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Quantitative study of gene regulation mediated by small RNA
EREL LEVINE, THOMAS KUHLMAN, Center for Theoretical Biological Physics, UCSD, ZHONGGE ZHANG, Division of Biological Sciences, UCSD, TERENCE HWA, Center for Theoretical Biological Physics, UCSD — The role of small regulatory RNAs (sRNA) in controlling many pathways in bacteria has been highlighted in recent years. Small RNAs have been found in regulating the response of *E. Coli* to various stress conditions, frequently by destabilizing the mRNA molecules of their target. Here we describe quantitatively the unique properties of this mode of regulation. We characterize - both theoretically and experimentally - the expression of a sRNA-regulated reporter, under different regulatory signals and genetic backgrounds. Our analysis predicts the existence of two regimes of gene expression, separated by a sharp transition: When the transcription rate of the sRNA exceeds that of its targets, we expect very low level of protein synthesis, with fluctuations strongly suppressed. However, when the sRNA transcription rate becomes lower than that of its target, a proportional fraction of target transcripts are expected to be stable, leading to protein expression. In the context of stress response, our results suggest a "stress-relief" mechanism, where gradual response is evoked only once a "tolerance threshold" is exceeded. We also characterized an intriguing *coupling* effect between the mRNA levels of different genes, arising from their shared regulatory sRNA. Such coupling may be used by the cell to create a hierarchy of responses to changes in regulatory signals.

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