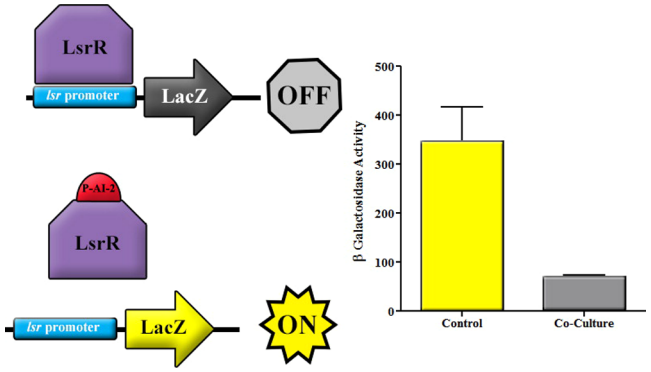
ACS SyntheticBiology

In This Issue

pubs.acs.org/synthbio

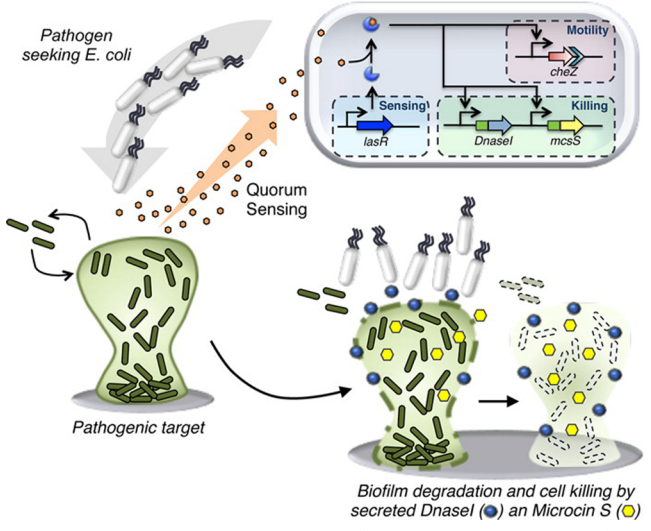
AN EVOLVED QUORUM SENSING REGULATOR FOR ALTERED SWITCHING FUNCTIONS



There are a limited number of transcriptional regulators available for use in the synthetic biology toolbox. Here, Adams *et al.* (DOI: 10.1021/sb400068z) expand this toolkit by developing the first ever, AI-2 controlled, synthetic switches capable of being tuned simultaneously in two distinct cell populations.

The authors used directed evolution to modify the *E. coli* quorum sensing transcriptional regulator, LsrR, in order to obtain variants with unique functions. They also used protein modeling of the different LsrRs to examine structural differences between the native repressor protein and the mutants and performed AI-2 docking studies to gain insight into the QS-signal binding. These quorum sensing-mediated switches allow for the creation of new synthetic networks capable of such complex functions and are necessary for the development of advanced synthetic products.

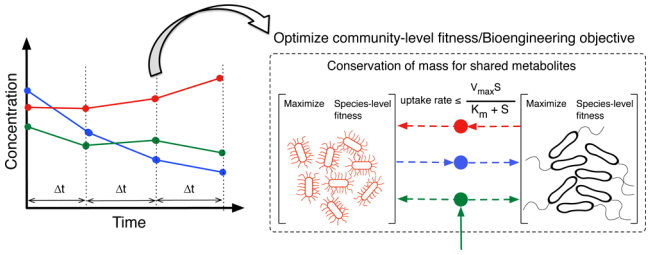
REPROGRAMMING MICROBES TO SEEK AND DESTROY PATHOGENS



Given the increasing development of antibiotic resistance and the persistence of chronic infections, novel therapeutic strategies are in demand. Here, Hwang *et al.* (DOI: 10.1021/sb400077j) provide an innovative example of localized pathogen destruction, for effective therapeutic treatment, mediated by directed cell migration.

Using a 2-fold antimicrobial strategy, the authors engineered *E. coli* to specifically recognize, migrate toward, and eradicate both dispersed and biofilm-encased pathogenic *Pseudomonas aeruginosa* cells. This novel antimicrobial strategy can be applied to tackling other infectious pathogens as well.

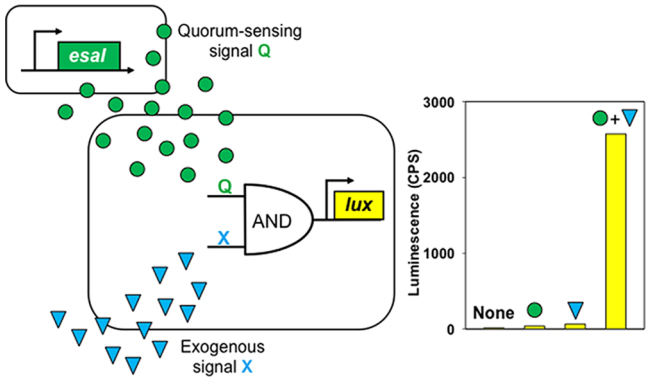
DYNAMIC MULTILEVEL, MULTIOBJECTIVE METABOLIC MODELING OF MICROBIAL COMMUNITIES



Microbial communities are involved in a variety of biological and biotechnological processes. They play fundamental roles in human health and disease as well as in the production of biofuels. However, changes in environmental conditions result in changes in these microbial communities, usually in their structure and function. Here, Zomorrodi, Islam, and Maranas (DOI: 10.1021/sb4001307) introduce a novel computational framework for the dynamic analysis of microbial communities using genome-scale metabolic models.

The authors describe d-OptCom, the first multilevel and multiobjective modeling suite for the dynamic modeling of microbial communities. d-OptCom enables the capture of temporal variations in interspecies metabolic interactions and community- and species-level fitness driving forces in response to variations/perturbations in environmental conditions, all in a unified framework.

CONTROL OF GENE EXPRESSION BY QUORUM SENSING-MODULATED AND-GATE PROMOTERS



Certain microbial communities use quorum sensing to regulate gene expression. In this paper, Shong and Collins

Special Issue: Cell-Cell Communication

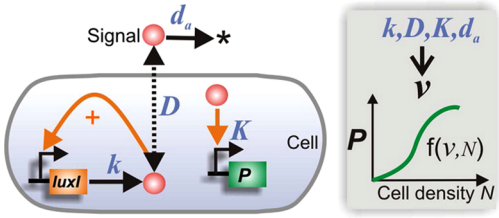
Received: March 26, 2014
Published: April 18, 2014

   dx.doi.org/10.1021/sb5002246 | *ACS Synth. Biol.* 2014, 3, 199–200

(DOI: 10.1021/sb4000965) describe the generation and characterization of a new set of two input AND-gate promoters that are regulated by the quorum-sensing regulator EsaR and either LacI or TetR.

The promoters described in this work demonstrate that EsaR and its target DNA sequence can be used to engineer new quorum sensing-dependent promoters. The AND-gate promoters described here may serve as a template for new regulatory systems that integrate quorum sensing and the presence of key metabolites or other environmental cues to enable dynamic changes in gene expression for metabolic engineering applications. Finally, such tools may broadly enable the development of novel density-dependent and/or multicellular systems for applications in synthetic biology.

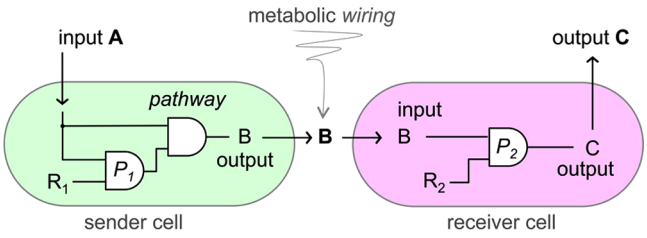
A GENERIC METRIC TO QUANTIFY QUORUM SENSING ACTIVATION DYNAMICS



Quorum sensing is a cell−cell communication mechanism that enables bacteria to sense and respond to changes in their population density using small signaling molecules. While most bacteria carry at least one quorum sensing system, these systems display a tremendous degree of variety in their signaling molecules, regulatory components, network architectures, and the target genes they control. In order to quantify density-dependent control characteristics of different quorum sensing systems or to make comparisons between their activation properties, Pai *et al.* (DOI: 10.1021/sb400069w) describe the development of a generic, quantitative metric for quorum sensing.

The authors show that this metric can reliably capture the dynamics of activation, irrespective of the specific parameters or architecture of the quorum sensing system and experimentally demonstrate how quorum sensing-mediated activation can be predictably modulated. The methodology described here could serve as a general way to quantify and choose quorum sensing systems for building engineered gene circuits of desired regulation characteristics.

ENGINEERING MULTICELLULAR LOGIC IN BACTERIA WITH METABOLIC WIRES



One of the challenges of synthetic biology is the engineering of complex synthetic circuits for biotechnological applications. The challenge arises from technical difficulties in the interconnection of different logic gates in an organism and the lack of different regulatory parts to assemble the system. Here, Silva-Rocha and de Lorenzo (DOI: 10.1021/sb400064y) report the engineering of a simple cell-to-cell communication device in *Pseudomonas putida* using pathways for toluene and benzoate degradation.

Unlike previous wiring approaches based on quorum-sensing molecules, the authors demonstrate the engineering of multicellular logic circuits using metabolites.

dx.doi.org/10.1021/sb5002246 | *ACS Synth. Biol.* 2014, 3, 199−200