PROTEOMICS

The condition-dependent proteome

Absolute levels of the *Escherichia coli* proteome measured under 22 different conditions represent a valuable resource.

Whereas the genome exists as a finite entity, the proteome of an organism is a nebulous thing. Even in a creature as tiny as *E. coli*, the proteome is always changing. Using mass spectrometry to take a snapshot of a proteome tells one only what is happening at that moment, under those experimental conditions.

This is why a recent effort to quantitatively profile the proteome of *E. coli* under 22 different experimental conditions represents an intriguing and important resource. In this work, a team of researchers led by Matthias Heinemann of the University of Groningen and Alexander Schmidt of the University of Basel developed a streamlined mass spectrometry–based proteomics platform that allowed them to amass a very large data set efficiently without compromising protein coverage.

The researchers varied the experimental conditions, including growing cells on minimal media while varying the energy source, providing limited glucose while varying the growth rate, providing excessive glucose while subjecting cells to different stresses, and growing cells on complex media. They also profiled the proteome on different days from the start of stationary phase. They developed optimized approaches for extracting membrane and ribosomal proteins, and they minimized sample prefractionation as much as possible for analysis by liquid chromatography coupled to high-resolution mass spectrometry. To determine absolute concentrations, they measured levels of 41 selected proteins with high accuracy and then used that information to calibrate the quantities of all identified proteins.

In total, the team measured the absolute amounts of 2,359 proteins, or about 55% of the predicted *E. coli* proteome, across all 22 conditions. They performed a number of analyses, which included profiling 11 different post-translational modifications, looking at how levels of certain classes of protein change with the growth rate, evaluating the role of transcriptional regulation in allowing the cell to adapt to new conditions, and understanding how proteins are distributed among cellular compartments, in particular the periplasm and cytoplasm, under differing conditions.

All of the data are available via ProteomeXchange and should be of value to systems biologists and *E. coli* researchers alike.

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RESEARCH PAPERS

Schmidt, A. *et al.* The quantitative and condition-dependent *Escherichia coli* proteome. *Nat. Biotechnol.* doi:10.1038/nbt.3418 (7 December 2015).