

Modularity of bacterial stress response evolution

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Responses to extracellular stress directly confer survival fitness by means of complex regulatory networks. Despite their complexity, the networks must be evolvable due to changing ecological and environmental pressures. Although the regulatory networks underlying stress responses are characterized extensively, their mechanism of evolution remains poorly understood. Here, we examine the evolution of three candidate stress response networks (chemotaxis, competence for DNA uptake, and endospore formation) by analyzing their phylogenetic distribution across several hundred diverse bacterial and archaeal lineages. We report that genes in the chemotaxis and sporulation networks group into well-defined evolutionary modules with distinct functions, phenotypes, and mutation rates as compared to control sets of randomly chosen genes. The evolutionary modules vary in both number and cohesiveness among the three pathways. Chemotaxis has five coherent modules whose distribution among species shows a clear pattern of interdependence and rewiring. Sporulation, by contrast, is nearly monolithic and appears to be inherited vertically, with three weak modules comprising early and late stages of the pathway. Competence does not exhibit well defined modules either at or below the pathway level. These three pathways are hence emblematic of different modes and constraints on evolution. Based on these findings, we derive a previously undescribed ontology that classifies gene function according to an engineering view of dynamical control, with roles such as "sensor," "regulator," and "actuator." Application of this ontology to the evolutionary modules reveals, surprisingly, that combinations of modules predict phenotype, and do not necessarily correlate with phylogenetic inheritance.

Bio:

Dr. Amoolya Singh is currently a postdoctoral researcher in the group of Peer Bork at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany. Born and raised in India in a family of scientists and artists, she was faced at age 17 with the difficult choice of a career in music vs. science. Science won out, and she graduated with honors in biology and computer science and a minor in environmental studies from Carnegie Mellon University. In 2006, she completed her PhD in computational biology from UC Berkeley under Richard Karp (CS/Math) and Adam Arkin (Bioengineering). Her doctoral studies were supported by a DoE Computational Science Graduate Fellowship (CSGF). As part of the CSGF program, she had the opportunity to spend a summer at the Pacific Northwest National Laboratory, near the Hanford nuclear waste site, studying the genetics and physiology of a uranium-eating bacterium. While a graduate student, she served as a Scientific Tour Guide for Lawrence Berkeley Laboratory, and won an LBL award for Excellence in Promoting Diversity. Her environmental leanings also led to several successful volunteer stints at local and international non-profit agencies. Dr. Singh's research interests are in the mathematical modeling and simulation of biological systems, dynamics and evolution of gene regulatory networks, bacterial stress response, bioremediation, and environmental metagenomics. She remains a serious student of music, and has finally stopped wondering if she made the right career choice.