government initiative. That allowed the White House to maintain that it hadn't handed NSF a blank check and to enshrine the concept that bigger budgets were a reward for good management. At the same time, congressional supporters of doubling could say that they had taken a big step toward raising NSF's budget from its current $4.8 billion to $9.8 billion in 2007.

The bill (H.R. 4664), now awaiting the president's signature, doesn't actually give NSF a dime, however. Annual spending is set by appropriators, who have yet to complete action on any domestic spending bill for the 2003 fiscal year that began 1 October. But "we think it's great," says NSF's David Stonner, head of legislative affairs. "It demonstrates strong congressional support for NSF." The bill is loaded with congressional demands, too, including more than a dozen reports on topics ranging from improving math and science education to building big research facilities.

–JEFFREY MERVIS

CELL BIOLOGY

Chaos Reigns in RNA Transcription

The critical job of transforming raw genetic information into proteins seems to call for a well-oiled machine. But one research team, pushing the boundaries of imaging technology and computer modeling, argues that this machine is the picture of inefficiency. Rather than smoothly assembling on a gene, the proteins that form a major transcription tool, called RNA polymerase I, collide without sticking and zoom off if their companions are seconds behind schedule.

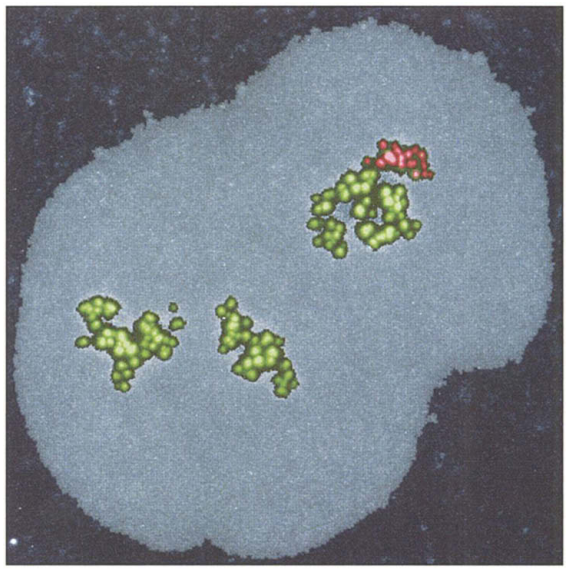
The research, reported on page 1623, is not without critics, who contend that the technology used in the study has not advanced enough to support such a model. But the work reflects an increasingly sophisticated effort to delineate the dance performed by transcription machinery. Two papers analyzing the other main transcription tool, RNA polymerase II, will be published next month. Although the three home in on different aspects, all find similar chaos.

"What they're saying is that things are just flying around, and they happen by accident to come together," says Joseph Gall of the Carnegie Institution of Washington's branch in Baltimore, Maryland, of the *Science* paper. "That's an extreme view ..., [but they're] such good data that you have to sit up and listen."

To gather these data, Tom Misteli and his colleagues at the National Cancer Institute (NCI) in Bethesda, Maryland, first conducted imaging experiments on animal cells. RNA polymerase I consists of at least a dozen different proteins; Misteli's group focused on nine of these that together make up the bulk of the polymerase. Using in vivo microscopy, they tagged one at a time with a fluorescent marker and followed each through the nucleus to the DNA. By watching how long each protein loitered by the gene and then overlaying that with the behavior of the eight others, the researchers could begin tracing polymerase assembly.

But imaging technology reveals only so much. The biologists were curious about a protein's chance of being welcomed into the polymerase if it surfaced in the right place at roughly the right time. For that, they turned to Robert Phair, a computer modeler at BioInformatics Services in Rockville, Maryland. The team plugged imaging data into a model Phair built to simulate the known stages of polymerase assembly. The model suggested that joining the polymerase was quite a challenge: A polymerase protein would wait for only 2 seconds for another to show up and bind to it before darting off.

Furthermore, the team discovered, a polymerase breaks apart once it has transcribed a gene, forcing reassembly to start from scratch. Despite this stunning inefficiency, the group found, a polymerase assembles every 1.5 seconds. Misteli theorizes that the system works because the polymerase proteins are so abundant.



Confused choreography. Tagging components of RNA polymerase I (red) revealed a jumbled transcription process in the nucleus (light blue).

CREDIT: MIREK DUNDR AND TOM MISTELI/NATIONAL CANCER INSTITUTE

But several researchers question whether imaging and mathematical models can provide such an unambiguous picture of assembly. NCI's Gordon Hager wonders whether the polymerase always comes together the way the model predicts. And other researchers point out that it's tricky with imaging to tell whether a protein is joining the polymerase. Misteli agrees that imaging and modeling a living cell isn't foolproof, but he still considers it superior to previous in vitro work.

Although Hager questions some of the details of protein motion reported by Misteli's team, his own paper, which will appear in December in *EMBO Reports*, supports the general theory that "everything is dynamic." It examines regulatory proteins for RNA polymerase II; although not part of the polymerase, these enzymes help launch transcription. His group reports that these proteins spend just seconds in transcription locales.

Another paper, by Oxford University's Peter Cook and his colleagues, will be published in the December *Journal of Cell Biology*. Cook's group studied a subunit of RNA polymerase II and saw many of the same inefficiencies as Misteli. This growing body of evidence might shift the debate about polymerase assembly and the stability of whole polymerases, says Cook: "A lot of what's driving everything is random chance events." The purpose scientists seek in cellular machinery, he adds, might be nowhere to be found.

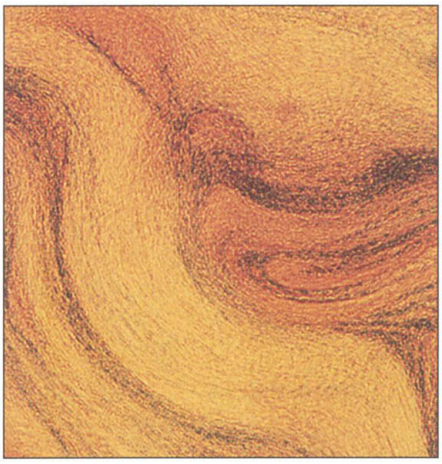
–JENNIFER COUZIN

EVOLUTIONARY BIOLOGY

Bacteria Shared Photosynthesis Genes

Historically, sun-loving microbes that convert solar energy to biomass, it seems, were quite promiscuous: They readily swapped DNA. Since then, they have been basking in the light for hundreds of millions of years, adding life-supporting energy and oxygen to the environment and making possible the variety of organisms on Earth today. Early on, these species were remarkably free, as researchers explain on page 1616, in sharing the photosynthesis genes that enable them to draw energy from sunlight—so free that it's hard to use these genes to trace the microbes' ancestry. "There's been massive horizontal gene transfer" among these organisms, says co-author Robert Blankenship, a biochemist at Arizona State University in Tempe.

Until about 5 years ago, researchers considered the transfer of genetic material from one species to another an oddity. Since then, genome studies have shown that some genes have moved around quite a bit. Even so, microbiologists assumed this would not be true for genes involved in translating DNA to RNA, for example, or sunlight to biomass; they couldn't see how genes of such mixed ancestry could possibly coordinate these



Swap meet. The *Chloroflexus aurantiacus* bacterium readily traded photosynthesis genes with other sun-loving microbes.

complex processes.

But that assumption "doesn't seem to be true," says W. Ford Doolittle, an evolutionary biologist at Dalhousie University in Halifax, Nova Scotia. The new work "clearly shows that photosynthesis genes have moved from one organism to another," adds Carl Bauer, a biochemist at Indiana University, Bloomington.

Five groups of bacteria use light as an energy source. To understand how photosynthesis genes could have evolved multiple times in these bacteria, Blankenship and others spent years studying the individual genes. But when bacterial genome sequences began pouring into public databases, they decided to take a global approach.

In the summer of 2001, graduate student Jason Raymond and his colleagues began to analyze the genome sequences of one organism from each of the five photosynthetic groups: a cyanobacterium, a filamentous green bacterium, a purple bacterium, a green sulfur bacterium, and a heliobacterium. Comparing the five genomes using several computer programs, including one called BLAST, they found 200 genes that were common to all.

Among those 200 shared genes, Raymond and his colleagues found about 50 photosynthesis genes. They compared the sequence differences of each gene among the five species; from those differences they built family trees that represented the relationships of the bacteria to one another. The approach is "very valuable," says Radhey Gupta, an evolutionary biologist at McMaster University in Hamilton, Ontario, because it takes into account all the available genetic information instead of just a few genes to determine which species are ancestral.

Had there been no gene swapping among the species, family trees based on each gene should have been the same. Instead, the researchers came up with 15 sets of relationships, the maximum possible with five species. "That suggested that different genes had different evolutionary histories," says Blankenship. These histories could differ only if the various genes had spent time in other organisms. "What this does is give us the first good data that genes were shuttled from one species to another," says Bauer.

The photosynthesis genes the researchers identified provided other clues to the microbes' photosynthetic past. For one, researchers learned about new support genes that might help repair or assemble photosynthetic machinery. Also, because photosynthesis requires many more proteins than the 50 genes can provide, it's likely that other genes have taken on double duty and help with photosynthesis. In looking for photosynthetic microbes' earliest ancestor, the best these data can advise, Blankenship thinks, is to lump together the cyanobacteria, green filamentous bacteria, and heliobacteria. "It's going to be very hard to pin down whether any one group was the first" to do photosynthesis. But this doesn't bother Doolittle. For him, "to find that [photosynthesis] is very extensively patched together from pieces is very exciting."

–ELIZABETH PENNISI

CREDITS: (TOP TO BOTTOM) J. RAYMOND *ET AL.*, *SCIENCE* 289, 1641 (2000); THOMAS HILDEBRANDT/INSTITUTE FOR ZOO AND WILDLIFE RESEARCH, BERLIN

WILDLIFE RESEARCH

New Rules Ease Specimen Shipments

CAMBRIDGE, U.K.—To the relief of scientists, an international trade body has decided to eliminate much of the red tape that has hindered the shipment of biological samples for research on endangered species. Although its action last week is not binding for individual nations, scientists say it will raise awareness of the pressing need for improved handling of the material.

The strict regulations of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) aim to prevent smuggling of animal parts. But as a side effect, they also hamper research on endangered species. Scientists often wait weeks or even months before being allowed to send blood, hair, or feathers from the field back to their home labs—no matter how urgent the need for diagnostic tests. The first proposal to simplify the procedure was rejected 2 years ago at the last CITES meeting in Nairobi (*Science*, 28 April 2000, p. 592), but it has since been refined in the organization's committees.

The new resolution, adopted during the parties' meeting in Santiago, Chile, lays out what kinds of samples, quantities, and purposes will qualify for a simplified and expedited permit. Biological samples must be "urgently required in the interest of an individual animal" and have a "negligible impact on the conservation of the species concerned." Every country participating in CITES must provide a list of eligible institutions. The proposal covers shipments of blood, secretions, hair, feathers, and tissues but excludes reproductive tissues—ova and sperm—and embryos. Nevertheless, the proposal had encountered strong opposition from countries such as Mexico, Brazil, and China, which feared that it could allow uncontrolled access to genetic resources.

"This is astonishingly far-reaching," beams elephant researcher Thomas Hildebrandt of the Institute for Zoo and Wildlife Research in Berlin. The proposal, he says, will greatly simplify the process of obtaining samples.

Even so, the declaration is just a recommendation to participating countries, warns Thomas Althaus of the Swiss Federal Veterinary Office, one of its authors. Many countries such as Thailand and the United States impose their own restrictions. But according to Hildebrandt, "the resolution gives us a stronger tool to pressure the authorities" to adopt compatible rules.

–PHILIPP WEIS

Philipp Weis is an intern in the Cambridge, U.K., office of *Science*.

Can't take that home. The new CITES rules won't ease the rules for transporting sperm.