

Poster A-26

Plasticity of transcriptional regulatory machinery revealed from whole genome comparison



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Short Abstract: We compare the repertoires of transcription factors (TFs) between model organisms *Escherichia coli* and *Bacillus subtilis* at different levels and present the first comprehensive and complete analysis of comparison of TFs between any two prokarya. We analyze and discuss the results in the light of the evolution of transcriptional regulatory networks.

Long Abstract:

Regulation of transcription can be viewed as a network of interactions between transcription factors (TFs) and their target genes (TGs) of which they regulate the transcription. Here we address the question of the degree to which transcription factors and their evolutionary families are shared between two prokaryotic model organisms, *Escherichia coli* [1] and *Bacillus subtilis* by using a compilation of the repertoire of TFs in the complete genomes. We first construct a repertoire of TFs from literature and knowledge bases like RegulonDB [2] and DBTBS [3] and then expand on the TFs collection across the genomes using family specific HMMs. 59 proteins and 28 families were found to be shared between the two bacteria, whereas different subsets were lineage-specific. Families in both bacteria were evaluated in terms of the global function of the regulated genes by using the transcriptional regulatory networks of these genomes. Although topologically the networks are similar in both the genomes we found that the players are different, suggesting different evolutionary origins for the transcriptional regulatory machinery in both bacteria. We show that global regulators have a tendency to be constrained to smaller regulatory families and generally originate from families which are lineage-specific or of recent origin and that although TF families may be conserved across genomes their functional roles might evolve in an organism-specific or lineage-specific manner and need not be conserved, indicating convergence to be a major phenomenon involved in the functional evolution of transcription factors of the same TF family. We also discuss the interaction of TFs within and across TF families and their evolutionary implications in the context of the evolution of transcriptional regulatory networks. Finally we measure the effect of lineage-specificity in predicting transcription factors from comparative genomic approaches.

References

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