Accelerating Microbial Engineering towards a Sustainable Bioeconomy
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The engineering of biological systems towards a sustainable bioeconomy requires a clear understanding of genetic function across scales. However, even in the most studied organisms, we still do not know the function of all genes in their genomes and how they are differentially regulated. Traditional functional genomics techniques to identify these genotype-phenotype linkages include a combination of adaptive evolution and rational design methods to screen or select for mutants with target phenotypes. While useful, these methods are limited by the ability to introduce synthetically designed, non-biased, trackable mutations to clearly link gene-to-trait. We have progressed towards the development of methods that allow rapid identification of these genotype-to-phenotype relationships under selective conditions such as growth, production of desired compounds, and tolerance in both model and non-model microbes. Here, I will discuss current efforts towards the development of a pipeline for the development of efficient genetic systems and tools (including CRISPR) in non-model microorganisms to enable accelerated, high throughput, genome scale gene-to-trait identification towards improving our understanding of these microbial systems, providing a platform for identifying variants for validation and engineering strategies as well as vast datasets for use in Machine Learning towards better predictive models.