

all matter gets completely diluted by the cosmic expansion, and an empty universe results. To fix this flaw, Steinhardt and Turok combined Abbott's model with the cyclic cosmological scenario (13), in which the universe goes through multiple cycles of expansion and contraction. The high density of matter is regenerated at the start of each cycle, so the empty universe problem is solved. Most of the cycles will occur while the universe is in the lowest Λ state, and Steinhardt and Turok argue that this state is most likely to be observed.

The cyclic model is still being developed and is not widely accepted. More importantly,

although Steinhardt and Turok's proposal may explain the smallness of Λ , it does not address the cosmic coincidence problem: Why should the smallest possible value of Λ be comparable to the present density of the universe? The anthropic explanation appears, therefore, to be more compelling.

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MATERIALS SCIENCE

High-Pressure Microscopy

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When materials are put under pressure, their structures can change dramatically. Such pressure-induced structural changes occur in many contexts, from materials synthesis to geophysics. Studies of these structural changes have mainly relied on diffraction and spectroscopic techniques. Electron microscopy—the only means to view atomic structure directly—must be conducted in a vacuum. It would therefore seem impossible to directly observe pressure-induced atomic motion. But on page 1199 of this issue, Sun *et al.* (1) show that transmission electron microscopy (TEM) can be used to induce self-compression of carbon nanotubes and hence to study the effect of pressure on materials trapped within the nanotubes.

The diamond anvil cell is currently the most widely used device for applying extreme pressures on a material (see the figure, left panel). In this method, two perfectly aligned gem diamond anvils squeeze a sample loaded within the gasket hole to achieve megabar pressure under a moderate loading force. Diamond anvil techniques have been used, for example, to produce metallic hydrogen and to study the melting of iron under pressure/temperature conditions resembling those in Earth's core (2–4).

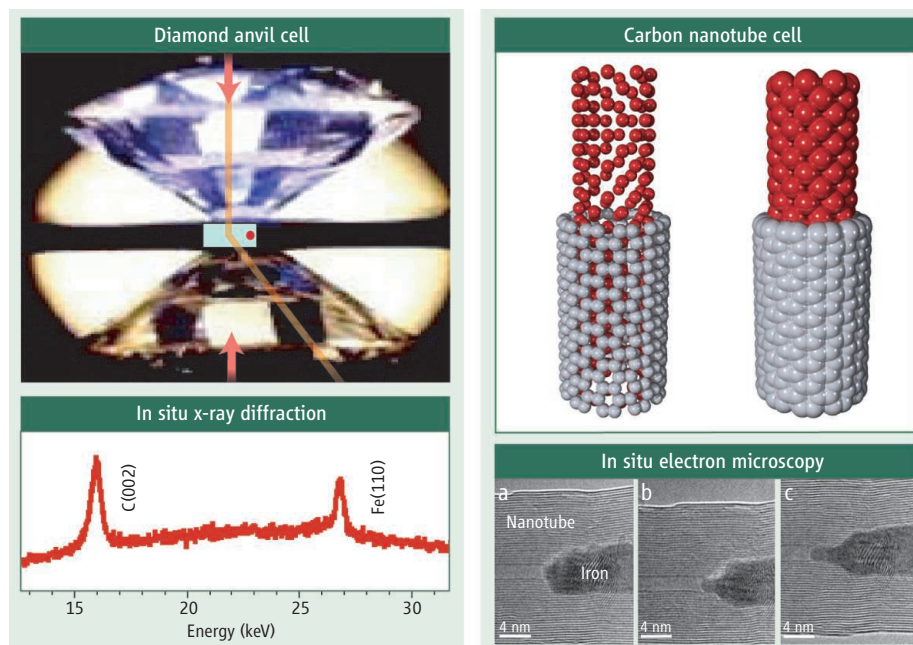
X-ray diffraction and Raman spectroscopic measurements can be performed within the diamond anvil cell, allowing crystal structures and transition pressures between different structures to be determined. For example, it has been shown that iron, which crystallizes in a cubic structure at ambient conditions, transforms to hexagonal phase at ~ 10 GPa (3, 4). Upon release

of pressure, the hexagonal iron transforms back to the starting cubic structure. However, the transformation mechanisms can only be conjectured. Recent syntheses of defect-free, nanometer-scale crystals have helped to elucidate the transformation mechanisms, but in situ spectroscopic measurements still cannot provide a definite answer (5, 6). Molecular dynamics simulations can also be used to study the transition mechanism and the resulting kinetics. However, it has been difficult to replicate complicated dynamic processes, such as the pressure-induced

When bombarded with electrons, carbon nanotubes shrink, creating high internal pressures. The effect on molecules within the tubes can be studied at atomic resolution.

transformations in iron and graphite, in simulations (4, 7, 8).

High-resolution TEM is the only analytical technique that provides a visual image of the atomic structure. Ten years ago, Banhart and Ajayan found that electron irradiation from a high-resolution TEM could induce self-compression of carbon nanotubes (9). More recent high-resolution TEM studies have observed atomic deformations of Mo and W nanocrystals encapsulated in carbon nanotubes, as a result of self-compression (10). These results provide important clues to



A matter of scale. (Left) A transparent diamond anvil cell allows in situ spectroscopic measurements of bulk samples. The red arrow represents an x-ray beam that is diffracted by the sample. (Right) A carbon nanotube self-compression cell enables in situ atomic-resolution snapshots at zero (a), intermediate (b), and high (~ 40 GPa) (c) pressure.

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how a carbon nanotube pressure cell for in situ high-resolution TEM observation can be built.

Such a pressure cell must meet four requirements: a strong elastic modulus to achieve maximum pressure; a hollow core to encapsulate materials; the ability to compress the sample through electron radiation; and a sufficiently small sample size for high-resolution TEM characterization. Sun *et al.* confirm that multiwalled carbon nanotubes are suitable for this task and document the atomic deformation of materials within the nanotubes (see the figure, right panel).

The authors created multiwalled carbon nanotubes filled with iron carbide, iron, and/or cobalt and placed them in a heating stage within their TEM. At a temperature of ~600°C, electron irradiation knocks carbon atoms off the nanotube lattices. Atomic-scale reconstruction results in the shrinkage of the nanotubes and consequently squeezes the encapsulated materials. Upon continuous electronic irradiation, the damage to and restructuring of the carbon lattice increases the pressure within the tubes; high-resolution TEM images recorded throughout this process provide a detailed record of the pressure buildup and resulting deformation of the encapsulated materials. The results show that even

hard materials such as iron carbide can be deformed, extruded, and broken by this method. The detailed deformation mechanisms appear to differ from that of macroscopic crystals, where defects—not observed in the current study—are known to play an important role.

How high is the pressure within the tubes? One way to reach an estimate is to measure the lattice spacings between the nanotube sheets and within the encapsulated materials; another is to perform computer simulations. Sun *et al.* show that both methods yield similar estimates of up to ~40 GPa. Although this is an order of magnitude below the highest pressure achieved in a diamond anvil cell, the phase-transformation pressures of many materials fall within this range (2–4), providing a route to explore the atomic-scale dynamics of these materials under pressure.

Carbon nanotubes have been filled with a wide range of materials, including gases, liquids, and solids (11, 12). The nanotube pressure cell opens up a window to directly watch atomic-scale development of pressure-induced phenomena in these samples, with applications in materials science, chemistry, condensed-matter physics, geophysics, planetary science, and nan-

otechnology. Understanding the driving mechanism of phase transformation at the atomic scale is important not only for optimizing the synthesis of novel functional materials, but also for developing robust theoretical models. Such insights will advance fundamental condensed-matter physics and will help to tune the properties of nanometer-scale crystals and composites and to explore the formation dynamics of Earth and other planets.

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MICROBIOLOGY

Bacteria Seize Control by Acetylating Host Proteins

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The devastation wreaked by the infamous bacterium *Yersinia pestis* in the Middle Ages altered the course of human history, as the plague or “black death” accounted for millions of deaths in what has been called one of the worst epidemics in history (1). Our molecular understanding of this bacterium and its pathogenic effects is helping us understand how it accomplished such a feat. *Y. pestis*, along with two related pathogens, *Y. pseudotuberculosis* and *Y. enterocolytica*, harbors a plasmid that encodes a secretion system that effectively delivers virulence factors into eukaryotic cells, where they can subvert key cellular systems for their own purposes. On page 1211 of this issue, Mukherjee *et al.* (2) report how one such virulence factor, YopJ, blocks the host’s immune response, allowing infection to prevail.

Yersinia’s type III secretion system is com-

monly described as a molecular pore or syringe-like structure that the bacterium uses to penetrate a host cell and inject virulence factors (referred to as *Yersinia* outer proteins or Yops). There are six well-defined Yops in *Yersinia*: YopO/YpkA, YopE, YopH, YopM, YopT, and YopJ. Early studies on YopJ showed that it prevents release of the cytokine tumor necrosis factor- α from host cells, thereby circumventing the body’s ability to mount an effective immune response (3).

Previous work demonstrated that YopJ blocks several cellular signaling pathways, including the extracellular signal-regulated kinase, c-Jun NH₂-terminal kinase, p38 mitogen-activated protein kinase (MAPK), and nuclear factor κ B (NF κ B) pathways (4, 5). Each of these pathways signals through a series of kinases, enzymes that catalyze protein phosphorylation. In the case of the MAPK signaling cascade (see the figure), an extracellular stimulus normally activates the pathway by inducing the phosphorylation of specific MAPK kinase kinases (MAPKKK or MKKK). These activated enzymes then phosphorylate their respective substrates, MAPK kinases (MAPKK or MKK) or I κ B kinase β (IKK β) in

The plague-causing bacterium *Yersinia pestis* injects toxic proteins into its hosts’ cells. One of these interferes with the host’s secretion of a protective factor by adding acetyl groups to a signaling kinase, blocking its activation.

the case of the NF κ B pathway. The MKKs and IKK β are activated by phosphorylation on two serine residues or a serine and threonine residue found in their activation loops. These activated kinases in turn phosphorylate and activate MAPK and NF κ B, resulting in the production of cytokines and antiapoptotic signals. Orth and colleagues (6) previously determined that YopJ can block these phosphorylation cascades. Using yeast two-hybrid analysis, they demonstrated that YopJ binds directly to MKK1. It turns out that YopJ also binds to several members of the MAPK kinase superfamily, but how this interaction blocks kinase activation has remained unresolved until now.

A search for proteins with amino acid sequence identity to YopJ identified several proteins from plant and animal pathogens, including adenovirus protease-2 (AVP), fowl *monas campestris* pv. *vesicatoria*, adenovirus 8-like-protease, AvrBst from *Xantho*AvrA from *Salmonella typhimurium*, and a potential protease from hemorrhagic enteritis virus (7). All of these proteins contain a conserved catalytic triad of amino acids (His, Asp/Glu, Cys) that is simi-

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