ACS SyntheticBiology

In This Issue

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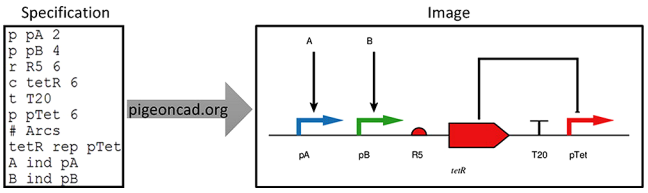
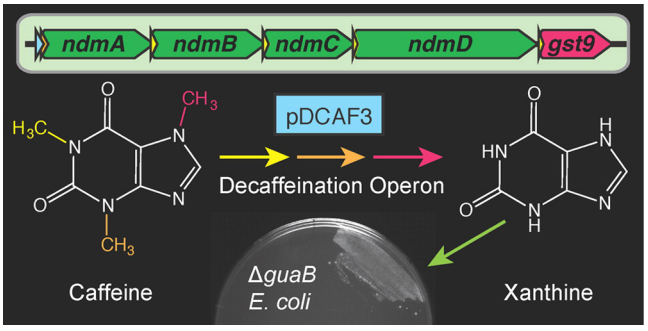
PIGEON: A DESIGN VISUALIZER



In this Technical Note, Bhatia and Densmore (DOI: 10.1021/sb400024s) describe the development of *Pigeon*, a new WWW software tool that accepts a textual description of a synthetic biology design and translates it into an image. It is easy to learn and has been used to quickly prototype genetic designs and share them with colleagues. *Pigeon* can also be connected to other software tools for visualizing their output.

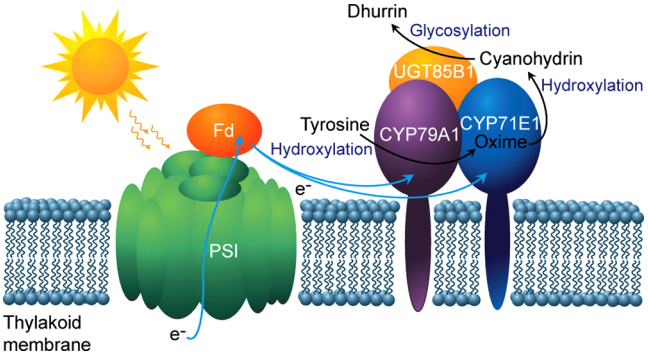
"ADDICTED" BACTERIA FOR DECAFFEINATION AND CAFFEINE MEASUREMENT



The abundance of caffeine in common beverages such as tea, coffee and energy drinks, in addition to its use in pharmaceuticals has led to significant environmental pollution. Byproducts of coffee bean processing and brewing are unsuitable for agricultural or biofuel feedstock due to the high caffeine content. Thus, a method to decaffeinate these waste products is extremely valuable. Here, Quandt et al. (DOI: 10.1021/sb4000146) describe the genetic refactoring of a decaffeination operon from an environmental isolate, *Pseudomonas putida* CBB5, so that the pathway functions in *E. coli*.

The authors describe how an "addicted" auxotrophic strain of *E. coli* was used to test several iterations of the operon and also how the resulting strain could be used to quantitatively measure the caffeine content of common energy drinks, thus functioning as a biosensor.

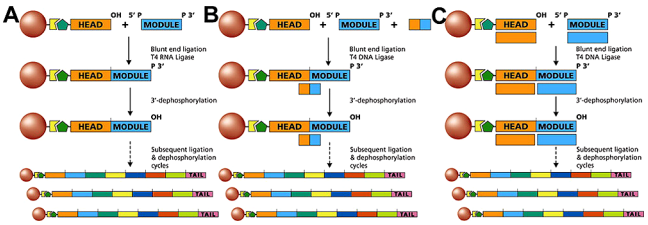
REDIRECTING PHOTOSYNTHESIS FOR NATURAL PRODUCT SYNTHESIS



Plants are unique in their ability to produce highly specialized bioactive natural products. However, these products are often too complex for chemists to synthesize de novo and difficult to isolate. They are usually produced in very small amounts along with a mixture of related, but undesirable, side products. Now, Nielsen et al. (DOI: 10.1021/sb300128r) demonstrate, for the first time, the exclusively light-driven biosynthesis of bioactive natural products.

The authors describe a synthetic biology approach to relocate an entire P450-dependent pathway to the chloroplast. This allowed them to directly tap into the reducing power of photosynthesis for the production of pharmaceutically relevant natural products using water as the primary electron donor.

A SOLID-PHASE PLATFORM FOR MULTIPART GENE ASSEMBLY



With an increase in the number of standardized genetic modules in the synthetic biology toolbox, there is a need for assembly protocols that are universal and easily automatable. While numerous methods have been developed, drawbacks such as the appearance of scar sequences still exist. Now, de Raad et al. (DOI: 10.1021/sb300122q) describe a method for the scarless ligation of multipart gene segments in a sequence-independent manner.

The authors based their method on the ligation of single- or double-stranded oligodeoxynucleotides and PCR products immobilized on a solid support. They tested various settings and also demonstrated proof of concept using a small library of four BioBrick modules.

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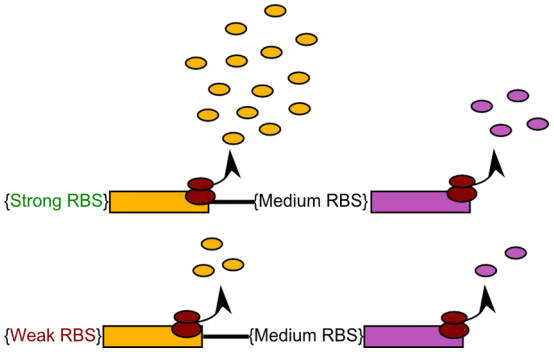
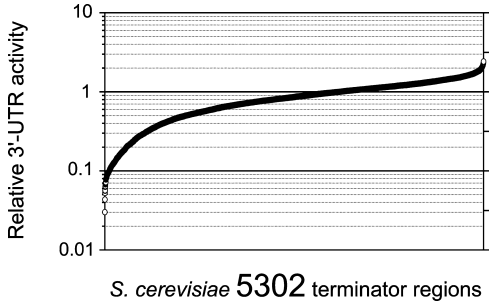
QUANTIFYING TRANSLATIONAL COUPLING IN *E. COLI*



The functionality of natural and synthetic biological circuits depends critically on tuning the expression of multiple genes. In bacteria, the final expression levels of proteins are dependent on post-transcriptional and translational effects, processes that remain poorly understood. Translational coupling, which is the interdependence of translation efficiency of neighboring genes encoded within a bacterial operon, is one such process. Here, Levin-Karp et al. (DOI: 10.1021/sb400002n) systematically quantify and characterize translational coupling in an *E. coli* synthetic operon using a library of plasmids carrying fluorescent reporter genes.

This study is a step toward the understanding of mechanisms involved in the modulation of translational expression and is useful for the accurate manipulation of gene expression in synthetic biology.

A "TERMINATOME" TOOLBOX



Terminators contain functional regions in the 3′-UTR that influence mRNA stability, thus modulating the rate of the protein synthesis. However, their utilization in genetic and metabolic engineering has been limited. Here, Yamanishi et al. (DOI: 10.1021/sb300116y) comprehensively evaluated the activity of 5302 terminators from a total of 5880 genes in *S. cerevisiae*, providing a new perspective on the role of the "terminatome" (or genome-wide set of terminators) in eukaryotes.

To evaluate terminator activity, the authors inserted each terminator region downstream of the P_{TDH3}- green fluorescent protein (GFP) reporter gene and measured the fluorescent intensity of GFP. The "terminatome" described here provides both important information regarding the modulatory roles of terminator regions as well as a useful toolbox for the development of metabolically and genetically engineered yeast.

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