Characterizing Strain Variation in Engineered E. coli Using a Multi-Omics-Based Workflow - DTU Orbit (09/11/2017)

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Understanding the complex interactions that occur between heterologous and native biochemical pathways represents a major challenge in metabolic engineering and synthetic biology. We present a workflow that integrates metabolomics, proteomics, and genome-scale models of *Escherichia coli* metabolism to study the effects of introducing a heterologous pathway into a microbial host. This workflow incorporates complementary approaches from computational systems biology, metabolic engineering, and synthetic biology; provides molecular insight into how the host organism microenvironment changes due to pathway engineering; and demonstrates how biological mechanisms underlying strain variation can be exploited as an engineering strategy to increase product yield. As a proof of concept, we present the analysis of eight engineered strains producing three biofuels: isopentenol, limonene, and bisabolene. Application of this workflow identified the roles of candidate genes, pathways, and biochemical reactions in observed experimental phenomena and facilitated the construction of a mutant strain with improved productivity. The contributed workflow is available as an open-source tool in the form of iPython notebooks.

General information

Publication information