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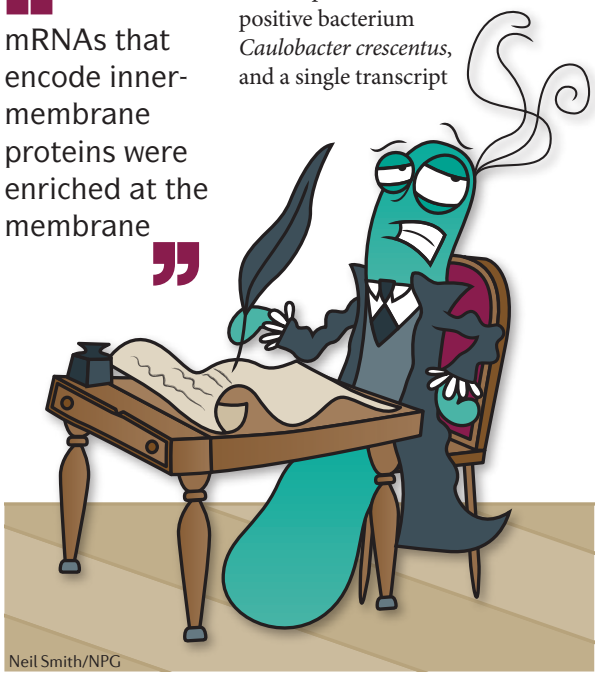
BACTERIAL TRANSCRIPTION

A tale of two specificities

In the past few years, several studies have reported the identification of bacterial mRNAs that, similarly to many eukaryotic mRNAs, have specific subcellular localizations. However, these studies examined only a small number of transcripts, and their conclusions seemed at odds with the relative lack of subcellular compartmentalization in bacterial cells. Now, Moffitt *et al.* use super-resolution microscopy to study the spatial organization of the *Escherichia coli* transcriptome at a near-global scale, finding that the localization of each mRNA in this bacterium is determined by whether the mRNA encodes an inner-membrane protein.

> “mRNAs that encode inner-membrane proteins were enriched at the membrane”

Previously, analysis of several transcripts in the Gram-positive bacterium *Caulobacter crescentus*, and a single transcript in *E. coli*, had suggested that bacterial mRNAs might localize in proximity to the genomic loci from which they are transcribed. To assess whether such a pattern characterizes the spatial distribution of *E. coli* mRNAs at a transcriptome-wide scale, 3D-STORM (sub-diffraction-limit imaging by stochastic optical reconstruction microscopy; a super-resolution microscopy technique) was used to image the subcellular localizations of 20 sets of fluorescently labelled *E. coli* mRNAs that were grouped by chromosomal region and accounted for nearly half of the chromosome. None of the sets of mRNAs had a localization that was enriched at the chromosome, yet alone a specific locus; instead, most sets of mRNAs were uniformly distributed in the cytoplasm, with the interesting exception of sets of mRNAs that had a subcellular localization that was enriched at the membrane. Notably, these membrane-enriched sets of mRNAs were also enriched for mRNAs that encode inner-membrane proteins, which was consistent with previous reports of a similar enrichment for a small number of mRNAs. By using 3D-STORM to image the subcellular localization of mRNAs that were grouped according to the desired localization of the cognate protein product at a near-global scale (76% of all mRNAs that were expressed under the growth conditions), the authors confirmed that mRNAs that encode inner-membrane proteins were enriched at the membrane. By contrast, mRNAs that encode periplasmic proteins, outer-membrane proteins or cytoplasmic proteins had a uniform spatial distribution.



Neil Smith/NPG

The signal-recognition particle (SRP), which is recruited by a leader sequence on inner-membrane proteins, is known to be responsible for the co-translational targeting of these proteins to the membrane. The authors of the study hypothesized that the SRP might co-translationally target mRNAs to the membrane, thus explaining the membrane enrichment of mRNAs that encode inner-membrane proteins. Experiments using fusion constructs that encoded different combinations of leader sequences and proteins confirmed that the SRP was responsible for targeting mRNAs to the membrane. Furthermore, the introduction of stop codons or the use of an inhibitor of translation initiation showed that translation of the SRP-recruiting leader sequence was required for this targeting. Finally, the authors were able to identify a physiological consequence of targeting mRNAs to the membrane. Genetic experiments showed that localization to the membrane substantially enhances the average degradation rate of mRNAs, and that the membrane-bound RNA degradosome complex is, at least in part, responsible for this enhanced degradation.

The authors conclude that *E. coli* mRNAs have, for the most part, a uniform subcellular distribution, but that mRNAs that encode inner-membrane proteins are a major exception that are co-translationally targeted to the membrane, where they can be more readily degraded by the RNA degradosome complex.

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ORIGINAL ARTICLE Moffitt, J. R. *et al.* Spatial organization shapes the turnover of a bacterial transcriptome. *eLife* **5**, e13065 (2016)