Biological Sciences Division
Research Highlights

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Just How Fast Can Bacteria Grow? It Depends.
Proteomics Data Validate Model of Bacterial Growth

Results: Proteomic research at Pacific Northwest National Laboratory is helping validate a bacterial metabolic model and is providing insights into the key proteins and metabolic pathways essential for encouraging and discouraging bacterial growth in a changing environment.

Why it matters: Bacteria are among the fastest reproducing organisms in the world, doubling every 4 to 20 minutes. Some fast-growing bacteria such as pathogenic strains of *E. coli* can sicken and kill us; other bacteria in a subsurface environment can be used to immobilize chemical contaminants, preventing their movement through groundwater and any associated negative ecosystem impacts. But whether bacteria are harmful or helpful, scientists need to be able to reliably predict how they will reproduce and grow in a particular environment.

Proteomics data from PNNL allowed scientists to map the abundance of 900 proteins identified in wild-type *E. coli* compared with *E. coli* that had been adapted for growth on either lactate or glycerol media. Enlarge Image
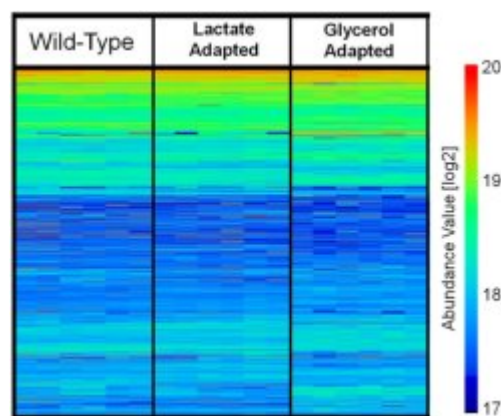
Internationally renowned researcher Bernhard Palsson and other researchers from the University of California San Diego led a team of scientists from PNNL, the University of Heidelberg, and the German Cancer Research Center to study how *E. coli* bacteria changed and evolved from one environment to another in a laboratory setting. The team then compared proteomics, genomic, and metabolic data from the study with a computational model for bacterial growth.

Methods: One of the key pieces of information was data generated using the unique high-throughput proteomics capability at EMSL, a Department of Energy scientific user facility located at PNNL. Using high-performance liquid chromatography coupled to mass spectrometry, the team gathered data on how the bacteria changed their protein profile as they grew and reproduced in different mediums. The scientists found that the data and model were correlated to a surprising degree (more than 98% in some cases), validating the model's ability to predict the growth of *E. coli* bacteria under specific conditions.

Being able to model the growth of *E. coli* will help scientists begin to develop reliable metabolic models for other more complex organisms. This work will also provide key insights into the best ways of integrating different complex datasets to more accurately predict how organisms respond to their environments at the molecular level.

What's next: Development of biological models will help scientists understand how organisms change their genetic make-up and gene and protein expression so that engineers can use better use biological organisms to improve our environment and health.

Science Foundation and National Institutes of Health. The PNNL team included Kim Hixson, Ashoka Polpitiya, Josh Adkins, Sam Purvine, Daniel Lopez-Ferrer, and Dick Smith.