1-6 Poster

IMPACT OF HIERARCHICAL STRUCTURE OF TRANSCRIPTIONAL REGULATORY NETWORKS ON THE EVOLUTION OF DRUG RESISTANCE

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A fundamental issue in evolutionary biology is the existence and nature of genes with large influence on the speed of evolutionary adaptation (evolvability). Recent studies indicate that complex adaptations are frequently accompanied by genome-wide changes in gene expression, possibly mediated by transcriptional regulatory genes. Taking advantage of the availability of *E.coli* knock-out libraries, here we ask how master transcriptional regulatory genes affect the tempo by which drug resistance can evolve by endogenous mutations. We initially performed large-scale automated phenotypic profiling to establish differences in basal drug tolerance across mutant strains. This procedure was followed by experimental evolution to determine the impact of various genes on the rate at which resistance emergences. Augmented with bioinformatics analyses, our work provides key insights on the impacts of regulatory network hierarchy, sign of regulation and the number of target genes.