

Employing Bacterial Microcompartments To Create Privileged Redox Pools

for Biofuel Production

Sasha Shirman,¹ Taylor Dickman,¹ Svetlana Ikonomova,¹ Keith Tyo,¹ Niall Mangan,¹ and **Danielle Tullman-Ercek**^{1*} (ercek@northwestern.edu)

¹Northwestern University, Evanston, Illinois

Project Goals: To compartmentalize metabolic pathways along with enzyme cofactor recycling pathways to increase the yield and efficiency of bioproduction processes

<https://dtelab.northwestern.edu/research/#nanobioreactors>

Metabolic engineering holds great promise for creating efficient, competitive routes for the production of biofuels and biochemicals without the necessity for harsh chemicals and hazardous byproducts. Successes in biochemical production include the production of Dupont's Sorona fibers from 1,3-propanediol from glucose using bacteria and the manufacture of the anti-malarial drug artemisinin from yeast. However, roadblocks to biosynthesis prevent many biochemicals from being produced biologically given current technology. Nature uses compartmentalization (eg in organelles in eukaryotes and in bacterial microcompartments in prokaryotes) to solve issues such as intermediate leakage, toxicity, and byproduct formation. Here we propose to deploy compartmentalization as a strategy to overcome a critical roadblock: the requirement for redox cofactor recycling. In traditional systems, redox cofactors are lost to cellular growth and maintenance needs. By compartmentalizing redox cofactors with the biochemical synthesis enzymes, we anticipate increasing the thermodynamic efficiency and preventing the loss of valuable intermediates and cofactors. If successful, it would be the first direct demonstration of this feature of a bacterial microcompartment, and would provide a tool for improving metabolic pathway performance for all enzymes with redox or other cofactors.

With this poster, we will describe how we are coupling modeling with experiments to improve the performance of our first target metabolic pathway: 1,3-propanediol production. We will also show how modeling is leading to new insight into the native function of these structures.

This material is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research, Genomic Science Program under Award Number DE-SC0019337.