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**Combining Genome-Scale Experimental and Computational Methods to Identify Essential Genes in Bacteria**

Tn-seq analysis software (TSAS) is a powerful tool for identifying essential genes and refining genome-scale metabolic models.

**The Science**

We used transposon sequencing (Tn-seq) to identify essential genes in the bacterium *Rhodobacter sphaeroides* under several growth conditions. We then used that data to evaluate and refine an existing genome-scale metabolic model, providing more precise systems-level understanding of the diverse metabolic lifestyles of this bacterium.

**The Impact**

Metabolic engineering of microbes for biofuel synthesis can be greatly aided by genome-scale models of cellular metabolism. TSAS is a new software tool that uses Tn-seq data to predict essential genes. The integration of this data into computational models allows more precise predictions of the impacts of biofuel synthesis on microbial physiology.

**Summary**

*Rhodobacter sphaeroides* is a bacterium with a high degree of metabolic flexibility that allows it to thrive in diverse environments. To gain a better systems-level understanding of this organism, we generated a large transposon mutant library and used transposon sequencing (Tn-seq) to identify genes that are essential under several growth conditions. Using newly developed Tn-seq analysis software (TSAS), we identified 493 genes as essential for aerobic growth on a rich medium. We then used the mutant library to identify conditionally essential genes under two laboratory growth conditions, identifying 85 additional genes required for aerobic growth in a minimal medium and 31 additional genes required for photosynthetic growth. In all instances, our analyses confirmed essentiality for many known genes and identified genes not previously considered to be essential. We used the resulting Tn-seq data to refine and improve a genome-scale metabolic network model (GEM) for *R. sphaeroides*. Together, we demonstrate how genetic, genomic, and computational approaches can be combined to obtain a systems-level understanding of the genetic framework underlying metabolic diversity in bacterial species. Moreover, detailed understanding of the underpinnings of *R. sphaeroides* metabolic flexibility can provide insight into how it and other alphaproteobacteria may be rationally engineered for biofuel production.

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**Publications**

Burger, B.T. et al, “Combining genome-scale experimental and computational methods to identify essential genes in *Rhodobacter sphaeroides*”, *mSystems* (2017), DOI:10.1128/mSystems.00015-17.

**Related Links**

**PM Recommendation for SC Web Publication**