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GENE EXPRESSION

Directly linking transcription and translation

In bacteria, transcription and translation are coupled in time and space. Two studies now show that transcription and translation are physically linked, which may be important for regulating bacterial gene expression in response to different environmental conditions.

Nudler and colleagues used an *in vivo* reporter gene system to monitor how altering the rate of translation affects transcription. They took advantage of a mutant bacterial strain in which ribosomes travel slowly, and showed that the transcription rate decreased proportionately with decreased translation. The slow translation phenotype of this mutant can be partially recovered using streptomycin, and under these conditions the speed of transcription increased proportionately. Moreover, the authors found that transcriptional and translational rates were perfectly matched under various nutrient conditions and in different stages of bacterial growth.

The codon composition of a transcript is known to affect the rate of translation, as rare codons pair with low-abundance transfer RNAs, delaying the passage of the ribosome. Does codon usage also affect the rate of transcription? Indeed, the authors found that the rates of transcription and translation for genes that have few rare codons were faster than for those that have a high frequency of rare codons.

Previously, Nudler and co-workers showed that transcription elongation complexes can spontaneously backtrack along a gene, but this effect can be rescued by lagging elongation complexes, which effectively push the backtracking elongation complex forward. A trailing ribosome might have a similar effect, which could explain transcription–translation coupling. To test this, the authors created a plasmid in which RNA polymerase (RNAP) was induced to backtrack owing to collision with a 'roadblock' consisting of bound lac repressor, leading to transcriptional stalling. When a strong ribosome-binding site was inserted upstream of the lac-binding site, backtracking was decreased, and RNAP could read through the roadblock. Therefore, a lagging ribosome physically stops RNAP backtracking and stimulates transcriptional readthrough.

A second paper by Burmann *et al.* provides insights into this physical link between RNAP and the ribosome. The authors used nuclear magnetic resonance spectroscopy to show that the *Escherichia coli* transcription factor NusG can bind to both the ribosome and RNAP. The carboxy-terminal domain (CTD) of NusG binds to the transcription factor NusE, which is part of the ribosomal 30S subunit, and the NusG amino-terminal domain contacts RNAP. Furthermore, the authors found that NusE competes for binding of the NusG CTD with the transcription termination factor Rho. As the uncoupling of transcription and translation at the ends of operons allows Rho to terminate transcription, they suggest that this competition between Rho and NusE may explain why Rho is unable to terminate translated transcripts.

In contrast to bacteria, transcription and translation in eukaryotes take place in different cellular compartments and are not coupled. This difference may be important for the bacterial lifestyle, as the precise tailoring of transcription in response to the codon usage and nutrient availability sensed by the ribosome could allow bacteria to adapt rapidly to various environmental conditions. In addition, this difference may allow the development of antimicrobial drugs targeted at transcription–translation coupling.

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ORIGINAL RESEARCH PAPERS Proshkin, S. *et al.* Cooperation between translating ribosomes and RNA polymerase in transcription elongation. *Science* 23 Apr 2010 (doi:10.1126/science.1184939) | Burmann, B. M. *et al.* A NusE:NusG complex links transcription and translation. *Science* 23 Apr 2010 (doi: 10.1126/science.1184953)