The yin and yang of gene expression

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The degradation of transcripts and transcription can be considered the yin and yang of gene expression. In this report, we outline our recent advances in understanding both of these processes using bacteria as model systems. Last year, we reported how we had used SELEX to identify sequences that are recognised by a transcription factor, called AtrA that controls the production of an antibiotic in *Streptomyces coelicolor*. Using bioinformatics, this had led to the identification of a target, *nagE2* that encodes the transporter of a key nutrient. This work has now been published. In an exciting twist, further refinement of the weighted matrix used for *in silico* scanning revealed multiple links to the metabolism of acetyl-CoA, the precursor of actinorhodin, and to additional morphogenes. The emerging picture is one of AtrA as a central coordinator of metabolism and morphological development. This has stimulated sufficient interest to initiate a collaboration to study AtrA on a systems/genome-wide level using chromatin-immunoprecipitation and transcriptomics.

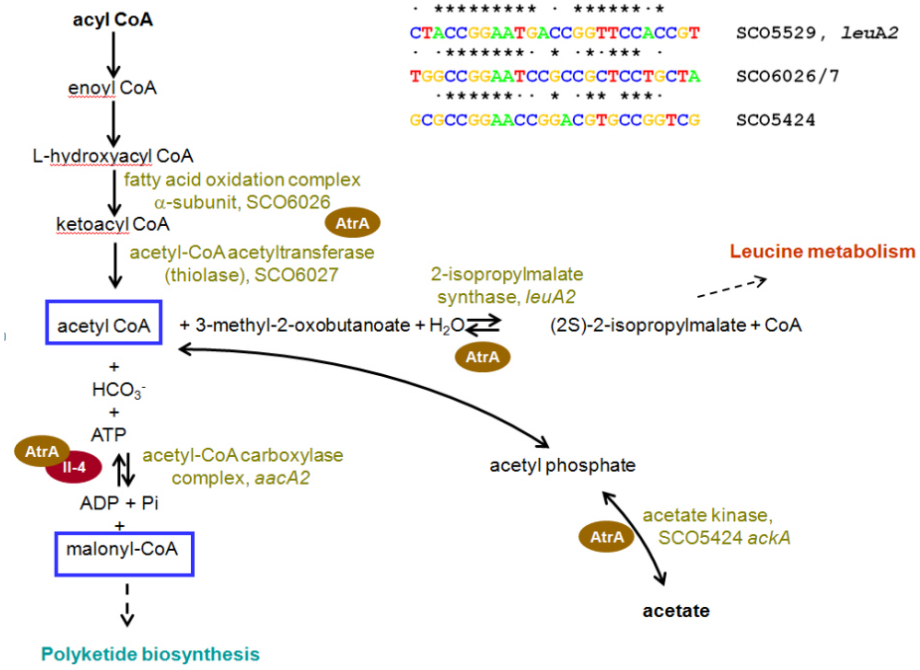

Figure 1: AtrA links to acetyl-CoA metabolism. Binding to promoters has been confirmed using electrophoretic mobility shift assays. The sequence of the binding sites is shown top right.

The degradation of mRNA is more than just a counterbalance; for example, it is the basis of the close coupling of translation to programs of transcription. Previously, we proposed here that the initiation of the degradation of many transcripts in *E. coli* is not dependent on "decapping", but endonucleolytic cleavages that are facilitated by the ability of the corresponding nuclease, RNase E to interact cooperatively with multiple single-stranded regions. This work has also now been published. This mode of recognition offers a simple explanation for the finding that in the absence of translating ribosomes many transcripts are highly susceptible to RNase E. We suggest that it might provide quality control by ensuring the rapid removal of defective mRNAs and reinforce the effects of small antisense RNAs that block translation.

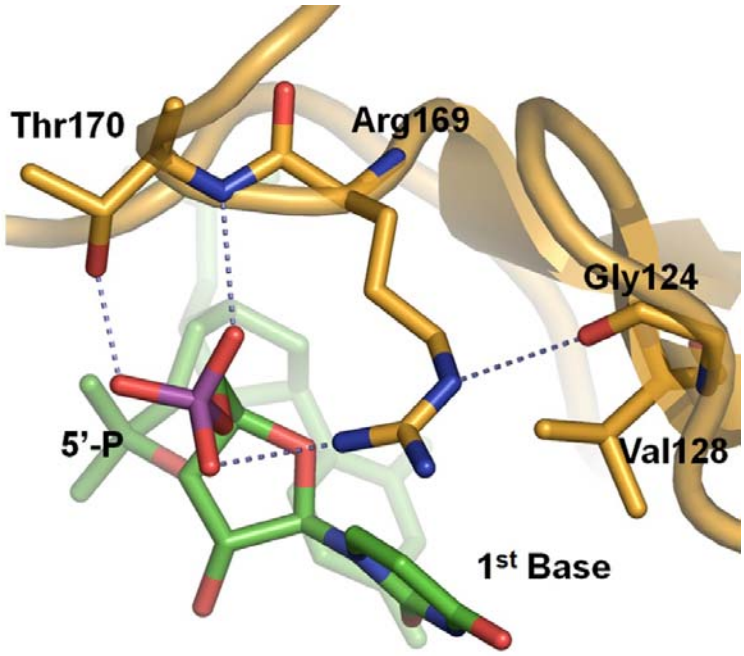

Figure 2: The interaction between the 5' end of an RNA substrate and RNase E. It now appears that this interaction can serve primarily as an additional foothold. While important for efficient cleavage in some circumstances, this interaction appears not to be universally required and not to serve as a critical allosteric switch.

Publications

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Collaborators

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