

Modular engineering of biomass degradation pathways

Background

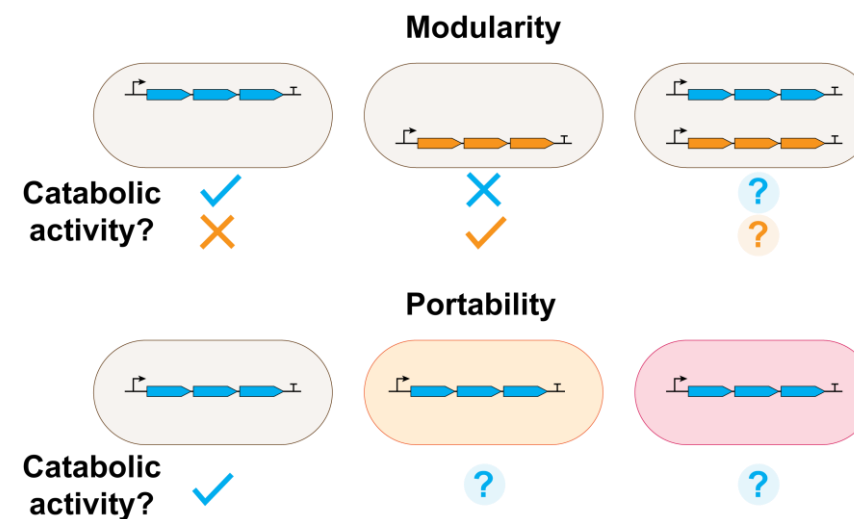
- Engineering bacteria to efficiently degrade biomass will require combining multiple heterologous assimilatory pathways (e.g., for hemicellulose-derived xylose/arabinose/galactose or a broad array of lignin-derived monomers and dimers)
- Pathways (or single genes) are usually built and tested in isolation, yet intended to be used in combination
- Similarly, pathways are usually tested in a single bacterial strain, yet might be useful in diverse engineered organisms

Conclusions

- At a minimum, consistently measuring pathway modularity and portability would allow rational pathway selection for compatibility with the host(s) and other engineered pathways
- Additional research into the fundamental causes of incompatibilities would aid in developing new generalizable design strategies to improve modularity and portability
- Existing biodesign strategies to minimize incompatibilities have not yet been tested consistently across pathways and organisms

Significance

- The Bioenergy Research Centers are engineering a broad range of assimilatory pathways into a diverse array of host microbes. The ability to rapidly and predictably combine pathways in different microbes would facilitate inter-BRC exchange and accelerate progress towards viable biomass conversion



Engineered metabolic pathways are rarely modular or portable by default. A modular pathway would function efficiently both in isolation and in combination; a portable pathway would function reliably in multiple host strains. These characteristics are rarely assessed, much less optimized.