Life Sciences Seminar

Computational analyses of the evolution of bacterial translation

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Translation is a central cellular process across the tree of life. Bacteria, which form a major portion of this tree, exhibit tremendous phenotypic and genomic diversity. An important question is how the process of translation has evolved given this large diversity of bacteria. So far, studies have analysed the evolution of codon usage, tRNA genes and tRNA modifications in only a few bacteria. Thus, a systematic and comprehensive study of these aspects across a large number of bacteria was lacking. I studied the evolution of three traits affecting translation elongation: tRNA modifications, tRNA gene complement, and internal Shine Dalgarno (SD)-like motifs, across a large number of bacteria. All three traits were correlated with the GC content of bacteria. For instance, high GC organisms possessed a larger set of tRNA genes and as a result, some high GC clades lost tRNA modifications. This is probably because a larger set of tRNA weakened selection on tRNA modifications and led to their loss. Differently AT rich bacteria lost several tRNA genes as well as tRNA modifications. This indicated that AT rich bacteria are unable to decode all 61 sense codons. Interestingly, across several species, the codons that were unreadable were used less frequently as compared with synonymous codons. Unreadable codons were also lost over evolutionary time indicating that codon use evolves in response to the gain/loss of tRNA genes. Finally, I found that the frequency of internal SD like motifs was correlated with the GC content of bacteria. However, the selection to avoid internal SD like motifs was higher for bacteria with high GC content. Interestingly, mesophiles and N-terminal regions of genes also showed a distinct signature of avoiding internal SD like motifs. This indicated that the frequency of internal SD like motifs is governed by multiple selection pressures. Overall, my thesis presents a nuanced view of the evolution of bacterial translation and demonstrates that translation mechanisms in diverse bacteria are extremely variable. I also describe interesting case studies for future work that could lead to further understanding of the evolution of bacterial translation.

Monday, April 15, 2019 11:00am - 12:00pm
Mondi Seminar Room 3, Central Building

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