CHEMINFORMATICS

Mars needs amino acids!

In the wake of renewed interest in the possibility of life on Mars, researchers have developed a chip-based system capable of highly sensitive detection of organic molecules.

The National Aeronautics and Space Administration (NASA) *Viking* Mars mission was both a historic landmark and a crushing disappointment. It generated striking images and offered invaluable geological and meteorological insights, but soil sample analyses revealed an apparent lack of organic molecules, suggesting an absence of life—little and green or otherwise. And so the quest for interplanetary life went on hiatus, or at least kept a low profile. "You kind of stayed in the closet," explains Berkeley chemist Richard Mathies, "[and] didn't really tell anybody you were doing exobiology, because you were afraid you were going to get branded as a complete crank!"

New inspiration came after analysis of Antarctica's Allen Hills 84001 meteorite yielded tantalizing geological data that helped revive hopes of finding martian life. More recently, the *Spirit* and *Opportunity* missions provided compelling, if not indisputable, evidence that the martian surface contained liquid water—at some point. Finally, various studies suggest that the *Viking* lander's analytical equipment lacked the sensitivity to quantify truly scarce molecules, and that soil samples were taken too close to the planet's surface, where organic molecules would have been thoroughly degraded by the highly oxidizing conditions (Benner *et al.*, 2000).

In 2009 or 2011, the European Space Agency (ESA) intends to embark on the *ExoMars* mobile rover mission, which will include a closer search for signs of life. To this end, Mathies and colleagues from several other institutions have developed the Mars Organic Analyzer (MOA), an innovative microfluidics-based capillary electophoresis system for the detection of amino acids—a prototype for the detector to be included in the *ExoMars* lander (Skelley *et al.*, 2005).

Earth's nearest equivalent to the martian surface lies in an inhospitable patch of Chile's Atacama desert, where the soil is highly oxidized and even bacterial life is extremely scarce. Levels of organic molecules there fall below the limits of the *Viking* system's detection capabilities—but MOA passed with flying colors, detecting traces of several amino acids. "The system we're running," says Mathies, "has low part-per-billion—to even tens-of-parts-per-trillion—sensitivity for these organic amines and amino acids. That's a sensitivity that's roughly 1,000 to 10,000 times better than *Viking*." The team is now scaling up to develop MOA systems capable of processing hundreds of samples.

Mathies believes the ESA and NASA now recognize the potential of new biological and chemical techniques, and beyond finding life on Mars, suggests that as a proving ground for microfluidics, MOA may also find new life in chemistry research: "The real trend is that this stuff is no longer just gee-whiz lab-on-a-chip stuff; it's starting to go mainstream... I see this as the start of a revolution in the way lots of people do chemistry."

Michael Eisenstein

RESEARCH PAPERS

Skelley, A.M. *et al.* Development and evaluation of a microdevice for amino acid biomarker detection and analysis on Mars. *Proc. Natl. Acad. Sci. USA* **102**, 1041–1046 (2005).

Benner, S.A. *et al.* The missing organic molecules on Mars. *Proc. Natl. Acad. Sci. USA* **97**, 2425–2430 (2000).

GENOMICS

More than an atlas of the brain

By pooling expertise and resources, a group of scientists have mapped the expression of mouse transcription factors in all major brain regions and in a variety of other tissues; thanks to their efforts, a plethora of information is now just a mouse-click away.

The nervous system in mammals has astounding diversity, with thousands of distinct neuronal cell types. The molecular basis for this diversity remains largely unknown; however, previous studies from different laboratories have pointed to transcription factors (TFs) as critical players in cell type specification. This motivated four groups at Harvard Medical School (led by Qiufu Ma, Charles Stiles, David Rowitch and Andy McMahon) to map TFs with spatially restricted expression in the nervous system and other tissues during mouse development, and a recent article in *Science* describes the results of this collaborative endeavor (Gray *et al.*, 2004).

Human genome sequence in hand, the researchers' first effort was to determine the number of human TFs and find their mouse orthologs. Using this sequence information, they cloned over 1,000 TFs and hybridized them to the major brain regions during different stages of development. Among the TFs, 27% showed expression that was restricted to certain regions of the central nervous system, and these TFs were thus deemed most likely to be involved in the development of this region. This project to systematically identify key developmental TFs also attracted scientists from outside the field of neuroscience. The team of Andrew McMahon used whole-mount embryos for *in situ* hybridization to add maps of TF expression in non-neuronal tissue. To guarantee easy access, the authors have compiled and posted all their data, including primer sequences and hybridization images, on a website (http://mahoney.chip.org/mahoney/). These maps provide powerful tools: scientists working on specific TFs can easily find the brain region or tissue of interest in which the TFs are active, and researchers interested in specific brain regions can search the website for relevant TFs.

When asked about the future of this collaborative effort, Stiles and Ma describe aspirations as big as their initial plan. They want to include maps obtained at a larger number of developmental stages and combine them with maps that show the expression of functional genes, such as those encoding neurotransmitter receptors. These plans are daunting in their time and labor intensity—but then again, so was the initial plan of mapping every TF in the mouse genome. Ma summarizes what made them succeed: "No lab can do it alone. You need a team!"

Nicole Rusk

RESEARCH PAPERS

Gray, P.A. *et al.* Mouse brain organization revealed through direct genome-scale TF expression analysis. *Science* **306**, 2255–2257 (2004).

WEB SITES

http://mahoney.chip.org/mahoney/