High-throughput evaluation of synthetic metabolic pathways

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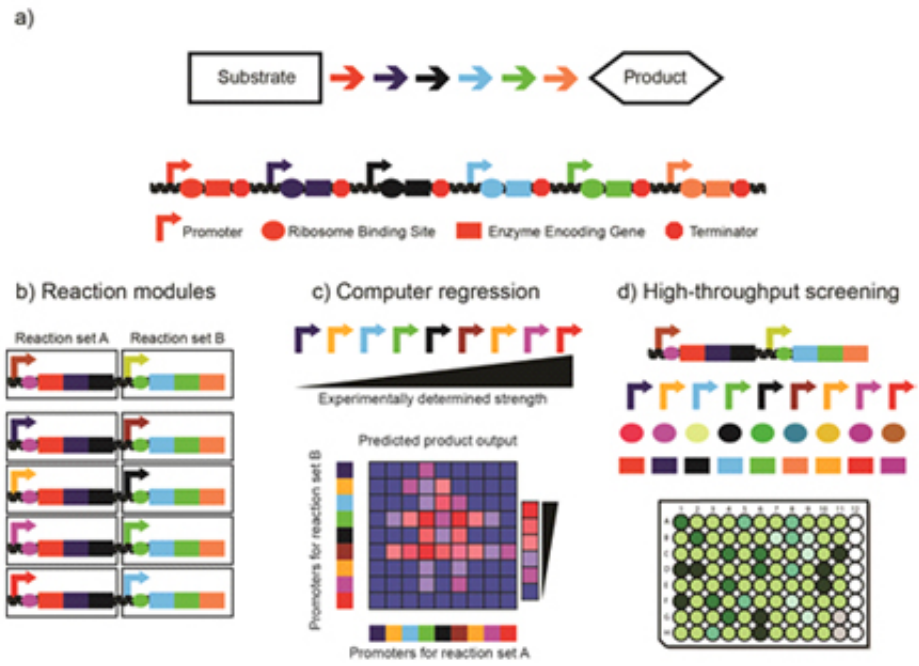

Three different strategies are reviewed for evaluation of synthetic metabolic pathways.

A central challenge in the field of metabolic engineering is the efficient identification of a metabolic pathway genotype that maximizes specific productivity over a robust range of process conditions. A review from researchers at Michigan State University in East Lansing, MI covers the challenges of optimizing specific productivity of metabolic pathways in cells and new advances in pathway creation and screening.

Current methods for optimizing specific productivity of metabolic pathways in living cells are reviewed. New tools for library generation, computational analysis of pathway sequence-flux space, and high-throughput screening and selection techniques are discussed. Current work on population-based measurements is reviewed and the current outlook for the field is presented. The review appears in *Technology* online ready.

"One major limitation of high-throughput screening is the inability to map a DNA sequence to the output phenotype in a high-throughput manner, as typically only a few winners of the selection are sequenced. This limits transferability of the winning genotype to alternate hosts as the winning genotype is typically strongly dependent on the particular screening conditions. Secondly this is difficult to do with pathways of moderate-length with standard Sanger sequencing methods. Work performed by many groups including ours have used advances in deep sequencing technologies to track tens of thousands of pathway variants in high-through screens enabling us to see hundreds of potential winners," says Justin Klesmith, the lead author on this review.

More information: Justin R. Klesmith et al. High-throughput evaluation of synthetic metabolic pathways, *TECHNOLOGY* (2015). DOI: 10.1142/S233954781640001X

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