Abstractions

PENULTIMATE AUTHOR

Mature proteins can be modified in several ways: the attachment of fats, for example, can facilitate their binding to cell membranes. Unusually, palmitoylation — attachment of the fat palmitic acid — is reversible, and so may regulate protein–membrane interactions. Last year, neuroscientist Alaa El-Husseini of the University of British Columbia in Canada teamed up with a group led by Nicholas Davis at Wayne State University in Detroit, Michigan, to use proteomics to explore the role of palmitoylation in the brain. They found significant involvement of this modification at synapses — junctions between nerves by which they signal to one another. Just a couple of days after submitting the paper on page 904, El-Husseini unexpectedly passed away. Davis discusses challenges the team faced.

What events led up to this work?

In 2002, Alaa showed that the firing of nerve impulses by synapses regulates the palmitoylation of a key synaptic protein called PSD-95. Palmitoylation has been remarkably understudied. My group developed a method for identifying palmitoylated proteins in yeast and Alaa was eager to apply it to the brain.

Were you pleased with the findings?

We were a bit overwhelmed to discover several hundred palmitoylated proteins participating in diverse areas of neuronal function, particularly at the synapse. Even more surprising was finding that the palmitoylation of the protein Cdc42 played a critical role in the formation of dendritic spines — tiny protrusions on neurons that change in number and shape in response to neuronal activity. Alaa was thrilled because he had long believed palmitoylation to be an important regulator of synapse function.

How did Dr El-Husseini's death affect publication?

We were all deeply saddened by Alaa's death. It also affected us on a professional level. When the reviewers asked for experiments to extend one of our findings, Alaa's students and postdocs really pulled together, driven by the prospect of having a *Nature* publication as tribute to him. They designed and performed a difficult series of experiments, which added a huge amount to the paper.

Where will you go from here?

I've worked with yeast for 20 years, but I am enjoying the foray into neuroscience. I'm intrigued by links that have been made between palmitoylation enzymes and various neurological diseases, including Huntington's disease and schizophrenia. We would like to apply quantitative proteomics to learn how changes in palmitoylation might participate in these diseases. ■

MAKING THE PAPER

Manolo Gouy

Genomic clues settle debate about ancestor of all life forms.

At the root of the tree of life is a hypothetical organism from which all life on Earth today is descended. This 'last universal common ancestor', or LUCA, as it is known, arose at an unknown point in time, probably in the oceans more than 3.5 billion years ago. Fossils from its distant era are few and far between, so Manolo Gouy, a molecular phylogeneticist at the University of Lyon in France, and his colleagues set about finding a different means of tracing LUCA.

They analysed sequences of ribosomal RNA and proteins from a variety of modern species using mathematical models of molecular evolution. Their work shows that LUCA was a mesophile — that is, grew best at temperatures approaching 50 °C — and its descendants then adapted to higher temperatures as Earth's environment changed. Not only do the results clear up a dispute about LUCA's temperature preference, but the group's approach could also be used to learn more about this intriguing species.

Because of the scarcity of fossils from LUCA's time, researchers have instead relied on indirect evidence, delving into the genomes of modern species, to uncover LUCA's features. To this end, about 10 years ago, Gouy's group studied ribosomal RNA, a part of the cell's protein-making machinery thought to have changed little over time. Thermophilic, or heat-loving, organisms carry ribosomal RNA rich in pairs of the nucleic acids guanine and cytosine. These have stronger bonds than do adenosine and uracil pairs, so are more stable at higher temperatures.

On the basis of their reconstruction of ancestral ribosomal-RNA sequences, Gouy and his colleagues posited that LUCA lived in cooler waters. "It was a surprise because there was a hypothesis that the origin of life would have occurred in a hot environment," says Gouy. In fact, another group of reseachers, who had reconstructed ancestral protein sequences, found just that — LUCA dwelled in a hot or thermophilic environment.

By analysing both protein and RNA sequences with new mathematical tools, Gouy and his team now show that there were two phases of environmental adaptation: first, a mesophilic LUCA, and second, its descendants, which adapted to higher temperatures (see page 942).

"We think we have demonstrated why there was a disagreement," says Gouy. "There was a difference in the method used to reconstruct the ancestral sequences. Some assume that the evolutionary process is constant, but that's an over-simplification." He attributes the leap forwards to computing power that didn't exist a decade ago, knowledge of many more genomic sequences and collaboration. "We can run models on much more data and our models can be much more complicated than they used to be," says Gouy. "And I was lucky enough to get a brilliant graduate student, Bastien Boussau, who was able to work out these new models."

As a LUCA-hunter, Gouy is after an elusive quarry. Many basic questions about LUCA remain, perhaps most importantly the date when it arose. "Any date would be unreliable, and it's a big problem," Gouy says. But he believes that he can apply his new method to learn more about LUCA's atmospheric environment, match it to the geological record for atmospheric oxygen concentration, and pinpoint a more reliable date. "If one really wants to understand the history of the evolution of life, one would really like to anchor it in time," he says. ■

FROM THE BLOGOSPHERE

Nautilus reports a call for authors to deposit supporting raw microarray data sets into a public database (http://tinyurl.com/6xugqy). After surveying papers from the 2007 issues of 20 journals for references to deposition of a microarray data set, Neil McKenna and colleagues write in *Nature Methods* (**5,** 991; 2008) that the rate of deposition was less than 50%. They also note that microarray data sets are not biologically interpretable unless accompanied by a description of the experimental details.

The researchers propose that journals require authors to identify a repository and accession number in their articles. (Of the 16 Nature journal papers that were part of the survey, such accession numbers were provided in 15 cases.) They also call for "a renewed collective effort from researchers, publishers and funding organizations to redress this situation and secure these data-rich research resources for posterity".

The Nature journals have for some years required authors to submit data compliant with MIAME (minimum information about a microarray) to a public repository (http://tinyurl.com/33fg2r). ■

Visit Nautilus for regular news relevant to *Nature* authors ▸ http://blogs.nature.com/nautilus and see Peer-to-Peer for news for peer reviewers and about peer review ▸ http://blogs.nature.com/peer-to-peer.