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## GENE REGULATION

# Translation steps up to a regulatory role

Although there is still much to learn, a lot is known about the regulation of gene expression at the level of transcription. However, regulation at the level of translation and its role in evolution remains somewhat a 'black box'. In two recent studies, Artieri and Fraser, and McManus *et al.* use the same approach in hybrid strains of yeast to identify a role for translational regulation in buffering gene expression in evolution.

Both groups analysed hybrids of *Saccharomyces cerevisiae* and *Saccharomyces paradoxus*. They carried out high-throughput sequencing of polyadenylated mRNA to determine mRNA abundances and ribosome profiling to characterize the ribosomal occupancy on these mRNAs; combining these data indicates the overall translational output from these mRNAs. The mRNA data allowed the authors to obtain data on transcript abundance, and the use of hybrid strains also enabled them to determine the haplotype phase of such data in

order to distinguish translation from each of the parental alleles. By observing whether translational efficiency and mRNA abundance alter in the same direction or in divergent directions between the species, the authors found that, remarkably, the two often went in the opposite direction, thus buffering potential protein expression differences that result from alterations in transcript abundance. Translational regulation may therefore buffer alterations that result from transcriptional changes, although Artieri and Fraser did also find instances in which selection acts in parallel on both transcription and translation in some genes.

The hybrid approach also allowed both groups to investigate the level of regulatory divergence at the *cis* and *trans* levels. Within the hybrids, as the *trans* backgrounds are the same, any differences in regulation between the alleles are due to *cis* effects. However, in the parental species, any differences that are not accountable by the *cis* differences

are due to effects in *trans*. McManus *et al.* found that *trans*-regulatory changes were mostly responsible for buffering species differences in gene expression, and Artieri and Fraser found that *cis* regulation was as pervasive at the level of translation as mRNA levels.

With regard to the more general mechanism of translational regulation, McManus *et al.* showed that differences in transcript leaders and codon bias contribute to translational regulation. However, Artieri and Fraser focused more on the role of stop codon readthrough, in which the stop codon is ignored by the ribosome to produce a longer peptide. They found that this mechanism may contribute to the regulation of biological function of 19 proteins.

These findings indicate that there is much for us to learn about translational regulation, particularly its role in evolution that adds to the layers upon which selection may act.

Hannah Stower

“ two recent studies ... use the same approach ... to identify a role for translational regulation in buffering gene expression in evolution ”

**ORIGINAL RESEARCH PAPERS** Artieri, C. G. & Fraser, H. B. Evolution at two levels of gene expression in yeast. *Genome Res.* <http://dx.doi.org/10.1101/gr.165522.113> (2013) | McManus, J. *et al.* Ribosome profiling reveals post-transcriptional buffering of divergent gene expression in yeast. *Genome Res.* <http://dx.doi.org/10.1101/gr.164996.113> (2013)