The Faculty of Biotechnology and Food Engineering

Seminar

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Intricate Networks of Small RNA-Mediated Regulation Revealed by RIL-seq

Abstract

Bacterial small RNAs (sRNAs) post-transcriptionally regulate their target mRNAs via base-pairing facilitated by RNA chaperones such as the well-studied Hfq and the under-studied ProQ. My colleagues and I recently developed RIL-seq (RNA Interaction by Ligation and sequencing) for global *in-vivo* identification of sRNA-RNA interactions, a valuable step towards understanding the roles of RNA chaperones and sRNAs in cellular networks [1, 2]. Application of RIL-seq to *Escherichia coli* Hfq revealed an extensive and dynamic network, recapitulating known interactions and revealing new interactions including those between novel sRNAs regulated by the flagella sigma factor (σ28) and their targets. Intriguingly, overexpression of each of these σ28-depednet sRNAs leads to a unique phenotype in terms of flagella length and number. These effects are mediated by regulation of target mRNAs encoding ribosomal proteins and transcription factors that control the flagellar regulon. We also applied RIL-seq to ProQ to gain deeper understanding of its role in *E. coli.* Interestingly, we found that there is a significant overlap between the ProQ- and the Hfq-bound RNA pairs. Further analysis of one RNA-RNA pair showed that while Hfq is required for downregulation of one of the RNAs, ProQ can block this effect [3]. Overall, these examples are only the tip of the iceberg of what can be learned from RIL-seq analysis, as this approach can be applied to different proteins and different bacteria, and as a tool to decipher the role of sRNAs in the communication of bacteria with their surroundings.

Monday, 20/1/2020, 13:00 – 14:00, Room 300

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