Materials science

Pore characterization

Porous materials are extremely useful in catalysis and selective molecular filtration, and can even serve as miniature laboratories for conducting chemistry with just a few molecules at a time.

Most natural porous minerals, such as zeolites, are laced with pores whose width is no greater than the size of small molecules (less than 2 nm). But materials scientists and chemical engineers want to make synthetic 'mesoporous' solids with larger pores (2–50 nm) that are selective for larger molecules.

Although much effort has gone into finding new ways of making such mesoporous solids, the atomic-scale structure of the pores is not well known and so refining their structure is a matter of trial-

and-error. This is due partly to the difficulty in obtaining large single crystals for conventional diffraction studies using X-rays or neutrons. Elsewhere in this issue (*Nature* **408**, 449–453; 2000), Galen Stucky and colleagues report a method that uses high-resolution electron microscopy to obtain images that can be mathematically treated to give a full three-dimensional (3D) structure of mesoporous materials.

Electron microscopy uses electrostatic lenses to form a magnified image of the sample (by recombining the diffracted electron beams). This has the advantage that it can be carried out on very small areas, because the focused electron beam is only a few micrometres in diameter. The technique does not depend on the actual resolution of

the images, but provides more complete information about the structure. So, compared with conventional methods for structural analysis of crystalline and amorphous materials, this approach is generally applicable to soft materials that have disorder at the atomic length scale, but order at the mesoscopic scale.

The picture here shows the 3D structure of a mesoporous silica material obtained by Stucky and colleagues. This image provides information about the sizes and shape of the pores at the nanoscale level, as well as their connectivity. Further analysis reveals an unusual bimodal structure, in which there are different sized micro- and mesopores.

What makes this imaging method so attractive is that, compared with

X-ray diffraction, it provides full structural information without using pre-assumed models or parameters. Moreover, it can reveal high-resolution details of pore structure at different scales in porous composites. The technique could be used to characterize the detailed structure of a wide range of composite materials.

Vincent Dusastre

virus vaccine. This virus often reverts to a more virulent form within the vaccinated person; such reversion does not harm the person concerned but can cause polio when transmitted to others who have not been vaccinated or previously infected⁵.

Teotónio and Rose conducted a large experiment using caged populations of *Drosophila* that were originally maintained for other purposes. For 25 years, one population has been kept under standard rearing conditions (the 'standard' line). Twenty years ago, a subset of the standard flies was used to start another population that was then selected for late-life fecundity (this line was originally used to test evolutionary theories of senescence). Eleven years ago, flies from the standard line were used to found two additional populations, one being selected for resistance to starvation, the other for intermediate generation time. Finally, eight years ago, a fourth population was started from the standard line, selecting for flies that developed into adults especially quickly.

About three years ago, flies from these four lines were returned to the original standard conditions. Since then, eight different phenotypic traits have been monitored across five replicates of each line: male and female development time; male and female resistance to starvation; early fecundity at high and low population densities; female dry body weight; and female lipid content. Teotónio and Rose observed three different patterns of reversibility: complete, partial and none. Most traits reversed completely, although the time taken for this varied from 20 to 50 generations. Partial reversals were not merely slower versions of complete

reversals, because their initial rate of reversal was rapid but then reached a plateau.

Why did some traits — such as fecundity at high population densities — fail to reverse at all or to completely attain the ancestral condition? The limitation could be genetic — that is, genetic variation was absent or exhausted by selection. Or epistasis could have blocked the return. Epistasis is an interaction in the effects of different mutations, such that the consequence of one mutation changes depending on whether another mutation is present or absent.

An example is seen in bacteria that have become resistant to antibiotics. Although mutations that give rise to drug resistance are, by themselves, generally deleterious in the absence of antibiotic, the ending of antibiotic treatment does not ensure the evolutionary reversal to antibiotic sensitivity. This is because drug-resistance mutations often impair essential cellular functions and so are followed by other, compensatory mutations that restore those functions. In the absence of antibiotics, the antibiotic-resistance gene and the compensatory mutations are each singly more harmful than they are in combination. So reverse evolution is blocked because neither gene can undergo reversal on its own⁶.

To explore similar possibilities in the fruitfly, Teotónio and Rose created hybrid populations between the selected and standard lines. These hybrid populations were genetically variable, and so should have reverted more easily because they lacked many types of genetic barriers to reversion. Correcting for the fact that the hybrid populations started their return from intermediate values, the replicates behaved essentially

as the evolved populations did, suggesting that genetic limitations did not explain the lack of reversion. Teotónio and Rose speculate that the form of selection was instead altered by the original evolution — that is, for some traits the nature of selection depended in subtle ways on the genetic background of the population, which changed over the course of the experiment.

But is phenotypic reversal accompanied by genetic reversal? Genetic reversal seems less likely than phenotypic reversal, because there are often several genetic routes to an adaptation, and because mutational biases and epistasis may effectively preclude a reversal back down the original pathway. Genetic reversions have been observed in microbes^{7,8}, but resolution of this question in *Drosophila* awaits further work. Nonetheless, Teotónio and Rose's study adds to a growing body of work on adaptation, in which natural or semi-natural replicates tend to reveal that natural selection has a powerful influence on phenotype. Their work suggests that there is essentially no intrinsic barrier opposing the return to formerly adaptive states, and that reversals of many types of phenotypic traits can occur. ■

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1. Teotónio, H. & Rose, M. R. *Nature* **408**, 463–466 (2000).
2. Gould, S. J. *J. Hist. Biol.* **3**, 189–212 (1970).
3. Minkoff, E. C. *Evolutionary Biology* (Addison Wesley, Reading, MA, 1983).
4. Hill, W. G. & Caballero, A. *Annu. Rev. Ecol. Syst.* **23**, 287–310 (1992).
5. Guillot, S. *et al. Vaccine* **12**, 503–507 (1994).
6. Schrag, S. J. *et al. Proc. R. Soc. Lond. B* **264**, 1287–1291 (1997).
7. Crill, W. D. *et al. Genetics* **154**, 27–37 (2000).
8. Levin, B. R. *et al. Genetics* **154**, 985–997 (2000).