11 November 2020

**Uncovering new features of bacterial control elements**

Collaboration could expand the industrial use of microbial chassis

**The Science**

Our society relies on a wide variety of chemicals with many uses and properties. Many chemicals and fuels that are currently made from oil could instead be made from plant material by microorganisms. The most promising microbes for this purpose have broad appetites and biosynthetic potential but have not been widely studied in research labs. In three recent studies, scientists report crucial information on how to control genes in unique and promising biosynthetic microbes—*Rhodobacter sphaeroides, Zymomonas mobilis,* and *Novosphingobium aromaticivorans*.

**The Impact**

A viable biofuels and bioproducts industry relies on large-scale, efficient production. Scientists can use genetic engineering to boost a microbe’s ability to make chemicals quickly and efficiently, but only if they understand the bacteria’s genes and the circuitry to control them. These papers report vital information that will enable genetic engineering in *Z. mobilis*, *R. sphaeroides*, and *N. aromaticivorans*. This is a crucial step for optimizing these bacteria for the bio-based production of fuels and chemicals.

**Summary**

There is a need for microbes that can transform abundant renewable materials into a wide variety of fuels and chemicals that are currently made from petroleum. Different microbes are likely needed to produce the suite of needed chemicals from a diverse array of renewable raw materials. There is significant industrial interest in a class of bacteria called Alphaproteobacteria for this purpose. They can break down a wide array of compounds and can potentially make fuels, chemicals, and materials from renewable resources. Efforts to optimize chemical production in these bacteria are impeded by a lack of knowledge about how to predictably and quantitatively control these poorly studied metabolic activities.

In a set of recent collaborative papers, researchers from the Great Lakes Bioenergy Research Center and the University of Wisconsin–Madison Departments of Bacteriology and Biochemistry report new information on the gene promoters in several alphaproteobacteria that are used or being developed for use by industry. Promoters are regions of DNA that direct proteins to start transcribing a gene into enzymes. The research teams combined genomic, genetic, and biochemical studies to demonstrate previously unknown differences between promoters of these alphaproteobacteria and those often used by industry. The newly discovered information presented in this work supplies crucial knowledge for engineering these bacteria to either produce new products or increase their yield in both laboratory and industrial settings. This information is vital as researchers develop species like *Z. mobilis, R. sphaeroides, and N. aromaticivorans* to produce fuels and chemicals from abundant renewable materials.

**Contacts**

**Program Manager**

N. Kent Peters
Program Manager, Office of Biological and Environmental Research
kent.peters@science.doe.gov, 301-903-5549

**Corresponding Authors**

Robert Landick
University of Wisconsin–Madison
landick@bact.wisc.edu

Timothy Donohue

University of Wisconsin-Madison

tdonohue@bact.wisc.edu

Richard L. Gourse
University of Wisconsin–Madison
rgourse@bact.wisc.edu

**Funding**

This research was supported by the Great Lakes Bioenergy Research Center, U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research (DE-SC0018409); the National Institutes of Health (NIH R01 GM37048 and T32GM007215); and the Jack Kent Cooke Foundation.

**Publications**

Vera, J.M., Ghosh, I.N., Zhang, Y., Hebert, A.S., Coon, J.J., Landick, R., “[Genome-Scale Transcription-Translation Mapping Reveals Features of *Zymomonas mobilis* Transcription Units and Promoters](https://www.osti.gov/pages/biblio/1639129-genome-scale-transcription-translation-mapping-reveals-features-zymomonas-mobilis-transcription-units-promoters),” *mSystems* **5**:e00250-20 (2020). [DOI: [10.1128/mSystems.00250-20](https://doi.org/10.1128/mSystems.00250-20)]

Myers, K.S., Vera, J.M., Lemmer, K.C., Linz, A.M., Landick, R., Noguera, D.R., Donohue, T.J., “[Genome-Wide Identification of Transcription Start Sites in Two *Alphaproteobacteria*, *Rhodobacter sphaeroides* 2.4.1 and *Novosphingobium aromaticivorans* DSM 12444](https://www.osti.gov/pages/biblio/1657307-genome-wide-identification-transcription-start-sites-two-alphaproteobacteria-rhodobacter-sphaeroides-novosphingobium-aromaticivorans-dsm),” *Microbiology Resource Announcements* **9** (36) e00880-20 (2020) [DOI: [10.1128/MRA.00880-20](https://doi.org/10.1128/MRA.00880-20)]

Henry, K.K., Ross, W., Myers, K.S., Lemmer, K.C., Vera, J.M., Landick. R., Donohue, T.J., Gourse, R.L., “A majority of *Rhodobacter sphaeroides* promoters lack a crucial RNA polymerase recognition feature, enabling coordinated transcription activation,” *Proceedings of the National Academy of Sciences* (2020) [DOI: [10.1073/pnas.2010087117](https://doi.org/10.1073/pnas.2010087117)]

**Related Links**

<https://www.glbrc.org/research/highlights/uncovering-new-features-of-bacterial-control-elements>