Changes in microbial metabolism upon introduction of heterologous reactions

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It has become a common practice to introduce heterologous genes into a microbial host in order to produce a variety of chemicals in metabolic engineering. However, effects of introducing heterologous reactions on microbial metabolism have not been studied sufficiently, especially when compared with gene knockouts and environmental perturbations. To this end, we study the effects of heterologous reactions on microbial metabolism using genome-scale metabolic simulations. As representative examples, *Escherichia coli* strains engineered to produce 1,4-butanediol, 1,3-propanediol, and amorphadiene are considered. The predicted changes in microbial metabolism upon introduction of heterologous biosynthetic pathways appear to be strain-specific, which contrasts with wild-type and single gene knockout mutants whose metabolic status can be overall generalized. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries from the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF) of Korea (NRF-2012M1A2A2026566).]