

166. Towards Engineering mRNA Stability: Global Analysis of mRNA Turnover in Cyanobacteria and *E. coli*

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Messenger RNA (mRNA) are labile intermediates that play critical roles in determining the translation rate and steady state protein concentrations in the cell. The majority of studies on mRNA turnover have focused on the model heterotrophic bacteria *Escherichia coli* and *Bacillus subtilis*. In contrast, much less is known about mRNA turnover in photosynthetic microbes. We generated a compendium of the RNases and provide an in-depth analysis of RNase III-like enzymes in commonly studied and diverse cyanobacteria. Furthermore, using targeted gene deletion, we genetically dissected the RNases in *Synechococcus* sp. PCC 7002, one of the fastest growing and industrially attractive cyanobacterial strains. We found that all three cyanobacterial homologs of RNase III and a member of the RNase II/R family are not essential under standard laboratory conditions, while homologs of RNase E/G, RNase J1/J2, PNPase, and a different member of the RNase II/R family appear to be essential for growth. These and other strains are being used to identify specific ribonuclease targets with base-pair resolution and determine genome-wide rates of mRNA turnover in *Synechococcus* sp. PCC 7002 and *E. coli* using Next-Gen sequencing. The principles of mRNA decay uncovered in this analysis are being used to construct designer transcripts with predictable lifetimes to enable precise control of gene expression for metabolic engineering.