MAR12-2011-006408

Abstract for an Invited Paper
for the MAR12 Meeting of
the American Physical Society

Mapping the environmental fitness landscape: Lessons from a noisy synthetic gene circuit[1]

GABOR BALAZSI, The University of Texas MD Anderson Cancer Center

Gene expression actualizes the organismal phenotypes encoded within the genome in an environment-dependent manner. Among all encoded phenotypes, cell population growth rate (cell population fitness) is perhaps the most important, since it determines how well-adapted a genotype is in various environments. Currently it remains unclear how a cell population's growth rate and its subpopulation fractions in specific environments emerge from the stochastic molecular-level kinetics of gene networks and the division rates of single cells. To address this question we developed and quantitatively characterized synthetic a gene circuit controlling the expression of a bifunctional antibiotic resistance gene in *Saccharomyces cerevisiae*. We found that knowing the cell division rates and nongenetic (cellular) memory of gene expression states were necessary for predicting the overall fitness of cell populations in specific antibiotic- and inducer-containing environments. We validated these predictions experimentally and identified environmental conditions that determined a "sweet spot" of drug resistance.

[1] This research was supported by the NIH Director's New Innovator Award Program [1DP2 OD006481-01].