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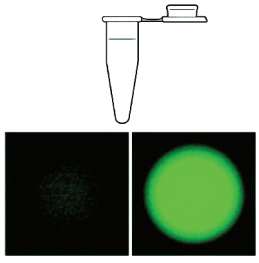
COMPUTER-AIDED DNA-ASSEMBLY DESIGN

The construction of the first synthetic microbial genome and the first synthetic eukaryotic chromosome were aided by the use of scar-less, multipart DNA-assembly techniques. Although these techniques are highly effective and of vital importance to synthetic biology projects, they are also error-prone, time-consuming, and labor-intensive. Hillson *et al.* (DOI: 10.1021/sb2000116) now describe the development and experimental validation of a web-based tool, j5, which automates the design process of DNA assembly.

For combinatorial DNA libraries of approximately 200 plasmids, the authors demonstrate that 10−20 times the cost associated with traditional approaches is saved through the use of a computer-aided approach. In addition, there are 3- to 10-fold savings in time. The computer aided design approach described here will be useful to researchers because it will result in a reduction of effort, time, and cost associated with DNA synthesis projects, as well as minimize frequency of errors, with a ultimate goal of allowing construction of synthetic genomes at unprecedented scales.

A NEW TOOLBOX FOR CELL-FREE SYNTHETIC BIOLOGY

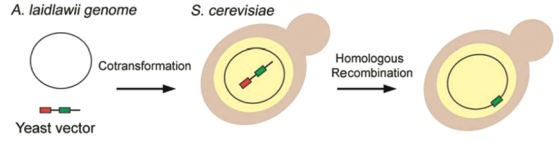
A central goal in synthetic biology is the quantitative analysis of molecular circuits in cell-free systems. To date, substantial progress has been made in the development of DNA and RNA circuits, which have successfully been used in interrogating the chemistry of certain biological processes. However, the lack of an extensive repertoire of effective cell-free transcription-translation systems has imposed limitations on the creation of synthetic creating gene circuits.



Now, Shin and Noireaux describe a molecular toolbox (DOI: 10.1021/sb200016s) that consists of major components of the transcription machinery of *Escherichia coli*. The authors also characterize synthetic gene circuits constructed using the cell-free transcription-translation toolbox.

BACTERIAL GENOMES AS YEAST CENTROMERIC PLASMIDS

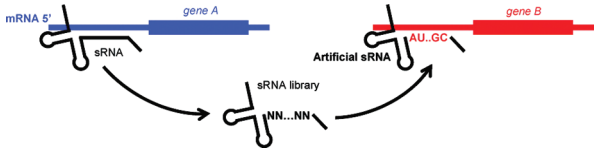
Cloning whole bacterial genomes in yeast is a key process that allows the replacement of a natural genome with a synthetic one. In *Mycoplasma mycoides*, which employs a nonstandard genetic code, the UGA codon encodes for the amino acid tryptophan instead of a translation stop signal. Karas *et al.* (DOI: 10.1021/sb200013j) demonstrate that it is possible to clone whole bacterial genomes, which utilize the standard genetic code, into yeast.



The authors cloned the whole bacterial genome of *Acholeplasma laidlawii* (with the exception of one toxic gene). The authors outline lessons learned during the process which will benefit other research groups attempting to clone whole or partial bacterial genomes in yeast.

ARTIFICIAL SMALL RNAS FOR CONDITIONAL GENE SILENCING

Post-transcriptional regulation of gene expression is modulated in many different species of bacteria through noncoding small RNAs that hybridize with mRNAs at the 5′ leader sequence. Small RNAs are often involved in the modulation of important physiological processes in bacteria, such as stress response and virulence. Taking a cue from natural small RNA riboregulators, Sharma, Yamamura, and Yokobayashi (DOI: 10.1021/sb200001q) now describe an efficient strategy for engineering artificial small RNA molecules that can modulate the expression of endogenous genes.



By exploiting natural small RNA scaffolds and high-throughput screening technology, the authors discovered artificial small RNAs that target specific genes in *Escherichia coli*. An artificial RNA molecule that was designed to target a component of bacterial flagella was able to render the cells immotile. Artificial small RNA molecules may prove to be useful as biological tools to study physiological processes, as well as in the creation of designer strains with biotechnological applications.

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