Surface physics

Hopping atoms in crystal growth

from Colin J. Humphreys

How do crystals grow? This question has fascinated people ever since the beautiful six-fold symmetry of a snow-flake was observed through a ten-times magnifying lens. The paper by Bovin et al. on page 47 of this issue presents dramatic new information about crystal growth from images of growing gold crystals, magnified over 30 million times using a high resolution electron microscope and real-time video-recording.

At this magnification, individual columns of atoms in the gold crystals are clearly revealed; it appears that not only are atoms on the surfaces of small crystals in constant motion, hopping from site to site, but also that the crystals are surrounded by clouds of atoms in constant interchange with atoms on the crystal surface. The clouds of gold atoms extended up to 9Å from the crystal surface, continually changing their shape and density.

Similar events have been observed independently by Sumio Iijima in Japan; a sequence of his micrographs showing very small gold crystals continually changing shape has already appeared in *Nature* (315, 628; 1985). Taken together, these observations may explain for the first time how atoms locate the most favourable positions during crystal growth.

Why have atom hopping and atom clouds not been observed before? The answer may be that so far most structural studies of crystal growth have involved techniques such as low-energy electron diffraction or X-ray diffraction, often using a synchrotron source. These techniques use relatively broad beams of electrons or X-rays, and the diffraction information is therefore averaged over a correspondingly large area of the specimen surface; local structural changes on a smaller scale than the incident-beam diameter cannot easily be detected. High resolution electron microscopy, on the other hand, produces images at atomic resolution, enabling atomic scale events on and above crystal surfaces to be detected.

Understanding how crystals grow is not only of scientific interest, but is also technologically important. Thus in the electronics industry, progress from very large scale integration to ultra large scale integration is constrained by the quality of the silicon crystals available, so that better knowledge of growth mechanisms in silicon and other semiconductors is essential. Similarly the behaviour of very small crystals is also of both scientific and technological interest. For example, many catalysts are composed of ultra-fine crystals whose activity is not well understood. The new ideas of atom hopping and atom clouds of Bovin et al. will have to be taken into account in catalysis.

Pertinently the work of Iijima on ultrafine particles is part of the Japanese government's Science and Technology Agency (STA) programme for Exploratory Research for Advanced Technology (ERATO), which specially supports materials research in areas selected for their intrinsic interest as well as strategic significance. Lack of British funds for this type of work was responsible for the emigration from Cambridge University to Arizona State University last summer of David Smith, a key member of the Bovin, Wallenberg and Smith team.

Finally, a word of caution about this elegant and important paper is in order.

Heisenberg, in his thought experiment to illustrate the Uncertainty Principle, argued that the position and momentum of a particle cannot simultaneously be measured precisely in an optical microscope because the incident photon beam interacts with the particle. To what extent, in the present work, does the interaction of the incident electron beam with the specimen influence the observed atom hopping and atom clouds, for example by momentum transfer and ionization? I believe that further experiments are needed to resolve this uncertainty, but the work reported is stimulating and may well have far-reaching scientific and technological implications.

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Transducing proteins

Yeast RAS and Tweedledee's logic

from Henry R. Bourne

THE discovery in yeast of genes with sequence homology to the ras oncogenes of mammals has raised the hope that the sophisticated genetic technology available for the analysis of yeast physiology might become directly applicable to the biochemical analysis of mammalian tumorigenesis. It is known that the yeast RAS proteins are essential for proliferation and that they are responsible for the GTPactivation of cyclase2. Thus many have speculated that adenylate cyclase, which is implicated in a number of cellular signal-transduction systems, may also be the target of the p21 proteins encoded by viral ras oncogenes and their normal cellular counterparts. It has recently become clear, however, that this attractive notion is wrong. This does not mean that yeast experiments cannot help to define the role of p21 in regulating cell proliferation and causing malignant transformation: merely that they will do so less directly than had been hoped.

Two sets of observations had suggested a direct functional homology between yeast and mammalian p21. First, p21 from the cellular gene c-Ha-ras can substitute for yeast RAS proteins as a stimulator of adenylate cyclase and in support of yeast-cell proliferation³. The second observation involves a mutation that substitutes valine for a specific glycine residue and is believed to confer oncogenic properties on the mammalian ras protein. The same amino-acid substitution affects the presumptive GTP-binding site of the yeast RAS proteins, and causes them to stimulate yeast adenylate cyclase much more

effectively, the consequent rise in cyclic AMP impairing the yeast cell's ability to stop proliferating when deprived of nutrition². The parallel with the oncogenic effects of the mutation in the animal protein is compelling.

All these observations had led to the supposition that yeast RAS might be functionally equivalent to the so-called G proteins that bind GTP and regulate the activity of adenylate cyclase in mammalian cells. But it is now clear from experiments in vitro that p21 does not in fact stimulate or inhibit mammalian adenylate cyclase. On page 71 of this issue⁴, Beckner et al. report studies of adenylate cyclase in membranes prepared from normal cells, from cells transformed by the viral oncogene v-Ha-ras, and from cells genetically deficient in the α subunit of G_s , the stimulatory GTP-binding regulatory protein of vertebrate adenylate cyclase. In all three cases, adenylate cyclase activity was unaffected by addition of relatively vast quantities of p21^{v-Ha-ras}, produced by expressing the oncogene in *Escherichia coli*. Because the E. coli-derived protein lacks a fatty acid modification that presumably facilitates membrane association of p21 in mammalian cells, Beckner et al. also tested smaller quantities of p21 (both c-Ha-ras and v-Ha-ras) purified from membranes of normal or v-Ha-ras-transformed mammalian cells, with the same result.

At the Cold Spring Harbor Symposium on Quantitative Biology in June, Michael Wigler reported a different kind of experiment: injection into frog oocytes of p21°-Ha-ras, obtained by expression in *E. coli*, caused no change in cAMP. The negative