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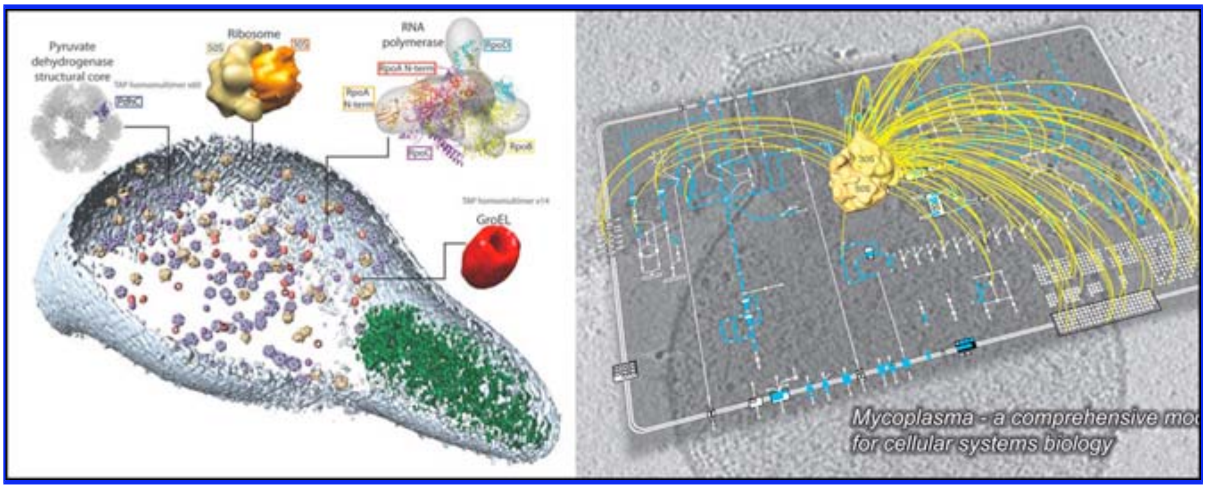
There’s No Such Thing as a ‘Simple’ Organism

By Brandon Keim November 30, 2009 | 5:15 pm | Categories: Biology, Genetics



What may be the most thorough study ever of a single organism has produced a beta code for life’s essential subroutines, and shown that even the simplest creatures are more complex than scientists suspected.

The analysis combined information about gene regulation, protein production and cell structure in *Mycoplasma pneumoniae*, one of the simplest self-sustaining microbes.

It’s far closer to a “blueprint” than a mere genome readout, and reveals processes “that are much more subtle and intricate than were previously considered possible in bacteria,” wrote University of Arizona biologists Howard Ochman and Rahul Raghavan in a commentary accompanying the findings, which were published last Thursday in *Science*.

M. pneumoniae has just one-fifth as many genes as *E. coli*, the traditional single-cell model organism. That makes it an ideal target for systems biologists who want to understand how cells function. To them, genome scans are just a first step. They don’t explain when or why genes are turned on and off, or how different genes interact at different times, or how cellular “machines” use proteins produced by gene instructions.

In the new studies, German and Spanish researchers documented almost every single protein used by *M. pneumoniae*. They looked up the known functions of each of its genes, and made recordings of gene activity. They documented all the chemical reactions inside *M. pneumoniae* and mapped its physical structure. Then they put all this together.

What emerged was a picture of surprising complexity. *M. pneumoniae* needs just eight gene “switches” to control its molecular activities, compared to 50 in *E. coli* — a number so low that it implies other, as-yet-unknown regulatory processes. Groups of genes thought to work in unison did so only intermittently. At other times they worked in isolation, or in unexpected configurations.

The findings also showed that chromosome topography — the actual, three-dimensional arrangement of an operating genome, rather than its linear laboratory readout — plays an important part in determining how genes interact.

In short, there was a lot going on in lowly, supposedly simple *M. pneumoniae*, and much of it is beyond the grasp of what’s now known about cell function.

Eventually, the thorough analytical approach used to study *M. pneumoniae* could be applied to other microbes. The findings could also be used by synthetic biologists trying to synthesize microbial life. But for now, they show just how much work remains to be done before life’s essential processes are understood.

“Linear mapping of genes to function rarely considers how a cell actually accomplishes the processes,” wrote Ochman and Raghavan. “There is no such thing as a ’simple’ bacterium.”

Image: From Science*, a 3-D reconstruction (left) of the* M. pneumoniae *cell; a map (right) of interactions between the amino-acid–making ribosome and the cell’s proteins.*

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Citations: “Proteome Organization in a Genome-Reduced Bacterium.” By Sebastian Kühner, Veravan Noort, Matthew J. Betts, Alejandra Leo-Macias, Claire Batisse, Michaela Rode, Takuji Yamada, Tobias Maier, Samuel Bader, Pedro Beltran-Alvarez, Daniel Castaño-Diez, Wei-Hua Chen, Damien Devos, Marc Güell, Tomas Norambuena, Ines Racke, Vladimir Rybin, Alexander Schmidt, Eva Yus, Ruedi Aebersold, Richard Herrmann, Bettina Böttcher, Achilleas S. Frangakis, Robert B. Russell, Luis Serrano, Peer Bork, Anne-Claude Gavin. Science*, Vol. 326 Issue 5957, Nov. 27, 2009.*

“Transcriptome Complexity in a Genome-Reduced Bacterium.” By Marc Güell, Vera van Noort, Eva Yus, Wei-Hua Chen, Justine Leigh-Bell, Konstantinos Michalodimitrakis, Takuji Yamada, Manimozhiyan Arumugam, Tobias Doerks, Sebastian Kühner, Michaela Rode, Mikita Suyama, Sabine Schmidt, Anne-Claude Gavin, Peer Bork and Luis Serrano. Science*, Vol. 326 Issue 5957, Nov. 27, 2009.*

“Impact of Genome Reduction on Bacterial Metabolism and Its Regulation.” By Eva Yus, Tobias Maier, Konstantinos Michalodimitrakis, Vera van Noort, Takuji Yamada, Wei-Hua Chen, Judith A. H. Wodke, Marc Güell, Sira Martínez, Ronan Bourgeois, Sebastian Kühner, Emanuele Raineri, Ivica Letunic, Olga V. Kalinina, Michaela Rode, Richard Herrmann, Ricardo Gutiérrez-Gallego, Robert B. Russell, Anne-Claude Gavin, Peer Bork and Luis Serrano. Science*, Vol. 326 Issue 5957, Nov. 27, 2009.*

“Excavating the Functional Landscape of Bacterial Cells.” By Howard Ochman and Rahul Raghavan. Science*, Vol. 326 Issue 5957, Nov. 27, 2009.*

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irreducible complexity anyone?

Posted by: ppetree | 11/30/09 | 7:25 pm

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Posted by: jfobigfoot | 11/30/09 | 8:41 pm

@ jjantos

I’ll second that.