

Thursday, September 27, 2018

3:00-3:30 p.m.

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Development of synthetic biology toolkits for non-model microbes

Engineering microorganisms for the production of desired chemicals at industrially relevant scales, rates, and titers often requires a combination of adaptive evolution and rational design methods to screen or select for mutants with optimized phenotypes. While useful, these methods are often limited by the ability to introduce non-biased, synthetically designed, and trackable mutations in multiplex and to identify clear gene-to-trait relationships. In model microbes such as *E. coli* or *S. cerevisiae*, there is an expanding range of cutting edge tools for the introduction of these targeted mutations and rapid genotype-to-phenotype identification. Unfortunately, the adaptation of these methods for use in non-model systems with complex phenotypes that are not easily tractable (e.g. photosynthesis, CO metabolism, biomass degradation, etc.) is still lacking due to limited basic genetic tools. I will discuss current progress for the development of expanded genome engineering tools in a variety of non-model, industrially relevant microbes to enable more robust gene editing and accelerated gene-to-trait identification for the production of a variety of fuels and chemicals from a broad range of feedstocks.