able to efficiently incorporate NSAAs. In their second study, the authors expanded on this work by re-assigning 13 rare codons in each of 42 highly expressed essential genes in 80 *E. coli* strains. Although this recoding was successful, most strains with recoded genes showed reduced fitness, which indicates that combining several recoded genes into one genome may not be feasible. Interestingly, they occasionally found that replacement of synonymous codons, such as that of CUU with UUG, did not produce the same effects as the native codon. Together, these studies show that recoding the bacterial genome is feasible and provide useful information for future genome-wide codon re-assignment designs.

ORIGINAL RESEARCH PAPERS Lajoie, M. J. *et al.* Genomically recoded organisms expand biological functions. *Science* **342**, 357–360 (2013) | Lajoie, M. J. *et al.* Probing the limits of genetic recoding in essential genes. *Science* **342**, 361–363 (2013)

MOLECULAR EVOLUTION

Bypassing indels

Insertions and deletions (indels) are prone to being formed at short sequence repeats owing to the misalignment of the DNA strands during replication, and a similar mechanism allows them to be bypassed in both transcription and translation. A recent study has investigated how well indels are tolerated in evolution as a result of transcriptional and translational bypassing. To identify how frequently these mutations occur, the authors mutated the *Haemophilus aegyptius* M.HaeIII gene *in vitro* using an error-prone polymerase followed by sequencing. They then expressed these mutated genes in *Escherichia coli* to ascertain the effect of natural selection. They found that the longer the repeats in M.HaeIII, the more frequently the mutations were formed and maintained in the *E. coli* population and were hence tolerated.

ORIGINAL RESEARCH PAPER Rockah-Shmuel, L. *et al.* Correlated occurrence and bypass of frame-shifting insertion-deletions (indels) to give functional proteins. *PLoS Genet.* **9**, e1003882 (2013)